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# OpenFF Toolkit Documentation

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Open Force Field Consortium

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## GETTING STARTED

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A modern, extensible library for molecular mechanics force field science from the [Open Force Field Initiative](#)



## INSTALLATION

### 1.1 Installing via conda

The simplest way to install the Open Force Field Toolkit is via the [conda](#) package manager. We publish [packages](#) via [conda-forge](#).

If you are using the [Anaconda](#) scientific Python distribution, you already have the conda package manager installed. If not, the quickest way to get started is to install the [Miniconda](#) distribution, a lightweight, minimal installation of Python and the Conda package manager. See the [conda](#) documentation for detailed installation instructions. We recommend [Miniforge](#), a drop-in replacement for Miniconda that uses the community-run conda-forge channel by default.

Once Conda is installed, use it to install the OpenFF Toolkit:

```
$ conda install -c conda-forge openff-toolkit
```

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**Note:** Installation via the Conda package manager is the preferred method since all dependencies are automatically fetched and installed for you.

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#### 1.1.1 OS support

The OpenFF Toolkit is pure Python, and we expect it to work on any platform that supports its dependencies. Our automated testing takes place on both (x86) MacOS and Ubuntu Linux.

##### Windows

For Windows support, we recommend using the [Windows Subsystem for Linux](#) (WSL) to run a Linux system integrated into Windows. We strongly suggest using WSL2, if your hardware supports it, for a smoother experience. WSL2 requires virtualization support in hardware. This is available on most modern CPUs, but may require activation in the BIOS.

Once WSL is configured, installing and using the Toolkit is done exactly as it would be for Linux. Note that by default, Jupyter Notebook will not be able to open a browser window and will log an error on startup; just ignore the error and open the link it provides in your ordinary Windows web browser.

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**Note:** WSL2 [does support](#) GPU compute, at least with nvidia cards, but setting it up [takes some work](#).

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## macOS with M1 chips

The Toolkit supports Apple Silicon (M1, M2, etc.), but only through [Rosetta](#) because (as of August 2022) some upstream dependencies are not yet built for the `osx-arm64` architecture. Conda can be configured to [use Rosetta](#) with the `CONDA_SUBDIR=osx-64` environment variable or the `subdir` Conda config variable. We recommend using this on a per-environment basis so that it persists across updates and new installs, but does not affect existing setups:

```
$ CONDA_SUBDIR=osx-64 conda create --name openff -c conda-forge openff-toolkit
$ conda activate
$ conda config --env --set subdir osx-64
```

Alternatively, make this setting the global default by updating the system Conda config:

```
$ conda config --system --set subdir osx-64
```

Note that this will affect how Conda behaves with other environments.

### 1.1.2 Conda environments

Conda environments that mix packages from the default channels and `conda-forge` can become inconsistent; to prevent this mixing, we recommend using `conda-forge` for all packages. The easiest way to do this is to install Conda with [Miniforge](#).

If you already have a complex environment, or you wish to install a version of the Toolkit that is incompatible with other software you have installed, you can install the Toolkit into a new environment:

```
$ conda create -c conda-forge --name offtk openff-toolkit
```

An environment must be activated in any new shell session to use the software installed in it:

```
$ conda activate offtk
```

### 1.1.3 Upgrading your installation

To update an earlier conda installation of `openff-toolkit` to the latest release version, you can use `conda update`:

```
$ conda update -c conda-forge openff-toolkit
```

Note that this may update other packages or install new packages if the most recent release of the Toolkit requires it.



## 1.2 Installing from source

The OpenFF Toolkit has a lot of dependencies, so we strongly encourage installation with a package manager. The [developer's guide](#) describes setting up a development environment. If you're sure you want to install from source, check the [conda-forge recipe](#) for current dependencies, install them, download and extract the source distribution from [GitHub](#), and then run pip:

```
$ cd openff-toolkit
$ python -m pip install .
```

## 1.3 Single-file installer

As of release 0.4.1, single-file installers are available for each Open Force Field Toolkit release. These are provided primarily for users who do not have access to the Anaconda cloud for installing packages. These installers have few requirements beyond a Linux or MacOS operating system and will, in one command, produce a functional Python executable containing the Open Force Field Toolkit, as well as all required dependencies. The installers are very similar to the widely-used Miniconda \*.sh files. Accordingly, installation using the “single-file installer” does not require root access.

The installers are between 200 and 300 MB each, and can be downloaded from the “Assets” section of the Toolkit's [GitHub Releases](#) page. They are generated using a [workflow](#) leveraging the Conda Constructor utility.

Please report any installer difficulties to the [OFF Toolkit issue tracker](#), as we hope to make this a major distribution channel for the toolkit moving forward.

### 1.3.1 Installation

Download the appropriate installer (openff-toolkit-<X.Y.Z>-<py3x>-<your platform>-x86\_64.sh.zip) from the “Assets” section at the bottom of the desired [release on GitHub](#). Then, install the toolkit with the following command:

```
$ bash openff-toolkit-<X.Y.Z>-py37-<your platform>-x86_64.sh
```

and follow the prompts.

---

**Note:** You must have write access to the installation directory. This is generally somewhere in the user's home directory. When prompted, we recommend NOT making modifications to your bash\_profile.

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**Warning:** We recommend that you do not install this package as root. Conda is intended to support on-the-fly creation of several independent environments, and managing a multi-user Conda installation is [complicated](#).

### 1.3.2 Usage

Any time you want to use this Conda environment in a terminal, run

```
$ source <install_directory>/etc/profile.d/conda.sh
$ conda activate base
```

Once the base environment is activated, your system will default to use Python (and other executables) from the newly installed Conda environment. For more information about Conda environments, see [Conda environments](#)

## 1.4 Optional dependencies (toolkits)

The OpenFF Toolkit outsources many common computational chemistry algorithms to other toolkits. Only one such toolkit is needed to gain access to all of the OpenFF Toolkit's features. If more than one is available, the Toolkit allows the user to specify their preference with the `toolkit_registry` argument to most functions and methods.

The `openff-toolkit` package installs everything needed to run the toolkit, including the optional dependencies RDKit and AmberTools. To install only the hard dependencies and provide your own optional dependencies, install the `openff-toolkit-base` package.

The OpenFF Toolkit requires an external toolkit for most functions. Though a builtin toolkit is provided, it implements only a small number of functions and is intended primarily for testing.

There are certain differences in toolkit behavior between RDKit/AmberTools and OpenEye when reading a small fraction of molecules, and we encourage you to report any unexpected behavior that may be caused by toolkit differences to our [issue tracker](#).

### 1.4.1 RDKit

RDKit is a free and open source chemistry toolkit installed by default with the `openff-toolkit` package. It provides most of the functionality that the OpenFF Toolkit relies on.

### 1.4.2 AmberTools

AmberTools is a collection of free tools provided with the Amber MD software and installed by default with the `openff-toolkit` package. It provides a free implementation of functionality required by OpenFF Toolkit and not provided by RDKit.

### 1.4.3 OpenEye

The OpenFF Toolkit can optionally make use of the [OpenEye toolkit](#) if the user has a license key installed. Academic laboratories intending to release results into the public domain can [obtain a free license key](#), while other users (including academics intending to use the software for purposes of generating protected intellectual property) must [pay to obtain a license](#).

To install the OpenEye toolkits:

```
$ conda install -c openeye -c conda-forge openeye-toolkits
```

Though OpenEye can be installed for free, using it requires a license file. No essential openff-toolkit release capabilities *require* the OpenEye toolkit, but the Open Force Field developers make use of it in parameterizing new open source force fields.

#### 1.4.4 Check installed toolkits

All available toolkits are automatically registered in the GLOBAL\_TOOLKIT\_REGISTRY. The available toolkits and their versions can be inspected through the registered\_toolkit\_versions dictionary:

```
from openff.toolkit import GLOBAL_TOOLKIT_REGISTRY
print(GLOBAL_TOOLKIT_REGISTRY.registered_toolkit_versions)
# {'The RDKit': '2022.03.5', 'AmberTools': '22.0', 'Built-in Toolkit': None}
```



## EXAMPLES USING SMIRNOFF WITH THE TOOLKIT

The following examples are available in [the OpenFF toolkit repository](#). Each can be run interactively in the browser with [binder](#), without installing anything on your computer.

### 2.1 Index of provided examples

- [toolkit\\_showcase](#) - parameterize a protein-ligand system with an OpenFF force field, simulate the resulting system, and visualize the result in the notebook
- [forcefield\\_modification](#) - modify force field parameters and evaluate how system energy changes
- [conformer\\_energies](#) - compute conformer energies of one or more small molecules using a SMIRNOFF force field
- [SMIRNOFF\\_simulation](#) - simulation of a molecule in the gas phase with the SMIRNOFF force field format
- [vsite\\_showcase](#) - two examples of using SMIRNOFF force fields virtual sites - a ligand with virtual sites on sulfur and chlorine and a comparison between the SMIRNOFF and OpenMM implementations of TIP5P
- [QCArchive\\_interface](#) - retrieving data from the QCArchive into Molecule objects
- [forcefield\\_modification](#) - modify force field parameters and evaluate how system energy changes
- [using\\_smirnoff\\_in\\_amber\\_or\\_gromacs](#) - convert a System generated with the Open Force Field Toolkit, which can be simulated natively with OpenMM, into AMBER prmtop/inpcrd and GROMACS top/gro input files through the ParmEd library.
- [swap\\_amber\\_parameters](#) - take a prepared AMBER protein-ligand system (prmtop and crd) along with a structure file of the ligand, and replace ligand parameters with OpenFF parameters.
- [inspect\\_assigned\\_parameters](#) - check which parameters are used in which molecules and generate parameter usage statistics.
- [using\\_smirnoff\\_with\\_amber\\_protein\\_forcefield](#) - use SMIRNOFF parameters for small molecules in combination with more conventional force fields for proteins and other components of your system (using ParmEd to combine parameterized structures)
- [visualization](#) - shows how rich representation of Molecule objects work in the context of Jupyter Notebooks.



## RELEASE HISTORY

Releases follow the `major.minor.micro` scheme recommended by [PEP440](#), where

- major increments denote a change that may break API compatibility with previous major releases
- minor increments add features but do not break API compatibility
- micro increments represent bugfix releases or improvements in documentation

### 3.1 0.12.1

#### 3.1.1 New features

- [PR #1502](#): Adds Gasteiger charge computation using the RDKit backend.
- [PR #1498](#): `Molecule.remap()` now supports partial mappings with the `partial` argument.
- [PR #1528](#): `Topology.box_vectors` are can now be set with `openmm.unit.Quantitys`, which are internally converted.

#### 3.1.2 Behavior changes

- [PR #1498](#): New, more complete, and more descriptive errors for `Molecule.remap()`.
- [PR #1525](#): Some unreleased force fields previously accessible from `"openff/toolkit/data/test_forcefields/"` are no longer implicitly available to the `ForceField` constructor.
- [PR #1545](#): Replaced the logic that sorts `HierarchyElements` with dedicated code in the OpenFF Toolkit instead of relying on deprecated features in the packaging module.

#### 3.1.3 Bugfixes

- [PR #1543](#): Fixes a bug in which plugins are not loaded if a `ForceField` is constructed prior without plugins.

### 3.1.4 Improved documentation and warnings

- [PR #1498](#): Improved documentation for `Molecule.remap()`, `Molecule.from_smiles()`, and `Molecule.from_mapped_smiles()`, emphasizing the relationships between these methods. In particular, the documentation now clearly states that `from_smiles()` will not reorder atoms based on SMILES atom mapping.
- [PR #1525](#): Improves reporting failures when loading force fields.
- [PR #1513](#): Improves error messages and documentation around supported aromaticity models (currently only “`OEAroModel_MDL`”).

## 3.2 0.12.0

### 3.2.1 New features

- [PR #1484](#): A `positions` argument has been added to `Topology.from_openmm()` and `Topology.from_mdtraj()`, which allows the topology’s positions to be set more conveniently.
- [PR #1468](#): Track which `ParameterHandlers` are loaded as plugins.

### 3.2.2 Behavior changes

- [PR #1481](#): Removes `compute_partial_charges_am1bcc`, which was deprecated in 0.11.0.
- [PR #1466](#): Replaces the use of `collections.OrderedDict` throughout the toolkit with the built-in `dict`. `attach_units`, `detach_units`, and `extract_serialized_units_from_dict` have been removed from `openff.toolkit.utils.utils`.
- [PR #1472](#): Removes `ParameterHandler._VALENCE_TYPE` and the same attribute of its subclasses, which were previously not used. Also deprecates `ChemicalEnvironment` and, by extension, the `openff.toolkit.typing.chemistry` submodule.

### 3.2.3 Bugfixes

- [PR #1476](#): Fixes [#1475](#) by also registering a `ParameterHandler`’s class when calling `ForceField.register_parameter_handler`.
- [PR #1480](#): Fixes [#1479](#) by requiring that `Atom.atomic_number` is a positive integer.
- [PR #1494](#): Fixes [#1493](#) in which some OFFXML file contents were parsed to `unit.Quantity` objects despite not representing physical quantities.

### 3.2.4 Improved documentation and warnings

- [PR #1484](#): The docstrings for `Topology.from_openmm()` and `Topology.from_mdtraj()` have been improved.
- [PR #1483](#): Simplified and clarified errors and warnings related to undefined stereochemistry with RDKit.



## 3.3 0.11.4 Bugfix release

### 3.3.1 Behavior changes

- [PR #1462](#): Makes residue numbers added by `Molecule.perceive_residues` strings (previously they were ints), to match the behavior of `Topology.from_openmm` and other hierarchy info-setting methods.

### 3.3.2 Bugfixes

- [PR #1459](#): Fixes [#1430](#), where `Topology.from_openmm` would mis-assign atom names (and probably also hierarchy metadata as well).
- [PR #1462](#): Fixes [#1461](#), where the default `Molecule.residues` iterator wouldn't sort by residue number correctly when residue information was added by `Molecule.perceive_residues`.

## 3.4 0.11.3 Bugfix release

- [PR #1460](#): Disables error causing [Issue #1432](#), where `Molecule.from_polymer_pdb` would sometimes issue stereochemistry errors when reading valid PDBs using the RDKit backend.

### 3.4.1 Bugfixes

- [PR #1436](#): Fix a small bug introduced in 0.11.2, where running with OpenEye installed but not licensed could lead to a crash.
- [PR #1444](#): Update for pint 0.20.

### 3.4.2 Examples updates

- [PR #1447](#): Fixed units of tolerance used in OpenMM minimization in Toolkit Showcase example notebook (from [@ziyuanzhao2000](#))

### 3.4.3 Improved documentation and warnings

- [PR #1442](#): Doctests added to CI, leading to numerous fixed docstrings and examples therein.

### 3.4.4 Miscellaneous

- [PR #1413](#): Remove some large and unused data files from the test suite.
- [PR #1434](#): Remove dependency on `typing_extensions`.

## 3.5 0.11.2 Bugfix release

### 3.5.1 Behavior changes

- [PR #1421](#): Allow `Molecule.from_rdkit()` to load D- and F- block radicals, which cannot have implicit hydrogens.

### 3.5.2 Bug fixes

- [PR #1417](#): Ensure the properties dict is copied when a `Molecule` is.

### 3.5.3 Improved documentation and warnings

- [PR #1426](#): A warning about OpenEye Toolkits being unavailable is only emitted when they are installed but the license file is not found.

## 3.6 0.11.1 Minor release forbidding loading radicals

### 3.6.1 Behavior changes

- [PR #1398](#): Updates the `Bond.bond_order` setter to only accept int values.
- [PR #1236](#): `from_rdkit` and `from_openeye` now raise an `RadicalsNotSupportedError` when loading radicals. It's not clear that the OpenFF Toolkit was ever safely handling radicals - they appear to be the root cause of many instances of unintended hydrogen addition and other connection table changes. If this change affects a workflow that was previously working correctly, please let us know on [this issue](#) so we can refine this behavior.

### 3.6.2 Examples changed

- [PR #1236](#): `examples/check_dataset_parameter_coverage` has been deprecated.

### 3.6.3 Bug fixes

- [PR #1400](#): Fixes a bug where `Molecule.from_pdb_and_smiles` could incorrectly order coordinates.
- [PR #1404](#): Support default hierarchy schemes in outputs of `Molecule.from_pdb_and_smiles()` and `Topology.from_openmm()`

## 3.7 0.11.0 Major release adding support for proteins and refactoring the Topology class.

### 3.8 Migration guide

#### 3.8.1 New `Molecule.from_polymer_pdb()` method for loading proteins from PDB files

The Toolkit now supports loading protein PDB files through the `Molecule.from_polymer_pdb()` class method. For now, PDB files must consist of only a single protein molecule composed only of the 20 standard amino acids, their common protonated and deprotonated conjugates, and the N-methyl and acetyl caps.

#### 3.8.2 Important API points re-exported from `openff.toolkit`

A number of commonly used API points have been re-exported from the package root. This should make using the Toolkit simpler for most people. The previous API points remain available. These API points are lazy-loaded so that parts of the toolkit can still be loaded without loading the entire code-base.

The most important of these are the `ForceField`, `Molecule`, and `Topology` classes:

```
- from openff.toolkit.typing.engines.smirnoff import ForceField
- from openff.toolkit.topology import Molecule, Topology
+ from openff.toolkit import ForceField, Molecule, Topology
```

A number of other useful API points are also available through this mechanism:

```
- from openff.toolkit.typing.engines.smirnoff import get_available_force_fields
- from openff.toolkit.utils.toolkits import (
-     GLOBAL_TOOLKIT_REGISTRY,
-     AmberToolsToolkitWrapper,
-     BuiltInToolkitWrapper,
-     OpenEyeToolkitWrapper,
-     RDKitToolkitWrapper,
-     ToolkitRegistry,
- )
+ from openff.toolkit import (
+     get_available_force_fields,
+     GLOBAL_TOOLKIT_REGISTRY,
+     AmberToolsToolkitWrapper,
+     BuiltInToolkitWrapper,
+     OpenEyeToolkitWrapper,
+     RDKitToolkitWrapper,
+     ToolkitRegistry,
+ )
```

The topology, typing, and utils modules can also be lazy loaded after importing only the top-level module:

```
- import openff.toolkit.topology
+ import openff.toolkit
  atom = openff.toolkit.topology.Atom()
```

### 3.8.3 Units

The use of OpenMM units has been replaced by the new OpenFF Units package, based on Pint.

Import the `unit registry` provided by `openff-units`:

```
from openff.units import unit
```

Create a `unit.Quantity` object:

```
value = unit.Quantity(1.0, unit.nanometer) # or 1.0 * unit.nanometer
```

Inspect the value and unit of this quantity:

```
print(value.magnitude) # or value.m
# 1.0
print(value.units)
# <Unit('nanometer')>
```

Convert to compatible units:

```
converted = value.to(unit.angstrom)
print(converted)
# 10.0 <Unit('angstrom')>
```

Report the value in compatible units:

```
print(value.m_as(unit.angstrom)) # Note that value.magnitude_as() does not exist
# 10.0 <Unit('angstrom')>
```

Convert to and from OpenMM quantities:

```
from openff.units.openmm import to_openmm, from_openmm
value_openmm = to_openmm(value)
print(value_openmm)
# Quantity(value=1.0, unit=nanometer)
print(type(value_openmm))
# 1.0 <Unit('nanometer')>
value_roundtrip = from_openmm(value_openmm)
print(value_roundtrip)
# 1.0 <Unit('nanometer')>
```

#### Breaking change: Removal of `openff.toolkit.utils.check_units_are_compatible()`

The `openff.toolkit.utils.check_units_are_compatible()` function has been removed. Use `openff.units.Quantity.is_compatible_with()` and `openff.units.openmm.from_openmm()` instead:

```
- check_units_are_compatible("length", length, openmm.unit.angstrom)
+ from_openmm(length).is_compatible_with(openff.units.unit.angstrom)
```

### 3.8.4 Breaking change: Interchange now responsible for system parametrization

Code for applying parameters to topologies has been removed from the Toolkit. This is now the responsibility of [OpenFF Interchange](#). This change improves support for working with parametrized systems (through the Interchange class), and adds support for working with simulation engines other than OpenMM.

The `ForceField.create_interchange()` method has been added, and the `ForceField.create_openmm_system()` method now uses Interchange under the hood.

As part of this change, the `UnsupportedKeywordArgumentsError` has been removed; passing unknown arguments to `create_openmm_system` now raises a `TypeError`, as is normal in Python.

The following classes and methods have been **removed** from `openff.toolkit.typing.engines.smirnoff.parameters`:

- `NonintegralMoleculeChargeException`
- `NonbondedMethod`
- `ParameterHandler.assign_parameters()`
- `ParameterHandler.postprocess_system()`
- `ParameterHandler.check_partial_bond_orders_from_molecules_duplicates()`
- `ParameterHandler.assign_partial_bond_orders_from_molecules()`

In addition, the `ParameterHandler.create_force()` method has been deprecated and its functionality has been removed. It will be removed in a future release.

The `return_topology` argument of `create_openmm_system` has also been deprecated, and will be removed in 0.12.0. To create an OpenMM topology, use Interchange:

```
- omm_sys, off_top = force_field.create_openmm_system(
-     topology,
-     return_topology=True,
- )
- omm_top = off_top.to_openmm()
+ interchange = force_field.create_interchange(topology)
+ omm_sys = interchange.to_openmm(combine_nonbonded_forces=True)
+ omm_top = interchange.to_openmm_topology()
```

If you need access to the modified OpenFF topology for some other reason, create an Interchange and retrieve it there:

```
- omm_sys, off_top = force_field.create_openmm_system(
-     topology,
-     return_topology=True,
- )
+ interchange = force_field.create_interchange(topology)
+ off_top = interchange.topology
+ omm_sys = interchange.to_openmm(combine_nonbonded_forces=True)
```

### 3.8.5 Breaking change: Topology molecule representation

Topology objects now store complete copies of their constituent Molecule objects, rather than using simplified classes specific to Topology. This dramatically simplifies the code base and allows the use of the full Molecule API on molecules inside topologies.

The following classes have been **removed**:

- TopologyAtom (use `Atom` instead)
- TopologyBond (use `Bond` instead)
- TopologyMolecule (use `Molecule` instead)

The following properties have been **deprecated** and will be removed in a future release:

- `Topology.n_topology_atoms` (use `Topology.n_atoms` instead)
- `Topology.topology_atoms` (use `Topology.atoms` instead)
- `Topology.n_topology_bonds` (use `Topology.n_bonds` instead)
- `Topology.topology_bonds` (use `Topology.bonds` instead)
- `Topology.n_topology_particles` (use `Topology.n_particles` instead)
- `Topology.topology_particles` (use `Topology.particles` instead)
- `Topology.reference_molecules` (use `Topology.unique_molecules` instead)
- `Topology.n_reference_molecules` (use `Topology.n_unique_molecules` instead)
- `Topology.n_topology_molecules` (use `Topology.n_molecules` instead)
- `Topology.topology_molecules` (use `Topology.molecules` instead)
- `Topology.n_particles` (use `Topology.n_atoms` instead)
- `Topology.particles` (use `Topology.atoms` instead)
- `Topology.particle_index` (use `Topology.atom_index` instead)

In addition, the `Topology.identical_molecule_groups` property has been added, to facilitate iterating over copies of isomorphic molecules in a Topology.

### 3.8.6 Breaking change: Removed virtual site handling from topologies

To maintain a clear distinction between a model and the chemistry it represents, virtual site handling has been removed from the Toolkit's Topology and Molecule classes. Virtual site support remains in the force field side of the toolkit, but creating virtual sites for particular molecules is now the responsibility of OpenFF Interchange. This allows the same Topology to be used for force fields that use different virtual sites; for example, a topology representing a solvated protein might be parametrized separately with a 3-point and 4-point water model.

As part of this change, the distinction between Atom and Particle is deprecated. The Particle class will be removed in a future release.

The following classes have been **removed**:

- BondChargeVirtualSite
- DivalentLonePairVirtualSite
- MonovalentLonePairVirtualSite

- `TrivalentLonePairVirtualSite`
- `VirtualParticle`
- `VirtualSite`
- `TopologyVirtualParticle`
- `TopologyVirtualSite`

The following methods and properties have been **removed**:

- `Atom.add_virtual_site()`
- `Atom.virtual_sites`
- `FrozenMolecule.compute_virtual_site_positions_from_conformer()`
- `FrozenMolecule.compute_virtual_site_positions_from_atom_positions()`
- `FrozenMolecule.n_virtual_sites`
- `FrozenMolecule.n_virtual_particles`
- `FrozenMolecule.virtual_sites()`
- `Molecule.add_bond_charge_virtual_site()`
- `Molecule.add_monovalent_lone_pair_virtual_site()`
- `Molecule.add_divalent_lone_pair_virtual_site()`
- `Molecule.add_trivalent_lone_pair_virtual_site()`
- `Molecule.add_bond_charge_virtual_site()`
- `Topology.n_topology_virtual_sites`
- `Topology.topology_virtual_sites`
- `Topology.virtual_site()`
- `Topology.add_particle()`

The following properties have been **deprecated** and will be removed in a future release:

- `Molecule.n_particles` (use `Molecule.n_atoms` instead)
- `Molecule.particles` (use `Molecule.atoms` instead)
- `Molecule.particle` (use `Molecule.atom` instead)
- `Molecule.particle_index` (use `Topology.n_atoms` instead)

### 3.8.7 Atom metadata and hierarchy schemes for iterating over residues, chains, etc.

The new `Atom.metadata` attribute is a dictionary that can store arbitrary metadata. Atom metadata commonly includes residue names, residue sequence numbers, chain identifiers, and other metadata that is not essential to the functioning of the Toolkit. Metadata can then be passed on when a `Molecule` is converted to another package; see [Molecule conversion to other packages](#).

Metadata can also support iteration through the `HierarchyScheme` class. A hierarchy scheme is defined by some uniqueness criteria. Iterating over the scheme iterates over groups of atoms that have identical metadata values for the defined uniqueness criteria. For more information, see the API docs for `HierarchyScheme` and its related methods.

### 3.8.8 Breaking change: Removed `Topology.charge_model` and `Topology.fractional_bond_order_model`

Due to flaws in previous versions of the OFF Toolkit, these properties never had an effect on the assigned parameters. To resolve this bug and maintain a clear distinction between a model and the chemistry it represents, the `Topology.charge_model` and `Topology.fractional_bond_order_model` properties have been removed. Charge models and FBOs are now the responsibility of the ForceField.

### 3.8.9 Breaking change: Removed `Atom.element`

`Atom.element` has been removed to reduce our dependency on OpenMM for core functions:

```
- atomic_number = atom.element.atomic_number
+ atomic_number = atom.atomic_number
- atom_mass = atom.element.mass
+ atom_mass = atom.mass
- atom_elem_symbol = atom.element.symbol
+ atom_elem_symbol = atom.symbol
```

### 3.8.10 `Topology.to_file()`

The `Topology.to_file()` method has been significantly revised, including three breaking changes.

#### Breaking change: `filename` argument renamed `file`

The `filename` argument has been renamed `file`, and now supports file-like objects in addition to file names:

```
- topology.to_file(filename="out.pdb", positions=xyz)
+ topology.to_file(file="out.pdb", positions=xyz)
```

#### Breaking change: Atom names guaranteed unique per residue by default

The default behavior is now to ensure that atom names are unique within a residue, rather than within a molecule. The `ensure_unique_atom_names` argument has been added to control this behavior. The previous behavior can be achieved by passing `True` to `ensure_unique_atom_names`:

```
- topology.to_file("out.pdb", xyz)
+ topology.to_file("out.pdb", xyz, ensure_unique_atom_names=True)
```

The `ensure_unique_atom_names` argument can also take the name of a `HierarchyScheme`, in which case atom names will be unique within the elements of that scheme (instead of within the atoms of a molecule). If the scheme is missing from a molecule, atom names will be unique within that molecule. The default value of this argument is `"residues"` to preserve atom names from the PDB.



### Breaking change: keepIds argument renamed keep\_ids

The keepIds argument has been renamed to the more Pythonic keep\_ids. Its behavior and position in the argument list has not changed.

```

- topology.to_file("out.pdb", xyz, keepIds=True)
+ topology.to_file("out.pdb", xyz, keep_ids=True)

```

### Non-breaking changes

In addition to these breaking changes, the positions argument is now optional. If it is not provided, positions will be taken from the first conformer of each molecule in the topology. If any molecule has no conformers, an error will be raised.

### 3.8.11 Positions in topologies

The `Topology.get_positions()` and `Topology.set_positions()` methods have been added to facilitate working with coordinates in topologies. A topology's positions are defined by the zeroth conformer of each molecule. If any molecule lacks conformers, the entire topology has no positions.

### 3.8.12 Parameter types moved out of handler classes

To facilitate their discovery and documentation, re-exports for the ParameterType classes have been added to the `openff.toolkit.typing.engines.smirnoff.parameters` module. Previously, they were accessible only within their associated ParameterHandler classes. This is not a breaking change.

```

- from openff.toolkit.typing.engines.smirnoff.parameters import BondHandler
- BondType = BondHandler.BondType
+ from openff.toolkit.typing.engines.smirnoff.parameters import BondType

```

### 3.8.13 Breaking change: MissingDependencyError renamed MissingPackageError

The MissingDependencyError exception has been renamed `MissingPackageError` to better reflect its purpose.

```

try:
    ...
- except MissingDependencyError:
+ except MissingPackageError:
    pass

```

### 3.8.14 `compute_partial_charges_am1bcc()` deprecated

The `compute_partial_charges_am1bcc()` methods of the `Molecule`, `AmberToolsToolkitWrapper` and `OpenEyeToolkitWrapper` classes have been deprecated and will be removed in a future release. Their functionality has been incorporated into `assign_partial_charges()` for more consistency with other charge generation methods:

```
- mol.compute_partial_charges_am1bcc()
+ mol.assign_partial_charges(partial_charge_method='am1bcc')
```

### 3.8.15 Additional changes and bugfixes

- PR #1105, PR #1195, PR #1301, PR #1331, PR #1322, PR #1372: Add `Molecule.from_polymer_pdb`
- PR #1377: Adds `Topology.unique_molecules`, which largely replaces `Topology.reference_molecules`.
- PR #1313: Fixes [Issue #1287](#), where `OpenEyeToolkitWrapper.assign_partial_charges` didn't request symmetrized charges when the charge model was set to AM1-Mulliken.
- PR #1348: Allows `pathlib.Path` objects to be passed to `Molecule.from_file`.
- PR #1276: Removes the `use_interchange` argument to `create_openmm_system`. Deletes the `create_force` and `postprocess_system` methods of `ParameterHandler` `ParameterHandler.create_force`, `ParameterHandler.postprocess_system` and other methods related to creating OpenMM systems and forces. This is now handled in Interchange.
- PR #1303: Deprecates `Topology.particles`, `Topology.n_particles`, `Topology.particle_index` as `Molecule` objects do not store virtual sites, only atoms.
- PR #1297: Drops support for Python 3.7, following [NEP-29](#).
- PR #1194: Adds `Topology.__add__`, allowing `Topology` objects to be added together, including added in-place, using the `+` operator.
- PR #1277: Adds support for version 0.4 of the <Electrostatics> section of the SMIRNOFF specification.
- PR #1279: `ParameterHandler.version` and the `.version` attribute of its subclasses is now a `Version` object. Previously it was a string, which is not safe for [PEP440](#)-style versioning.
- PR #1250: Adds support for `return_topology` in the Interchange code path in `create_openmm_system`.
- PR #964: Adds initial implementation of atom metadata dictionaries.
- PR #1097: Deprecates `TopologyMolecule`.
- PR #1097: `Topology.from_openmm` is no longer guaranteed to maintain the ordering of bonds, but now explicitly guarantees that it maintains the order of atoms (Neither of these ordering guarantees were explicitly documented before, but this may be a change from the previous behavior).
- PR #1165: Adds the boolean argument `use_interchange` to `create_openmm_system` with a default value of `False`. Setting it to `True` routes openmm.System creation through Interchange.
- PR #1192: Add re-exports for core classes to the new `openff.toolkit.app` module and re-exports for parameter types to the new `openff.toolkit.topology.parametertypes` module. This does not affect existing paths and gives some new, easier to remember paths to core objects.
- PR #1198: Ensure the vdW switch width is correctly set and enabled.
- PR #1213: Removes `Topology.charge_model` and `Topology.fractional_bond_order_model`.

- [PR #1140](#): Adds the `Topology.identical_molecule_groups` property, which provides a way of grouping the instances of a specific chemical species in the topology.
- [PR #1200](#): Fixes a bug ([Issue #1199](#)) in which library charges were ignored in some force fields, including openff-2.0.0 code name “Sage.” This resulted in the TIP3P partial charges included Sage not being applied correctly in versions 0.10.1 and 0.10.2 of the OpenFF Toolkit. This regression was not present in version 0.10.0 and earlier and therefore is not believed to have any impact on the fitting or benchmarking of the first release of Sage (version 2.0.0). The change causing regression only affected library charges and therefore no other parameter types are believed to be affected.
- [PR #1346](#): Conformer generation with RDKit will use `useRandomCoords=True` on a second attempt if the first attempt fails, which sometimes happens with large molecules.
- [PR #1277](#): Version 0.3 `<Electrostatics>` sections of OFFXML files will automatically be up-converted (in memory) to version 0.4 according to the recommendations provided in [OFF-EP 0005](#). Note this means the method attribute is replaced by `periodic_potential`, `nonperiodic_potential`, and `exception_potential`.
- [PR #1277](#): Fixes a bug in which attempting to convert `ElectrostaticsHandler.switch_width` did nothing.
- [PR #1130](#): Running unit tests will no longer generate force field files in the local directory.
- [PR #1182](#): Removes `Atom.element`, thereby also removing `Atom.element.symbol`, `Atom.element.mass` and `Atom.element.atomic_number`. These are replaced with corresponding properties directly on the `Atom` class: `Atom.symbol`, `Atom.mass`, and `Atom.atomic_number`.
- [PR #1209](#): Fixes [Issue #1073](#), where the `fractional_bondorder_method` kwarg to the `BondHandler` initializer was being ignored.
- [PR #1214](#): A long overdue fix for [Issue #837](#)! If OpenEye is available, the `ToolkitAM1BCCHandler` will use the ELF10 method to select conformers for AM1BCC charge assignment.
- [PR #1160](#): Fixes the bug identified in [Issue #1159](#), in which the order of atoms defining a `BondChargeVirtualSite` (and possibly other virtual sites types too) might be reversed if the `match` attribute of the virtual site has a value of “once”.
- [PR #1231](#): Fixes [Issue #1181](#) and [Issue #1190](#), where in rare cases double bond stereo would cause `to_rdkit` to raise an error. The transfer of double bond stereochemistry from OpenFF’s E/Z representation to RDKit’s local representation is now handled as a constraint satisfaction problem.
- [PR #1368](#): Adds the `Topology.get_positions()` and `Topology.set_positions()` methods for working with topology positions. Positions are represented as the first conformer of each molecule in the topology.
- [PR #1368](#): Allows setting the `ensure_unique_atom_names` argument of `Topology.to_openmm()` to the name of a hierarchy scheme, in which case atom names are guaranteed unique per element of that scheme rather than per molecule. Changes the default value to “residues”.
- [PR #1368](#): Adds the `ensure_unique_atom_names` argument to the `Topology.to_file()`, which mimics the same argument in `Topology.to_openmm()`. Renames the `keepIds` argument to `keep_ids`. Renames the `filename` argument to `file` and allows a file-like object to be passed instead of a filename. Makes the `positions` argument optional; if it is not given, positions are taken from the first conformer of each molecule in the Topology.
- [PR #1290](#): Fixes [Issue #1216](#) by adding internal logic to handle the possibility that multiple `vsites` share the same parent atom, and makes the return value of `VirtualSiteHandler.find_matches` be closer to the base class.

### 3.8.16 Examples added

- [PR #1113](#): Updates the Amber/GROMACS example to use Interchange.
- [PR #1368](#): Updates the Toolkit showcase with the new polymer handling and Interchange support

### 3.8.17 Tests updated

- [PR #1188](#): Add an `<Electrostatics>` section to the TIP3P force field file used in testing (`test_forcefields/tip3p.offxml`)

## 3.9 0.10.5 Bugfix release

- [PR #1252](#): Refactors virtual site support, resolving [Issue #1235](#), [Issue #1233](#), [Issue #1222](#), [Issue #1221](#), and [Issue #1206](#).
  - Attempts to make virtual site handler more resilient through code simplification.
  - Virtual sites are now associated with a particular ‘parent’ atom, rather than with a set of atoms. In particular, when checking if a v-site has been assigned we now only check the main ‘parent’ atom associated with the v-site, rather than all additional orientation atoms. As an example, if a force field contained a bond-charge v-site that matches `[O:1]=[C:2]` and a monovalent lone pair that matches `[O:1]=[C:2]-[*:3]` in that order, then only the monovalent lone pair will be assigned to formaldehyde as the oxygen is the main atom that would be associated with both v-sites, and the monovalent lone pair appears later in the hierarchy. This constitutes a behaviour change over previous versions.
  - All v-site exclusion policies have been removed except for ‘parents’ which has been updated to match [OFF-EP 0006](#).
  - checks have been added to enforce that the ‘match’ keyword complies with the SMIRNOFF spec.
  - Molecule virtual site classes no longer store FF data such as epsilon and sigma.
  - Sanity checks have been added when matching chemical environments for v-sites that ensure the environment looks like one of our expected test cases.
  - Fixes di- and trivalent lone pairs mixing the `:1` and `:2` indices.
  - Fixes trivalent v-site positioning.
  - Correctly splits `TopologyVirtualSite` and `TopologyVirtualParticle` so that virtual particles no longer have attributes such as `particles`, and ensure that indexing methods now work correctly.

## 3.10 0.10.4 Bugfix release

### 3.10.1 Critical bugfixes

- [PR #1242](#): Fixes [Issue #837](#). If OpenEye Toolkits are available, `ToolkitAM1BCCHandler` will use the ELF10 method to select conformers for AM1-BCC charge assignment.
- [PR #1184](#): Fixes [Issue #1181](#) and [Issue #1190](#), where in rare cases double bond stereochemistry would cause `Molecule.to_rdkit` to raise an error. The transfer of double bond stereochemistry from OpenFF’s E/Z representation to RDKit’s local representation is now handled as a constraint satisfaction problem.

## 3.11 0.10.3 Bugfix release

### 3.11.1 Critical bugfixes

- [PR #1200](#): Fixes a bug ([Issue #1199](#)) in which library charges were ignored in some force fields, including openff-2.0.0 code name “Sage.” This resulted in the TIP3P partial charges included Sage not being applied correctly in versions 0.10.1 and 0.10.2 of the OpenFF Toolkit. This regression was not present in version 0.10.0 and earlier and therefore is not believed to have any impact on the fitting or benchmarking of the first release of Sage (version 2.0.0). The change causing the regression only affected library charges and therefore no other parameter types are believed to be affected.

### 3.11.2 API breaking changes

- [PR #855](#): In earlier versions of the toolkit, we had mistakenly made the assumption that cheminformatics toolkits agreed on the number and membership of rings. However we later learned that this was not true. This PR removes `Molecule.rings` and `Molecule.n_rings`. To find rings in a molecule, directly use a cheminformatics toolkit after using `Molecule.to_rdkit` or `Molecule.to_openeye`. `Atom.is_in_ring` and `Bond.is_in_ring` are now methods, not properties.

### 3.11.3 Behaviors changed and bugfixes

- [PR #1171](#): Failure of `Molecule.apply_elf_conformer_selection()` due to excluding all available conformations ([Issue #428](#)) now provides a better error. The `make_carboxylic_acids_cis` argument (False by default) has been added to `Molecule.generate_conformers()` to mitigate a common cause of this error. By setting this argument to True in internal use of this method, trans carboxylic acids are no longer generated in `Molecule.assign_partial_charges()` and `Molecule.assign_fractional_bond_orders()` methods (though users may still pass trans conformers in, they’ll just be pruned by ELF methods). This should work around most instances of the OpenEye Omega bug where trans carboxylic acids are more common than they should be.

### 3.11.4 Behaviors changed and bugfixes

- [PR #1185](#): Removed length check in `ValenceDict` and fixed checking the permutations of dihedrals

### 3.11.5 Improved documentation and warnings

- [PR #1172](#): Adding discussion about constraints to the FAQ
- [PR #1173](#): Expand on the SMIRNOFF section of the toolkit docs
- [PR #855](#): Refactors `Atom.is_in_ring` and `Bond.is_in_ring` to use corresponding functionality in OpenEye and RDKit wrappers.

### 3.11.6 API breaking changes

- [PR #855](#): Removes `Molecule.rings` and `Molecule.n_rings`. To find rings in a molecule, directly use a cheminformatics toolkit after using `Molecule.to_rdkit` or `Molecule.to_openeye`. `Atom.is_in_ring` and `Bond.is_in_ring` are now methods, not properties.

## 3.12 0.10.2 Bugfix release

### 3.12.1 API-breaking changes

- [PR #1118](#): `Molecule.to_hill_formula` is now a class method and no longer accepts input of NetworkX graphs.

### 3.12.2 Behaviors changed and bugfixes

- [PR #1160](#): Fixes a major bug identified in [Issue #1159](#), in which the order of atoms defining a `BondChargeVirtualSite` (and possibly other virtual sites types too) might be reversed if the `match` attribute of the virtual site has a value of "once".
- [PR #1130](#): Running unit tests will no longer generate force field files in the local directory.
- [PR #1148](#): Adds a new exception `UnsupportedFileTypeError` and descriptive error message when attempting to use `Molecule.from_file` to parse XYZ/.xyz files.
- [PR #1153](#): Fixes [Issue #1152](#) in which running `Molecule.generate_conformers` using the OpenEye backend would use the stereochemistry from an existing conformer instead of the stereochemistry from the molecular graph, leading to undefined behavior if the molecule had a 2D conformer.
- [PR #1158](#): Fixes the default representation of `Molecule` failing in Jupyter notebooks when NGLview is not installed.
- [PR #1151](#): Fixes [Issue #1150](#), in which calling `Molecule.assign_fractional_bond_orders` with all default arguments would lead to an error as a result of trying to lowercase `None`.
- [PR #1149](#): `TopologyAtom`, `TopologyBond`, and `TopologyVirtualSite` now properly reference their reference molecule from their `.molecule` attribute.
- [PR #1155](#): Ensures big-endian byte order of NumPy arrays when serialized to dictionaries or files formats except JSON.
- [PR #1163](#): Fixes the bug identified in [Issue #1161](#), which was caused by the use of the deprecated `pkg_resources` package. Now the recommended `importlib_metadata` package is used instead.

### 3.12.3 Breaking changes

- [PR #1118](#): `Molecule.to_hill_formula` is now a class method and no longer accepts input of NetworkX graphs.
- [PR #1156](#): Removes `ParseError` and `MessageException`, which has been deprecated since version 0.10.0.

### 3.12.4 Examples added

- [PR #1113](#): Updates the Amber/GROMACS example to use Interchange.

## 3.13 0.10.1 Minor feature and bugfix release

### 3.13.1 Behaviors changed and bugfixes

- [PR #1096](#): Atom names generated by `Molecule.generate_unique_atom_names` are now appended with an "x". See the linked issue for more details.
- [PR #1050](#): In `Molecule.generate_conformers`, a single toolkit wrapper failing to generate conformers is no longer fatal, but if all wrappers in a registry fail, then a `ValueError` will be raised. This mirrors the behavior of `Molecule.assign_partial_charges`.
- [PR #1050](#): Conformer generation failures in `OpenEyeToolkitWrapper.generate_conformers`, and `RDKitToolkitWrapper.generate_conformers` now each raise `openff.toolkit.utils.exceptions.ConformerGenerationError` if conformer generation fails. The same behavior occurs in `Molecule.generate_conformers`, but only when the `toolkit_registry` argument is a `ToolkitWrapper`, not when it is a `ToolkitRegistry`.
- [PR #1046](#): Changes OFFXML output to replace tabs with 4 spaces to standardize representation in different text viewers.
- [PR #1001](#): RDKit Mol objects created through the `Molecule.to_rdkit()` method have the `NoImplicit` property set to `True` on all atoms. This prevents RDKit from incorrectly adding hydrogen atoms to to molecule.
- [PR #1058](#): Removes the unimplemented methods `ForceField.create_parmed_structure`, `Topology.to_parmed`, and `Topology.from_parmed`.
- [PR #1065](#): The example `conformer_energies.py` script now uses the Sage 2.0.0 force field.
- [PR #1036](#): SMARTS matching logic for library charges was updated to use only one unique match instead of enumerating all possible matches. This results in faster matching, particularly with larger molecules. No adverse side effects were found in testing, but bad behavior may possibly exist in some unknown cases. Note that the default behavior for other parameter handlers was not updated.
- [PR #1001](#): Revamped the `Molecule.visualize()` method's rdkit backend for more pleasing and idiomatic 2D visualization by default.
- [PR #1087](#): Fixes [Issue #1073](#) in which `Molecule.__repr__` fails if the molecule can not be represented as a SMILES pattern. Now, if SMILES generation fails, the molecule will be described by its Hill formula.
- [PR #1052](#): Fixes [Issue #986](#) by raising a subclass of `AttributeError` in `_ParameterAttributeHandler.__getattr__`.
- [PR #1030](#): Fixes a bug in which the expectations for capitalization for values of `bond_order_model` attributes and keywords are inconsistent.
- [PR #1101](#): Fixes a bug in which calling `to_qcschema` on a molecule with no connectivity feeds `QCElemental.Molecule` an empty list for the connectivity field; now feeds `None`.



### 3.13.2 Tests updated

- [PR #1017](#): Ensures that OpenEye-only CI builds really do lack both AmberTools and RDKit.

### 3.13.3 Improved documentation and warnings

- [PR #1065](#): Example notebooks were updated to use the Sage Open Force Field
- [PR #1062](#): Rewrote installation guide for clarity and comprehensiveness.

## 3.14 0.10.0 Improvements for force field fitting

### 3.14.1 Behaviors changed

- [PR #1021](#): Renames `openff.toolkit.utils.exceptions.ParseError` to `openff.toolkit.utils.exceptions.SMILESParseError` to avoid a conflict with an identically-named exception in the SMIRNOFF XML parsing code.
- [PR #1021](#): Renames and moves `openff.toolkit.typing.engines.smirnoff.forcefield.ParseError` to `openff.toolkit.utils.exceptions.SMIRNOFFParseError`. This `ParseError` is deprecated and will be removed in a future release.

### 3.14.2 New features and behaviors changed

- [PR #1027](#): Corrects interconversion of Molecule objects with OEMol objects by ensuring atom names are correctly accessible via the `OEAtomBase.GetName()` and `OEAtomBase.SetName()` methods, rather than the non-standard `OEAtomBase.GetData("name")` and `OEAtomBase.SetData("name", name)`.
- [PR #1007](#): Resolves [Issue #456](#) by adding the `normalize_partial_charges` (default is `True`) keyword argument to `Molecule.assign_partial_charges`, `AmberToolsToolkitWrapper.assign_partial_charges`, `OpenEyeToolkitWrapper.assign_partial_charges`, `RDKitToolkitWrapper.assign_partial_charges`, and `BuiltInToolkitWrapper.assign_partial_charges`. This adds an offset to each atom's partial charge to ensure that their sum is equal to the net charge on the molecule (to the limit of a python float's precision, generally less than 1e-6 electron charge). **Note that, because this new behavior is ON by default, it may slightly affect the partial charges and energies of systems generated by running `create_openmm_system`.**
- [PR #954](#): Adds `LibraryChargeType.from_molecule` which returns a `LibraryChargeType` object that will match the full molecule being parameterized, and assign it the same partial charges as are set on the input molecule.
- [PR #923](#): Adds `Molecule.nth_degree_neighbors`, `Topology.nth_degree_neighbors`, `TopologyMolecule.nth_degree_neighbors`, which returns pairs of atoms that are separated in a molecule or topology by *exactly* N atoms.
- [PR #917](#): `ForceField.create_openmm_system` now ensures that the cutoff of the `NonbondedForce` is set to the cutoff of the `vdWHandler` when it and a `Electrostatics` handler are present in the force field.
- [PR #850](#): `OpenEyeToolkitWrapper.is_available` now returns `True` if *any* OpenEye tools are licensed (and installed). This allows, i.e, use of functionality that requires OEChem without having an OEOmega license.



- [PR #909](#): Virtual site positions can now be computed directly in the toolkit. This functionality is accessed through
  - `FrozenMolecule.compute_virtual_site_positions_from_conformer`
  - `VirtualSite.compute_positions_from_conformer`
  - `VirtualParticle.compute_position_from_conformer`
  - `FrozenMolecule.compute_virtual_site_positions_from_atom_positions`
  - `VirtualSite.compute_positions_from_atom_positions`
  - `VirtualParticle.compute_position_from_atom_positions` where the positions can be computed from a stored conformer, or an input vector of atom positions.
  - Tests have been added (`TestMolecule.test_*_virtual_site_position`) to check for sane behavior. The tests do not directly compare OpenMM position equivalence, but offline tests show that they are equivalent.
  - The helper method `VirtualSiteHandler.create_openff_virtual_sites` is now public, which returns a modified topology with virtual sites added.
  - Virtual sites now expose the parameters used to create its local frame via the read-only properties
    - \* `VirtualSite.local_frame_weights`
    - \* `VirtualSite.local_frame_position`
  - Adding virtual sites via the Molecule API now have defaults for `sigma`, `epsilon`, and `charge_increment` set to 0 with appropriate units, rather than None
- [PR #956](#): Added `ForceField.get_partial_charges()` to more easily compute the partial charges assigned by a force field for a molecule.
- [PR #1006](#): Two behavior changes in the SMILES output for `to_file()` and `to_file_obj()`:
  - The RDKit and OpenEye wrappers now output the same SMILES as `to_smiles()`. This uses explicit hydrogens rather than the toolkit's default of implicit hydrogens.
  - The RDKit wrapper no longer includes a header line. This improves the consistency between the OpenEye and RDKit outputs.

### 3.14.3 Bugfixes

- [PR #1024](#): Small changes for compatibility with OpenMM 7.6.
- [PR #1003](#): Fixes [Issue #1000](#), where a stereochemistry warning is sometimes erroneously emitted when loading a stereogenic molecule using `Molecule.from_pdb_and_smiles`
- [PR #1002](#): Fixes a bug in which OFFXML files could inadvertently be loaded from subdirectories.
- [PR #969](#): Fixes a bug in which the cutoff distance of the NonbondedForce generated by `ForceField.create_openmm_system` was not set to the value specified by the vdW and Electrostatics handlers.
- [PR #909](#): Fixed several bugs related to creating an OpenMM system with virtual sites created via the Molecule virtual site API
- [PR #1006](#): Many small fixes to the toolkit wrapper I/O for better error handling, improved consistency between reading from a file vs. file object, and improved consistency between the RDKit and OEChem toolkit wrappers. For the full list see [Issue #1005](#). Some of the more significant fixes are:
  - `RDKitToolkitWrapper.from_file_obj()` now uses the same structure normalization as `from_file()`.

- `from_smiles()` now raises an `openff.toolkit.utils.exceptions.SMILESParsingError` if the SMILES could not be parsed.
- OEChem input and output files now raise an `OSError` if the file could not be opened.
- All input file object readers now support file objects open in binary mode.

### 3.14.4 Examples added

- [PR #763](#): Adds an introductory example showcasing the toolkit parameterizing a protein-ligand simulation.
- [PR #955](#): Refreshed the force field modification example
- [PR #934](#) and [conda-forge/openff-toolkit-feedstock#9](#): Added `openff-toolkit-examples` Conda package for easy installation of examples and their dependencies. Simply `conda install -c conda-forge openff-toolkit-examples` and then run the `openff-toolkit-examples` script to copy the examples suite to a convenient place to run them!

### 3.14.5 Tests updated

- [PR #963](#): Several tests modules used functions from `test_forcefield.py` that created an OpenFF Molecule without a toolkit. These functions are now in their own module so they can be imported directly, without the overhead of going through `test_forcefield`.
- [PR #997](#): Several XML snippets in `test_forcefield.py` that were scattered around inside of classes and functions are now moved to the module level.

## 3.15 0.9.2 Minor feature and bugfix release

### 3.15.1 New features and behaviors changed

- [PR #762](#): `Molecule.from_rdkit` now converts implicit hydrogens into explicit hydrogens by default. This change may affect `RDKitToolkitWrapper/Molecule.from_smiles`, `from_mapped_smiles`, `from_file`, `from_file_obj`, `from_inchi`, and `from_qcschema`. This new behavior can be disabled using the `hydrogens_are_explicit=True` keyword argument to `from_smiles`, or loading the molecule into the desired explicit protonation state in RDKit, then calling `from_rdkit` on the RDKit molecule with `hydrogens_are_explicit=True`.
- [PR #894](#): Calls to `Molecule.from_openeye`, `Molecule.from_rdkit`, `Molecule.from_smiles`, `OpenEyeToolkitWrapper.from_smiles`, and `RDKitToolkitWrapper.from_smiles` will now load atom maps into the the resulting Molecule's `offmol.properties['atom_map']` field, even if not all atoms have map indices assigned.
- [PR #904](#): `TopologyAtom` objects now have an element getter `TopologyAtom.element`.

### 3.15.2 Bugfixes

- [PR #891](#): Calls to `Molecule/OpenEyeToolkitWrapper.from_openeye` no longer mutate the input OE molecule.
- [PR #897](#): Fixes enumeration of stereoisomers for molecules with already defined stereochemistry using `RDKitToolkitWrapper.enumerate_stereoisomers`.
- [PR #859](#): Makes `RDKitToolkitWrapper.enumerate_tautomers` actually use the `max_states` keyword argument during tautomer generation, which will reduce resource use in some cases.

### 3.15.3 Improved documentation and warnings

- [PR #862](#): Clarify that System objects produced by the toolkit are OpenMM Systems in anticipation of forthcoming OpenFF Systems. Fixes [Issue #618](#).
- [PR #863](#): Documented how to build the docs in the developers guide.
- [PR #870](#): Reorganised documentation to improve discoverability and allow future additions.
- [PR #871](#): Changed Markdown parser from m2r2 to MyST for improved documentation rendering.
- [PR #880](#): Cleanup and partial rewrite of the developer's guide.
- [PR #906](#): Cleaner instructions on how to setup development environment.

## 3.16 Earlier releases

### 3.16.1 0.9.1 - Minor feature and bugfix release

#### New features

- [PR #839](#): Add support for computing WBOs from multiple conformers using the AmberTools and OpenEye toolkits, and from ELF10 conformers using the OpenEye toolkit wrapper.
- [PR #832](#): Expose ELF conformer selection through the Molecule API via a new `apply_elf_conformer_selection` function.
- [PR #831](#): Expose ELF conformer selection through the OpenEye wrapper.
- [PR #790](#): Fixes [Issue #720](#) where qcschema roundtrip to/from results in an error due to missing cmiles entry in attributes.
- [PR #793](#): Add an initial ELF conformer selection implementation which uses RDKit.
- [PR #799](#): Closes [Issue #746](#) by adding `Molecule.smirnoff_impropers`, `Molecule.amber_impropers`, `TopologyMolecule.smirnoff_impropers`, `TopologyMolecule.amber_impropers`, `Topology.smirnoff_impropers`, and `Topology.amber_impropers`.
- [PR #847](#): Instances of `ParameterAttribute` documentation can now specify their docstrings with the optional docstring argument to the `__init__()` method.
- [PR #827](#): The setter for `Topology.box_vectors` now infers box vectors when box lengths are pass as a list of length 3.

### Behavior changed

- [PR #802](#): Fixes [Issue #408](#). The 1-4 scaling factor for electrostatic interactions is now properly set by the value specified in the force field. Previously it fell back to a default value of 0.83333. The toolkit may now produce slightly different energies as a result of this change.
- [PR #839](#): The average WBO will now be returned when multiple conformers are provided to `assign_fractional_bond_orders` using `use_conformers`.
- [PR #816](#): Force field file paths are now loaded in a case-insensitive manner.

### Bugfixes

- [PR #849](#): Changes `create_openmm_system` so that it no longer uses the conformers on existing reference molecules (if present) to calculate Wiberg bond orders. Instead, new conformers are always generated during parameterization.

### Improved documentation and warnings

- [PR #838](#): Corrects spacing of “forcefield” to “force field” throughout documentation. Fixes [Issue #112](#).
- [PR #846](#): Corrects dead links throughout release history. Fixes [Issue #835](#).
- [PR #847](#): Documentation now compiles with far fewer warnings, and in many cases more correctly. Additionally, `ParameterAttribute` documentation no longer appears incorrectly in classes where it is used. Fixes [Issue #397](#).

## 3.16.2 0.9.0 - Namespace Migration

This release marks the transition from the old `openforcefield` branding over to its new identity as `openff-toolkit`. This change has been made to better represent the role of the toolkit, and highlight its place in the larger Open Force Field (OpenFF) ecosystem.

From version 0.9.0 onwards the toolkit will need to be imported as `import openff.toolkit.XXX` and from `openff.toolkit import XXX`.

### API-breaking changes

- [PR #803](#): Migrates `openforcefield` imports to `openff.toolkit`.

## 3.16.3 0.8.4 - Minor feature and bugfix release

**This release is intended to be functionally identical to 0.9.1. The only difference is that it uses the “`openforcefield`” namespace.**

This release is a final patch for the 0.8.X series of releases of the toolkit, and also marks the last version of the toolkit which will be imported as `import openforcefield.XXX` / `from openforcefield import XXX`. From version 0.9.0 onwards the toolkit will be importable only as `import openff.toolkit.XXX` / `from openff.toolkit import XXX`.

**Note** This change will also be accompanied by a renaming of the package from `openforcefield` to `openff-toolkit`, so users need not worry about accidentally pulling in a version with changed imports. Users will have to explicitly choose to install the `openff-toolkit` package once released which will contain the breaking import changes.

### 3.16.4 0.8.3 - Major bugfix release

This release fixes a critical bug in van der Waals parameter assignment.

This release is also a final patch for the 0.8.X series of releases of the toolkit, and also marks the last version of the toolkit which will be imported as `import openforcefield.XXX / from openforcefield import XXX`. From version 0.9.0 onwards the toolkit will be importable only as `import openff.toolkit.XXX / from openff.toolkit import XXX`.

**Note** This change will also be accompanied by a renaming of the package from `openforcefield` to `openff-toolkit`, so users need not worry about accidentally pulling in a version with changed imports. Users will have to explicitly choose to install the `openff-toolkit` package once released which will contain the breaking import changes.

#### Bugfixes

- [PR #808](#): Fixes [Issue #807](#), which tracks a major bug in the interconversion between a vdW sigma and `rmin_half` parameter.

#### New features

- [PR #794](#): Adds a decorator `@requires_package` that denotes a function requires an optional dependency.
- [PR #805](#): Adds a deprecation warning for the up-coming release of the `openff-toolkit` package and its import breaking changes.

### 3.16.5 0.8.2 - Bugfix release

**WARNING:** This release was later found to contain a major bug, [Issue #807](#), and produces incorrect energies.

#### Bugfixes

- [PR #786](#): Fixes [Issue #785](#) where `RDKitToolkitWrapper` would sometimes expect stereochemistry to be defined for non-stereogenic bonds when loading from SDF.
- [PR #786](#): Fixes an issue where using the `Molecule` copy constructor (`newmol = Molecule(oldmol)`) would result in the copy sharing the same `.properties` dict as the original (as in, changes to the `.properties` dict of the copy would be reflected in the original).
- [PR #789](#): Fixes a regression noted in [Issue #788](#) where creating `vdWHandler.vdWType` or setting sigma or `rmin_half` using Quantities represented as strings resulted in an error.

### 3.16.6 0.8.1 - Bugfix and minor feature release

**WARNING:** This release was later found to contain a major bug, [Issue #807](#), and produces incorrect energies.

#### API-breaking changes

- [PR #757](#): Renames `test_forcefields/smirnoff99Frosst.offxml` to `test_forcefields/test_forcefield.offxml` to avoid confusion with any of the ACTUAL released FFs in the `smirnoff99Frosst` line
- [PR #751](#): Removes the optional `oetools=("oechem", "oequacpac", "oeiupac", "oeomega")` keyword argument from `OpenEyeToolkitWrapper.is_available`, as there are no special behaviors that are accessed in the case of partially-licensed OpenEye backends. The new behavior of this method is the same as if the default value above is always provided.

#### Behavior Changed

- [PR #583](#): Methods such as `Molecule.from_rdkit` and `Molecule.from_openeye`, which delegate their internal logic to `ToolkitRegistry` functions, now guarantee that they will return an object of the correct type when being called on `Molecule`-derived classes. Previously, running these constructors using subclasses of `FrozenMolecule` would not return an instance of that subclass, but rather just an instance of a `Molecule`.
- [PR #753](#): `ParameterLookupError` is now raised when passing to `ParameterList.index` a SMIRKS pattern not found in the parameter list.

#### New features

- [PR #751](#): Adds `LicenseError`, a subclass of `ToolkitUnavailableException` which is raised when attempting to add a cheminformatics `ToolkitWrapper` for a toolkit that is installed but unlicensed.
- [PR #678](#): Adds `ForceField.deregister_parameter_handler`.
- [PR #730](#): Adds `Topology.is_periodic`.
- [PR #753](#): Adds `ParameterHandler.__getitem__` to look up individual `ParameterType` objects.

#### Bugfixes

- [PR #745](#): Fixes bug when serializing molecule with conformers to JSON.
- [PR #750](#): Fixes a bug causing either `sigma` or `rmin_half` to sometimes be missing on `vdWHandler.vdWType` objects.
- [PR #756](#): Fixes bug when running `vdWHandler.create_force` using a `vdWHandler` that was initialized using the API.
- [PR #776](#): Fixes a bug in which the `Topology.from_openmm` and `Topology.from_mdtraj` methods would dangerously allow `unique_molecules=None`.
- [PR #777](#): `RDKitToolkitWrapper` now outputs the full warning message when `allow_undefined_stereo=True` (previously the description of which stereo was undefined was squelched)

### 3.16.7 0.8.0 - Virtual Sites

#### Major Feature: Support for the SMIRNOFF VirtualSite tag

This release implements the SMIRNOFF virtual site specification. The implementation enables support for models using off-site charges, including 4- and 5-point water models, in addition to lone pair modeling on various functional groups. The primary focus was on the ability to parameterize a system using virtual sites, and generating an OpenMM system with all virtual sites present and ready for evaluation. Support for formats other than OpenMM has not been implemented in this release, but may come with the appearance of the OpenFF system object. In addition to implementing the specification, the toolkit `Molecule` objects now allow the creation and manipulation of virtual sites.

This change is documented in the [Virtual sites page](#) of the user guide.

#### Minor Feature: Support for the 0.4 ChargeIncrementModel tag

To allow for more convenient fitting of ChargeIncrement parameters, it is now possible to specify one less charge\_increment value than there are tagged atoms in a ChargeIncrement's smirks. The missing charge\_increment value will be calculated at parameterization-time to make the sum of the charge contributions from a ChargeIncrement parameter equal to zero. Since this change allows for force fields that are incompatible with the previous specification, this new style of ChargeIncrement must specify a ChargeIncrementModel section version of 0.4. All 0.3-compatible ChargeIncrement parameters are compatible with the 0.4 ChargeIncrementModel specification.

More details and examples of this change are available in [The ChargeIncrementModel tag in the SMIRNOFF specification](#)

#### New features

- [PR #726](#): Adds support for the 0.4 ChargeIncrementModel spec, allowing for the specification of one fewer charge\_increment values than there are tagged atoms in the smirks, and automatically assigning the final atom an offsetting charge.
- [PR #548](#): Adds support for the VirtualSites tag in the SMIRNOFF specification
- [PR #548](#): Adds replace and all\_permutations kwarg to
  - `Molecule.add_bond_charge_virtual_site`
  - `Molecule.add_monovalent_lone_pair_virtual_site`
  - `Molecule.add_divalent_lone_pair_virtual_site`
  - `Molecule.add_trivalent_lone_pair_virtual_site`
- [PR #548](#): Adds orientations to
  - `BondChargeVirtualSite`
  - `MonovalentLonePairVirtualSite`
  - `DivalentLonePairVirtualSite`
  - `TrivalentLonePairVirtualSite`
- [PR #548](#): Adds
  - `VirtualParticle`
  - `TopologyVirtualParticle`
  - `BondChargeVirtualSite.get_openmm_virtual_site`
  - `MonovalentLonePairVirtualSite.get_openmm_virtual_site`

- `DivalentLonePairVirtualSite.get_openmm_virtual_site`
- `TrivalentLonePairVirtualSite.get_openmm_virtual_site`
- `ValenceDict.key_transform`
- `ValenceDict.index_of`
- `ImproperDict.key_transform`
- `ImproperDict.index_of`
- [PR #705](#): Adds interpolation based on fractional bond orders for harmonic bonds. This includes interpolation for both the force constant  $k$  and/or equilibrium bond distance length. This is accompanied by a bump in the `<Bonds>` section of the SMIRNOFF spec (but not the entire spec).
- [PR #718](#): Adds `.rings` and `.n_rings` to `Molecule` and `.is_in_ring` to `Atom` and `Bond`

### Bugfixes

- [PR #682](#): Catches failures in `Molecule.from_iupac` instead of silently failing.
- [PR #743](#): Prevents the non-bonded (vdW) cutoff from silently falling back to the OpenMM default of 1 nm in `Forcefield.create_openmm_system` and instead sets its to the value specified by the force field.
- [PR #737](#): Prevents `OpenEye` from incidentally being used in the conformer generation step of `AmberToolsToolkitWrapper.assign_fractional_bond_orders`.

### Behavior changed

- [PR #705](#): Changes the default values in the `<Bonds>` section of the SMIRNOFF spec to `fractional_bondorder_method="AM1-Wiberg"` and `potential="(k/2)*(r-length)^2"`, which is backwards-compatible with and equivalent to `potential="harmonic"`.

### Examples added

- [PR #548](#): Adds a virtual site example notebook to run an OpenMM simulation with virtual sites, and compares positions and potential energy of TIP5P water between OpenFF and OpenMM force fields.

### API-breaking changes

- [PR #548](#): Methods
  - `Molecule.add_bond_charge_virtual_site`
  - `Molecule.add_monovalent_lone_pair_virtual_site`
  - `Molecule.add_divalent_lone_pair_virtual_site`
  - `Molecule.add_trivalent_lone_pair_virtual_site` now only accept a list of atoms, not a list of integers, to define to parent atoms
- [PR #548](#): Removes `VirtualParticle.molecule_particle_index`
- [PR #548](#): Removes `outOfPlaneAngle` from
  - `DivalentLonePairVirtualSite`
  - `TrivalentLonePairVirtualSite`



- [PR #548](#): Removes `inPlaneAngle` from `TrivalentLonePairVirtualSite`
- [PR #548](#): Removes weights from
  - `BondChargeVirtualSite`
  - `MonovalentLonePairVirtualSite`
  - `DivalentLonePairVirtualSite`
  - `TrivalentLonePairVirtualSite`

#### Tests added

- [PR #548](#): Adds test for
  - The virtual site parameter handler
  - TIP5P water dimer energy and positions
  - Adds tests to for virtual site/particle indexing/counting

### 3.16.8 0.7.2 - Bugfix and minor feature release

#### New features

- [PR #662](#): Adds `.aromaticity_model` of `ForceField` and `.TAGNAME` of `ParameterHandler` as public attributes.
- [PR #667](#) and [PR #681](#) linted the codebase with `black` and `isort`, respectively.
- [PR #675](#) adds `.toolkit_version` to `ToolkitWrapper` and `.registered_toolkit_versions` to `ToolkitRegistry`.
- [PR #696](#) Exposes a setter for `ForceField.aromaticity_model`
- [PR #685](#) Adds a custom `__hash__` function to `ForceField`

#### Behavior changed

- [PR #684](#): Changes `ToolkitRegistry` to return an empty registry when initialized with no arguments, i.e. `ToolkitRegistry()` and makes the `register_imported_toolkit_wrappers` argument private.
- [PR #711](#): The setter for `Topology.box_vectors` now infers box vectors (a 3x3 matrix) when box lengths (a 3x1 array) are passed, assuming an orthogonal box.
- [PR #649](#): Makes SMARTS searches stereochemistry-specific (if stereo is specified in the SMARTS) for both OpenEye and RDKit backends. Also ensures molecule aromaticity is re-perceived according to the `ForceField`'s specified aromaticity model, which may overwrite user-specified aromaticity on the `Molecule`
- [PR #648](#): Removes the `utils.structure` module, which was deprecated in 0.2.0.
- [PR #670](#): Makes the `Topology` returned by `create_openmm_system` contain the partial charges and partial bond orders (if any) assigned during parameterization.
- [PR #675](#) changes the exception raised when no antechamber executable is found from `IOError` to `AntechamberNotFoundError`
- [PR #696](#) Adds an `aromaticity_model` keyword argument to the `ForceField` constructor, which defaults to `DEFAULT_AROMATICITY_MODEL`.

### Bugfixes

- [PR #715](#): Closes issue [Issue #475](#) writing a “PDB” file using OE backend rearranges the order of the atoms by pushing the hydrogens to the bottom.
- [PR #649](#): Prevents 2020 OE toolkit from issuing a warning caused by doing stereo-specific smarts searches on certain structures.
- [PR #724](#): Closes issue [Issue #502](#) Adding a utility function `Topology.to_file()` to write topology and positions to a “PDB” file using openmm backend for pdb file write.

### Tests added

- [PR #694](#): Adds automated testing to code snippets in docs.
- [PR #715](#): Adds tests for pdb file writes using OE backend.
- [PR #724](#): Adds tests for the utility function `Topology.to_file()`.

## 3.16.9 0.7.1 - OETK2020 Compatibility and Minor Update

This is the first of our patch releases on our new planned monthly release schedule.

Detailed release notes are below, but the major new features of this release are updates for compatibility with the new 2020 OpenEye Toolkits release, the `get_available_force_fields` function, and the disregarding of pyrimidal nitrogen stereochemistry in molecule isomorphism checks.

### Behavior changed

- [PR #646](#): Checking for `Molecule` equality using the `==` operator now disregards all pyrimidal nitrogen stereochemistry by default. To re-enable, use `Molecule.{is|are}_isomorphic` with the `strip_pyrimidal_n_atom_stereo=False` keyword argument.
- [PR #646](#): Adds an optional `toolkit_registry` keyword argument to `Molecule.are_isomorphic`, which identifies the toolkit that should be used to search for pyrimidal nitrogens.

### Bugfixes

- [PR #647](#): Updates `OpenEyeToolkitWrapper` for 2020.0.4 OpenEye Toolkit behavior/API changes.
- [PR #646](#): Fixes a bug where `Molecule.chemical_environment_matches` was not able to accept a `ChemicalEnvironment` object as a query.
- [PR #634](#): Fixes a bug in which calling `RDKitToolkitWrapper.from_file` directly would not load files correctly if passed lowercase `file_format`. Note that this bug did not occur when calling `Molecule.from_file`.
- [PR #631](#): Fixes a bug in which calling `unit_to_string` returned `None` when the unit is dimensionless. Now “dimensionless” is returned.
- [PR #630](#): Closes issue [Issue #629](#) in which the wrong exception is raised when attempting to instantiate a `ForceField` from an unparsable string.

## New features

- [PR #632](#): Adds `ForceField.registered_parameter_handlers`
- [PR #614](#): Adds `ToolkitRegistry.deregister_toolkit` to de-register registered toolkits, which can include toolkit wrappers loaded into `GLOBAL_TOOLKIT_REGISTRY` by default.
- [PR #656](#): Adds a new allowed `am1elf10` option to the OpenEye implementation of `assign_partial_charges` which calculates the average partial charges at the AM1 level of theory using conformers selected using the ELF10 method.
- [PR #643](#): Adds `openforcefield.typing.engines.smirnoff.forcefield.get_available_force_fields`, which returns paths to the files of force fields available through entry point plugins.

### 3.16.10 0.7.0 - Charge Increment Model, Proper Torsion interpolation, and new Molecule methods

This is a relatively large release, motivated by the idea that changing existing functionality is bad so we shouldn't do it too often, but when we do change things we should do it all at once.

Here's a brief rundown of what changed, migration tips, and how to find more details in the full release notes below:

- To provide more consistent partial charges for a given molecule, existing conformers are now disregarded by default by `Molecule.assign_partial_charges`. Instead, new conformers are generated for use in semiempirical calculations. Search for `use_conformers`.
- Formal charges are now always returned as `simtk.unit.Quantity` objects, with units of elementary charge. To convert them to integers, use `from simtk import unit` and `atom.formal_charge.value_in_unit(unit.elementary_charge)` or `mol.total_charge.value_in_unit(unit.elementary_charge)`. Search `atom.formal_charge`.
- The OpenFF Toolkit now automatically reads and writes partial charges in SDF files. Search for `atom.dprop.PartialCharges`.
- The OpenFF Toolkit now has different behavior for handling multi-molecule and multi-conformer SDF files. Search `multi-conformer`.
- The OpenFF Toolkit now distinguishes between partial charges that are all-zero and partial charges that are unknown. Search `partial_charges = None`.
- `Topology.to_openmm` now assigns unique atoms names by default. Search `ensure_unique_atom_names`.
- Molecule equality checks are now done by graph comparison instead of SMILES comparison. Search `Molecule.are_isomorphic`.
- The `ChemicalEnvironment` module was almost entirely removed, as it is an outdated duplicate of some Chemper functionality. Search `ChemicalEnvironment`.
- `TopologyMolecule.topology_particle_start_index` has been removed from the `TopologyMolecule` API, since atoms and virtualsites are no longer contiguous in the `Topology` particle indexing system. Search `topology_particle_start_index`.
- `compute_wiberg_bond_orders` has been renamed to `assign_fractional_bond_orders`.

There are also a number of new features, such as:

- Support for `ChargeIncrementModel` sections in force fields.
- Support for `ProperTorsion` k interpolation in force fields using fractional bond orders.

- Support for AM1-Mulliken, Gasteiger, and other charge methods using the new `assign_partial_charges` methods.
- Support for AM1-Wiberg bond order calculation using either the OpenEye or RDKit/AmberTools backends and the `assign_fractional_bond_orders` methods.
- Initial (limited) interoperability with QCArchive, via `Molecule.to_qcschema` and `from_qcschema`.
- A `Molecule.visualize` method.
- Several additional `Molecule` methods, including state enumeration and mapped SMILES creation.

### Major Feature: Support for the SMIRNOFF `ChargeIncrementModel` tag

The `ChargeIncrementModel` tag in the SMIRNOFF specification provides analogous functionality to AM1-BCC, except that instead of AM1-Mulliken charges, a number of different charge methods can be called, and instead of a fixed library of two-atom charge corrections, an arbitrary number of SMIRKS-based, N-atom charge corrections can be defined in the SMIRNOFF format.

The initial implementation of the SMIRNOFF `ChargeIncrementModel` tag accepts keywords for `version`, `partial_charge_method`, and `number_of_conformers`. `partial_charge_method` can be any string, and it is up to the `ToolkitWrapper`'s `compute_partial_charges` methods to understand what they mean. For geometry-independent `partial_charge_method` choices, `number_of_conformers` should be set to zero.

SMIRKS-based parameter application for `ChargeIncrement` parameters is different than other SMIRNOFF sections. The initial implementation of `ChargeIncrementModelHandler` follows these rules:

- an atom can be subject to many `ChargeIncrement` parameters, which combine additively.
- a `ChargeIncrement` that matches a set of atoms is overwritten only if another `ChargeIncrement` matches the same group of atoms, regardless of order. This overriding follows the normal SMIRNOFF hierarchy.

To give a concise example, what if a molecule A-B(-C)-D were being parametrized, and the force field defined `ChargeIncrement` SMIRKS in the following order?

- 1) [A:1]-[B:2]
- 2) [B:1]-[A:2]
- 3) [A:1]-[B:2]-[C:3]
- 4) [\*:1]-[B:2](-[\*:3])-[\*:4]
- 5) [D:1]-[B:2](-[\*:3])-[\*:4]

In the case above, the `ChargeIncrement` from parameters 1 and 4 would NOT be applied to the molecule, since another parameter matching the same set of atoms is specified further down in the parameter hierarchy (despite those subsequent matches being in a different order).

Ultimately, the `ChargeIncrement` contributions from parameters 2, 3, and 5 would be summed and applied.

It's also important to identify a behavior that these rules were written to *avoid*: if not for the “regardless of order” clause in the second rule, parameters 4 and 5 could actually have been applied six and two times, respectively (due to symmetry in the SMIRKS and the use of wildcards). This situation could also arise as a result of molecular symmetry. For example, a methyl group could match the SMIRKS [C:1]([H:2])([H:3])([H:4]) six ways (with different orderings of the three hydrogen atoms), but the user would almost certainly not intend for the charge increments to be applied six times. The “regardless of order” clause was added specifically to address this.

In short, the first time a group of atoms becomes involved in a `ChargeIncrement` together, the OpenMM System gains a new parameter “slot”. Only another `ChargeIncrement` which applies to the exact same group of atoms (in any order) can take over the “slot”, pushing the original `ChargeIncrement` out.

### Major Feature: Support for ProperTorsion k value interpolation

Chaya Stern's work showed that we may be able to produce higher-quality proper torsion parameters by taking into account the "partial bond order" of the torsion's central bond. We now have the machinery to compute AM1-Wiberg partial bond orders for entire molecules using the `assign_fractional_bond_orders` methods of either `OpenEyeToolkitWrapper` or `AmberToolsToolkitWrapper`. The thought is that, if some simple electron population analysis shows that a certain aromatic bond's order is 1.53, maybe rotations about that bond can be described well by interpolating 53% of the way between the single and double bond  $k$  values.

Full details of how to define a torsion-interpolating SMIRNOFF force fields are available in the [ProperTorsions](#) section of the SMIRNOFF specification.

### Behavior changed

- **PR #508:** In order to provide the same results for the same chemical species, regardless of input conformation, `Molecule` `assign_partial_charges`, `compute_partial_charges_am1bcc`, and `assign_fractional_bond_orders` methods now default to ignore input conformers and generate new conformer(s) of the molecule before running semiempirical calculations. Users can override this behavior by specifying the keyword argument `use_conformers=molecule.conformers`.
- **PR #281:** Closes [Issue #250](#) by adding support for partial charge I/O in SDF. The partial charges are stored as a property in the SDF molecule block under the tag `<atom.dprop.PartialCharge>`.
- **PR #281:** If a `Molecule`'s `partial_charges` attribute is set to `None` (the default value), calling `to_openeye` will now produce a OE molecule with partial charges set to `nan`. This would previously produce an OE molecule with partial charges of `0.0`, which was a loss of information, since it wouldn't be clear whether the original OFFMol's partial charges were REALLY all-zero as opposed to `None`. OpenEye toolkit wrapper methods such as `from_smiles` and `from_file` now produce OFFMols with `partial_charges = None` when appropriate (previously these would produce OFFMols with all-zero charges, for the same reasoning as above).
- **PR #281:** `Molecule` `to_rdkit` now sets partial charges on the `RDAtom`'s `PartialCharges` property (this was previously set on the `partial_charges` property). If the `Molecule`'s `partial_charges` attribute is `None`, this property will not be defined on the `RDAtoms`.
- **PR #281:** Enforce the behavior during SDF I/O that a SDF may contain multiple *molecules*, but that the OFF Toolkit does not assume that it contains multiple *conformers of the same molecule*. This is an important distinction, since otherwise there is ambiguity around whether properties of one entry in a SDF are shared among several molecule blocks or not, or how to resolve conflicts if properties are defined differently for several "conformers" of chemically-identical species (More info [here](#)). If the user requests the OFF Toolkit to write a multi-conformer `Molecule` to SDF, only the first conformer will be written. For more fine-grained control of writing properties, conformers, and partial charges, consider using `Molecule.to_rdkit` or `Molecule.to_openeye` and using the functionality offered by those packages.
- **PR #281:** Due to different constraints placed on the data types allowed by external toolkits, we make our best effort to preserve `Molecule` properties when converting molecules to other packages, but users should be aware that no guarantee of data integrity is made. The only data format for keys and values in the property dict that we will try to support through a roundtrip to another toolkit's `Molecule` object is `string`.
- **PR #574:** Removed check that all partial charges are zero after assignment by `quacpac` when `AM1BCC` used for charge assignment. This check fails erroneously for cases in which the partial charge assignments are correctly all zero, such as for `N#N`. It is also an unnecessary check given that `quacpac` will reliably indicate when it has failed to assign charges.
- **PR #597:** Energy-minimized sample systems with Parsley 1.1.0.
- **PR #558:** The `Topology` particle indexing system now orders `TopologyVirtualSites` after all atoms.

- [PR #469](#): When running `Topology.to_openmm`, unique atom names are generated if the provided atom names are not unique (overriding any existing atom names). This uniqueness extends only to atoms in the same molecule. To disable this behavior, set the kwarg `ensure_unique_atom_names=False`.
- [PR #472](#): `Molecule.__eq__` now uses the new `Molecule.are_isomorphic` to perform the similarity checking.
- [PR #472](#): The `Topology.from_openmm` and `Topology.add_molecule` methods now use the `Molecule.are_isomorphic` method to match molecules.
- [PR #551](#): Implemented the `ParameterHandler.get_parameter` function (would previously return `None`).

### API-breaking changes

- [PR #471](#): Closes [Issue #465](#). `atom.formal_charge` and `molecule.total_charge` now return `simtk.unit.Quantity` objects instead of integers. To preserve backward compatibility, the setter for `atom.formal_charge` can accept either a `simtk.unit.Quantity` or an integer.
- [PR #601](#): Removes almost all of the previous `ChemicalEnvironment` API, since this entire module was simply copied from `Chemper` several years ago and has fallen behind on updates. Currently only `ChemicalEnvironment.get_type`, `ChemicalEnvironment.validate`, and an equivalent classmethod `ChemicalEnvironment.validate_smirks` remain. Also, please comment on [this GitHub issue](#) if you HAVE been using the previous extra functionality in this module and would like us to prioritize creation of a `Chemper` conda package.
- [PR #558](#): Removes `TopologyMolecule.topology_particle_start_index`, since the `Topology` particle indexing system now orders `TopologyVirtualSites` after all atoms. `TopologyMolecule.atom_start_topology_index` and `TopologyMolecule.virtual_particle_start_topology_index` are still available to access the appropriate values in the respective topology indexing systems.
- [PR #508](#): `OpenEyeToolkitWrapper.compute_wiberg_bond_orders` is now `OpenEyeToolkitWrapper.assign_fractional_bond_orders`. The `charge_model` keyword is now `bond_order_model`. The allowed values of this keyword have changed from `am1` and `pm3` to `am1-wiberg` and `pm3-wiberg`, respectively.
- [PR #508](#): `Molecule.compute_wiberg_bond_orders` is now `Molecule.assign_fractional_bond_orders`.
- [PR #595](#): Removed functions `openforcefield.utils.utils.temporary_directory` and `openforcefield.utils.utils.temporary_cd` and replaced their behavior with `tempfile.TemporaryDirectory()`.

### New features

- [PR #471](#): Closes [Issue #208](#) by implementing support for the `ChargeIncrementModel` tag in the `SMIRNOFF` specification.
- [PR #471](#): Implements `Molecule.assign_partial_charges`, which calls one of the newly-implemented `OpenEyeToolkitWrapper.assign_partial_charges`, and `AmberToolsToolkitWrapper.assign_partial_charges`. `strict_n_conformers` is a optional boolean keyword argument indicating whether an `IncorrectNumConformersError` should be raised if an invalid number of conformers is supplied during partial charge calculation. For example, if two conformers are supplied, but `partial_charge_method="AM1BCC"` is also set, then there is no clear use for the second conformer. The previous behavior in this case was to raise a warning, and to preserve that behavior, `strict_n_conformers` defaults to a value of `False`.
- [PR #471](#): Adds keyword argument `raise_exception_types` (default: `[Exception]`) to `ToolkitRegistry.call`. The default value will provide the previous OpenFF Toolkit behavior, which is that the first `ToolkitWrapper` that can provide the requested method is called, and it either returns



on success or raises an exception. This new keyword argument allows the ToolkitRegistry to *ignore* certain exceptions, but treat others as fatal. If `raise_exception_types = []`, the ToolkitRegistry will attempt to call each ToolkitWrapper that provides the requested method and if none succeeds, a single `ValueError` will be raised, with text listing the errors that were raised by each ToolkitWrapper.

- PR #601: Adds `RDKitToolkitWrapper.get_tagged_smarts_connectivity` and `OpenEyeToolkitWrapper.get_tagged_smarts_connectivity`, which allow the use of either toolkit for smirks/tagged smarts validation.
- PR #600: Adds `ForceField.__getitem__` to look up `ParameterHandler` objects based on their string names.
- PR #508: Adds `AmberToolsToolkitWrapper.assign_fractional_bond_orders`.
- PR #469: The `Molecule` class adds `Molecule.has_unique_atom_names` and `Molecule.has_unique_atom_names`.
- PR #472: Adds to the `Molecule` class `Molecule.are_isomorphic` and `Molecule.is_isomorphic_with` and `Molecule.hill_formula` and `Molecule.to_hill_formula` and `Molecule.to_qcschema` and `Molecule.from_qcschema` and `Molecule.from_mapped_smiles` and `Molecule.from_pdb_and_smiles` and `Molecule.canonical_order_atoms` and `Molecule.remap`

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**Note:** The `to_qcschema` method accepts an extras dictionary which is passed into the validated `qcelestial.models.Molecule` object.

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- PR #506: The `Molecule` class adds `Molecule.find_rotatable_bonds`
- PR #521: Adds `Molecule.to_inchi` and `Molecule.to_inchikey` and `Molecule.from_inchi`

**Warning:** InChI was not designed as an molecule interchange format and using it as one is not recommended. Many round trip tests will fail when using this format due to a loss of information. We have also added support for fixed hydrogen layer nonstandard InChI which can help in the case of tautomers, but overall creating molecules from InChI should be avoided.

- PR #529: Adds the ability to write out to XYZ files via `Molecule.to_file` Both single frame and multiframe XYZ files are supported. Note reading from XYZ files will not be supported due to the lack of connectivity information.
- PR #535: Extends the the API for the `Molecule.to_smiles` to allow for the creation of cmiles identifiers through combinations of isomeric, explicit hydrogen and mapped smiles, the default settings will return isomeric explicit hydrogen smiles as expected.

**Warning:** Atom maps can be supplied to the properties dictionary to modify which atoms have their map index included, if no map is supplied all atoms will be mapped in the order they appear in the `Molecule`.

- PR #563: Adds `test_forcefields/ion_charges.offxml`, giving `LibraryCharges` for monatomic ions.
- PR #543: Adds 3 new methods to the `Molecule` class which allow the enumeration of molecule states. These are `Molecule.enumerate_tautomers`, `Molecule.enumerate_stereoisomers`, `Molecule.enumerate_protomers`

**Warning:** Enumerate protomers is currently only available through the OpenEye toolkit.

- [PR #573](#): Adds quacpac error output to quacpac failure in `Molecule.compute_partial_charges_ambcc`.
- [PR #560](#): Added visualization method to the `Molecule` class.
- [PR #620](#): Added the ability to register parameter handlers via entry point plugins. This functionality is accessible by initializing a `ForceField` with the `load_plugins=True` keyword argument.
- [PR #582](#): Added fractional bond order interpolation Adds `return_topology` kwarg to `Forcefield.create_openmm_system`, which returns the processed topology along with the OpenMM System when `True` (default `False`).

### Tests added

- [PR #558](#): Adds tests ensuring that the new Topology particle indexing system are properly implemented, and that `TopologyVirtualSites` reference the correct `TopologyAtoms`.
- [PR #469](#): Added round-trip SMILES test to add coverage for `Molecule.from_smiles`.
- [PR #469](#): Added tests for unique atom naming behavior in `Topology.to_openmm`, as well as tests of the `ensure_unique_atom_names=False` kwarg disabling this behavior.
- [PR #472](#): Added tests for `Molecule.hill_formula` and `Molecule.to_hill_formula` for the various supported input types.
- [PR #472](#): Added round-trip test for `Molecule.from_qcschema` and `Molecule.to_qcschema`.
- [PR #472](#): Added tests for `Molecule.is_isomorphic_with` and `Molecule.are_isomorphic` with various levels of isomorphic graph matching.
- [PR #472](#): Added toolkit dependent tests for `Molecule.canonical_order_atoms` due to differences in the algorithms used.
- [PR #472](#): Added a test for `Molecule.from_mapped_smiles` using the molecule from issue #412 to ensure it is now fixed.
- [PR #472](#): Added a test for `Molecule.remap`, this also checks for expected error when the mapping is not complete.
- [PR #472](#): Added tests for `Molecule.from_pdb_and_smiles` to check for a correct combination of smiles and PDB and incorrect combinations.
- [PR #509](#): Added test for `Molecule.chemical_environment_matches` to check that the complete set of matches is returned.
- [PR #509](#): Added test for `Forcefield.create_openmm_system` to check that a protein system can be created.
- [PR #506](#): Added a test for the molecule identified in issue #513 as losing aromaticity when converted to rdkit.
- [PR #506](#): Added a verity of toolkit dependent tests for identifying rotatable bonds while ignoring the user requested types.
- [PR #521](#): Added toolkit independent round-trip InChI tests which add coverage for `Molecule.to_inchi` and `Molecule.from_inchi`. Also added coverage for bad inputs and `Molecule.to_inchikey`.
- [PR #529](#): Added to XYZ file coverage tests.



- [PR #563](#): Added *LibraryCharges* parameterization test for monatomic ions in `test_forcefields/ion_charges.offxml`.
- [PR #543](#): Added tests to assure that state enumeration can correctly find molecules tautomers, stereoisomers and protomers when possible.
- [PR #573](#): Added test for quacpac error output for quacpac failure in `Molecule.compute_partial_charges_ambcc`.
- [PR #579](#): Adds regression tests to ensure RDKit can be used to write multi-model PDB files.
- [PR #582](#): Added fractional bond order interpolation tests, tests for `ValidatedDict`.

## Bugfixes

- [PR #558](#): Fixes a bug where `TopologyVirtualSite.atoms` would not correctly apply `TopologyMolecule` atom ordering on top of the reference molecule ordering, in cases where the same molecule appears multiple times, but in a different order, in the same `Topology`.
- [Issue #460](#): Creates unique atom names in `Topology.to_openmm` if the existing ones are not unique. The lack of unique atom names had been causing problems in workflows involving downstream tools that expect unique atom names.
- [Issue #448](#): We can now make molecules from mapped smiles using `Molecule.from_mapped_smiles` where the order will correspond to the indexing used in the smiles. Molecules can also be re-indexed at any time using the `Molecule.remap`.
- [Issue #462](#): We can now instance the `Molecule` from a QCArchive entry record instance or dictionary representation.
- [Issue #412](#): We can now instance the `Molecule` using `Molecule.from_mapped_smiles`. This resolves an issue caused by RDKit considering atom map indices to be a distinguishing feature of an atom, which led to erroneous definition of chirality (as otherwise symmetric substituents would be seen as different). We anticipate that this will reduce the number of times you need to type `allow_undefined_stereo=True` when processing molecules that do not actually contain stereochemistry.
- [Issue #513](#): The `Molecule.to_rdkit` now re-sets the aromaticity model after sanitizing the molecule.
- [Issue #500](#): The `Molecule.find_rotatable_bonds` has been added which returns a list of rotatable `Bond` instances for the molecule.
- [Issue #491](#): We can now parse large molecules without hitting a match limit cap.
- [Issue #474](#): We can now convert molecules to InChI and InChIKey and from InChI.
- [Issue #523](#): The `Molecule.to_file` method can now correctly write to MOL files, in line with the supported file type list.
- [Issue #568](#): The `Molecule.to_file` can now correctly write multi-model PDB files when using the RDKit backend toolkit.

### Examples added

- [PR #591](#) and [PR #533](#): Adds an [example notebook](#) and utility to compute conformer energies. This example is made to be reverse-compatible with the 0.6.0 OpenFF Toolkit release.
- [PR #472](#): Adds an example notebook [QCarchive\\_interface.ipynb](#) which shows users how to instance the [Molecule](#) from a QCarchive entry level record and calculate the energy using RDKit through QCEngine.

### 3.16.11 0.6.0 - Library Charges

This release adds support for a new SMIRKS-based charge assignment method, [Library Charges](#). The addition of more charge assignment methods opens the door for new types of experimentation, but also introduces several complex behaviors and failure modes. Accordingly, we have made changes to the charge assignment infrastructure to check for cases when partial charges do not sum to the formal charge of the molecule, or when no charge assignment method is able to generate charges for a molecule. More detailed explanation of the new errors that may be raised and keywords for overriding them are in the “Behavior Changed” section below.

With this release, we update `test_forcefields/tip3p.offxml` to be a working example of assigning `LibraryCharges`. However, we do not provide any force field files to assign protein residue `LibraryCharges`. If you are interested in translating an existing protein FF to SMIRNOFF format or developing a new one, please feel free to contact us on the [Issue tracker](#) or open a [Pull Request](#).

### New features

- [PR #433](#): Closes [Issue #25](#) by adding initial support for the [LibraryCharges](#) tag in the SMIRNOFF specification using `LibraryChargeHandler`. For a molecule to have charges assigned using `LibraryCharges`, all of its atoms must be covered by at least one `LibraryCharge`. If an atom is covered by multiple `LibraryCharge`s, then the last `LibraryCharge` matched will be applied (per the hierarchy rules in the SMIRNOFF format).

This functionality is thus able to apply per-residue charges similar to those in traditional protein force fields. At this time, there is no concept of “residues” or “fragments” during parametrization, so it is not possible to assign charges to *some* atoms in a molecule using `LibraryCharge`s, but calculate charges for other atoms in the same molecule using a different method. To assign charges to a protein, `LibraryCharges` SMARTS must be provided for the residues and protonation states in the molecule, as well as for any capping groups and post-translational modifications that are present.

It is valid for `LibraryCharge` SMARTS to *partially* overlap one another. For example, a molecule consisting of atoms A-B-C connected by single bonds could be matched by a SMIRNOFF `LibraryCharges` section containing two `LibraryCharge` SMARTS: A-B and B-C. If listed in that order, the molecule would be assigned the A charge from the A-B `LibraryCharge` element and the B and C charges from the B-C element. In testing, these types of partial overlaps were found to frequently be sources of undesired behavior, so it is recommended that users define whole-molecule `LibraryCharge` SMARTS whenever possible.

- [PR #455](#): Addresses [Issue #393](#) by adding `ParameterHandler.attribute_is_cosmetic` and `ParameterType.attribute_is_cosmetic`, which return True if the provided attribute name is defined for the queried object but does not correspond to an allowed value in the SMIRNOFF spec.

## Behavior changed

- [PR #433](#): If a molecule can not be assigned charges by any charge-assignment method, an `openforcefield.typing.engines.smirnoff.parameters.UnassignedMoleculeChargeException` will be raised. Previously, creating a system without either `ToolkitAM1BCCHandler` or the `charge_from_molecules` keyword argument to `ForceField.create_openmm_system` would produce an OpenMM System where the molecule has zero charge on all atoms. However, given that we will soon be adding more options for charge assignment, it is important that failures not be silent. Molecules with zero charge can still be produced by setting the `Molecule.partial_charges` array to be all zeroes, and including the molecule in the `charge_from_molecules` keyword argument to `create_openmm_system`.
- [PR #433](#): Due to risks introduced by permitting charge assignment using partially-overlapping `LibraryCharges`, the toolkit will now raise a `openforcefield.typing.engines.smirnoff.parameters.NonIntegralMoleculeChargeException` if the sum of partial charges on a molecule are found to be more than 0.01 elementary charge units different than the molecule's formal charge. This exception can be overridden by providing the `allow_nonintegral_charges=True` keyword argument to `ForceField.create_openmm_system`.

## Tests added

- [PR #430](#): Added test for Wiberg Bond Order implemented in OpenEye Toolkits. Molecules taken from DOI:10.5281/zenodo.3405489 . Added by Sukanya Sasmal.
- [PR #569](#): Added round-trip tests for more serialization formats (dict, YAML, TOML, JSON, BSON, messagepack, pickle). Note that some are unsupported, but the tests raise the appropriate error.

## Bugfixes

- [PR #431](#): Fixes an issue where `ToolkitWrapper` objects would improperly search for functionality in the `GLOBAL_TOOLKIT_REGISTRY`, even though a specific `ToolkitRegistry` was requested for an operation.
- [PR #439](#): Fixes [Issue #438](#), by replacing call to `NetworkX Graph.node` with call to `Graph.nodes`, per [2.4 migration guide](#).

## Files modified

- [PR #433](#): Updates the previously-nonfunctional `test_forcefields/tip3p.offxml` to a functional state by updating it to the SMIRNOFF 0.3 specification, and specifying atomic charges using the `LibraryCharges` tag.

### 3.16.12 0.5.1 - Adding the parameter coverage example notebook

This release contains a new notebook example, [check\\_parameter\\_coverage.ipynb](#), which loads sets of molecules, checks whether they are parameterizable, and generates reports of chemical motifs that are not. It also fixes several simple issues, improves warnings and docstring text, and removes unused files.

The parameter coverage example notebook goes hand-in-hand with the release candidate of our initial force field, [openff-1.0.0-RC1.offxml](#) , which will be temporarily available until the official force field release is made in October. Our goal in publishing this notebook alongside our first major refitting is to allow interested users to check whether there is parameter coverage for their molecules of interest. If the force field is unable to parameterize a molecule, this notebook will generate reports of the specific chemistry that is not covered. We understand that many organizations in our field have restrictions about sharing specific molecules, and

the outputs from this notebook can easily be cropped to communicate unparameterizable chemistry without revealing the full structure.

The force field release candidate is in our new refit force field package, [openforcefields](#). This package is now a part of the Open Force Field Toolkit conda recipe, along with the original [smirnoff99Frosst](#) line of force fields.

Once the openforcefields conda package is installed, you can load the release candidate using:

```
ff = ForceField('openff-1.0.0-RC1.offxml')
```

The release candidate will be removed when the official force field, openff-1.0.0.offxml, is released in early October.

Complete details about this release are below.

### Example added

- [PR #419](#): Adds an example notebook [check\\_parameter\\_coverage.ipynb](#) which shows how to use the toolkit to check a molecule dataset for missing parameter coverage, and provides functionality to output tagged SMILES and 2D drawings of the unparameterizable chemistry.

### New features

- [PR #419](#): Unassigned valence parameter exceptions now include a list of tuples of `TopologyAtom` which were unable to be parameterized (`exception.unassigned_topology_atom_tuples`) and the class of the `ParameterHandler` that raised the exception (`exception.handler_class`).
- [PR #425](#): Implements Trevor Gokey's suggestion from [Issue #411](#), which enables pickling of `ForceFields` and `ParameterHandlers`. Note that, while XML representations of `ForceFields` are stable and conform to the SMIRNOFF specification, the pickled `ForceFields` that this functionality enables are not guaranteed to be compatible with future toolkit versions.

### Improved documentation and warnings

- [PR #425](#): Addresses [Issue #410](#), by explicitly having toolkit warnings print `Warning:` at the beginning of each warning, and adding clearer language to the warning produced when the OpenEye Toolkits can not be loaded.
- [PR #425](#): Addresses [Issue #421](#) by adding type/shape information to all `Molecule` partial charge and conformer docstrings.
- [PR #425](#): Addresses [Issue #407](#) by providing a more extensive explanation of why we don't use RDKit's mol2 parser for molecule input.

### Bugfixes

- [PR #419](#): Fixes [Issue #417](#) and [Issue #418](#), where `RDKitToolkitWrapper.from_file` would disregard the `allow_undefined_stereo` kwarg and skip the first molecule when reading a SMILES file.

## Files removed

- [PR #425](#): Addresses [Issue #424](#) by deleting the unused files `openforcefield/typing/engines/smirnoff/gbsaforces.py` and `openforcefield/tests/test_smirnoff.py`. `gbsaforces.py` was only used internally and `test_smirnoff.py` tested unsupported functionality from before the 0.2.0 release.

### 3.16.13 0.5.0 - GBSA support and quality-of-life improvements

This release adds support for the [GBSA tag in the SMIRNOFF specification](#). Currently, the HCT, OBC1, and OBC2 models (corresponding to AMBER keywords `igb=1`, `2`, and `5`, respectively) are supported, with the OBC2 implementation being the most flexible. Unfortunately, systems produced using these keywords are not yet transferable to other simulation packages via ParmEd, so users are restricted to using OpenMM to simulate systems with GBSA.

OFFXML files containing GBSA parameter definitions are available, and can be loaded in addition to existing parameter sets (for example, with the command `ForceField('test_forcefields/smirnoff99Frosst.offxml', 'test_forcefields/GBSA_OBC1-1.0.offxml')`). A manifest of new SMIRNOFF-format GBSA files is below.

Several other user-facing improvements have been added, including easier access to indexed attributes, which are now accessible as `torsion.k1`, `torsion.k2`, etc. (the previous access method `torsion.k` still works as well). More details of the new features and several bugfixes are listed below.

## New features

- [PR #363](#): Implements [GBSAHandler](#), which supports the [GBSA tag in the SMIRNOFF specification](#). Currently, only [GBSAHandlers](#) with `gb_model="OBC2"` support setting non-default values for the `surface_area_penalty` term (default  $5.4 \times \text{calories/mole/angstroms}^2$ ), though users can zero the SA term for OBC1 and HCT models by setting `sa_model="None"`. No model currently supports setting `solvent_radius` to any value other than  $1.4 \times \text{angstroms}$ . Files containing experimental SMIRNOFF-format implementations of HCT, OBC1, and OBC2 are included with this release (see below). Additional details of these models, including literature references, are available on the [SMIRNOFF specification page](#).

**Warning:** The current release of ParmEd can not transfer GBSA models produced by the Open Force Field Toolkit to other simulation packages. These GBSA forces are currently only computable using OpenMM.

- [PR #363](#): When using `Topology.to_openmm()`, periodic box vectors are now transferred from the Open Force Field Toolkit Topology into the newly-created OpenMM Topology.
- [PR #377](#): Single indexed parameters in [ParameterHandler](#) and [ParameterType](#) can now be get/set through normal attribute syntax in addition to the list syntax.
- [PR #394](#): Include element and atom name in error output when there are missing valence parameters during molecule parameterization.

## Bugfixes

- [PR #385](#): Fixes [Issue #346](#) by having `OpenEyeToolkitWrapper.compute_partial_charges_am1bcc` fall back to using standard AM1-BCC if AM1-BCC ELF10 charge generation raises an error about “trans COOH conformers”
- [PR #399](#): Fixes issue where `ForceField` constructor would ignore `parameter_handler_classes` kwarg.
- [PR #400](#): Makes link-checking tests retry three times before failing.

## Files added

- [PR #363](#): Adds `test_forcefields/GBSA_HCT-1.0.offxml`, `test_forcefields/GBSA_OBC1-1.0.offxml`, and `test_forcefields/GBSA_OBC2-1.0.offxml`, which are experimental implementations of GBSA models. These are primarily used in validation tests against OpenMM’s models, and their version numbers will increment if bugfixes are necessary.

## 3.16.14 0.4.1 - Bugfix Release

This update fixes several toolkit bugs that have been reported by the community. Details of these bugfixes are provided below.

It also refactors how `ParameterType` and `ParameterHandler` store their attributes, by introducing `ParameterAttribute` and `IndexedParameterAttribute`. These new attribute-handling classes provide a consistent backend which should simplify manipulation of parameters and implementation of new handlers.

## Bug fixes

- [PR #329](#): Fixed a bug where the two `BondType` parameter attributes `k` and `length` were treated as indexed attributes. (`k` and `length` values that correspond to specific bond orders will be indexed under `k_bondorder1`, `k_bondorder2`, etc when implemented in the future)
- [PR #329](#): Fixed a bug that allowed setting indexed attributes to single values instead of strictly lists.
- [PR #370](#): Fixed a bug in the API where `BondHandler`, `ProperTorsionHandler`, and `ImproperTorsionHandler` exposed non-functional indexed parameters.
- [PR #351](#): Fixes [Issue #344](#), in which the main `FrozenMolecule` constructor and several other Molecule-construction functions ignored or did not expose the `allow_undefined_stereo` keyword argument.
- [PR #351](#): Fixes a bug where a molecule which previously generated a SMILES using one cheminformatics toolkit returns the same SMILES, even though a different toolkit (which would generate a different SMILES for the molecule) is explicitly called.
- [PR #354](#): Fixes the error message that is printed if an unexpected parameter attribute is found while loading data into a `ForceField` (now instructs users to specify `allow_cosmetic_attributes` instead of `permit_cosmetic_attributes`)
- [PR #364](#): Fixes [Issue #362](#) by modifying `OpenEyeToolkitWrapper.from_smiles` and `RDKitToolkitWrapper.from_smiles` to make implicit hydrogens explicit before molecule creation. These functions also now raise an error if the optional keyword `hydrogens_are_explicit=True` but the SMILES are interpreted by the backend cheminformatic toolkit as having implicit hydrogens.
- [PR #371](#): Fixes error when reading early SMIRNOFF 0.1 spec files enclosed by a top-level SMIRFF tag.

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**Note:** The enclosing SMIRFF tag is present only in legacy files. Since developing a formal specification, the only acceptable top-level tag value in a SMIRNOFF data structure is SMIRNOFF.

---

### Code enhancements

- [PR #329](#): `ParameterType` was refactored to improve its extensibility. It is now possible to create new parameter types by using the new descriptors `ParameterAttribute` and `IndexedParameterAttribute`.
- [PR #357](#): Addresses [Issue #356](#) by raising an informative error message if a user attempts to load an OpenMM topology which is probably missing connectivity information.

### Force fields added

- [PR #368](#): Temporarily adds `test_forcefields/smirnoff99frosst_experimental.offxml` to address hierarchy problems, redundancies, SMIRKS pattern typos etc., as documented in [issue #367](#). Will ultimately be propagated to an updated force field in the `openforcefield/smirnoff99frosst` repo.
- [PR #371](#): Adds `test_forcefields/smirnoff99frosst_reference_0_1_spec.offxml`, a SMIRNOFF 0.1 spec file enclosed by the legacy SMIRFF tag. This file is used in backwards-compatibility testing.

## 3.16.15 0.4.0 - Performance optimizations and support for SMIRNOFF 0.3 specification

This update contains performance enhancements that significantly reduce the time to create OpenMM systems for topologies containing many molecules via `ForceField.create_openmm_system`.

This update also introduces the [SMIRNOFF 0.3 specification](#). The spec update is the result of discussions about how to handle the evolution of data and parameter types as further functional forms are added to the SMIRNOFF spec.

We provide methods to convert SMIRNOFF 0.1 and 0.2 force fields written with the XML serialization (`.offxml`) to the SMIRNOFF 0.3 specification. These methods are called automatically when loading a serialized SMIRNOFF data representation written in the 0.1 or 0.2 specification. This functionality allows the toolkit to continue to read files containing SMIRNOFF 0.2 spec force fields, and also implements backwards-compatibility for SMIRNOFF 0.1 spec force fields.

**Warning:** The SMIRNOFF 0.1 spec did not contain fields for several energy-determining parameters that are exposed in later SMIRNOFF specs. Thus, when reading SMIRNOFF 0.1 spec data, the toolkit must make assumptions about the values that should be added for the newly-required fields. The values that are added include 1-2, 1-3 and 1-5 scaling factors, cutoffs, and long-range treatments for nonbonded interactions. Each assumption is printed as a warning during the conversion process. Please carefully review the warning messages to ensure that the conversion is providing your desired behavior.



### SMIRNOFF 0.3 specification updates

- The SMIRNOFF 0.3 spec introduces versioning for each individual parameter section, allowing asynchronous updates to the features of each parameter class. The top-level SMIRNOFF tag, containing information like `aromaticity_model`, `Author`, and `Date`, still has a version (currently 0.3). But, to allow for independent development of individual parameter types, each section (such as Bonds, Angles, etc) now has its own version as well (currently all 0.3).
- All units are now stored in expressions with their corresponding values. For example, distances are now stored as `1.526*angstrom`, instead of storing the unit separately in the section header.
- The current allowed value of the potential field for `ProperTorsions` and `ImproperTorsions` tags is no longer `charmm`, but is rather `k*(1+cos(periodicity*theta-phase))`. It was pointed out to us that CHARMM-style torsions deviate from this formula when the periodicity of a torsion term is 0, and we do not intend to reproduce that behavior.
- SMIRNOFF spec documentation has been updated with tables of keywords and their defaults for each parameter section and parameter type. These tables will track the allowed keywords and default behavior as updated versions of individual parameter sections are released.

### Performance improvements and bugfixes

- [PR #329](#): Performance improvements when creating systems for topologies with many atoms.
- [PR #347](#): Fixes bug in charge assignment that occurs when charges are read from file, and reference and charge molecules have different atom orderings.

### New features

- [PR #311](#): Several new experimental functions.
  - Adds `convert_0_2_smirnoff_to_0_3`, which takes a SMIRNOFF 0.2-spec data dict, and updates it to 0.3. This function is called automatically when creating a `ForceField` from a SMIRNOFF 0.2 spec OFFXML file.
  - Adds `convert_0_1_smirnoff_to_0_2`, which takes a SMIRNOFF 0.1-spec data dict, and updates it to 0.2. This function is called automatically when creating a `ForceField` from a SMIRNOFF 0.1 spec OFFXML file.
  - NOTE: The format of the “SMIRNOFF data dict” above is likely to change significantly in the future. Users that require a stable serialized `ForceField` object should use the output of `ForceField.to_string('XML')` instead.
  - Adds `ParameterHandler` and `ParameterType` `add_cosmetic_attribute` and `delete_cosmetic_attribute` functions. Once created, cosmetic attributes can be accessed and modified as attributes of the underlying object (eg. `ParameterType.my_cosmetic_attr = 'blue'`) These functions are experimental, and we are interested in feedback on how cosmetic attribute handling could be improved. (See [Issue #338](#)) Note that if a new cosmetic attribute is added to an object without using these functions, it will not be recognized by the toolkit and will not be written out during serialization.
  - Values for the top-level `Author` and `Date` tags are now kept during SMIRNOFF data I/O. If multiple data sources containing these fields are read, the values are concatenated using “AND” as a separator.



### API-breaking changes

- `ForceField.to_string` and `ForceField.to_file` have had the default value of their `discard_cosmetic_attributes` kwarg set to `False`.
- `ParameterHandler` and `ParameterType` constructors now expect the `version` kwarg (per the SMIRNOFF spec change above) This requirement can be skipped by providing the kwarg `skip_version_check=True`
- `ParameterHandler` and `ParameterType` functions no longer handle `X_unit` attributes in SMIRNOFF data (per the SMIRNOFF spec change above).
- The scripts in `utilities/convert_frosst` are now deprecated. This functionality is important for provenance and will be migrated to the `openforcefield/smirnoff99Frosst` repository in the coming weeks.
- `ParameterType` `._SMIRNOFF_ATTRIBS` is now `ParameterType` `._REQUIRED_SPEC_ATTRIBS`, to better parallel the structure of the `ParameterHandler` class.
- `ParameterType` `._OPTIONAL_ATTRIBS` is now `ParameterType` `._OPTIONAL_SPEC_ATTRIBS`, to better parallel the structure of the `ParameterHandler` class.
- Added class-level dictionaries `ParameterHandler` `._DEFAULT_SPEC_ATTRIBS` and `ParameterType` `._DEFAULT_SPEC_ATTRIBS`.

### 3.16.16 0.3.0 - API Improvements

Several improvements and changes to public API.

#### New features

- [PR #292](#): Implement `Topology.to_openmm` and remove `ToolkitRegistry.toolkit_is_available`
- [PR #322](#): Install directories for the lookup of OFFXML files through the entry point group `openforcefield.smirnoff_forcefield_directory`. The `ForceField` class doesn't search in the `data/forcefield/` folder anymore (now renamed `data/test_forcefields/`), but only in `data/`.

#### API-breaking Changes

- [PR #278](#): Standardize variable/method names
- [PR #291](#): Remove `ForceField.load/to_smirnoff_data`, add `ForceField.to_file/string` and `ParameterHandler.add_parameters`. Change behavior of `ForceField.register_X_handler` functions.

#### Bugfixes

- [PR #327](#): Fix units in `tip3p.offxml` (note that this file is still not loadable by current toolkit)
- [PR #325](#): Fix solvent box for provided test system to resolve periodic clashes.
- [PR #325](#): Add informative message containing Hill formula when a molecule can't be matched in `Topology.from_openmm`.
- [PR #325](#): Provide warning or error message as appropriate when a molecule is missing stereochemistry.
- [PR #316](#): Fix formatting issues in GBSA section of SMIRNOFF spec
- [PR #308](#): Cache molecule SMILES to improve system creation speed

- [PR #306](#): Allow single-atom molecules with all zero coordinates to be converted to OE/RDK mols
- [PR #313](#): Fix issue where constraints are applied twice to constrained bonds

### 3.16.17 0.2.2 - Bugfix release

This release modifies an example to show how to parameterize a solvated system, cleans up backend code, and makes several improvements to the README.

#### Bugfixes

- [PR #279](#): Cleanup of unused code/warnings in main package `__init__`
- [PR #259](#): Update T4 Lysozyme + toluene example to show how to set up solvated systems
- [PR #256](#) and [PR #274](#): Add functionality to ensure that links in READMEs resolve successfully

### 3.16.18 0.2.1 - Bugfix release

This release features various documentation fixes, minor bugfixes, and code cleanup.

#### Bugfixes

- [PR #267](#): Add neglected `<ToolkitAM1BCC>` documentation to the SMIRNOFF 0.2 spec
- [PR #258](#): General cleanup and removal of unused/inaccessible code.
- [PR #244](#): Improvements and typo fixes for BRD4:inhibitor benchmark

### 3.16.19 0.2.0 - Initial RDKit support

This version of the toolkit introduces many new features on the way to a 1.0.0 release.

#### New features

- Major overhaul, resulting in the creation of the [SMIRNOFF 0.2 specification](#) and its XML representation
- Updated API and infrastructure for reference SMIRNOFF [ForceField](#) implementation
- Implementation of modular [ParameterHandler](#) classes which process the topology to add all necessary forces to the system.
- Implementation of modular [ParameterIOHandler](#) classes for reading/writing different serialized SMIRNOFF force field representations
- Introduction of [Molecule](#) and [Topology](#) classes for representing molecules and biomolecular systems
- New [ToolkitWrapper](#) interface to RDKit, OpenEye, and AmberTools toolkits, managed by [ToolkitRegistry](#)
- API improvements to more closely follow [PEP8](#) guidelines
- Improved documentation and examples

### 3.16.20 0.1.0

This is an early preview release of the toolkit that matches the functionality described in the preprint describing the SMIRNOFF v0.1 force field format: [\[DOI\]](#).

#### New features

This release features additional documentation, code comments, and support for automated testing.

#### Bugfixes

##### Treatment of improper torsions

A significant (though currently unused) problem in handling of improper torsions was corrected. Previously, non-planar impropers did not behave correctly, as six-fold impropers have two potential chiralities. To remedy this, SMIRNOFF impropers are now implemented as three-fold impropers with consistent chirality. However, current force fields in the SMIRNOFF format had no non-planar impropers, so this change is mainly aimed at future work.



## FREQUENTLY ASKED QUESTIONS (FAQ)

### 4.1 What kinds of input files can I apply SMIRNOFF parameters to?

SMIRNOFF force fields use direct chemical perception meaning that, unlike many molecular mechanics (MM) force fields, they apply parameters based on substructure searches acting directly on molecules. This creates unique opportunities and allows them to encode a great deal of chemistry quite simply, but it also means that the *starting point* for parameter assignment must be well-defined chemically, giving not just the elements and connectivity for all of the atoms of all of the components of your system, but also providing the formal charges and bond orders.

Specifically, to apply SMIRNOFF to a system, you must either:

1. Provide Open Force Field Toolkit [Molecule](#) objects corresponding to the components of your system, or
2. Provide an OpenMM [Topology](#) which includes bond orders and thus can be converted to molecules corresponding to the components of your system

Without this information, our direct chemical perception cannot be applied to your molecule, as it requires the chemical identity of the molecules in your system – that is, bond order and formal charge as well as atoms and connectivity. Unless you provide the full chemical identity in this sense, we must attempt to guess or infer the chemical identity of your molecules, which is a recipe for trouble. Different molecules can have the same chemical graph but differ in bond order and formal charge, or different resonance structures may be treated rather differently by some force fields (e.g. c1cc(ccc1c2cc[nH+]cc2)[O-] vs C1=CC(C=CC1=C2C=CNC=C2)=O, where the central bond is rotatable in one resonance structure but not in the other) even though they have identical formal charge and connectivity (chemical graph). A force field which uses the chemical identity of molecules to assign parameters needs to know the exact chemical identity of the molecule you are intending to parameterize.

### 4.2 Can I use an AMBER (or GROMACS) topology/coordinate file as a starting point for applying a SMIRNOFF force field?

In a word, “no”.

Parameter files used by typical molecular dynamics simulation packages do not currently encode enough information to identify the molecules chemically present, or at least not without drawing inferences. For example, one could take a structure file and infer bond orders based on bond lengths, or attempt to infer bond orders from force constants in a parameter file. Such inference work is outside the scope of SMIRNOFF.

## 4.3 What about starting from a PDB file?

PDB files do not in general provide the chemical identity of small molecules contained therein, and thus do not provide suitable starting points for applying SMIRNOFF to small molecules. This is especially problematic for PDB files from X-ray crystallography which typically do not include proteins, making the problem even worse. For our purposes here, however, we assume you begin with the coordinates of all atoms present and the full topology of your system.

Given a PDB file of a hypothetical biomolecular system of interest containing a small molecule, there are several routes available to you for treating the small molecule present:

- Use a cheminformatics toolkit (see below) to infer bond orders
- Identify your ligand from a database; e.g. if it is in the Protein Data Bank (PDB), it will be present in the [Ligand Expo](#) meaning that it has a database entry and code you can use to look up its putative chemical identity
- Identify your ligand by name or SMILES string (or similar) from the literature or your collaborators

## 4.4 What about starting from an XYZ file?

XYZ files generally only contain elements and positions, and are therefore similar in content to PDB files. See the above section “What about starting from a PDB file?” for more information.

## 4.5 What do you recommend as a starting point?

For application of SMIRNOFF force fields, we recommend that you begin your work with formats which provide the chemical identity of your small molecule (including formal charge and bond order). This means we recommend one of the following or equivalent:

- A .sdf, .mol, or .mol2 file or files for the molecules comprising your system, with correct bond orders and formal charges. (Note: Do NOT generate this from a simulation package or tool which does not have access to bond order information; you may end up with a correct-seeming file, but the bond orders will be incorrect)
- Isomeric SMILES strings for the components of your system
- InChi strings for the components of your system
- Chemical Identity Registry numbers for the components of your system
- IUPAC names for the components of your system

Essentially, anything which provides the full identity of what you want to simulate (including stereochemistry) should work, though it may require more or less work to get it into an acceptable format.

## 4.6 I understand the risks and want to perform bond and formal charge inference anyway

If you are unable to provide a molecule in the formats recommended above and want to attempt to infer the bond orders and atomic formal charges, there are tools available elsewhere that can provide guesses for this problem. These tools are not perfect, and the inference problem itself is poorly defined, so you should review each output closely (see our [Core Concepts](#) for an explanation of what information is needed to construct an OpenFF Molecule). Some tools we know of include:

- the OpenEye Toolkit's [OEPeceiveBondOrders](#) functionality
- [MDAnalysis'](#) RDKit converter, with an [example here](#)
- the Jensen group's [xyz2mol](#) program

## 4.7 I'm getting stereochemistry errors when loading a molecule from a SMILES string.

By default, the OpenFF Toolkit throws an error if a molecule with undefined stereochemistry is loaded. This is because the stereochemistry of a molecule may affect its partial charges, and assigning parameters using [direct chemical perception](#) may require knowing the stereochemistry of chiral centers. In addition, coordinates generated by the Toolkit for undefined chiral centers may have any combination of stereochemistries; the toolkit makes no guarantees about consistency, uniformity, or randomness. Note that the main-line OpenFF force fields currently use a stereochemistry-dependent charge generation method, but do not include any other stereospecific parameters.

This behavior is in line with OpenFF's general attitude of requiring users to explicitly acknowledge actions that may cause silent errors later on. If you're confident a Molecule with unassigned stereochemistry is acceptable, pass `allow_undefined_stereo=True` to molecule loading methods like [Molecule.from\\_smiles](#) to downgrade the exception to a warning. For an example, see the "SMILES without stereochemistry" section in the [Molecule cookbook](#). Where possible, our parameter assignment infrastructure will gracefully handle molecules with undefined stereochemistry that are loaded this way, though they will be missing any stereospecific parameters.

## 4.8 I'm having troubles installing the OpenFF Toolkit on my Apple Silicon Mac.

As of August 2022, some upstreams (at least AmberTools, possibly more) are not built on `osx-arm64`, so installing the OpenFF stack is only possible with [Rosetta](#). See the [platform support](#) section of the installation documentation for more.

(Keywords `osx-arm64`, M1 Mac, M2 Mac)

## 4.9 My conda installation of the toolkit doesn't appear to work. What should I try next?

We recommend that you install the toolkit in a fresh conda environment, explicitly passing the channels to be used, in-order:

```
conda create -n <my_new_env> -c conda-forge openff-toolkit
conda activate <my_new_env>
```

Installing into a new environment avoids forcing conda to satisfy the dependencies of both the toolkit and all existing packages in that environment. Taking the approach that conda environments are generally disposable, even ephemeral, minimizes the chances for hard-to-diagnose dependency issues.

## 4.10 My conda installation of the toolkit STILL doesn't appear to work.

Many of our users encounter issues that are ultimately due to their terminal finding a different conda at higher priority in their PATH than the conda deployment where OpenFF is installed. To fix this, find the conda deployment where OpenFF is installed. Then, if that folder is something like ~/miniconda3, run in the terminal:

```
source ~/miniconda3/etc/profile.d/conda.sh
```

and then try rerunning and/or reinstalling the Toolkit.

## 4.11 The partial charges generated by the toolkit don't seem to depend on the molecule's conformation! Is this a bug?

No! This is the intended behavior. The force field parameters of a molecule should be independent of both their chemical environment and conformation so that they can be used and compared across different contexts. When applying AM1BCC partial charges, the toolkit achieves a deterministic output by ignoring the input conformation and producing several new conformations for the same molecule. Partial charges are then computed based on these conformations. This behavior can be controlled with the `use_conformers` argument to `Molecule.assign_partial_charges()`.

## 4.12 Parameterizing my system, which contains a large molecule, is taking forever. What's wrong?

The mainline OpenFF force fields use AM1-BCC to assign partial charges (via the `<ToolkitAM1BCCHandler>` tag in the OFFXML file). This method unfortunately scales poorly with the size of a molecule and ligands roughly 100 atoms (about 40 heavy atoms) or larger may take so long (i.e. 10 minutes or more) that it seems like your code is simply hanging indefinitely. If you have an OpenEye license and OpenEye Toolkits *installed*, the OpenFF Toolkit will instead use quacpac, which can offer better performance on large molecules. Otherwise, it uses AmberTools' `sqm`, which is free to use.

In the future, the use of AM1-BCC in OpenFF force fields may be replaced with method(s) that perform better and scale better with molecule size, but (as of April 2022) these are still in an experimental phase.



## 4.13 How can I distribute my own force fields in SMIRNOFF format?

We support conda data packages for distribution of force fields in .offxml format! Just add the relevant entry point to setup.py and distribute via a conda (or PyPI) package:

```
entry_points={
    'openforcefield.smirnoff_forcefield_directory' : [
        'my_new_force_field_paths = my_package:get_my_new_force_field_paths',
    ],
}
```

Where `get_my_new_force_field_paths` is a function in the `my_package` module providing a list of strings holding the paths to the directories to search. You should also rename `my_new_force_field_paths` to suit your force field. See [openff-forcefields](#) for an example.

## 4.14 What does “unconstrained” mean in a force field name?

Each release of an [OpenFF force field](#) has two associated .offxml files: one unadorned (for example, `openff-2.0.0.offxml`) and one labeled “unconstrained” (`openff_unconstrained-2.0.0.offxml`). This reflects the presence or absence of holonomic constraints on hydrogen-involving bonds in the force field specification.

Typically, OpenFF force fields treat bonds with a harmonic potential according to Hooke’s law. With this treatment, bonds involving hydrogen atoms have a much higher vibration frequency than any other part of a typical biochemical system. By constraining these bonds to a fixed length, MD time steps can be increased past 1 fs, improving simulation performance. These bond vibrations are not structurally important to proteins so can usually be ignored.

While we recommend hydrogen-involving bond constraints and a time step of 2 fs for ordinary use, some other specialist uses require a harmonic treatment. The unconstrained force fields are provided for these uses.

Use the constrained force field:

- When running MD with a time step greater than 1 fs

Use the unconstrained force field:

- When computing single point energy calculations or energy minimization
- When running MD with a time step of 1 fs (or less)
- When bond lengths may deviate from equilibrium
- When fitting a force field, both because many fitting techniques require continuity and because deviations from equilibrium bond length may be important
- Any other circumstance when forces or energies must be defined or continuous for any possible position of a hydrogen atom

Starting with v2.0.0 (Sage), TIP3P water is included in OpenFF force fields. The geometry of TIP3P water is always constrained, even in the unconstrained force fields.

## 4.15 How do I add or remove constraints from my own force field?

To make applying or removing bond constraints easy, constrained force fields released by OpenFF always include full bond parameters. Constraints on Hydrogen-involving bonds inherit their lengths from the harmonic parameters also included in the force field. To restore the harmonic treatment, simply remove the appropriate constraint entry from the force field.

Hydrogen-involving bonds are constrained with a single constraint entry in a .offxml file:

```
<Constraints version="0.3">
  <!-- constrain all bonds to hydrogen to their equilibrium bond length -->
  <Constraint smirks="#1:1]-[*:2]" id="c1"></Constraint>
</Constraints>
```

Adding or removing the inner `<Constraint...>` line will convert a force field between being constrained and unconstrained. A `ForceField` object can constrain its bonds involving hydrogen by adding the relevant parameter to its 'Constraints' parameter handler:

```
ch = force_field.get_parameter_handler('Constraints')
ch.add_parameter(smirks="#1:1]-[*:2]")
```

Constraints can be removed from bonds involving hydrogen by removing the corresponding parameter:

```
del forcefield['Constraints'][ "#1:1]-[*:2]"]
```

## CORE CONCEPTS

**OpenFF Molecule** A graph representation of a molecule containing enough information to unambiguously parametrize it. Required data fields for a Molecule are:

- atoms: element (integer), formal\_charge (integer), is\_aromatic (boolean), stereochemistry ('R'/'S'/None)
- bonds: order (integer), is\_aromatic (boolean), stereochemistry ('E'/'Z'/None)

There are several other optional attributes such as conformers and partial\_charges that may be populated in the Molecule data structure. These are considered “optional” because they are not required for system creation, however if those fields are populated, the user MAY use them to override values that would otherwise be generated during system creation.

A dictionary, `Molecule.properties` is exposed, which is a Python dict that can be populated with arbitrary data. This data should be considered cosmetic and should not affect system creation. Whenever possible, molecule serialization or format conversion should preserve this data.

**OpenFF Topology** A collection of molecules, as well as optional box vector, positions, and other information. A Topology describes the chemistry of a system, but has no force field parameters.

**OpenFF ForceField** An object generated from an OFFXML file (or other source of SMIRNOFF data). Most information from the SMIRNOFF data source is stored in this object’s several `ParameterHandlers`, however some top-level SMIRNOFF data is stored in the `ForceField` object itself.

**OpenFF Interchange** A Topology that has been parametrized by a `ForceField`. An `Interchange` contains all the information needed to calculate an energy or start a simulation. `Interchange` also provides methods to export this information to MD simulation engines.



## COOKBOOK: EVERY WAY TO MAKE A MOLECULE

Every pathway through the OpenFF Toolkit boils down to four steps:

1. Using other tools, assemble a graph of a molecule, including all of its atoms, bonds, bond orders, formal charges, and stereochemistry<sup>1</sup>
2. Use that information to construct a `Molecule`
3. Combine a number of `Molecule` objects to construct a `Topology`
4. Call `ForceField.create_openmm_system(topology)` to create an OpenMM `System` (or, in the near future, an OpenFF `Interchange` for painless conversion to all sorts of MD formats)

So let's take a look at every way there is to construct a molecule! We'll use zwitterionic L-alanine as an example biomolecule with all the tricky bits - a stereocenter, non-zero formal charges, and bonds of different orders.

### 6.1 From SMILES

SMILES is the classic way to create a `Molecule`. SMILES is a widely-used compact textual representation of arbitrary molecules. This lets us specify an exact molecule, including stereochemistry and bond orders, very easily — though they may not be the most human-readable format.

The `Molecule.from_smiles()` method is used to create a `Molecule` from a SMILES code.

#### 6.1.1 Implicit hydrogens SMILES

```
zw_l_alanine = Molecule.from_smiles("C[C@H]([NH3+])C(=O)[O-]")  
  
zw_l_alanine.visualize()
```

```
<IPython.core.display.SVG object>
```

---

<sup>1</sup> Note that this stereochemistry must be defined on the *graph* of the molecule. It's not good enough to just co-ordinates with the correct stereochemistry. But if you have the co-ordinates, you can try getting the stereochemistry automatically with `rdkit` or `openeye` — If you dare!

### 6.1.2 Explicit hydrogens SMILES

```
smiles_explicit_h = Molecule.from_smiles(
    "[H][C]([H])([H])[C@@]([H])([C](=[O])[O-])[N+](H)(H)H",
    hydrogens_are_explicit=True
)

assert zw_l_alanine.is_isomorphic_with(smiles_explicit_h)

smiles_explicit_h.visualize()
```

```
<IPython.core.display.SVG object>
```

### 6.1.3 Mapped SMILES

By default, no guarantees are made about the indexing of atoms from a SMILES string. If the indexing is important, a mapped SMILES string may be used. In this case, Hydrogens must be explicit. Note that though mapped SMILES strings must start at index 1, Python lists start at index 0.

```
mapped_smiles = Molecule.from_mapped_smiles(
    "[H:10][C:2]([H:7])([H:8])[C@@:4]([H:9])([C:3](=[O:5])[O-:6])[N+:1]([H:11])([H:12])[H:13]
    ↪"
)

assert zw_l_alanine.is_isomorphic_with(mapped_smiles)

assert mapped_smiles.atoms[0].atomic_number == 7 # First index is the Nitrogen
assert all([a.atomic_number==1 for a in mapped_smiles.atoms[6:]]) # Final indices are all H

mapped_smiles.visualize()
```

```
<IPython.core.display.SVG object>
```

### 6.1.4 SMILES without stereochemistry

The Toolkit won't accept an ambiguous SMILES. This SMILES could be L- or D- alanine; rather than guess, the Toolkit throws an error:

```
smiles_non_isomeric = Molecule.from_smiles(
    "CC([NH3+])C(=O)[O-]"
)
```

```
UndefinedStereochemistryError: Unable to make OFFMol from OEMol: OEMol has unspecified_
↪ stereochemistry. oemol.GetTitle():
Problematic atoms are:
Atom atomic num: 6, name: , idx: 1, aromatic: False, chiral: True with bonds:
bond order: 1, chiral: False to atom atomic num: 6, name: , idx: 0, aromatic: False, chiral:
↪ False
bond order: 1, chiral: False to atom atomic num: 7, name: , idx: 2, aromatic: False, chiral:
↪ False
```

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```
bond order: 1, chiral: False to atom atomic num: 6, name: , idx: 3, aromatic: False, chiral:↵
↵False
bond order: 1, chiral: False to atom atomic num: 1, name: , idx: 9, aromatic: False, chiral:↵
↵False
```

We can downgrade this error to a warning with the `allow_undefined_stereo` argument. This will create a molecule with undefined stereochemistry, which might lead to incorrect parametrization or surprising conformer generation. See the [FAQ](#) for more details.

```
smiles_non_isomeric = Molecule.from_smiles(
    "CC([NH3+])C(=O)[O-]",
    allow_undefined_stereo=True
)

assert not zw_l_alanine.is_isomorphic_with(smiles_non_isomeric)

smiles_non_isomeric.visualize()
```

```
Warning (not error because allow_undefined_stereo=True): OEMol has unspecified↵
↵stereochemistry. oemol.GetTitle():
Problematic atoms are:
Atom atomic num: 6, name: , idx: 1, aromatic: False, chiral: True with bonds:
bond order: 1, chiral: False to atom atomic num: 6, name: , idx: 0, aromatic: False, chiral:↵
↵False
bond order: 1, chiral: False to atom atomic num: 7, name: , idx: 2, aromatic: False, chiral:↵
↵False
bond order: 1, chiral: False to atom atomic num: 6, name: , idx: 3, aromatic: False, chiral:↵
↵False
bond order: 1, chiral: False to atom atomic num: 1, name: , idx: 9, aromatic: False, chiral:↵
↵False
```

```
<IPython.core.display.SVG object>
```

## 6.2 By hand

You can always construct a `Molecule` by building it up from individual atoms and bonds. Other methods are generally easier, but it's a useful fallback for when you need to write your own constructor for an unsupported source format.

The `Molecule()` constructor and the `add_atom()` and `add_bond()` methods are used to construct a `Molecule` by hand.

```
by_hand = Molecule()
by_hand.name = "Zwitterionic l-Alanine"

by_hand.add_atom(
    atomic_number = 8, # Atomic number 8 is Oxygen
    formal_charge = -1, # Formal negative charge
    is_aromatic = False, # Atom is not part of an aromatic system
    stereochemistry = None, # Optional argument; "R" or "S" stereochemistry
```

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```

    name = "O-" # Optional argument; descriptive name for the atom
)
by_hand.add_atom(6, 0, False, name="C")
by_hand.add_atom(8, 0, False, name="O")
by_hand.add_atom(6, 0, False, stereochemistry="S", name="CA")
by_hand.add_atom(1, 0, False, name="CAH")
by_hand.add_atom(6, 0, False, name="CB")
by_hand.add_atom(1, 0, False, name="HB1")
by_hand.add_atom(1, 0, False, name="HB2")
by_hand.add_atom(1, 0, False, name="HB3")
by_hand.add_atom(7, +1, False, name="N+")
by_hand.add_atom(1, 0, False, name="HN1")
by_hand.add_atom(1, 0, False, name="HN2")
by_hand.add_atom(1, 0, False, name="HN3")

by_hand.add_bond(
    atom1 = 0, # First (zero-indexed) atom specified above ("O-")
    atom2 = 1, # Second atom specified above ("C")
    bond_order = 1, # Single bond
    is_aromatic = False, # Bond is not aromatic
    stereochemistry = None, # Optional argument; "E" or "Z" stereochemistry
    fractional_bond_order = None # Optional argument; Wiberg (or similar) bond order
)
by_hand.add_bond( 1, 2, 2, False) # C = O
by_hand.add_bond( 1, 3, 1, False) # C - CA
by_hand.add_bond( 3, 4, 1, False) # CA - CAH
by_hand.add_bond( 3, 5, 1, False) # CA - CB
by_hand.add_bond( 5, 6, 1, False) # CB - HB1
by_hand.add_bond( 5, 7, 1, False) # CB - HB2
by_hand.add_bond( 5, 8, 1, False) # CB - HB3
by_hand.add_bond( 3, 9, 1, False) # CB - N+
by_hand.add_bond( 9, 10, 1, False) # N+ - HN1
by_hand.add_bond( 9, 11, 1, False) # N+ - HN2
by_hand.add_bond( 9, 12, 1, False) # N+ - HN3

assert zw_l_alanine.is_isomorphic_with(by_hand)

by_hand.visualize()

```

```
<IPython.core.display.SVG object>
```



### 6.2.1 From a dictionary

Rather than build up the Molecule one method at a time, the `Molecule.from_dict()` method can construct a Molecule in one shot from a Python dict that describes the molecule in question. This allows Molecule objects to be written to and read from disk in any format that can be interpreted as a dict; this mechanism underlies the `from_bson()`, `from_json()`, `from_messagepack()`, `from_pickle()`, `from_toml()`, `from_xml()`, and `from_yaml()` methods.

This format can get very verbose, as it is intended for serialization, so this example uses hydrogen cyanide rather than alanine.

```
molecule_dict = {
    "name": "",
    "atoms": [
        {
            "atomic_number": 1,
            "formal_charge": 0,
            "is_aromatic": False,
            "stereochemistry": None,
            "name": "H",
        },
        {
            "atomic_number": 6,
            "formal_charge": 0,
            "is_aromatic": False,
            "stereochemistry": None,
            "name": "C",
        },
        {
            "atomic_number": 7,
            "formal_charge": 0,
            "is_aromatic": False,
            "stereochemistry": None,
            "name": "N",
        },
    ],
    "virtual_sites": [],
    "bonds": [
        {
            "atom1": 0,
            "atom2": 1,
            "bond_order": 1,
            "is_aromatic": False,
            "stereochemistry": None,
            "fractional_bond_order": None,
        },
        {
            "atom1": 1,
            "atom2": 2,
            "bond_order": 3,
            "is_aromatic": False,
            "stereochemistry": None,
            "fractional_bond_order": None,
        },
    ],
}
```

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```
],
  "properties": {},
  "conformers": None,
  "partial_charges": None,
  "partial_charges_unit": None,
  "hierarchy_schemes": {},
}

from_dictionary = Molecule.from_dict(molecule_dict)

from_dictionary.visualize()
```

&lt;IPython.core.display.SVG object&gt;

## 6.3 From a file

We can construct a Molecule from a file or file-like object with the `from_file()` method. We're a bit constrained in what file formats we can accept, because they need to provide all the information needed to construct the molecular graph; not just coordinates, but also elements, formal charges, bond orders, and stereochemistry.

### 6.3.1 From SDF file

We generally recommend the SDF format. The SDF file used here can be found [on GitHub](#)

```
sdf_path = Molecule.from_file("zw_l_alanine.sdf")
assert zw_l_alanine.is_isomorphic_with(sdf_path)
sdf_path.visualize()
```

&lt;IPython.core.display.SVG object&gt;

### 6.3.2 From SDF file object

`from_file()` can also take a file object, rather than a path. Note that the object must be in binary mode!

```
with open("zw_l_alanine.sdf", mode="rb") as file:
    sdf_object = Molecule.from_file(file, file_format="SDF")

assert zw_l_alanine.is_isomorphic_with(sdf_object)
sdf_object.visualize()
```

&lt;IPython.core.display.SVG object&gt;

### 6.3.3 From protein PDB file

The `from_polymer_pdb()` method can interpret a protein from a PDB file as a molecule. It can infer the full chemical graph of the canonical amino acids (26 including protonation states) in capped and uncapped forms. It does this according to the [RCSB chemical component dictionary](#) — the information is not explicitly in the PDB. For the moment, it's quite slow, but this is the easiest way to get a full protein into the OpenFF ecosystem:

```
from openff.toolkit.utils import get_data_file_path

path = get_data_file_path('proteins/T4-protein.pdb')
protein = Molecule.from_polymer_pdb(path)
protein.visualize("nglview")
```

```
NGLWidget()
```

### 6.3.4 From small molecule PDB file

Using PDB files for small molecules is not recommended, even if they have CONECT records, as they do not provide stereoisomeric information or bond orders. The RDKit backend assumes that bond orders are 1, so the toolkit refuses to use it:

```
from openff.toolkit.utils.toolkits import RDKitToolkitWrapper

pdb = Molecule.from_file("zw_l_alanine.pdb", "pdb", toolkit_registry=RDKitToolkitWrapper())
```

```
NotImplementedError: Toolkit The RDKit can not read file zw_l_alanine.pdb (format PDB).
↳ Supported formats for this toolkit are ['SDF', 'MOL', 'SMI']. RDKit can however read PDBs
↳ with a valid smiles string using the Molecule.from_pdb_and_smiles(file_path, smiles)
↳ constructor
```

OpenEye can infer bond orders and stereochemistry from the structure. This is not recommended, as it can make mistakes that may be difficult to catch. Note also that this requires a license for OpenEye, as this is proprietary software.

If we instead provide a SMILES code, a PDB file can be used to populate the `Molecule` object's conformers attribute and provide atom ordering, as well as check that the SMILES code matches the PDB file. This method is the recommended way to create a `Molecule` from a PDB file. The PDB file used here can be found [on GitHub](#)

**Important:** Note that the Toolkit doesn't guarantee that the coordinates in the PDB are correctly assigned to atoms. It makes an effort, but you should check that the results are reasonable.

```
pdb_with_smiles = Molecule.from_pdb_and_smiles(
    "zw_l_alanine.pdb",
    "C[C@H]([NH3+])C(=O)[O-]"
)
```

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```
assert zw_l_alanine.is_isomorphic_with(pdb_with_smiles)

pdb_with_smiles.visualize()
```

```
<IPython.core.display.SVG object>
```

## 6.4 Other string identification formats

The OpenFF Toolkit supports a few text based molecular identity formats other than SMILES ([see above](#))

### 6.4.1 From InChI

The `Molecule.from_inchi()` method constructs a `Molecule` from an IUPAC InChI string. Note that InChI cannot distinguish the zwitterionic form of alanine from the neutral form (see section 13.2 of the [InChI Technical FAQ](#)), so the toolkit defaults to the neutral form.

**Warning:** The OpenFF Toolkit makes no guarantees about the atomic ordering produced by the `from_inchi` method. InChI is not intended to be an interchange format.

```
inchi = Molecule.from_inchi("InChI=1S/C3H7NO2/c1-2(4)3(5)6/h2H,4H2,1H3,(H,5,6)/t2-m/s1")

inchi.visualize()
```

```
<IPython.core.display.SVG object>
```

### 6.4.2 From IUPAC name

The `Molecule.from_iupac()` method constructs a `Molecule` from an IUPAC name.

---

**Important:** This code requires the OpenEye toolkit.

---

```
iupac = Molecule.from_iupac("(2S)-2-azaniumylpropanoate")

assert zw_l_alanine.is_isomorphic_with(iupac)

iupac.visualize()
```

```
<IPython.core.display.SVG object>
```

## 6.5 Re-ordering atoms in an existing Molecule

Most Molecule creation methods don't specify the ordering of atoms in the new Molecule. The `Molecule.remap()` method allows a new ordering to be applied to an existing Molecule.

See also *Mapped SMILES*.

**Warning:** The `Molecule.remap()` method is experimental and subject to change.

```
# Note that this mapping is off-by-one from the mapping taken
# by the remap method, as Python indexing is 0-based but SMILES
# is 1-based
print("Before remapping:", zw_l_alanine.to_smiles(mapped=True))

# Flip the order of the carbonyl carbon and oxygen
remapped = zw_l_alanine.remap({0: 0, 1: 1, 2: 2, 3: 4, 4: 3, 5: 5, 6: 6, 7: 7, 8: 8, 9: 9,
↪ 10: 10, 11: 11, 12: 12})
#                                     ^-----^

print("After remapping: ", remapped.to_smiles(mapped=True))

# Doesn't affect the identity of the molecule
assert zw_l_alanine.is_isomorphic_with(remapped)
remapped.visualize()
```

```
Before remapping: [H:3][C@@:2][C:5](=[O:6])[O-
↪:7])([C:1]([H:8])([H:9])[H:10])[N+:4]([H:11])([H:12])[H:13]
After remapping: [H:3][C@@:2][C:4](=[O:6])[O-
↪:7])([C:1]([H:8])([H:9])[H:10])[N+:5]([H:11])([H:12])[H:13]
```

```
<IPython.core.display.SVG object>
```

## 6.6 Via Topology objects

The `Topology` class represents a biomolecular system; it is analogous to the similarly named objects in GROMACS, MDTraj or OpenMM. Notably, it does not include co-ordinates and may represent multiple copies of a particular molecular species or even more complex mixtures of molecules. Topology objects are usually built up one species at a time from Molecule objects.

Molecule objects can be retrieved from a Topology via the `Topology.molecule()` method by providing the index of the molecule within the topology. For a topology consisting of a single molecule, this is just `topology.molecule(0)`.

Constructor methods that are available for Topology but not Molecule generally require a Molecule to be provided via the `unique_molecules` keyword argument. The provided Molecule is used to provide the identity of the molecule, including aromaticity, bond orders, formal charges, and so forth. These methods therefore don't provide a route to the graph of the molecule, but can be useful for reordering atoms to match another software package.

### 6.6.1 From an OpenMM Topology

The `Topology.from_openmm()` method constructs an OpenFF Topology from an OpenMM `Topology`. The method requires that all the unique molecules in the Topology are provided as OpenFF `Molecule` objects, as the structure of an OpenMM Topology doesn't include the concept of a molecule. When using this method to create a `Molecule`, this limitation means that the method really only offers a pathway to reorder the atoms of a `Molecule` to match that of the OpenMM Topology.

```
from openmm.app.pdbfile import PDBFile

openmm_topology = PDBFile('zw_l_alanine.pdb').getTopology()
openff_topology = Topology.from_openmm(openmm_topology, unique_molecules=[zw_l_alanine])

from_openmm_topology = openff_topology.molecule(0)

assert zw_l_alanine.is_isomorphic_with(from_openmm_topology)

from_openmm_topology.visualize()
```

```
<IPython.core.display.SVG object>
```

### 6.6.2 From an MDTraj Topology

The `Topology.from_mdtraj()` method constructs an OpenFF Topology from an MDTraj `Topology`. The method requires that all the unique molecules in the Topology are provided as OpenFF `Molecule` objects to ensure that the graph of the molecule is correct. When using this method to create a `Molecule`, this limitation means that the method really only offers a pathway to reorder the atoms of a `Molecule` to match that of the MDTraj Topology.

```
from mdtraj import load_pdb

mdtraj_topology = load_pdb('zw_l_alanine.pdb').topology
openff_topology = Topology.from_openmm(mdtraj_topology, unique_molecules=[zw_l_alanine])

from_mdtraj_topology = openff_topology.molecule(0)

assert zw_l_alanine.is_isomorphic_with(from_mdtraj_topology)

from_mdtraj_topology.visualize()
```

```
<IPython.core.display.SVG object>
```

## 6.7 From Toolkit objects

The OpenFF Toolkit calls out to other software to perform low-level tasks like reading SMILES or files. These external software packages are called toolkits, and presently include [RDKit](#) and the [OpenEye Toolkit](#). OpenFF Molecule objects can be created from the equivalent objects in these toolkits.

### 6.7.1 From RDKit Mol

The `Molecule.from_rdkit()` method converts an `rdkit.Chem.rdchem.Mol` object to an OpenFF Molecule.

```
from rdkit import Chem
rdmol = Chem.MolFromSmiles("C[C@H]([NH3+])C([O-])=O")

print("rdmol is of type", type(rdmol))

from_rdmol = Molecule.from_rdkit(rdmol)

assert zw_l_alanine.is_isomorphic_with(from_rdmol)
from_rdmol.visualize()
```

```
rdmol is of type <class 'rdkit.Chem.rdchem.Mol'>
```

```
<IPython.core.display.SVG object>
```

### 6.7.2 From OpenEye OEMol

The `Molecule.from_openeye()` method converts an object that inherits from `openeye.oechem.OEMolBase` to an OpenFF Molecule.

```
from openeye import oechem

oemol = oechem.OEGraphMol()
oechem.OESmilesToMol(oemol, "C[C@H]([NH3+])C([O-])=O")

assert isinstance(oemol, oechem.OEMolBase)

from_oemol = Molecule.from_openeye(oemol)

assert zw_l_alanine.is_isomorphic_with(from_oemol)
from_oemol.visualize()
```

```
<IPython.core.display.SVG object>
```

## 6.8 From QCArchive

QCArchive is a repository of quantum chemical calculations on small molecules. The `Molecule.from_qcschema()` method creates a `Molecule` from a record from the archive. Because the identity of a molecule can change of the course of a QC calculation, the Toolkit accepts records only if they contain a hydrogen-mapped SMILES code.

---

**Note:** These examples use molecules other than l-Alanine because of their availability in QCArchive

---

### 6.8.1 From a QCArchive molecule record

The `Molecule.from_qcschema()` method can take a molecule record queried from the QCArchive and create a `Molecule` from it.

```
from qcportal import FractalClient

client = FractalClient()
query = client.query_molecules(molecular_formula="C16H20N3O5")

from_qcarchive = Molecule.from_qcschema(query[0])

from_qcarchive.visualize()
```

```
<IPython.core.display.SVG object>
```

### 6.8.2 From a QCArchive optimisation record

`Molecule.from_qcschema()` can also take an optimisation record and create the corresponding `Molecule`.

```
optimization_dataset = client.get_collection(
    "OptimizationDataset",
    "SMIRNOFF Coverage Set 1"
)
dimethoxymethanol_optimization = optimization_dataset.get_entry('coc(o)oc-0')

from_optimisation = Molecule.from_qcschema(dimethoxymethanol_optimization)

from_optimisation.visualize()
```

```
<IPython.core.display.SVG object>
```



## SMIRNOFF (SMIRKS NATIVE OPEN FORCE FIELD)

### 7.1 The SMIRNOFF specification

The SMIRNOFF specification can be found in the OpenFF [standards repository](#).

### 7.2 SMIRNOFF and the Toolkit

OpenFF releases all its force fields in SMIRNOFF format. SMIRNOFF is a format developed by OpenFF; its specification can be found in our [standards repository](#). SMIRNOFF-format force fields are distributed as XML files with the .offxml extension. Instead of using atom types like traditional force field formats, SMIRNOFF associates parameters directly with chemical groups using [SMARTS](#) and [SMIRKS](#), which are extensions of the popular SMILES serialization format for molecules. SMIRNOFF goes to great lengths to ensure reproducibility of results generated from its force fields.

The OpenFF Toolkit is the reference implementation of the SMIRNOFF spec. The toolkit is responsible for reading and writing .offxml files, for facilitating their modification, and for applying them to a molecular system in order to produce an Interchange object. The OpenFF Interchange project then takes over and is responsible for [producing input files and data](#) for actual MD software. The toolkit strives to be backwards compatible with old versions of the spec, but owing to the vagaries of the arrow of time cannot be forward compatible. Trying to use an old version of the toolkit to load an .OFFXML file created with a new version of the spec will lead to an error.

A simplified .offxml file for TIP3P water might look like this:

```
<?xml version="1.0" encoding="utf-8"?>
<SMIRNOFF version="0.3" aromaticity_model="OEAroModel_MDL">
  <Author>The Open Force Field Initiative</Author>
  <Date>2021-08-16</Date>
  <Constraints version="0.3">
    <Constraint smirks="[#1:1]-[#8X2H2+0:2]-[#1]" id="c-tip3p-H-O"
      distance="0.9572 * angstrom"></Constraint>
    <Constraint smirks="[#1:1]-[#8X2H2+0]-[#1:2]" id="c-tip3p-H-O-H"
      distance="1.5139006545247014 * angstrom"></Constraint>
  </Constraints>
  <vdW version="0.3" potential="Lennard-Jones-12-6" combining_rules="Lorentz-Berthelot"
    scale12="0.0" scale13="0.0" scale14="0.5" scale15="1.0" cutoff="9.0 * angstrom"
    switch_width="1.0 * angstrom" method="cutoff">
    <Atom smirks="[#1]-[#8X2H2+0:1]-[#1]" epsilon="0.1521 * mole**-1 * kilocalorie"
      id="n-tip3p-O" sigma="3.1507 * angstrom"></Atom>
    <Atom smirks="[#1:1]-[#8X2H2+0]-[#1]" epsilon="0 * mole**-1 * kilocalorie"
```

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```
        id="n-tip3p-H" sigma="1 * angstrom"></Atom>
</vdW>
<Electrostatics version="0.3" scale12="0.0" scale13="0.0" scale14="0.833333333"
    scale15="1.0" cutoff="9.0 * angstrom" switch_width="0.0 * angstrom"
    method="PME"></Electrostatics>
<LibraryCharges version="0.3">
    <LibraryCharge smirks="#1]-[#8X2H2+0:1]-[#1]" charge1="-0.834 * elementary_charge"
        id="q-tip3p-O"></LibraryCharge>
    <LibraryCharge smirks="#1:1]-[#8X2H2+0:1]-[#1]" charge1="0.417 * elementary_charge"
        id="q-tip3p-H"></LibraryCharge>
</LibraryCharges>
</SMIRNOFF>
```

---

**Note:** TIP3P's geometry is specified entirely by constraints, but SMIRNOFF certainly supports a wide variety of bonded parameters and functional forms.

---

Note that this format specifies not just the individual parameters, but also their functional forms and units in very explicit terms. This both makes it easy to read and means that the correct implementation of each force is specifically defined, rather than being left up to the MD engine.

The complicated part is that each parameter is specified by a SMIRKS code. These codes are SMARTS codes with an optional numerical index on some atoms given after a colon. This indexing system comes from SMIRKS. Each parameter expects a certain number of indexed atoms, and applies the force accordingly. Unindexed atoms are used to match the chemistry, but forces are not applied to them. SMARTS/SMIRKS codes are less intimidating than they look; [#1] matches any Hydrogen atom (atomic number 1), while [#8X2H2+0] matches an oxygen atom (atomic number 8) with some additional constraints. Dashes represent bonds. So [#1]-[#8X2H2+0:1]-[#1] represents an oxygen atom indexed as 1 connected to two unindexed hydrogen atoms. This system allows individual parameters to be as general or as specific as needed.

---

**Hint:** This page is not the SMIRNOFF spec; it has been moved to the [standards repository](#).

---

## VIRTUAL SITES

The Open Force Field Toolkit fully supports the SMIRNOFF virtual site specification for models using off-site charges, including 4- and 5-point water models, in addition to lone pair modelling on various functional groups. The primary focus is on the ability to add virtual sites to a system as part of system parameterization

Virtual sites are treated as massless particles whose positions are computed directly from the 3D coordinates of a set of atoms in the parent molecule. The number of atoms that are required to define the position will depend on the exact type of virtual site being used

Fig. 1: Examples of each type of virtual site with ‘orientation’ atoms colored blue and ‘parent’ atoms colored green.

Those atoms used to position the virtual site are referred to as ‘orientation’ atoms. Further, each type of virtual site will denote one of these orientation atoms to be the ‘parent’, which conceptually corresponds to the atom that the virtual site is ‘attached to’.

### 8.1 Applying virtual site parameters

Virtual sites are incorporated into a force field by adding a [VirtualSites tag], which specifies both the parameters associated with the different virtual sites and how they should be applied to a molecule according to SMARTS-based rules.

As with all parameters in the SMIRNOFF specification, each virtual site parameter has an associated SMIRKS pattern with a number of atoms tagged with map indices. Each mapped atom corresponds to one of the atoms used to orientate the virtual site, and for all the currently supported types, the atom matched as atom :1 is denoted the parent.

Fig. 2: The mappings between SMIRKS map indices to orientation particle

Virtual site parameters are applied by trying to match every associated SMIRKS pattern with the molecule of interest. In cases where multiple parameters *with the same name* would designate the same atom as a parent (i.e. an atom that a virtual site will be ‘attached’ to), then the last parameter to match will be assigned.

Fig. 3: The last parameter to match a particular parent atom wins. Here the monovalent lone parameter would be assigned rather than the bond charge parameter as it appears later in the parameter list.

In cases where the same parameter matches the same parent atom multiple times, as is the case in the above example of formaldehyde, the value of the match keyword will determine the outcome.

The "match" attribute accepts either "once" or "all\_permutations", offering control for situations where a SMARTS pattern can possibly match the same group of atoms in different orders (either due to wildcards or local symmetry) and it is desired to either add just one or all of the possible virtual particles.

- once - only one of the possible matches will yield a virtual site being added to the system. This keyword is only valid for types virtual site whose coordinates are invariant to the ordering of the orientation atoms, e.g. the trivalent lone pair type, to avoid ambiguity as to which atom ordering to retain.
- all\_permutations - all the possible matches will yield a virtual site being added to the system, such as in the monovalent lone pair example above.

If multiple parameters with different names would designate the same atom as a parent then the last matched parameter for each value of name would be assigned and yield a new virtual site being added.

Fig. 4: Multiple parameters can be used to create virtual sites on the same parent atom by giving them different names, e.g. in the case of a TIP6P model.

The following cases exemplify our reasoning in implementing this behavior, and should draw caution to complex issues that may arise when designing virtual site parameters. Let us consider 4-, 5-, and 6-point water models:

- A 4-point water model with a DivalentLonePair: This can be implemented by specifying `match="once"`, `outOfPlaneAngle="0*degree"`, and `distance=-.15*angstrom"`. Since the SMIRKS pattern `"[#1:1]-[#8X2:2]-[#1:3]"` would match water twice and would create two particles in the exact same position if `all_permutations` was specified, we specify "once" to have only one particle generated. Although having two particles in the same position should not affect the physics if the proper exclusion policy is applied, it would effectively make the 4-point model just as expensive as 5-point models.
- A 5-point water model with a DivalentLonePair: This can be implemented by using `match="all_permutations"` (unlike the 4-point model), `outOfPlaneAngle="56.26*degree"`, and `distance=0.7*angstrom`, for example. Here the permutations will cause particles to be placed at  $\pm 56.26$  degrees.
- A 6-point water model with both DivalentLonePair sites above. Since these two parameters look identical, it is unclear whether they should both be applied or if one should override the other. The toolkit never compares the physical numbers to determine equality as this can lead to instability during e.g. parameter fitting. To get this to work, we specify `name="EP1"` for the first parameter, and `name="EP2"` for the second parameter. This instructs the parameter handler keep them separate, and therefore both are applied. If both had the same name, then the typical SMIRNOFF hierarchy rules are used, and only the last matched parameter would be applied.

## 8.2 Ordering of atoms and virtual sites

The toolkit handles the orders the atoms and virtual sites in a topology in a specific manner for internal convenience.

In addition, due to the fact that a virtual site may contain multiple particles coupled to single parameters, the toolkit makes a distinction between a virtual *site*, and a virtual *particle*. A virtual site may represent multiple virtual particles, so the total number of particles cannot be directly determined by simply summing the number of atoms and virtual sites in a molecule. This is taken into account, however, and the `Molecule` and `Topology` classes both implement `particle` iterators.

---

**Note:** The distinction between a virtual site and virtual particle is due to be removed in a future version of

the toolkit, and a ‘virtual site’ will simply refer to one massless particle placed on a parent atom rather than to a collection of massless particles.

### Intramolecular interactions

The virtual site specification allows a [virtual site section](#) to define the policy that should be used to handle intramolecular interactions (exclusions). The toolkit currently only supports the parent's policy as outline in the [virtual site section](#) of the SMIRNOFF specification, which states that each virtual site should inherit their 1-2, 1-3, 1-4, and 1-n exclusions directly from the parent atom.

---



## DEVELOPING FOR THE TOOLKIT

- *Overview*
  - *Philosophy*
  - *Terminology*
    - \* *SMIRNOFF and the OpenFF Toolkit*
    - \* *Development Infrastructure*
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- *Contributing*
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- *Checking code coverage locally*
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This guide is written with the understanding that our contributors are NOT professional software developers, but are instead computational chemistry trainees and professionals. With this in mind, we aim to use a minimum of bleeding-edge technology and alphabet soup, and we will define any potentially unfamiliar processes or technologies the first time they are mentioned. We enforce use of certain practices (tests, formatting, coverage analysis, documentation) primarily because they are worthwhile upfront investments in the long-term sustainability of this project. The resources allocated to this project will come and go, but we hope that following these practices will ensure that minimal developer time will maintain this software

far into the future.

The process of contributing to the OpenFF Toolkit is more than just writing code. Before contributing, it is a very good idea to start a discussion on the [Issue tracker](#) about the functionality you'd like to add. This Issue discussion will help us decide with you where in the codebase it should go, any overlapping efforts with other developers, and what the user experience should be. Please note that the OpenFF Toolkit is intended to be used primarily as one piece of larger workflows, and that simplicity and reliability are two of our primary goals. Often, the cost/benefit of new features must be discussed, as a complex codebase is harder to maintain. When new functionality is added to the OpenFF Toolkit, it becomes our responsibility to maintain it, so it's important that we understand contributed code and are in a position to keep it up to date.

## 9.1 Overview

### 9.1.1 Philosophy

- The *core functionality* of the OpenFF Toolkit is to combine an Open Force Field [ForceField](#) and [Topology](#) to create an OpenMM [System](#).
- An OpenMM [System](#) contains *everything* needed to compute the potential energy of a system, except the coordinates and (optionally) box vectors.
- The OpenFF toolkit employs a modular “plugin” architecture wherever possible, providing a standard interface for contributed features.

### 9.1.2 Terminology

For high-level toolkit concepts and terminology important for both development and use of the Toolkit, see the [core concepts page](#).

#### SMIRNOFF and the OpenFF Toolkit

**SMIRNOFF data** A hierarchical data structure that complies with the [SMIRNOFF specification](#). This can be serialized in many formats, including XML (OFFXML). The subsections in a SMIRNOFF data source generally correspond to one energy term in the functional form of a force field.

**Cosmetic attribute** Data in a SMIRNOFF data source that does not correspond to a known attribute. These have no functional effect, but several programs use the extensibility of the OFFXML format to define additional attributes for their own use, and their workflows require the OFF toolkit to process the files while retaining these keywords.

#### Development Infrastructure

**Continuous Integration (CI)** Tests that run frequently while the code is undergoing changes, ensuring that the codebase still installs and has the intended behavior. Currently, we use a service called [GitHub Actions](#) for this. CI jobs run every time a commit is made to the main branch of the openff-toolkit GitHub repository or in a PR opened against it. These runs start by booting virtual machines that mimic brand new Linux and macOS computers. They then follow build instructions (see the `.github/workflows/CI.yml` file) to install the toolkit. After installing the OpenFF Toolkit and its dependencies, these virtual machines run our test suite. If the tests all pass, the build “passes” (returns a green check mark on GitHub).



If all the tests for a specific change to the main branch return green, then we know that the change has not broken the toolkit's existing functionality. When proposing code changes, we ask that contributors open a Pull Request (PR) on GitHub to merge their changes into the main branch. When a pull request is open, CI will run on the latest set of proposed changes and indicate whether they are safe to merge through status checks, summarized as a green check mark or red cross.

**CodeCov** An extension to our testing framework that reports the fraction of our source code lines that were run during the tests (our "code coverage"). This functionality is actually the combination of several components – GitHub Actions runners run the tests using `pytest` with the `pytest-cov` plugin, and then coverage reports are uploaded to [CodeCov's website](#). This analysis is re-run alongside the rest of our CI, and a badge showing our coverage percentage is in the project README.

**"Looks Good To Me" (LGTM)** A service that analyzes the code in our repository for simple style and formatting issues. This service assigns a letter grade to the codebase, and a badge showing our LGTM report is in the project README.

**ReadTheDocs (RTD)** A service that compiles and renders the package's documentation (from the `docs/` folder). The documentation itself can be accessed from the ReadTheDocs badge in the README. It is compiled by RTD alongside the other CI checks, and the compiled documentation for a pull request can be viewed by clicking the "details" link after the status.

### 9.1.3 User Experience

One important aspect of how we make design decisions is by asking "who do we envision using this software, and what would they want it to do here?". There is a wide range of possible users, from non-chemists, to students/trainees, to expert computational medicinal chemists. We have decided to build functionality intended for use by *expert medicinal chemists*, and whenever possible, add fatal errors if the toolkit risks doing the wrong thing. So, for example, if a molecule is loaded with an odd ionization state, we assume that the user has input it this way intentionally.

This design philosophy inevitably has trade-offs — For example, the OpenFF Toolkit will give the user a hard time if they try to load a "dirty" molecule dataset, where some molecules have errors or are not described in enough detail for the toolkit to unambiguously parametrize them. If there is risk of misinterpreting the molecule (for example, bond orders being undefined or chiral centers without defined stereochemistry), the toolkit should raise an error that the user can override. In this regard we differ from RDKit, which is more permissive in the level of detail it requires when creating molecules. This makes sense for RDKit's use cases, as several of its analyses can operate with a lower level of detail about the molecules. Often, the same design decision is the best for all types of users, but when we do need to make trade-offs, we assume the user is an expert.

At the same time, we aim for "automagic" behavior whenever a decision will clearly go one way over another. System parameterization is an inherently complex topic, and the OFF toolkit would be nearly unusable if we required the user to explicitly approve every aspect of the process. For example, if a Topology has its `box_vectors` attribute defined, we assume that the resulting OpenMM System should be periodic.

## 9.2 Modular design features

There are a few areas where we've designed the toolkit with extensibility in mind. Adding functionality at these interfaces should be considerably easier than in other parts of the toolkit, and we encourage experimentation and contribution on these fronts.

These features have occasionally confusing names. “Parameter” here refers to a single value in a force field, as it is generally used in biophysics; it does not refer to an argument to a function. “Attribute” is used to refer to an XML attribute, which allows data to be defined for a particular tag; it does not refer to a member of a Python class or object. For example, in the following XML excerpt the `<SMIRNOFF>` tag has the attributes `version` and `aromaticity_model`:

```
<SMIRNOFF version="0.3" aromaticity_model="OEAroModel_MDL">
...
</SMIRNOFF>
```

“Member” is used here to describe Python attributes. This terminology is borrowed for the sake of clarity in this section from languages like C++ and Java.

### 9.2.1 ParameterAttribute

A `ParameterAttribute` is a single value that can be validated at runtime.

A `ParameterAttribute` can be instantiated as Python class or instance members to define the kinds of value that a particular parameter can take. They are used in the definitions of both `ParameterHandler` and `ParameterType`. The sorts of values a `ParameterAttribute` can take on are restricted by runtime validation. This validation is highly customizable, and may do things like allowing only certain values for a string or enforcing the correct units or array dimensions on the value; in fact, the validation can be defined using arbitrary code. The name of a `ParameterAttribute` should correspond exactly to the corresponding attribute in an OFFXML file.

#### IndexedParameterAttribute

An `IndexedParameterAttribute` is a `ParameterAttribute` with a sequence of values, rather than just one. Each value in the sequence is indexed by an integer.

The exact name of an `IndexedParameterAttribute` is NOT expected to appear verbatim in a OFFXML file, but instead should appear with a numerical integer suffix. For example the `IndexedParameterAttribute k` should only appear as `k1`, `k2`, `k3`, and so on in an OFFXML. The current implementation requires this indexing to start at 1 and subsequent values be contiguous (no skipping numbers), but does not enforce an upper limit on the integer.

For example, dihedral torsions are often parameterized as the sum of several sine wave terms. Each of the parameters of the sine wave `k`, periodicity, and phase is implemented as an `IndexedParameterAttribute`.

### MappedParameterAttribute

A `MappedParameterAttribute` is a `ParameterAttribute` with several values, with some arbitrary mapping to access values.

### IndexedMappedParameterAttribute

An `IndexedMappedParameterAttribute` is a `ParameterAttribute` with a sequence of maps of values.

## 9.2.2 ParameterHandler

`ParameterHandler` is a generic base class for objects that perform parameterization for one section in a SMIRNOFF data source. A `ParameterHandler` has the ability to produce one component of an OpenMM System. Extend this class to add a support for a new force or energy term to the toolkit.

Each `ParameterHandler`-derived class MUST implement the following methods and define the following attributes:

- Class members `ParameterAttributes`: These correspond to the header-level attributes in a SMIRNOFF data source. For example, the Bonds tag in the SMIRNOFF spec has an optional `fractional_bondorder_method` field, which corresponds to the line `fractional_bondorder_method = ParameterAttribute(default=None)` in the `BondHandler` class definition. The `ParameterAttribute` and `IndexedParameterAttribute` classes offer considerable flexibility for validating inputs. Defining these attributes at the class level implements the corresponding behavior in the default `__init__` function.
- Class members `_MIN_SUPPORTED_SECTION_VERSION` and `_MAX_SUPPORTED_SECTION_VERSION`. `ParameterHandler` versions allow us to evolve `ParameterHandler` behavior in a controlled, recorded way. Force field development is experimental by nature, and it is unlikely that the initial choice of header attributes is suitable for all use cases. Recording the “versions” of a SMIRNOFF spec tag allows us to encode the default behavior and API of a specific generation of a `ParameterHandler`, while allowing the safe addition of new attributes and behaviors. If these attributes are not defined, defaults in the base class will apply and updates introducing new versions may break the existing code.

Each `ParameterHandler`-derived class MAY implement:

- `_KWARGS`: Keyword arguments passed to `ForceField.create_openmm_system` are validated against the `_KWARGS` lists of each `ParameterHandler` that the `ForceField` owns. If present, these keyword arguments and their values will be passed on to the `ParameterHandler`.
- `_TAGNAME`: The name of the SMIRNOFF OFFXML tag used to parameterize the class. This tag should appear in the top level within the `<SMIRNOFF>` tag; see the [Parameter generators](#) section of the SMIRNOFF specification.
- `_INFOTYPE`: The `ParameterType` subclass used to parse the elements in the `ParameterHandler`’s parameter list.
- `_DEPENDENCIES`: A list of `ParameterHandler` subclasses that, when present, must run before this one. Note that this is *not* a list of `ParameterHandler` subclasses that are required by this one. Ideally, child classes of `ParameterHandler` are entirely independent, and energy components of a force field form distinct terms; when this is impossible, `_DEPENDENCIES` may be used to guarantee execution order.
- `to_dict`: converts the `ParameterHandler` to a hierarchical dict compliant with the SMIRNOFF specification. The default implementation of this function should suffice for most developers.
- `check_handler_compatibility`: Checks whether this `ParameterHandler` is “compatible” with another. This function is used when a `ForceField` is attempted to be constructed from *multiple* SMIRNOFF data sources, and it is necessary to check that two sections with the same tag name can be combined in

a sane way. For example, if the user instructed two vdW sections to be read, but the sections defined different vdW potentials, then this function should raise an Exception indicating that there is no safe way to combine the parameters. The default implementation of this function should suffice for most developers.

### 9.2.3 ParameterType

`ParameterType` is a base class for the SMIRKS-based parameters of a `ParameterHandler`. Extend this alongside `ParameterHandler` to define and validate the force field parameters of a new force. This is analogous to ParmEd's XType classes, like `BondType`. A `ParameterType` should correspond to a single SMARTS-based parameter.

For example, the Lennard-Jones potential can be parameterized through either the size `ParameterAttribute` `sigma` or `r_min`, alongside the energy `ParameterAttribute` `epsilon`. Both options are handled through the `vdWType` class, a subclass of `ParameterType`.

### 9.2.4 Non-bonded methods as implemented in OpenMM

The SMIRNOFF specification describes the contents of a force field, which can be implemented in a number of different ways in different molecular simulation engines. The OpenMM implementation provided by the OpenFF Toolkit either produces an `openmm.System` containing a `openmm.NonbondedForce` object or raises an exception depending on how the non-bonded parameters are specified. Exceptions are raised when parameters are incompatible with OpenMM (`IncompatibleParameterError`) or otherwise against spec (`SMIRNOFFSpecError`), and also when they are appropriate for the spec but not yet implemented in the toolkit (`SMIRNOFFSpecUnimplementedError`). This table describes which `NonbondedMethod` is used in the produced `NonbondedForce`, or else which exception is raised.

vdw_method	electrostatics_method	periodic	OpenMM Nonbonded method or exception	Common case
cutoff	Coulomb	True	raises <code>IncompatibleParameterError</code>	
cutoff	Coulomb	False	<code>openmm.NonbondedForce.NoCutoff</code>	
cutoff	reaction-field	True	raises <code>SMIRNOFFSpecUnimplementedError</code>	
cutoff	reaction-field	False	raises <code>SMIRNOFFSpecError</code>	
cutoff	PME	True	<code>openmm.NonbondedForce.PME</code>	*
cutoff	PME	False	<code>openmm.NonbondedForce.NoCutoff</code>	
LJPME	Coulomb	True	raises <code>IncompatibleParameterError</code>	
LJPME	Coulomb	False	<code>openmm.NonbondedForce.NoCutoff</code>	
LJPME	reaction-field	True	raises <code>IncompatibleParameterError</code>	
LJPME	reaction-field	False	raises <code>SMIRNOFFSpecError</code>	
LJPME	PME	True	<code>openmm.NonbondedForce.LJPME</code>	
LJPME	PME	False	<code>openmm.NonbondedForce.NoCutoff</code>	

Notes:

- The most commonly-used case (including the Parsley line) is in the fifth row (cutoff vdW, PME electrostatics, periodic topology) and marked with an asterisk.
- For all cases included a non-periodic topology, `openmm.NonbondedForce.NoCutoff` is currently used.
- Electrostatics method reaction-field can only apply to periodic systems, however it is not currently implemented.
- LJPME (particle mesh ewald for LJ/vdW interactions) is not yet fully described in the SMIRNOFF specification.
- In the future, the OpenFF Toolkit may create multiple `CustomNonbondedForce` objects in order to better de-couple vdW and electrostatic interactions.

## 9.3 Contributing

We always welcome [GitHub pull requests](#). For bug fixes, major feature additions, or refactoring, please raise an issue on the [GitHub issue tracker](#) first to ensure the design will be amenable to current developer plans. Development of new toolkit features generally proceeds in the following stages:

- Begin a discussion on the [GitHub issue tracker](#) to determine big-picture “what should this feature do?” and “does it fit in the scope of the OpenFF Toolkit?”
  - “... typically, for existing water models, we want to assign library charges”
- Start identifying details of the implementation that will be clear from the outset
  - “Create a new “special section” in the SMIRNOFF format (kind of analogous to the Bond-ChargeCorrections section) which allows SMIRKS patterns to specify use of library charges for specific groups
  - “Following #86, here’s how library charges might work: ...”
- Create a branch or fork for development
  - The OpenFF Toolkit has one unusual aspect of its CI build process, which is that certain functionality requires the OpenEye toolkits, so the builds must contain a valid OpenEye license file. An OpenEye license is stored as an encrypted token within the openforcefield organization on GitHub. For security reasons, builds run from forks cannot access this key. Therefore, tests that depend on the OpenEye Toolkits will be skipped on forks. Contributions run on forks are still welcome, especially as features that do not interact directly with the OpenEye Toolkits are not likely affected by this limitation.

### 9.3.1 Setting up a development environment

1. Install the conda package manager as part of the Anaconda Distribution from [here](#)
2. Set up conda environment:

```
git clone https://github.com/openforcefield/openff-toolkit
cd openff-toolkit/
# Create a conda environment with dependencies from env/YAML file
conda env create -n openff-dev -f devtools/conda-envs/test_env.yaml
conda activate openff-dev
# Perform editable/dirty dev install
pip install -e .
```

3. Obtain and store Open Eye license somewhere like `~/.oe_license.txt`. Optionally store the path in environmental variable `OE_LICENSE`, i.e. using a command like `echo "export OE_LICENSE=/Users/yournamehere/.oe_license.txt" >> ~/.bashrc`

## Building the Docs

The documentation is composed of two parts, a hand-written user guide and an auto-generated API reference. Both are compiled by Sphinx, and can be automatically served and regenerated on changes with `sphinx-autobuild`. Documentation for released versions is available at [ReadTheDocs](#). ReadTheDocs also builds the documentation for each Pull Request opened on GitHub and keeps the output for 90 days.

To add the documentation dependencies to your existing `openff-dev` Conda environment:

```
# Add the documentation requirements to your Conda environment
conda env update --name openff-dev --file docs/environment.yml
conda install --name openff-dev -c conda-forge sphinx-autobuild
```

To build the documentation from scratch:

```
# Build the documentation
# From the openff-toolkit root directory
conda activate openff-dev
cd docs
make html
# Documentation can be found in docs/_build/html/index.html
```

To watch the source directory for changes and automatically rebuild the documentation and refresh your browser:

```
# Host the docs on a local HTTP server and rebuild when a source file is changed
# Works best when the docs have already been built
# From the openff-toolkit root directory
conda activate openff-dev
sphinx-autobuild docs docs/_build/html --watch openff
# Then navigate your web browser to http://localhost:8000
```

## 9.3.2 Style guide

Development for the `openff-toolkit` conforms to the recommendations given by the [Software Development Best Practices for Computational Chemistry](#) guide.

The naming conventions of classes, functions, and variables follows [PEP8](#), consistently with the best practices guide. The naming conventions used in this library not covered by PEP8 are:

- Use `file_path`, `file_name`, and `file_stem` to indicate path/to/stem.extension, stem.extension, and stem respectively, consistent with the variables in the `pathlib` module of the standard library.
- Use `n_x` to abbreviate “number of *x*” (e.g. `n_atoms`, `n_molecules`).

We place a high priority on code cleanliness and readability, even if code could be written more compactly. For example, 15-character variable names are fine. Triply nested list comprehensions are not.

The `openff-toolkit` has adopted code formatting tools (“linters”) to maintain consistent style and remove the burden of adhering to these standards by hand. Currently, two are employed:

1. [Black](#), the uncompromising code formatter, automatically formats code with a consistent style.

## 2. `isort`, sorts imports

There is a step in CI that uses these tools to check for a consistent style (see the file [.github/workflows/lint.yml](#)). These checks will use the most recent versions of each linter. To ensure that changes follow these standards, you can install and run these tools locally:

```
conda install black isort -c conda-forge
black openff
isort openff
```

Anything not covered above is currently up to personal preference, but this may change as new linters are added.

### 9.3.3 Pre-commit

The `pre-commit` tool can *optionally* be used to automate some or all of the above style checks. It automatically runs other programs (“hooks”) when you run `git commit`. It aborts the commit with an exit code if any of the hooks fail, i.e. if `black` reformats code. This project uses `pre-commit ci`, a free service that enforces style on GitHub using the `pre-commit` framework in CI.

To use `pre-commit` locally, first install it:

```
conda install pre-commit -c conda-forge # also available via pip
```

Then, install the pre-commit hooks (note that it installs the linters into an isolated virtual environment, not the current conda environment):

```
pre-commit install
```

Hooks will now run automatically before commits. Once installed, they should run in a total of a few seconds.

If `pre-commit` is not used by the developer and style issues are found, a `pre-commit.ci` bot may commit directly to a PR to make these fixes. This bot should only ever alter styl and never make functional changes to code.

Note that tests (too slow) and type-checking (weird reasons) are not run by `pre-commit`. You should still manually run tests before committing code.

## 9.4 Checking code coverage locally

Run something like

```
$ python -m pytest --cov=openff --cov-config=setup.cfg --cov-report html openff
$ open htmlcov/index.html
```

to see a code coverage report. This uses [Coverage.py](#) and also requires a pytest plugin (`pytest-cov`), both of which should be installed if you are using the provided conda environments. CodeCov provides this as an automated service with their own web frontend using a similar file generated by our CI. However, it can be useful to run this locally to check coverage changes (i.e. “is this function I added sufficiently covered by tests?”) without waiting for CI to complete.

## 9.5 Supported Python versions

The OpenFF Toolkit roughly follows [NEP 29](#). As of version 0.11.0 (June 2022) this means Python 3.8-3.9 are officially supported. We develop, test, and distribute on macOS and Linux-based operating systems. We do not currently support Windows. Some CI builds run using only RDKit as a backend, some run using only OpenEye Toolkits, and some run using both installed at once.

The CI matrix is currently as follows:

	Linux			macOS		
	RDKit	OpenEye	RDKit + OE	RDKit	OpenEye	RDKit + OE
Python 3.7 and older	No support after 0.11.0 (March 2021)					
Python 3.8	<b>Test</b>	<b>Test</b>	<b>Test</b>	<b>Test</b>	<b>Test</b>	<b>Test</b>
Python 3.9	<b>Test</b>	Skip	Skip	<b>Test</b>	Skip	Skip
Python 3.10	<b>Test</b>	Skip	Skip	<b>Test</b>	Skip	Skip
Python 3.11 and newer	Pending official releases and/or upstream support					



## MOLECULE CONVERSION TO OTHER PACKAGES

Molecule conversion spec

### 10.1 Hierarchy data (chains and residues)

Note that the representations of hierarchy data (namely, chains and residues) in different software packages have different expectations. For example, in OpenMM, the atoms of a single residue must be contiguous. In RDKit, it is permissible to have an atom with no PDB residue information, whereas in OpenEye the fields must be populated. In most packages, it is expected that any atom with a residue name defined will also have a residue number.

The OpenFF toolkit does not have these restrictions, and records hierarchy metadata almost entirely for interoperability and user convenience reasons. No code paths in the OpenFF Toolkit consider hierarchy metadata during parameter assignment. While users should expect hierarchy metadata to be correctly handled in simple loading operations and export to other packages, *modifying* hierarchy metadata in the OpenFF Toolkit may lead to unexpected incompatibilities with other packages/representations.

Another consequence of this difference in representations is that hierarchy iterators (like `Molecule.residues` and `Topology.chains`) are not accessed during conversion to other packages. Only the underlying hierarchy metadata from the atoms is transferred, and the OpenFF Toolkit makes no attempt to match the behavior of iterators in other packages.

In cases where only *some* common metadata fields are set (but not others), the following calls happen during conversion TO other packages

- RDKit - We run `rdatom.SetPDBMetadata` if ANY of `residue_name`, `residue_number`, or `chain_id` are set on the OpenFF Atom. This means that, in cases where only one or two of those fields are filled, the others will be set to be the default values in RDKit
- OpenEye - We always run `oechem.OEAtomSetResidue(oe_atom, res)`. If the metadata values are not defined in OpenFF, we assign default values (`residue_name="UNL"`, `residue_number=1`, `chain_id=" "`)
- OpenMM - OpenMM *requires* identification of chains and residues when constructing a Topology, and residues must be entirely contained within their parent chain. Our `Topology.to_openmm` method creates at least one chain for each OpenFF Molecule. Contiguously-indexed atoms with the same `chain_id` value within a OpenFF Molecule will be assigned to a single OpenMM chain. Continuously indexed atoms with the same `residue_name`, `residue_number`, and `chain_id` will be assigned to the same OpenMM residue.



Toolkit	residue_name	residue_number	insertion_code	chain_id
PDB file ATOM/HETATM columns	Columns 18-20 (resName)	Columns 23-26 (resSeq)	Columns 27 (iCode)	Columns 22 (chainID)
PDBx/MMCIF fields	label_comp_id	label_seq_id	label_ins_code	label_asym_id
OpenFF getter (defined)	atom.metadata[ ↪ "residue_name" ↪ ]	atom.metadata[ ↪ "residue_ ↪ number"]	atom.metadata[ ↪ "insertion_ ↪ code"]	atom.metadata[ ↪ "chain_id"]
OpenFF getter (undefined)	"residue_name" ↪ ↪ not in atom. ↪ metadata	"residue_number" ↪ ↪ not in atom. ↪ metadata	"insertion_code" ↪ ↪ not in atom. ↪ metadata	"chain_id" not ↪ ↪ in atom. ↪ metadata
OpenFF setter (de- fined)	atom.metadata[ ↪ "residue_name" ↪ ] = X	atom.metadata[ ↪ "residue_ ↪ number"] = X	atom.metadata[ ↪ "insertion_ ↪ code"] = X	atom.metadata[ ↪ "chain_id"] = ↪ ↪ X
OpenFF setter (un- defined)	del atom. ↪ metadata[ ↪ 'residue_name' ↪ ]	del atom. ↪ metadata[ ↪ 'residue_ ↪ number']	del atom. ↪ metadata[ ↪ 'insertion_ ↪ code']	del atom. ↪ metadata[ ↪ 'chain_id']
OpenMM getter (defined)	omm_atom. ↪ residue.name	omm_atom. ↪ residue.id	omm_atom. ↪ residue. ↪ insertionCode	omm_atom. ↪ residue.chain. ↪ id
OpenMM getter (undefined)	All particles in an OpenMM Topol- ogy belong to a chain and residue	All particles in an OpenMM Topol- ogy belong to a chain and residue	All particles in an OpenMM Topol- ogy belong to a chain and residue	All particles in an OpenMM Topol- ogy belong to a chain and residue
OpenMM setter (defined)	omm_atom. ↪ residue.name ↪ ↪ = X	omm_atom. ↪ residue.id = X	omm_atom. ↪ residue. ↪ insertionCode ↪ ↪ = X	omm_atom. ↪ residue.chain. ↪ id = X
OpenMM setter (undefined)	omm_atom. ↪ residue.name ↪ ↪ = "UNL"	omm_atom. ↪ residue.id = 0	omm_atom. ↪ residue. ↪ insertionCode ↪ ↪ = " "	omm_atom. ↪ residue.chain. ↪ id = "X"
RDKit getter (de- fined)	rda. ↪ GetPDBResidueInfo ↪ GetResidueName()	rda. ↪ GetPDBResidueInfo ↪ GetResidueNumber	rda. ↪ GetPDBResidueInfo ↪ GetInsertionCode	rda. ↪ GetPDBResidueInfo(). ↪ GetChainId()
RDKit getter (un- defined)	rda. ↪ GetPDBResidueInfo ↪ is None	rda. ↪ GetPDBResidueInfo ↪ is None	rda. ↪ GetPDBResidueInfo ↪ is None	rda. ↪ GetPDBResidueInfo(). ↪ is None
RDKit setter (de- fined)	res = rda. ↪ GetPDBResidueInfo( ↪ chain_id, res_id)	res = rda. ↪ GetPDBResidueInfo( ↪ chain_id, res_id)	res = rda. ↪ GetPDBResidueInfo( ↪ chain_id, res_id)	res = rda. ↪ GetPDBResidueInfo( ↪ chain_id, res_id)

## 10.1. Hierarchy data (chains and residues)



## MOLECULAR TOPOLOGY REPRESENTATIONS

This module provides pure-Python classes for representing molecules and molecular systems. These classes offer several advantages over corresponding Topology objects in [OpenMM](#) and [MDTraj](#), including offering serialization to a variety of standard formats (including [XML](#), [JSON](#), [YAML](#), [BSON](#), [TOML](#), and [MessagePack](#)).

### 11.1 Primary objects

<a href="#">FrozenMolecule</a>	Immutable chemical representation of a molecule, such as a small molecule or biopolymer.
<a href="#">Molecule</a>	Mutable chemical representation of a molecule, such as a small molecule or biopolymer.
<a href="#">Topology</a>	A Topology is a chemical representation of a system containing one or more molecules appearing in a specified order.

#### 11.1.1 FrozenMolecule

```
class openff.toolkit.topology.FrozenMolecule(other=None, file_format: Optional[str] = None,  
                                              toolkit_registry: Union[ToolkitRegistry, ToolkitWrapper]  
                                              = GLOBAL_TOOLKIT_REGISTRY,  
                                              allow_undefined_stereo: bool = False)
```

Immutable chemical representation of a molecule, such as a small molecule or biopolymer.

#### Examples

Create a molecule from a sdf file

```
>>> from openff.toolkit.utils import get_data_file_path  
>>> sdf_filepath = get_data_file_path('molecules/ethanol.sdf')  
>>> molecule = FrozenMolecule.from_file(sdf_filepath)
```

Convert to OpenEye OEMol object

```
>>> oemol = molecule.to_openeye()
```

Create a molecule from an OpenEye molecule

```
>>> molecule = FrozenMolecule.from_openeye(oemol)
```

Convert to RDKit Mol object

```
>>> rdmol = molecule.to_rdkit()
```

Create a molecule from an RDKit molecule

```
>>> molecule = FrozenMolecule.from_rdkit(rdmol)
```

Create a molecule from IUPAC name (requires the OpenEye toolkit)

```
>>> molecule = FrozenMolecule.from_iupac('imatinib')
```

Create a molecule from SMILES

```
>>> molecule = FrozenMolecule.from_smiles('Cc1ccccc1')
```

**Warning:** This API is experimental and subject to change.

```
__init__(other=None, file_format: Optional[str] = None, toolkit_registry: Union[ToolkitRegistry, ToolkitWrapper] = GLOBAL_TOOLKIT_REGISTRY, allow_undefined_stereo: bool = False)
```

Create a new FrozenMolecule object

#### Parameters

- **other** (optional, default=None) – If specified, attempt to construct a copy of the molecule from the specified object. This can be any one of the following:
  - a `Molecule` object
  - a file that can be used to construct a `Molecule` object
  - an `openeye.ochem.OEMol`
  - an `rdkit.Chem.rdchem.Mol`
  - a serialized `Molecule` object
- **file\_format** (`str`, optional, default=None) – If providing a file-like object, you must specify the format of the data. If providing a file, the file format will attempt to be guessed from the suffix.
- **toolkit\_registry** (a `ToolkitRegistry` or `ToolkitWrapper` object, optional, default=`GLOBAL_TOOLKIT_REGISTRY`) – `ToolkitRegistry` or `ToolkitWrapper` to use for I/O operations
- **allow\_undefined\_stereo** (`bool`, default=False) – If loaded from a file and False, raises an exception if undefined stereochemistry is detected during the molecule's construction.

## Examples

Create an empty molecule:

```
>>> empty_molecule = FrozenMolecule()
```

Create a molecule from a file that can be used to construct a molecule, using either a filename or file-like object:

```
>>> from openff.toolkit.utils import get_data_file_path
>>> sdf_filepath = get_data_file_path('molecules/ethanol.sdf')
>>> molecule = FrozenMolecule(sdf_filepath)
>>> molecule = FrozenMolecule(open(sdf_filepath, 'r'), file_format='sdf')
```

```
>>> import gzip
>>> mol2_gz_filepath = get_data_file_path('molecules/toluene.mol2.gz')
>>> molecule = FrozenMolecule(gzip.GzipFile(mol2_gz_filepath, 'r'), file_format=
↳ 'mol2')
```

Create a molecule from another molecule:

```
>>> molecule_copy = FrozenMolecule(molecule)
```

Convert to OpenEye OEMol object

```
>>> oemol = molecule.to_openeye()
```

Create a molecule from an OpenEye molecule:

```
>>> molecule = FrozenMolecule(oemol)
```

Convert to RDKit Mol object

```
>>> rdmol = molecule.to_rdkit()
```

Create a molecule from an RDKit molecule:

```
>>> molecule = FrozenMolecule(rdmol)
```

Convert the molecule into a dictionary and back again:

```
>>> serialized_molecule = molecule.to_dict()
>>> molecule_copy = FrozenMolecule(serialized_molecule)
```

## Methods

<code>__init__([other, file_format, ...])</code>	Create a new FrozenMolecule object
<code>add_default_hierarchy_schemes([...])</code>	Adds chain and residue hierarchy schemes.
<code>add_hierarchy_scheme(uniqueness_criteria, ...)</code>	Use the molecule's metadata to facilitate iteration over its atoms.
<code>apply_elf_conformer_selection([percentage, ...])</code>	Select a set of diverse conformers from the molecule's conformers with ELF.

continues on next page

Table 1 – continued from previous page

<code>are_isomorphic(mol1, mol2[, ...])</code>	Determine if mol1 is isomorphic to mol2.
<code>assign_fractional_bond_orders([...])</code>	Update and store list of bond orders this molecule.
<code>assign_partial_charges(partial_charge_method)</code>	Calculate partial atomic charges and store them in the molecule.
<code>atom(index)</code>	Get the atom with the specified index.
<code>atom_index(atom)</code>	Returns the index of the given atom in this molecule
<code>bond(index)</code>	Get the bond with the specified index.
<code>canonical_order_atoms([toolkit_registry])</code>	Produce a copy of the molecule with the atoms reordered canonically.
<code>chemical_environment_matches(query[, ...])</code>	Find matches in the molecule for a SMARTS string
<code>delete_hierarchy_scheme(iter_name)</code>	Remove an existing HierarchyScheme specified by its iterator name.
<code>enumerate_protomers([max_states])</code>	Enumerate the formal charges of a molecule to generate different protomoers.
<code>enumerate_stereoisomers([undefined_only, ...])</code>	Enumerate the stereocenters and bonds of the current molecule.
<code>enumerate_tautomers([max_states, ...])</code>	Enumerate the possible tautomers of the current molecule
<code>find_rotatable_bonds([...])</code>	Find all bonds classed as rotatable ignoring any matched to the <code>ignore_functional_groups</code> list.
<code>from_bson(serialized)</code>	Instantiate an object from a BSON serialized representation.
<code>from_dict(molecule_dict)</code>	Create a new Molecule from a dictionary representation
<code>from_file(file_path[, file_format, ...])</code>	Create one or more molecules from a file
<code>from_inchi(inchi[, allow_undefined_stereo, ...])</code>	Construct a Molecule from a InChI representation
<code>from_iupac(iupac_name[, toolkit_registry, ...])</code>	Generate a molecule from IUPAC or common name
<code>from_json(serialized)</code>	Instantiate an object from a JSON serialized representation.
<code>from_mapped_smiles(mapped_smiles[, ...])</code>	Create a Molecule from a SMILES string, ordering atoms from mappings
<code>from_messagepack(serialized)</code>	Instantiate an object from a MessagePack serialized representation.
<code>from_openeye(oemol[, allow_undefined_stereo])</code>	Create a Molecule from an OpenEye molecule.
<code>from_pdb_and_smiles(file_path, smiles[, ...])</code>	Create a Molecule from a pdb file and a SMILES string using RDKit.
<code>from_pickle(serialized)</code>	Instantiate an object from a pickle serialized representation.
<code>from_polymer_pdb(file_path[, toolkit_registry])</code>	Loads a polymer from a PDB file.
<code>from_qcschema(qca_record[, client, ...])</code>	Create a Molecule from a QCArchive molecule record or dataset entry based on attached cmiles information.
<code>from_rdkit(rdmol[, allow_undefined_stereo, ...])</code>	Create a Molecule from an RDKit molecule.

continues on next page



Table 1 – continued from previous page

<code>from_smiles(smiles[, ...])</code>	Construct a Molecule from a SMILES representation
<code>from_toml(serialized)</code>	Instantiate an object from a TOML serialized representation.
<code>from_topology(topology)</code>	Return a Molecule representation of an OpenFF Topology containing a single Molecule object.
<code>from_xml(serialized)</code>	Instantiate an object from an XML serialized representation.
<code>from_yaml(serialized)</code>	Instantiate from a YAML serialized representation.
<code>generate_conformers([toolkit_registry, ...])</code>	Generate conformers for this molecule using an underlying toolkit.
<code>generate_unique_atom_names()</code>	Generate unique atom names from the element symbol and count.
<code>get_bond_between(i, j)</code>	Returns the bond between two atoms
<code>is_isomorphic_with(other, **kwargs)</code>	Check if the molecule is isomorphic with the other molecule which can be an <code>openff.toolkit.topology.Molecule</code> or <code>nx.Graph()</code> .
<code>nth_degree_neighbors(n_degrees)</code>	Return canonicalized pairs of atoms whose shortest separation is <i>exactly</i> n bonds.
<code>ordered_connection_table_hash()</code>	Compute an ordered hash of the atoms and bonds in the molecule
<code>particle(index)</code>	Deprecated since version 0.11.0.
<code>particle_index(particle)</code>	Deprecated since version 0.11.0.
<code>remap(mapping_dict[, current_to_new, partial])</code>	Reorder the atoms in the molecule according to the given mapping dict.
<code>strip_atom_stereochemistry(smarts[, ...])</code>	Delete stereochemistry information for certain atoms, if it is present.
<code>to_bson()</code>	Return a BSON serialized representation.
<code>to_dict()</code>	Return a dictionary representation of the molecule.
<code>to_file(file_path, file_format[, ...])</code>	Write the current molecule to a file or file-like object
<code>to_hill_formula()</code>	Generate the Hill formula of this molecule.
<code>to_inchi([fixed_hydrogens, toolkit_registry])</code>	Create an InChI string for the molecule using the requested toolkit backend.
<code>to_inchikey([fixed_hydrogens, toolkit_registry])</code>	Create an InChIKey for the molecule using the requested toolkit backend.
<code>to_iupac([toolkit_registry])</code>	Generate IUPAC name from Molecule
<code>to_json([indent])</code>	Return a JSON serialized representation.
<code>to_messagepack()</code>	Return a MessagePack representation.
<code>to_networkx()</code>	Generate a NetworkX undirected graph from the molecule.
<code>to_openeye([toolkit_registry, aromaticity_model])</code>	Create an OpenEye molecule
<code>to_pickle()</code>	Return a pickle serialized representation.
<code>to_qcschema([multiplicity, conformer, extras])</code>	Create a QCElemental Molecule.

continues on next page

Table 1 – continued from previous page

<code>to_rdkit([aromaticity_model, toolkit_registry])</code>	Create an RDKit molecule
<code>to_smiles([isomeric, explicit_hydrogens, ...])</code>	Return a canonical isomeric SMILES representation of the current molecule.
<code>to_toml()</code>	Return a TOML serialized representation.
<code>to_topology()</code>	Return an OpenFF Topology representation containing one copy of this molecule
<code>to_xml([indent])</code>	Return an XML representation.
<code>to_yaml()</code>	Return a YAML serialized representation.
<code>update_hierarchy_schemes([iter_names])</code>	Infer a hierarchy from atom metadata according to the existing hierarchy schemes.

## Attributes

<code>amber_impropers</code>	Iterate over all impropers with trivalent centers, reporting the central atom first.
<code>angles</code>	Get an iterator over all i-j-k angles.
<code>atoms</code>	Iterate over all Atom objects in the molecule.
<code>bonds</code>	Iterate over all Bond objects in the molecule.
<code>conformers</code>	Returns the list of conformers for this molecule.
<code>has_unique_atom_names</code>	True if the molecule has unique atom names, False otherwise.
<code>hierarchy_schemes</code>	The hierarchy schemes available on the molecule.
<code>hill_formula</code>	Get the Hill formula of the molecule
<code>impropers</code>	Iterate over all improper torsions in the molecule.
<code>n_angles</code>	Number of angles in the molecule.
<code>n_atoms</code>	The number of Atom objects.
<code>n_bonds</code>	The number of Bond objects in the molecule.
<code>n_conformers</code>	The number of conformers for this molecule.
<code>n_impropers</code>	Number of possible improper torsions in the molecule.
<code>n_particles</code>	Deprecated since version 0.11.0.
<code>n_propers</code>	Number of proper torsions in the molecule.
<code>name</code>	The name (or title) of the molecule
<code>partial_charges</code>	Returns the partial charges (if present) on the molecule.
<code>particles</code>	Deprecated since version 0.11.0.
<code>propers</code>	Iterate over all proper torsions in the molecule
<code>properties</code>	The properties dictionary of the molecule
<code>smirnoff_impropers</code>	Iterate over all impropers with trivalent centers, reporting the central atom second.
<code>torsions</code>	Get an iterator over all i-j-k-l torsions.
<code>total_charge</code>	Return the total charge on the molecule

property `has_unique_atom_names`: `bool`

True if the molecule has unique atom names, False otherwise.

**generate\_unique\_atom\_names()**

Generate unique atom names from the element symbol and count.

Names are generated from the elemental symbol and the number of times that element is found in the molecule. The character 'x' is appended to these generated names to reduce the odds that they clash with an atom name or type imported from another source. For example, generated atom names might begin 'C1x', 'H1x', 'O1x', 'C2x', etc.

**strip\_atom\_stereochemistry**(*smarts*: *str*, *toolkit\_registry*: *Union*[*ToolkitRegistry*, *ToolkitWrapper*] = *GLOBAL\_TOOLKIT\_REGISTRY*)

Delete stereochemistry information for certain atoms, if it is present. This method can be used to “normalize” molecules imported from different cheminformatics toolkits, which differ in which atom centers are considered stereogenic.

#### Parameters

- **smarts** (*str*) – Tagged SMARTS with a single atom with index 1. Any matches for this atom will have any assigned stereochemistry information removed.
- **toolkit\_registry** (a *ToolkitRegistry* or *ToolkitWrapper* object, optional,) – default=*GLOBAL\_TOOLKIT\_REGISTRY* *ToolkitRegistry* or *ToolkitWrapper* to use for I/O operations

**to\_dict()** → *dict*

Return a dictionary representation of the molecule.

**Returns** **molecule\_dict** (*dict*) – A dictionary representation of the molecule.

**ordered\_connection\_table\_hash()**

Compute an ordered hash of the atoms and bonds in the molecule

**classmethod from\_dict**(*molecule\_dict*: *dict*)

Create a new Molecule from a dictionary representation

**Parameters** **molecule\_dict** (*dict*) – A dictionary representation of the molecule.

**Returns** **molecule** (*Molecule*) – A Molecule created from the dictionary representation

**add\_default\_hierarchy\_schemes**(*overwrite\_existing*=*True*)

Adds chain and residue hierarchy schemes.

The Open Force Field Toolkit has no native understanding of hierarchical atom organisation schemes common to other biomolecular software, such as “residues” or “chains” (see [Hierarchy data \(chains and residues\)](#)). Hierarchy schemes allow iteration over groups of atoms according to their metadata. For more information, see [HierarchyScheme](#).

If a Molecule with the default hierarchy schemes changes, [Molecule.update\\_hierarchy\\_schemes\(\)](#) must be called before the residues or chains are iterated over again or else the iteration may be incorrect.

**Parameters** **overwrite\_existing** (*bool*, default=*True*) – Whether to overwrite existing instances of the *residue* and *chain* hierarchy schemes. If this is *False* and either of the hierarchy schemes are already defined on this molecule, an exception will be raised.

**Raises** [HierarchySchemeWithIteratorNameAlreadyRegisteredException](#) – When *overwrite\_existing=False* and either the chains or residues hierarchy scheme is already configured.

See also:

`HierarchyScheme`, `Molecule.add_hierarchy_scheme`, `Molecule.update_hierarchy_schemes`,  
`Molecule.perceive_residues`

**add\_hierarchy\_scheme**(*uniqueness\_criteria*, *iterator\_name*)

Use the molecule's metadata to facilitate iteration over its atoms.

This method will add an attribute with the name given by the *iterator\_name* argument that provides an iterator over groups of atoms. Atoms are grouped by the values in their `atom.metadata` dictionary; any atoms with the same values for the keys given in the *uniqueness\_criteria* argument will be in the same group. These groups have the type `HierarchyElement`.

Hierarchy schemes are not updated dynamically; if a `Molecule` with hierarchy schemes changes, `Molecule.update_hierarchy_schemes()` must be called before the scheme is iterated over again or else the grouping may be incorrect.

Hierarchy schemes allow iteration over groups of atoms according to their metadata. For more information, see `HierarchyScheme`.

#### Parameters

- **uniqueness\_criteria** (tuple of str) – The names of Atom metadata entries that define this scheme. An atom belongs to a `HierarchyElement` only if its metadata has the same values for these criteria as the other atoms in the `HierarchyElement`.
- **iterator\_name** (str) – Name of the iterator that will be exposed to access the hierarchy elements generated by this scheme.

**Returns** **new\_hier\_scheme** (`openff.toolkit.topology.HierarchyScheme`) – The newly created `HierarchyScheme`

See also:

`Molecule.add_default_hierarchy_schemes`, `Molecule.hierarchy_schemes`, `Molecule.delete_hierarchy_scheme`, `Molecule.update_hierarchy_schemes`, `HierarchyScheme`

**property hierarchy\_schemes:** `Dict[str, HierarchyScheme]`

The hierarchy schemes available on the molecule.

Hierarchy schemes allow iteration over groups of atoms according to their metadata. For more information, see `HierarchyScheme`.

**Returns** **A dict of the form {str (HierarchyScheme)}** – The `HierarchySchemes` associated with the molecule.

See also:

`Molecule.add_hierarchy_scheme`, `Molecule.delete_hierarchy_scheme`, `Molecule.update_hierarchy_schemes`, `Topology.hierarchy_iterator`, `HierarchyScheme`

**delete\_hierarchy\_scheme**(*iter\_name*)

Remove an existing `HierarchyScheme` specified by its iterator name.

Hierarchy schemes allow iteration over groups of atoms according to their metadata. For more information, see `HierarchyScheme`.

**Parameters** **iter\_name** (str) –

See also:

`Molecule.add_hierarchy_scheme`, `Molecule.update_hierarchy_schemes`, `Molecule.hierarchy_schemes`, `HierarchyScheme`

**update\_hierarchy\_schemes**(*iter\_names=None*)

Infer a hierarchy from atom metadata according to the existing hierarchy schemes.

Hierarchy schemes allow iteration over groups of atoms according to their metadata. For more information, see [HierarchyScheme](#).

**Parameters** *iter\_names* (Iterable of str, Optional) – Only perceive hierarchy for HierarchySchemes that expose these iterator names. If not provided, all known hierarchies will be perceived, overwriting previous results if applicable.

**See also:**

[Molecule.add\\_hierarchy\\_scheme](#), [Molecule.delete\\_hierarchy\\_schemes](#), [Molecule.hierarchy\\_schemes](#), [HierarchyScheme](#)

**to\_smiles**(*isomeric: bool = True, explicit\_hydrogens: bool = True, mapped: bool = False, toolkit\_registry: Union[ToolkitRegistry, ToolkitWrapper] = GLOBAL\_TOOLKIT\_REGISTRY*)

Return a canonical isomeric SMILES representation of the current molecule. A partially mapped smiles can also be generated for atoms of interest by supplying an *atom\_map* to the properties dictionary.

---

**Note:** RDKit and OpenEye versions will not necessarily return the same representation.

---

#### Parameters

- **isomeric** (bool optional, default= True) – return an isomeric smiles
- **explicit\_hydrogens** (bool optional, default=True) – return a smiles string containing all hydrogens explicitly
- **mapped** (bool optional, default=False) – return a explicit hydrogen mapped smiles, the atoms to be mapped can be controlled by supplying an atom map into the properties dictionary. If no mapping is passed all atoms will be mapped in order, else an atom map dictionary from the current atom index to the map id should be supplied with no duplicates. The map ids (values) should start from 0 or 1.
- **toolkit\_registry** ([openff.toolkit.utils.toolkits.ToolkitRegistry](#) or [openff.toolkit.utils.toolkits.ToolkitWrapper](#), optional, default=None) – [ToolkitRegistry](#) or [ToolkitWrapper](#) to use for SMILES conversion

**Returns** *smiles* (str) – Canonical isomeric explicit-hydrogen SMILES

#### Examples

```
>>> from openff.toolkit.utils import get_data_file_path
>>> sdf_filepath = get_data_file_path('molecules/ethanol.sdf')
>>> molecule = Molecule(sdf_filepath)
>>> smiles = molecule.to_smiles()
```

**classmethod** **from\_inchi**(*inchi: str, allow\_undefined\_stereo: bool = False, toolkit\_registry: ~typing.Union[~openff.toolkit.utils.toolkit\_registry.ToolkitRegistry, ~openff.toolkit.utils.base\_wrapper.ToolkitWrapper] = <ToolkitRegistry containing The RDKit, AmberTools, Built-in Toolkit>*)

Construct a Molecule from a InChI representation

### Parameters

- **inchi** (*str*) – The InChI representation of the molecule.
- **allow\_undefined\_stereo** (*bool*, default=False) – Whether to accept InChI with undefined stereochemistry. If False, an exception will be raised if a InChI with undefined stereochemistry is passed into this function.
- **toolkit\_registry** (`openff.toolkit.utils.toolkits.ToolRegistry`) – or `openff.toolkit.utils.toolkits.ToolkitWrapper`, optional, default=None `ToolkitRegistry` or `ToolkitWrapper` to use for InChI-to-molecule conversion

**Returns** *molecule* (`openff.toolkit.topology.Molecule`)

### Examples

Make cis-1,2-Dichloroethene:

```
>>> molecule = Molecule.from_inchi('InChI=1S/C2H2Cl2/c3-1-2-4/h1-2H/b2-1-')
```

**to\_inchi**(*fixed\_hydrogens*: *bool* = False, *toolkit\_registry*: `Union[ToolkitRegistry, ToolkitWrapper]` = `GLOBAL_TOOLKIT_REGISTRY`) → *str*

Create an InChI string for the molecule using the requested toolkit backend. InChI is a standardised representation that does not capture tautomers unless specified using the fixed hydrogen layer.

For information on InChi see here <https://iupac.org/who-we-are/divisions/division-details/inchi/>

### Parameters

- **fixed\_hydrogens** (*bool*, default=False) – If a fixed hydrogen layer should be added to the InChI, if *True* this will produce a non standard specific InChI string of the molecule.
- **toolkit\_registry** (`openff.toolkit.utils.toolkits.ToolRegistry`) – or `openff.toolkit.utils.toolkits.ToolkitWrapper`, optional, default=None `ToolkitRegistry` or `ToolkitWrapper` to use for molecule-to-InChI conversion

**Returns** *inchi* (*str*) – The InChI string of the molecule.

**Raises** `InvalidToolkitRegistryError` – If an invalid object is passed as the `toolkit_registry` parameter

**to\_inchikey**(*fixed\_hydrogens*: *bool* = False, *toolkit\_registry*: `Union[ToolkitRegistry, ToolkitWrapper]` = `GLOBAL_TOOLKIT_REGISTRY`)

Create an InChIKey for the molecule using the requested toolkit backend. InChIKey is a standardised representation that does not capture tautomers unless specified using the fixed hydrogen layer.

For information on InChi see here <https://iupac.org/who-we-are/divisions/division-details/inchi/>

### Parameters

- **fixed\_hydrogens** (*bool*, default=False) – If a fixed hydrogen layer should be added to the InChI, if *True* this will produce a non standard specific InChI string of the molecule.

- **toolkit\_registry** (openff.toolkit.utils.toolkits.ToolRegistry) – or openff.toolkit.utils.toolkits.ToolkitWrapper, optional, default=None ToolkitRegistry or ToolkitWrapper to use for molecule-to-InChIKey conversion

**Returns** **inchi\_key** (*str*) – The InChIKey representation of the molecule.

**Raises** **InvalidToolkitRegistryError** – If an invalid object is passed as the **toolkit\_registry** parameter

```
classmethod from_smiles(smiles: str, hydrogens_are_explicit: bool = False, toolkit_registry:
    ~typing.Union[~openff.toolkit.utils.toolkit_registry.ToolkitRegistry,
    ~openff.toolkit.utils.base_wrapper.ToolkitWrapper] = <ToolkitRegistry
    containing The RDKit, AmberTools, Built-in Toolkit>,
    allow_undefined_stereo: bool = False) → Molecule
```

Construct a Molecule from a SMILES representation

The order of atoms in the Molecule is unspecified and may change from version to version or with different toolkits. SMILES atom indices (also known as atom maps) are not used to order atoms; instead, they are stored in the produced molecule's properties attribute, accessible via `molecule.properties["atom_map"]`. The atom map is stored as a dictionary mapping molecule atom indices to SMILES atom maps. To order atoms according to SMILES atom indices, see `Molecule.from_mapped_smiles()`, which helpfully raises an exception if any atom map is missing, duplicated, or out-of-range, or else `Molecule.remap()` for arbitrary remaps.

#### Parameters

- **smiles** – The SMILES representation of the molecule.
- **hydrogens\_are\_explicit** – If True, forbid the cheminformatics toolkit from inferring hydrogen atoms not explicitly specified in the SMILES.
- **toolkit\_registry** – The cheminformatics toolkit to use to interpret the SMILES.
- **allow\_undefined\_stereo** – Whether to accept SMILES with undefined stereochemistry. If False, an exception will be raised if a SMILES with undefined stereochemistry is passed into this function.

**Raises** **RadicalsNotSupportedError** – If any atoms in the input molecule contain radical electrons.

#### Examples

Create a Molecule representing toluene from SMILES:

```
>>> molecule = Molecule.from_smiles('Cc1ccccc1')
```

Create a Molecule representing phenol from SMILES with the oxygen at atom index 0 (SMILES indices begin at 1):

```
>>> molecule = Molecule.from_smiles('c1ccccc1[OH:1]')
>>> molecule = molecule.remap(
...     {k: v - 1 for k, v in molecule.properties["atom_map"].items()},
...     partial=True,
... )
>>> assert molecule.atom(0).symbol == "O"
```



See also:

`from_mapped_smiles`, `remap`

```
static are_isomorphic(mol1: Union[FrozenMolecule, Graph], mol2: Union[FrozenMolecule,
    Graph], return_atom_map: bool = False, aromatic_matching: bool = True,
    formal_charge_matching: bool = True, bond_order_matching: bool = True,
    atom_stereochemistry_matching: bool = True,
    bond_stereochemistry_matching: bool = True, strip_pyrimidal_n_atom_stereo:
    bool = True, toolkit_registry: Union[ToolkitRegistry, ToolkitWrapper] =
    GLOBAL_TOOLKIT_REGISTRY)
```

Determine if mol1 is isomorphic to mol2.

`are_isomorphic()` compares two molecule's graph representations and the chosen node/edge attributes. Connections and atomic numbers are always checked.

If `nx.Graphs()` are given they must at least have `atomic_number` attributes on nodes. Other attributes that `are_isomorphic()` can optionally check...

- ... in nodes are:
  - `is_aromatic`
  - `formal_charge`
  - `stereochemistry`
- ... in edges are:
  - `is_aromatic`
  - `bond_order`
  - `stereochemistry`

By default, all attributes are checked, but stereochemistry around pyrimidal nitrogen is ignored.

**Warning:** This API is experimental and subject to change.

#### Parameters

- **mol1** (an `openff.toolkit.topology.molecule.FrozenMolecule` or `nx.Graph()`) – The first molecule to test for isomorphism.
- **mol2** (an `openff.toolkit.topology.molecule.FrozenMolecule` or `nx.Graph()`) – The second molecule to test for isomorphism.
- **return\_atom\_map** (`bool`, default=False, optional) – Return a dict containing the atomic mapping instead of a bool.
- **aromatic\_matching** (`bool`, default=True, optional) – If False, aromaticity of graph nodes and edges are ignored for the purpose of determining isomorphism.
- **formal\_charge\_matching** (`bool`, default=True, optional) – If False, formal charges of graph nodes are ignored for the purpose of determining isomorphism.
- **bond\_order\_matching** (`bool`, default=True, optional) – If False, bond orders of graph edges are ignored for the purpose of determining isomorphism.
- **atom\_stereochemistry\_matching** (`bool`, default=True, optional) – If False, atoms' stereochemistry is ignored for the purpose of determining isomorphism.



- **bond\_stereochemistry\_matching** (*bool*, default=True, optional) – If False, bonds' stereochemistry is ignored for the purpose of determining isomorphism.
- **strip\_pyrimidal\_n\_atom\_stereo** (*bool*, default=True, optional) – If True, any stereochemistry defined around pyrimidal nitrogen stereocenters will be disregarded in the isomorphism check.
- **toolkit\_registry** (*ToolkitRegistry*) – or `openff.toolkit.utils.toolkits.ToolkitWrapper`, optional, default=None *ToolkitRegistry* or *ToolkitWrapper* to use for removing stereochemistry from pyrimidal nitrogens.

#### Returns

- **molecules\_are\_isomorphic** (*bool*)
- **atom\_map** (*default=None, Optional,*) – [Dict[int,int]] ordered by mol1 indexing {mol1\_index: mol2\_index} If molecules are not isomorphic given input arguments, will return None instead of dict.

**is\_isomorphic\_with**(*other: Union[FrozenMolecule, Graph], \*\*kwargs*)

Check if the molecule is isomorphic with the other molecule which can be an `openff.toolkit.topology.Molecule` or `nx.Graph()`. Full matching is done using the options described below.

**Warning:** This API is experimental and subject to change.

#### Parameters

- **other** (*Molecule* or `nx.Graph()`) –
- **aromatic\_matching** (*bool*, default=True, optional) –
- **atoms.** (compare the formal charges attributes of the) –
- **formal\_charge\_matching** (*bool*, default=True, optional) –
- **atoms.** –
- **bond\_order\_matching** (*bool*, default=True, optional) –
- **bonds.** (compare the bond order on attributes of the) –
- **atom\_stereochemistry\_matching** (*bool*, default=True, optional) – If False, atoms' stereochemistry is ignored for the purpose of determining equality.
- **bond\_stereochemistry\_matching** (*bool*, default=True, optional) – If False, bonds' stereochemistry is ignored for the purpose of determining equality.
- **strip\_pyrimidal\_n\_atom\_stereo** (*bool*, default=True, optional) – If True, any stereochemistry defined around pyrimidal nitrogen stereocenters will be disregarded in the isomorphism check.
- **toolkit\_registry** (*ToolkitRegistry*) – or `openff.toolkit.utils.toolkits.ToolkitWrapper`, optional, default=None *ToolkitRegistry* or *ToolkitWrapper* to use for removing stereochemistry from pyrimidal nitrogens.

Returns **isomorphic** (*bool*)

```
generate_conformers(toolkit_registry: Union[ToolkitRegistry, ToolkitWrapper] =  
    GLOBAL_TOOLKIT_REGISTRY, n_conformers: int = 10, rms_cutoff:  
    Optional[Quantity] = None, clear_existing: bool = True,  
    make_carboxylic_acids_cis: bool = True)
```

Generate conformers for this molecule using an underlying toolkit.

If `n_conformers=0`, no toolkit wrapper will be called. If `n_conformers=0` and `clear_existing=True`, `molecule.conformers` will be set to `None`.

#### Parameters

- **toolkit\_registry** (openff.toolkit.utils.toolkits.ToolkitRegistry or) – openff.toolkit.utils.toolkits.ToolkitWrapper, optional, default=None ToolkitRegistry or ToolkitWrapper to use for SMILES-to-molecule conversion
- **n\_conformers** (int, default=1) – The maximum number of conformers to produce
- **rms\_cutoff** (openff.unit.Quantity-wrapped float, in units of distance, optional, default=None) – The minimum RMS value at which two conformers are considered redundant and one is deleted. Precise implementation of this cutoff may be toolkit-dependent. If None, the cutoff is set to be the default value for each ToolkitWrapper (generally 1 Angstrom).
- **clear\_existing** (bool, default=True) – Whether to overwrite existing conformers for the molecule
- **make\_carboxylic\_acids\_cis** (bool, default=True) – Guarantee all conformers have exclusively cis carboxylic acid groups (COOH) by rotating the proton in any trans carboxylic acids 180 degrees around the C-O bond. Works around a bug in conformer generation by the OpenEye toolkit where trans COOH is much more common than it should be.

#### Examples

```
>>> molecule = Molecule.from_smiles('CCCCC')  
>>> molecule.generate_conformers()
```

Raises **InvalidToolkitRegistryError** – If an invalid object is passed as the `toolkit_registry` parameter

```
apply_elf_conformer_selection(percentage: float = 2.0, limit: int = 10, toolkit_registry:  
    Optional[Union[ToolkitRegistry, ToolkitWrapper]] =  
    GLOBAL_TOOLKIT_REGISTRY, **kwargs)
```

Select a set of diverse conformers from the molecule's conformers with ELF.

Applies the [Electrostatically Least-interacting Functional groups method](#) to select a set of diverse conformers which have minimal electrostatically strongly interacting functional groups from the molecule's conformers.

#### Parameters

- **toolkit\_registry** – The underlying toolkit to use to select the ELF conformers.
- **percentage** – The percentage of conformers with the lowest electrostatic interaction energies to greedily select from.
- **limit** – The maximum number of conformers to select.

## Notes

- The input molecule should have a large set of conformers already generated to select the ELF conformers from.
- The selected conformers will be retained in the *conformers* list while unselected conformers will be discarded.

## See also:

`openff.toolkit.utils.toolkits.OpenEyeToolkitWrapper.apply_elf_conformer_selection`,  
`openff.toolkit.utils.toolkits.RDKitToolkitWrapper.apply_elf_conformer_selection`

**assign\_partial\_charges**(*partial\_charge\_method*: *str*, *strict\_n\_conformers*: *bool* = *False*,  
*use\_conformers*: *Optional[List[Quantity]]* = *None*, *toolkit\_registry*:  
*Union[ToolkitRegistry, ToolkitWrapper]* = *GLOBAL\_TOOLKIT\_REGISTRY*,  
*normalize\_partial\_charges*: *bool* = *True*)

Calculate partial atomic charges and store them in the molecule.

`assign_partial_charges` computes charges using the specified toolkit and assigns the new values to the `partial_charges` attribute. Supported charge methods vary from toolkit to toolkit, but some supported methods are:

- "am1bcc"
- "am1bccelf10" (requires OpenEye Toolkits)
- "am1-mulliken"
- "mmff94"
- "gasteiger"

For more supported charge methods and details, see the corresponding methods in each toolkit wrapper:

- `OpenEyeToolkitWrapper.assign_partial_charges`
- `RDKitToolkitWrapper.assign_partial_charges`
- `AmberToolsToolkitWrapper.assign_partial_charges`
- `BuiltInToolkitWrapper.assign_partial_charges`

## Parameters

- **partial\_charge\_method** (string) – The partial charge calculation method to use for partial charge calculation.
- **strict\_n\_conformers** (*bool*, default=False) – Whether to raise an exception if an invalid number of conformers is provided for the given charge method. If this is False and an invalid number of conformers is found, a warning will be raised.
- **use\_conformers** (iterable of `openff.unit.Quantity`-wrapped numpy arrays, each with shape (n\_atoms, 3) and) – dimension of distance. Optional, default=None Coordinates to use for partial charge calculation. If None, an appropriate number of conformers will be generated.
- **toolkit\_registry** (`openff.toolkit.utils.toolkits.ToolkitRegistry` or) – `openff.toolkit.utils.toolkits.ToolkitWrapper`, optional, default=None `ToolkitRegistry` or `ToolkitWrapper` to use for the calculation.

- **normalize\_partial\_charges** (*bool*, default=True) – Whether to offset partial charges so that they sum to the total formal charge of the molecule. This is used to prevent accumulation of rounding errors when the partial charge assignment method returns values at limited precision.

### Examples

```
>>> molecule = Molecule.from_smiles('CCCCC')
>>> molecule.assign_partial_charges('am1-mulliken')
```

Raises **InvalidToolkitRegistryError** – If an invalid object is passed as the `toolkit_registry` parameter

### See also:

`openff.toolkit.utils.toolkits.OpenEyeToolkitWrapper.assign_partial_charges`, `openff.toolkit.utils.toolkits.RDKitToolkitWrapper.assign_partial_charges`, `openff.toolkit.utils.toolkits.AmberToolsToolkitWrapper.assign_partial_charges`, `openff.toolkit.utils.toolkits.BuiltInToolkitWrapper.assign_partial_charges`

**assign\_fractional\_bond\_orders**(*bond\_order\_model=None*,  
                                  *toolkit\_registry=GLOBAL\_TOOLKIT\_REGISTRY*,  
                                  *use\_conformers=None*)

Update and store list of bond orders this molecule.

Bond orders are stored on each bond, in the `bond.fractional_bond_order` attribute.

**Warning:** This API is experimental and subject to change.

### Parameters

- **toolkit\_registry** (`openff.toolkit.utils.toolkits.ToolkitRegistry` or) – `openff.toolkit.utils.toolkits.ToolkitWrapper`, optional, default=None `ToolkitRegistry` or `ToolkitWrapper` to use for SMILES-to-molecule conversion
- **bond\_order\_model** (string, optional. Default=None) – The bond order model to use for fractional bond order calculation. If None, "am1-wiberg" is used.
- **use\_conformers** (iterable of `openff.unit.Quantity(np.array)` with shape (n\_atoms, 3) and dimension of distance,) – optional, default=None The conformers to use for fractional bond order calculation. If None, an appropriate number of conformers will be generated by an available `ToolkitWrapper`.

## Examples

```
>>> from openff.toolkit import Molecule
>>> molecule = Molecule.from_smiles('CCCCC')
>>> molecule.assign_fractional_bond_orders()
```

Raises `InvalidToolkitRegistryError` – If an invalid object is passed as the `toolkit_registry` parameter

### `to_networkx()`

Generate a NetworkX undirected graph from the molecule.

Nodes are Atoms labeled with atom indices and atomic elements (via the `element` node attribute). Edges denote chemical bonds between Atoms.

**Returns graph** (*networkx.Graph*) – The resulting graph, with nodes (atoms) labeled with atom indices, elements, stereochemistry and aromaticity flags and bonds with two atom indices, bond order, stereochemistry, and aromaticity flags

## Examples

Retrieve the bond graph for imatinib (OpenEye toolkit required)

```
>>> molecule = Molecule.from_iupac('imatinib')
>>> nxgraph = molecule.to_networkx()
```

**find\_rotatable\_bonds**(*ignore\_functional\_groups=None*,  
*toolkit\_registry=GLOBAL\_TOOLKIT\_REGISTRY*)

Find all bonds classed as rotatable ignoring any matched to the `ignore_functional_groups` list.

### Parameters

- **ignore\_functional\_groups** (optional, `List[str]`, `default=None`,) – A list of bond SMARTS patterns to be ignored when finding rotatable bonds.
- **toolkit\_registry** (`ToolkitRegistry`) – or `openff.toolkit.utils.toolkits.ToolkitWrapper`, optional, `default=None` `ToolkitRegistry` or `ToolkitWrapper` to use for SMARTS matching

**Returns bonds** (*List[openff.toolkit.topology.molecule.Bond]*) – The list of `openff.toolkit.topology.molecule.Bond` instances which are rotatable.

### **property partial\_charges**

Returns the partial charges (if present) on the molecule.

**Returns partial\_charges** (*a openff.unit.Quantity - wrapped numpy array [1 x n\_atoms] or None*) – The partial charges on the molecule's atoms. Returns `None` if no charges have been specified.

### **property n\_particles: int**

Deprecated since version 0.11.0: This property has been deprecated and will soon be removed. Use `Molecule.n_atoms()` instead.

### **property n\_atoms: int**

The number of Atom objects.

**property** `n_bonds`: `int`

The number of Bond objects in the molecule.

**property** `n_angles`: `int`

Number of angles in the molecule.

**property** `n_propers`: `int`

Number of proper torsions in the molecule.

**property** `n_impropers`: `int`

Number of possible improper torsions in the molecule.

**property** `particles`: `List[Atom]`

Deprecated since version 0.11.0: This property has been deprecated and will soon be removed. Use `Molecule.atoms()` instead.

**particle**(`index`: `int`) → `Atom`

Deprecated since version 0.11.0: This method has been deprecated and will soon be removed. Use `Molecule.atom()` instead.

**particle\_index**(`particle`: `Atom`) → `int`

Deprecated since version 0.11.0: This method has been deprecated and will soon be removed. Use `Molecule.atom_index()` instead.

**property** `atoms`

Iterate over all Atom objects in the molecule.

**atom**(`index`: `int`) → `Atom`

Get the atom with the specified index.

**Parameters** `index` (`int`) –

**Returns** `atom` (`openff.toolkit.topology.Atom`)

**atom\_index**(`atom`: `Atom`) → `int`

Returns the index of the given atom in this molecule

**Parameters** `atom` (`Atom`) –

**Returns** `index` (`int`) – The index of the given atom in this molecule

**property** `conformers`

Returns the list of conformers for this molecule.

Conformers are presented as a list of Quantity-wrapped NumPy arrays, of shape (3 x n\_atoms) and with dimensions of [Distance]. The return value is the actual list of conformers, and changes to the contents affect the original FrozenMolecule.

**property** `n_conformers`: `int`

The number of conformers for this molecule.

**property** `bonds`: `List[Bond]`

Iterate over all Bond objects in the molecule.

**bond**(`index`: `int`) → `Bond`

Get the bond with the specified index.

**Parameters** `index` (`int`) –

**Returns** `bond` (`openff.toolkit.topology.Bond`)

**property angles:** `Set[Tuple[Atom, Atom, Atom]]`

Get an iterator over all i-j-k angles.

**property torsions:** `Set[Tuple[Atom, Atom, Atom, Atom]]`

Get an iterator over all i-j-k-l torsions. Note that i-j-k-i torsions (cycles) are excluded.

**Returns torsions** (*iterable of 4-Atom tuples*)

**property propers:** `Set[Tuple[Atom, Atom, Atom, Atom]]`

Iterate over all proper torsions in the molecule

**property impropers:** `Set[Tuple[Atom, Atom, Atom, Atom]]`

Iterate over all improper torsions in the molecule.

**Returns impropers** (*set of tuple*) – An iterator of tuples, each containing the atoms making up a possible improper torsion.

**See also:**

`smirnoff_improvers`, `amber_improvers`

**property smirnoff\_improvers:** `Set[Tuple[Atom, Atom, Atom, Atom]]`

Iterate over all improvers with trivalent centers, reporting the central atom second.

The central atom is reported second in each torsion. This method reports an improper for each trivalent atom in the molecule, whether or not any given force field would assign it improper torsion parameters.

Also note that this will return 6 possible atom orderings around each improper center. In current SMIRNOFF parameterization, three of these six orderings will be used for the actual assignment of the improper term and measurement of the angles. These three orderings capture the three unique angles that could be calculated around the improper center, therefore the sum of these three terms will always return a consistent energy.

The exact three orderings that will be applied during parameterization can not be determined in this method, since it requires sorting the atom indices, and those indices may change when this molecule is added to a Topology.

For more details on the use of three-fold (‘trefoil’) improvers, see <https://openforcefield.github.io/standards/standards/smirnoff/#improvertorsions>

**Returns improvers** (*set of tuple*) – An iterator of tuples, each containing the indices of atoms making up a possible improper torsion. The central atom is listed second in each tuple.

**See also:**

`improvers`, `amber_improvers`

**property amber\_improvers:** `Set[Tuple[Atom, Atom, Atom, Atom]]`

Iterate over all improvers with trivalent centers, reporting the central atom first.

The central atom is reported first in each torsion. This method reports an improper for each trivalent atom in the molecule, whether or not any given force field would assign it improper torsion parameters.

Also note that this will return 6 possible atom orderings around each improper center. In current AMBER parameterization, one of these six orderings will be used for the actual assignment of the improper term and measurement of the angle. This method does not encode the logic to determine which of the six orderings AMBER would use.

**Returns** **impropers** (*set of tuple*) – An iterator of tuples, each containing the indices of atoms making up a possible improper torsion. The central atom is listed first in each tuple.

**See also:**

`impropers`, `smirnoff_impropers`

**nth\_degree\_neighbors**(*n\_degrees*)

Return canonicalized pairs of atoms whose shortest separation is *exactly* n bonds. Only pairs with increasing atom indices are returned.

**Parameters** **n** (*int*) – The number of bonds separating atoms in each pair

**Returns** **neighbors** (*iterator of tuple of Atom*) – Tuples (len 2) of atom that are separated by n bonds.

## Notes

The criteria used here relies on minimum distances; when there are multiple valid paths between atoms, such as atoms in rings, the shortest path is considered. For example, two atoms in “meta” positions with respect to each other in a benzene are separated by two paths, one length 2 bonds and the other length 4 bonds. This function would consider them to be 2 apart and would not include them if n=4 was passed.

**property** **total\_charge**

Return the total charge on the molecule

**property** **name:** `str`

The name (or title) of the molecule

**property** **properties:** `Dict[str, Any]`

The properties dictionary of the molecule

**property** **hill\_formula:** `str`

Get the Hill formula of the molecule

**to\_hill\_formula**()  $\rightarrow$  `str`

Generate the Hill formula of this molecule.

**Returns** **formula** (*the Hill formula of the molecule*)

:raises `NotImplementedError` : if the molecule is not of one of the specified types.:

**chemical\_environment\_matches**(*query: str, unique: bool = False,*  
*toolkit\_registry=GLOBAL\_TOOLKIT\_REGISTRY*)

Find matches in the molecule for a SMARTS string

**Parameters**

- **query** (`str`) – SMARTS string (with one or more tagged atoms).
- **unique** (`bool`, default=False) –
- **toolkit\_registry** (`ToolkitRegistry`) – or `openff.toolkit.utils.toolkits.ToolkitWrapper`, optional, default=`GLOBAL_TOOLKIT_REGISTRY` `ToolkitRegistry` or `ToolkitWrapper` to use for chemical environment matches

**Returns** **matches** (*list of atom index tuples*) – A list of tuples, containing the indices of the matching atoms.



## Examples

Retrieve all the carbon-carbon bond matches in a molecule

```
>>> molecule = Molecule.from_iupac('imatinib')
>>> matches = molecule.chemical_environment_matches('[#6X3:1]~[#6X3:2]')
```

**classmethod** `from_iupac`(*iupac\_name*, *toolkit\_registry*=<ToolkitRegistry containing The RDKit, AmberTools, Built-in Toolkit>, *allow\_undefined\_stereo*=False, *\*\*kwargs*)

Generate a molecule from IUPAC or common name

---

**Note:** This method requires the OpenEye toolkit to be installed.

---

### Parameters

- **iupac\_name** (*str*) – IUPAC name of molecule to be generated
- **toolkit\_registry** (*ToolkitRegistry*) – or `openff.toolkit.utils.toolkits.ToolkitWrapper`, optional, default=`GLOBAL_TOOLKIT_REGISTRY` *ToolkitRegistry* or *ToolkitWrapper* to use for chemical environment matches
- **allow\_undefined\_stereo** (*bool*, default=False) – If false, raises an exception if molecule contains undefined stereochemistry.

**Returns** *molecule* (*Molecule*) – The resulting molecule with position

## Examples

Create a molecule from an IUPAC name

```
>>> molecule = Molecule.from_iupac('4-[(4-methylpiperazin-1-yl)methyl]-N-(4-methyl-3-{[4-(pyridin-3-yl)pyrimidin-2-yl]amino}phenyl)benzamide') # noqa
```

Create a molecule from a common name

```
>>> molecule = Molecule.from_iupac('imatinib')
```

**to\_iupac**(*toolkit\_registry*=*GLOBAL\_TOOLKIT\_REGISTRY*)

Generate IUPAC name from Molecule

### Returns

- **iupac\_name** (*str*) – IUPAC name of the molecule
- .. note :: This method requires the OpenEye toolkit to be installed.

## Examples

```
>>> from openff.toolkit.utils import get_data_file_path
>>> sdf_filepath = get_data_file_path('molecules/ethanol.sdf')
>>> molecule = Molecule(sdf_filepath)
>>> iupac_name = molecule.to_iupac()
```

### classmethod `from_topology(topology)`

Return a Molecule representation of an OpenFF Topology containing a single Molecule object.

**Parameters** `topology` (`Topology`) – The `Topology` object containing a single `Molecule` object. Note that OpenMM and MDTraj Topology objects are not supported.

**Returns** `molecule` (`openff.toolkit.topology.Molecule`) – The Molecule object in the topology

**Raises** `ValueError` – If the topology does not contain exactly one molecule.

## Examples

Create a molecule from a Topology object that contains exactly one molecule

```
>>> from openff.toolkit import Molecule, Topology
>>> topology = Topology.from_molecules(Molecule.from_smiles('[CH4]'))
>>> molecule = Molecule.from_topology(topology)
```

### `to_topology()`

Return an OpenFF Topology representation containing one copy of this molecule

**Returns** `topology` (`openff.toolkit.topology.Topology`) – A Topology representation of this molecule

## Examples

```
>>> from openff.toolkit import Molecule
>>> molecule = Molecule.from_iupac('imatinib')
>>> topology = molecule.to_topology()
```

### classmethod `from_file(file_path, file_format=None, toolkit_registry=<ToolkitRegistry containing The RDKit, AmberTools, Built-in Toolkit>, allow_undefined_stereo=False)`

Create one or more molecules from a file

#### Parameters

- **file\_path** (`str` or file-like object) – The path to the file or file-like object to stream one or more molecules from.
- **file\_format** (`str`, optional, default=None) – Format specifier, usually file suffix (eg. 'MOL2', 'SMI') Note that not all toolkits support all formats. Check `ToolkitWrapper.toolkit_file_read_formats` for your loaded toolkits for details.
- **toolkit\_registry** (`openff.toolkit.utils.toolkits.ToolkitRegistry` or `openff.toolkit.utils.toolkits.ToolkitWrapper`, optional, default=`GLOBAL_TOOLKIT_REGISTRY` `ToolkitRegistry` or `ToolkitWrapper` to use for file loading. If a Toolkit is passed, only the highest-precedence toolkit is used

- **allow\_undefined\_stereo** (*bool*, default=False) – If false, raises an exception if oemol contains undefined stereochemistry.

**Returns molecules** (*Molecule or list of Molecules*) – If there is a single molecule in the file, a Molecule is returned; otherwise, a list of Molecule objects is returned.

### Examples

```
>>> from openff.toolkit import Molecule
>>> from openff.toolkit.utils.utils import get_data_file_path
>>> sdf_file_path = get_data_file_path("molecules/toluene.sdf")
>>> molecule = Molecule.from_file(sdf_file_path)
```

**classmethod from\_polymer\_pdb**(*file\_path: ~typing.Union[str, ~typing.TextIO]*,  
*toolkit\_registry=<ToolkitRegistry containing The RDKit, AmberTools, Built-in Toolkit>*)

Loads a polymer from a PDB file.

Currently only supports proteins with canonical amino acids that are either uncapped or capped by ACE/NME groups, but may later be extended to handle other common polymers, or accept user-defined polymer templates. Only one polymer chain may be present in the PDB file, and it must be the only molecule present.

Connectivity and bond orders are assigned by matching SMARTS codes for the supported residues against atom names. The PDB file must include all atoms with the correct standard atom names described in the [PDB Chemical Component Dictionary](#). Residue names are used to assist troubleshooting failed assignments, but are not used in the actual assignment process.

Metadata such as residues, chains, and atom names are recorded in the `Atom.metadata` attribute, which is a dictionary mapping from strings like “residue\_name” to the appropriate value. `from_polymer_pdb` returns a molecule that can be iterated over with the `.residues` and `.chains` attributes, as well as the usual `.atoms`.

### Parameters

- **file\_path** (*str* or *file* object) – PDB information to be passed to OpenMM PDBFile object for loading
- **None** (*toolkit\_registry = ToolkitWrapper or ToolkitRegistry. Default =*) – Either a ToolkitRegistry, ToolkitWrapper

**Returns molecule** (*openff.toolkit.topology.Molecule*)

### Raises

- **UnassignedChemistryInPDBError** – If an atom or bond could not be assigned; the exception will provide a detailed diagnostic of what went wrong.
- **MultipleMoleculesInPDBError** – If all atoms and bonds could be assigned, but the PDB includes multiple chains or molecules.

**to\_file**(*file\_path, file\_format, toolkit\_registry=GLOBAL\_TOOLKIT\_REGISTRY*)

Write the current molecule to a file or file-like object

### Parameters

- **file\_path** (*str* or *file-like* object) – A file-like object or the path to the file to be written.

- **file\_format** (*str*) – Format specifier, one of ['MOL2', 'MOL2H', 'SDF', 'PDB', 'SMI', 'CAN', 'TDT'] Note that not all toolkits support all formats
- **toolkit\_registry** (*ToolkitRegistry*) – or `openff.toolkit.utils.toolkits.ToolkitWrapper`, optional, default=`GLOBAL_TOOLKIT_REGISTRY` *ToolkitRegistry* or *ToolkitWrapper* to use for file writing. If a *Toolkit* is passed, only the highest-precedence toolkit is used

**Raises** *ValueError* – If the requested `file_format` is not supported by one of the installed cheminformatics toolkits

### Examples

```
>>> molecule = Molecule.from_iupac('imatinib')
>>> molecule.to_file('imatinib.mol2', file_format='mol2')
>>> molecule.to_file('imatinib.sdf', file_format='sdf')
>>> molecule.to_file('imatinib.pdb', file_format='pdb')
```

**enumerate\_tautomers**(*max\_states=20, toolkit\_registry=GLOBAL\_TOOLKIT\_REGISTRY*)

Enumerate the possible tautomers of the current molecule

#### Parameters

- **max\_states** (int optional, default=20) – The maximum amount of molecules that should be returned
- **toolkit\_registry** (*ToolkitRegistry*) – or `openff.toolkit.utils.toolkits.ToolkitWrapper`, default=`GLOBAL_TOOLKIT_REGISTRY` *ToolkitRegistry* or *ToolkitWrapper* to use to enumerate the tautomers.

**Returns** *molecules* (*List[openff.toolkit.topology.Molecule]*) – A list of `openff.toolkit.topology.Molecule` instances not including the input molecule.

**enumerate\_stereoisomers**(*undefined\_only=False, max\_isomers=20, rationalise=True, toolkit\_registry=GLOBAL\_TOOLKIT\_REGISTRY*)

Enumerate the stereocenters and bonds of the current molecule.

#### Parameters

- **undefined\_only** (bool optional, default=False) – If we should enumerate all stereocenters and bonds or only those with undefined stereochemistry
- **max\_isomers** (int optional, default=20) – The maximum amount of molecules that should be returned
- **rationalise** (bool optional, default=True) – If we should try to build and rationalise the molecule to ensure it can exist
- **toolkit\_registry** (*openff.toolkit.utils.toolkits.ToolkitRegistry* or *openff.toolkit.utils.toolkits.ToolkitWrapper*, default=`GLOBAL_TOOLKIT_REGISTRY` *ToolkitRegistry* or *ToolkitWrapper* to use to enumerate the stereoisomers.

**Returns** *molecules* (*List[openff.toolkit.topology.Molecule]*) – A list of *Molecule* instances not including the input molecule.

**enumerate\_protomers**(*max\_states=10*)

Enumerate the formal charges of a molecule to generate different protomoers.

**Parameters** `max_states` (int optional, default=10,) – The maximum number of protomer states to be returned.

**Returns** `molecules` (*List[openff.toolkit.topology.Molecule]*,) – A list of the protomers of the input molecules not including the input.

**classmethod** `from_rdmol(rdmol, allow_undefined_stereo=False, hydrogens_are_explicit=False)`

Create a Molecule from an RDKit molecule.

Requires the RDKit to be installed.

**Parameters**

- `rdmol` (`rdkit.RDMol`) – An RDKit molecule
- `allow_undefined_stereo` (bool, default=False) – If False, raises an exception if `rdmol` contains undefined stereochemistry.
- `hydrogens_are_explicit` (bool, default=False) – If False, RDKit will perform hydrogen addition using `Chem.AddHs`

**Returns** `molecule` (*openff.toolkit.topology.Molecule*) – An OpenFF molecule

### Examples

Create a molecule from an RDKit molecule

```
>>> from openff.toolkit import Molecule
>>> from rdkit import Chem
>>> rdmol = Chem.MolFromSmiles("CCO")
>>> molecule = Molecule.from_rdmol(rdmol)
```

**to\_rdmol**(*aromaticity\_model=DEFAULT\_AROMATICITY\_MODEL*,  
*toolkit\_registry=GLOBAL\_TOOLKIT\_REGISTRY*)

Create an RDKit molecule

Requires the RDKit to be installed.

**Parameters** `aromaticity_model` (str, optional, default="OEAroModel\_MDL") – The aromaticity model to use. Only OEAroModel\_MDL is supported.

**Returns** `rdmol` (`rdkit.RDMol`) – An RDKit molecule

### Examples

Convert a molecule to RDKit

```
>>> from openff.toolkit.utils import get_data_file_path
>>> sdf_filepath = get_data_file_path('molecules/ethanol.sdf')
>>> molecule = Molecule(sdf_filepath)
>>> rdmol = molecule.to_rdmol()
```

**classmethod** `from_openeye(oemol, allow_undefined_stereo=False)`

Create a Molecule from an OpenEye molecule.

Requires the OpenEye toolkit to be installed.

**Parameters**

- **oemol** (openeye.oechem.OEMol) – An OpenEye molecule
- **allow\_undefined\_stereo** (bool, default=False) – If False, raises an exception if oemol contains undefined stereochemistry.

**Returns** molecule (*openff.toolkit.topology.Molecule*) – An OpenFF molecule

### Examples

Create a Molecule from an OpenEye OEMol

```
>>> from openff.toolkit import Molecule
>>> from openeye import oechem
>>> oemol = oechem.OEMol()
>>> oechem.OESmilesToMol(oemol, '[H]C([H])([H])C([H])([H])O[H]')
True
>>> molecule = Molecule.from_openeye(oemol)
```

**to\_qcschema**(multiplicity=1, conformer=0, extras=None)

Create a QCElemental Molecule.

**Warning:** This API is experimental and subject to change.

### Parameters

- **multiplicity** (int, default=1,) – The multiplicity of the molecule; sets molecular\_multiplicity field for QCElemental Molecule.
- **conformer** (int, default=0,) – The index of the conformer to use for the QCElemental Molecule geometry.
- **extras** (dict, default=None) – A dictionary that should be included in the extras field on the QCElemental Molecule. This can be used to include extra information, such as a smiles representation.

**Returns** *qcelemental.models.Molecule* – A validated QCElemental Molecule.

### Examples

Create a QCElemental Molecule:

```
>>> import qcelemental as qcel
>>> mol = Molecule.from_smiles('CC')
>>> mol.generate_conformers(n_conformers=1)
>>> qcemol = mol.to_qcschema()
```

### Raises

- **MissingOptionalDependencyError** – If qcelemental is not installed, the qcschema can not be validated.
- **InvalidConformerError** – No conformer found at the given index.

```
classmethod from_mapped_smiles(mapped_smiles: str, toolkit_registry:
    ~typing.Union[~openff.toolkit.utils.toolkit_registry.ToolkitRegistry,
    ~openff.toolkit.utils.base_wrapper.ToolkitWrapper] =
    <ToolkitRegistry containing The RDKit, AmberTools, Built-in
    Toolkit>, allow_undefined_stereo: bool = False)
```

Create a Molecule from a SMILES string, ordering atoms from mappings

SMILES strings support mapping integer indices to each atom by ending a bracketed atom declaration with a colon followed by a 1-indexed integer:

This method creates a Molecule from such a SMILES string whose atoms are ordered according to the mapping. Each atom must be mapped exactly once; any duplicate, missing, or out-of-range mappings will cause the method to fail.

**Warning:** This API is experimental and subject to change.

### Parameters

- **mapped\_smiles** (*str*) – A mapped SMILES string with explicit hydrogens.
- **toolkit\_registry** – Cheminformatics toolkit to use for SMILES-to-molecule conversion
- **allow\_undefined\_stereo** – If false, raise an exception if the SMILES contains undefined stereochemistry.

**Returns** *offmol* – An OpenFF molecule instance.

### Raises

- **SmilesParsingError** – If the given SMILES had no indexing picked up by the toolkits, or if the indexing is missing indices.
- **RemapIndexError** – If the mapping has duplicate or out-of-range indices.

### Examples

Create a mapped chlorofluoroiodomethane molecule and check the atoms are placed accordingly:

```
>>> molecule = Molecule.from_mapped_smiles(
...     "[Cl:2][C@:1]([F:3])([I:4])[H:5]"
... )
>>> assert molecule.atom(0).symbol == "C"
>>> assert molecule.atom(1).symbol == "Cl"
>>> assert molecule.atom(2).symbol == "F"
>>> assert molecule.atom(3).symbol == "I"
>>> assert molecule.atom(4).symbol == "H"
```

See also:

[from\\_smiles](#), [remap](#)

```
classmethod from_qcschema(qca_record, client=None, toolkit_registry=<ToolkitRegistry containing
    The RDKit, AmberTools, Built-in Toolkit>, allow_undefined_stereo=False)
```

Create a Molecule from a QCArchive molecule record or dataset entry based on attached cmiles information.

For a molecule record, a conformer will be set from its geometry.

For a dataset entry, if a corresponding client instance is provided, the starting geometry for that entry will be used as a conformer.

A QCElemental Molecule produced from `Molecule.to_qcschema` can be round-tripped through this method to produce a new, valid Molecule.

#### Parameters

- **qca\_record** (*dict*) – A QCArchive molecule record or dataset entry.
- **client** (optional, *default=None*,) – A `qcportal.FractalClient` instance to use for fetching an initial geometry. Only used if `qca_record` is a dataset entry.
- **toolkit\_registry** (`openff.toolkit.utils.toolkits.ToolkitRegistry` or `openff.toolkit.utils.toolkits.ToolkitWrapper`, optional `ToolkitRegistry` or `ToolkitWrapper` to use for SMILES-to-molecule conversion
- **allow\_undefined\_stereo** (*bool*, *default=False*) – If false, raises an exception if `qca_record` contains undefined stereochemistry.

**Returns** **molecule** (*openff.toolkit.topology.Molecule*) – An OpenFF molecule instance.

#### Examples

Get Molecule from a QCArchive molecule record:

```
>>> from qcportal import FractalClient
>>> client = FractalClient()
>>> offmol = Molecule.from_qcschema(
...     client.query_molecules(molecular_formula="C16H20N3O5")[0]
... )
```

Get Molecule from a QCArchive optimization entry:

```
>>> from qcportal import FractalClient
>>> client = FractalClient()
>>> optds = client.get_collection(
...     "OptimizationDataset",
...     "SMIRNOFF Coverage Set 1"
... )
>>> offmol = Molecule.from_qcschema(optds.get_entry('coc(o)oc-0'))
```

Same as above, but with conformer(s) from initial molecule(s) by providing client to database:

```
>>> offmol = Molecule.from_qcschema(
...     optds.get_entry('coc(o)oc-0'),
...     client=client
... )
```

#### Raises

- **AttributeError** – If the record dict can not be made from `qca_record`, or if the provided client could not retrieve the initial molecule.
- **KeyError** – If the record does not contain the `canonical_isomeric_explicit_hydrogen_mapped_smiles`.



- **InvalidConformerError** – Silent error, if the conformer could not be attached.

**classmethod** `from_pdb_and_smiles(file_path, smiles, allow_undefined_stereo=False)`

Create a Molecule from a pdb file and a SMILES string using RDKit.

Requires RDKit to be installed.

**Warning:** This API is experimental and subject to change.

The molecule is created and sanitised based on the SMILES string, we then find a mapping between this molecule and one from the PDB based only on atomic number and connections. The SMILES molecule is then reindexed to match the PDB, the conformer is attached, and the molecule returned.

Note that any stereochemistry in the molecule is set by the SMILES, and not the coordinates of the PDB.

#### Parameters

- **file\_path** (*str*) – PDB file path
- **smiles** (*str*) – a valid smiles string for the pdb, used for stereochemistry, formal charges, and bond order
- **allow\_undefined\_stereo** (*bool*, default=False) – If false, raises an exception if SMILES contains undefined stereochemistry.

**Returns** *molecule* (*openff.toolkit.Molecule*) – An OFFMol instance with ordering the same as used in the PDB file.

**Raises** **InvalidConformerError** – If the SMILES and PDB molecules are not isomorphic.

**canonical\_order\_atoms**(*toolkit\_registry=GLOBAL\_TOOLKIT\_REGISTRY*)

Produce a copy of the molecule with the atoms reordered canonically.

Each toolkit defines its own canonical ordering of atoms. The canonical order may change from toolkit version to toolkit version or between toolkits.

**Warning:** This API is experimental and subject to change.

**Parameters** **toolkit\_registry** (*openff.toolkit.utils.toolkits.ToolkitRegistry* or) – *openff.toolkit.utils.toolkits.ToolkitWrapper*, optional *ToolkitRegistry* or *ToolkitWrapper* to use for SMILES-to-molecule conversion

**Returns** *molecule* (*openff.toolkit.topology.Molecule*) – An new OpenFF style molecule with atoms in the canonical order.

**remap**(*mapping\_dict: Dict[int, int]*, *current\_to\_new: bool = True*, *partial: bool = False*)

Reorder the atoms in the molecule according to the given mapping dict.

The mapping dict must be a dictionary mapping atom indices to atom indices. Each atom index must be an integer in the half-open interval  $[0, n\_atoms)$ ; ie, it must be a valid index into the `self.atoms` list. All atom indices in the molecule must be mapped from and to exactly once unless `partial=True` is given, in which case they must be mapped no more than once. Missing (unless `partial=True`), out-of-range (including non-integer), or duplicate indices are not allowed in the `mapping_dict` and will lead to an exception.

By default, the mapping dict's keys are the source indices and its values are destination indices, but this can be changed with the `current_to_new` argument.

The keys of the `self.properties["atom_map"]` property are updated for the new ordering. Other values of the properties dictionary are transferred unchanged.

**Warning:** This API is experimental and subject to change.

#### Parameters

- **mapping\_dict** – A dictionary of the mapping between indices. The mapping should be indexed starting from 0 for both the source and destination; note that SMILES atom mapping is typically 1-based.
- **current\_to\_new** – If this is `True`, then `mapping_dict` is of the form `{current_index: new_index}`; otherwise, it is of the form `{new_index: current_index}`.
- **partial** – If `False` (the default), an exception will be raised if any atom is lacking a destination in the atom map. Note that if this is `True`, atoms without entries in the mapping dict may be moved in addition to those in the dictionary. Note that partial maps must still be in-range and not include duplicates.

**Returns** `new_molecule` (*openff.toolkit.topology.molecule.Molecule*) – A copy of the molecule in the new order.

**Raises** `RemapIndexError` – When an out-of-range, duplicate, or missing index is found in the `mapping_dict`.

See also:

`from_mapped_smiles`

`to_openeye(toolkit_registry=GLOBAL_TOOLKIT_REGISTRY,  
aromaticity_model=DEFAULT_AROMATICITY_MODEL)`

Create an OpenEye molecule

Requires the OpenEye toolkit to be installed.

**Parameters** `aromaticity_model` (`str`, optional, default="OEAroModel\_MDL") – The aromaticity model to use. Only `OEAroModel_MDL` is supported.

**Returns** `oemol` (*openeye.oechem.OEMol*) – An OpenEye molecule

#### Examples

Create an OpenEye molecule from a Molecule

```
>>> molecule = Molecule.from_smiles('CC')
>>> oemol = molecule.to_openeye()
```

`get_bond_between(i: Union[int, Atom], j: Union[int, Atom]) → Bond`

Returns the bond between two atoms

#### Parameters

- **i** (`int` or `Atom`) – Atoms or atom indices to check
- **j** (`int` or `Atom`) – Atoms or atom indices to check

**Returns** **bond** (*Bond*) – The bond between i and j.

**classmethod** **from\_bson**(*serialized*)

Instantiate an object from a BSON serialized representation.

Specification: <http://bsonspec.org/>

**Parameters** **serialized** (*bytes*) – A BSON serialized representation of the object

**Returns** **instance** (*cls*) – An instantiated object

**classmethod** **from\_json**(*serialized: str*)

Instantiate an object from a JSON serialized representation.

Specification: <https://www.json.org/>

**Parameters** **serialized** (*str*) – A JSON serialized representation of the object

**Returns** **instance** (*cls*) – An instantiated object

**classmethod** **from\_messagepack**(*serialized*)

Instantiate an object from a MessagePack serialized representation.

Specification: <https://msgpack.org/index.html>

**Parameters** **serialized** (*bytes*) – A MessagePack-encoded bytes serialized representation

**Returns** **instance** (*cls*) – Instantiated object.

**classmethod** **from\_pickle**(*serialized*)

Instantiate an object from a pickle serialized representation.

**Warning:** This is not recommended for safe, stable storage since the pickle specification may change between Python versions.

**Parameters** **serialized** (*str*) – A pickled representation of the object

**Returns** **instance** (*cls*) – An instantiated object

**classmethod** **from\_toml**(*serialized*)

Instantiate an object from a TOML serialized representation.

Specification: <https://github.com/toml-lang/toml>

**Parameters** **serialized** (*str*) – A TOML serialized representation of the object

**Returns** **instance** (*cls*) – An instantiated object

**classmethod** **from\_xml**(*serialized*)

Instantiate an object from an XML serialized representation.

Specification: <https://www.w3.org/XML/>

**Parameters** **serialized** (*bytes*) – An XML serialized representation

**Returns** **instance** (*cls*) – Instantiated object.

**classmethod** **from\_yaml**(*serialized*)

Instantiate from a YAML serialized representation.

Specification: <http://yaml.org/>

**Parameters** `serialized` (*str*) – A YAML serialized representation of the object

**Returns** `instance` (*cls*) – Instantiated object

**to\_bson()**

Return a BSON serialized representation.

Specification: <http://bsonspec.org/>

**Returns** `serialized` (*bytes*) – A BSON serialized representation of the object

**to\_json(indent=None)** → *str*

Return a JSON serialized representation.

Specification: <https://www.json.org/>

**Parameters** `indent` (*int*, optional, default=None) – If not None, will pretty-print with specified number of spaces for indentation

**Returns** `serialized` (*str*) – A JSON serialized representation of the object

**to\_messagepack()**

Return a MessagePack representation.

Specification: <https://msgpack.org/index.html>

**Returns** `serialized` (*bytes*) – A MessagePack-encoded bytes serialized representation of the object

**to\_pickle()**

Return a pickle serialized representation.

**Warning:** This is not recommended for safe, stable storage since the pickle specification may change between Python versions.

**Returns** `serialized` (*str*) – A pickled representation of the object

**to\_toml()**

Return a TOML serialized representation.

Specification: <https://github.com/toml-lang/toml>

**Returns** `serialized` (*str*) – A TOML serialized representation of the object

**to\_xml(indent=2)**

Return an XML representation.

Specification: <https://www.w3.org/XML/>

**Parameters** `indent` (*int*, optional, default=2) – If not None, will pretty-print with specified number of spaces for indentation

**Returns** `serialized` (*bytes*) – A MessagePack-encoded bytes serialized representation.

**to\_yaml()**

Return a YAML serialized representation.

Specification: <http://yaml.org/>

**Returns** `serialized` (*str*) – A YAML serialized representation of the object

### 11.1.2 Molecule

**class** openff.toolkit.topology.Molecule(\*args, \*\*kwargs)

Mutable chemical representation of a molecule, such as a small molecule or biopolymer.

#### Examples

Create a molecule from an sdf file

```
>>> from openff.toolkit.utils import get_data_file_path
>>> sdf_filepath = get_data_file_path('molecules/ethanol.sdf')
>>> molecule = Molecule(sdf_filepath)
```

Convert to OpenEye OEMol object

```
>>> oemol = molecule.to_openeye()
```

Create a molecule from an OpenEye molecule

```
>>> molecule = Molecule.from_openeye(oemol)
```

Convert to RDKit Mol object

```
>>> rdmol = molecule.to_rdkit()
```

Create a molecule from an RDKit molecule

```
>>> molecule = Molecule.from_rdkit(rdmol)
```

Create a molecule from IUPAC name (requires the OpenEye toolkit)

```
>>> molecule = Molecule.from_iupac('imatinib')
```

Create a molecule from SMILES

```
>>> molecule = Molecule.from_smiles('Cc1ccccc1')
```

**Warning:** This API is experimental and subject to change.

**\_\_init\_\_**(\*args, \*\*kwargs)

Create a new Molecule object

**Parameters** **other** (optional, default=None) – If specified, attempt to construct a copy of the molecule from the specified object. This can be any one of the following:

- a [Molecule](#) object
- a file that can be used to construct a [Molecule](#) object
- an openeye.oechem.OEMol
- an rdkit.Chem.rdchem.Mol
- a serialized [Molecule](#) object

## Examples

Create an empty molecule:

```
>>> empty_molecule = Molecule()
```

Create a molecule from a file that can be used to construct a molecule, using either a filename or file-like object:

```
>>> from openff.toolkit.utils import get_data_file_path
>>> sdf_filepath = get_data_file_path('molecules/ethanol.sdf')
>>> molecule = Molecule(sdf_filepath)
>>> molecule = Molecule(open(sdf_filepath, 'r'), file_format='sdf')
```

```
>>> import gzip
>>> mol2_gz_filepath = get_data_file_path('molecules/toluene.mol2.gz')
>>> molecule = Molecule(gzip.GzipFile(mol2_gz_filepath, 'r'), file_format='mol2')
```

Create a molecule from another molecule:

```
>>> molecule_copy = Molecule(molecule)
```

Convert to OpenEye OEMol object

```
>>> oemol = molecule.to_openeye()
```

Create a molecule from an OpenEye molecule:

```
>>> molecule = Molecule(oemol)
```

Convert to RDKit Mol object

```
>>> rdmol = molecule.to_rdkit()
```

Create a molecule from an RDKit molecule:

```
>>> molecule = Molecule(rdmol)
```

Convert the molecule into a dictionary and back again:

```
>>> serialized_molecule = molecule.to_dict()
>>> molecule_copy = Molecule(serialized_molecule)
```

## Methods

<code>__init__(*args, **kwargs)</code>	Create a new Molecule object
<code>add_atom(atomic_number, formal_charge, ...)</code>	Add an atom to the molecule.
<code>add_bond(atom1, atom2, bond_order, is_aromatic)</code>	Add a bond between two specified atom indices
<code>add_conformer(coordinates)</code>	Add a conformation of the molecule
<code>add_default_hierarchy_schemes([...])</code>	Adds chain and residue hierarchy schemes.

continues on next page

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<code>add_hierarchy_scheme(uniqueness_criteria, ...)</code>	Use the molecule's metadata to facilitate iteration over its atoms.
<code>apply_elf_conformer_selection([percentage, ...])</code>	Select a set of diverse conformers from the molecule's conformers with ELF.
<code>are_isomorphic(mol1, mol2[, ...])</code>	Determine if mol1 is isomorphic to mol2.
<code>assign_fractional_bond_orders([...])</code>	Update and store list of bond orders this molecule.
<code>assign_partial_charges(partial_charge_method)</code>	Calculate partial atomic charges and store them in the molecule.
<code>atom(index)</code>	Get the atom with the specified index.
<code>atom_index(atom)</code>	Returns the index of the given atom in this molecule
<code>bond(index)</code>	Get the bond with the specified index.
<code>canonical_order_atoms([toolkit_registry])</code>	Produce a copy of the molecule with the atoms reordered canonically.
<code>chemical_environment_matches(query[, ...])</code>	Find matches in the molecule for a SMARTS string
<code>delete_hierarchy_scheme(iter_name)</code>	Remove an existing HierarchyScheme specified by its iterator name.
<code>enumerate_protomers([max_states])</code>	Enumerate the formal charges of a molecule to generate different protomoers.
<code>enumerate_stereoisomers([undefined_only, ...])</code>	Enumerate the stereocenters and bonds of the current molecule.
<code>enumerate_tautomers([max_states, ...])</code>	Enumerate the possible tautomers of the current molecule
<code>find_rotatable_bonds([...])</code>	Find all bonds classed as rotatable ignoring any matched to the ignore_functional_groups list.
<code>from_bson(serialized)</code>	Instantiate an object from a BSON serialized representation.
<code>from_dict(molecule_dict)</code>	Create a new Molecule from a dictionary representation
<code>from_file(file_path[, file_format, ...])</code>	Create one or more molecules from a file
<code>from_inchi(inchi[, allow_undefined_stereo, ...])</code>	Construct a Molecule from a InChI representation
<code>from_iupac(iupac_name[, toolkit_registry, ...])</code>	Generate a molecule from IUPAC or common name
<code>from_json(serialized)</code>	Instantiate an object from a JSON serialized representation.
<code>from_mapped_smiles(mapped_smiles[, ...])</code>	Create a Molecule from a SMILES string, ordering atoms from mappings
<code>from_messagepack(serialized)</code>	Instantiate an object from a MessagePack serialized representation.
<code>from_openeye(oemol[, allow_undefined_stereo])</code>	Create a Molecule from an OpenEye molecule.
<code>from_pdb_and_smiles(file_path, smiles[, ...])</code>	Create a Molecule from a pdb file and a SMILES string using RDKit.
<code>from_pickle(serialized)</code>	Instantiate an object from a pickle serialized representation.
<code>from_polymer_pdb(file_path[, toolkit_registry])</code>	Loads a polymer from a PDB file.

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<code>from_qcschema(qca_record[, client, ...])</code>	Create a Molecule from a QCArchive molecule record or dataset entry based on attached cmiles information.
<code>from_rdkit(rdmol[, allow_undefined_stereo, ...])</code>	Create a Molecule from an RDKit molecule.
<code>from_smiles(smiles[, ...])</code>	Construct a Molecule from a SMILES representation
<code>from_toml(serialized)</code>	Instantiate an object from a TOML serialized representation.
<code>from_topology(topology)</code>	Return a Molecule representation of an OpenFF Topology containing a single Molecule object.
<code>from_xml(serialized)</code>	Instantiate an object from an XML serialized representation.
<code>from_yaml(serialized)</code>	Instantiate from a YAML serialized representation.
<code>generate_conformers([toolkit_registry, ...])</code>	Generate conformers for this molecule using an underlying toolkit.
<code>generate_unique_atom_names()</code>	Generate unique atom names from the element symbol and count.
<code>get_bond_between(i, j)</code>	Returns the bond between two atoms
<code>is_isomorphic_with(other, **kwargs)</code>	Check if the molecule is isomorphic with the other molecule which can be an <code>openff.toolkit.topology.Molecule</code> or <code>nx.Graph()</code> .
<code>nth_degree_neighbors(n_degrees)</code>	Return canonicalized pairs of atoms whose shortest separation is <i>exactly</i> n bonds.
<code>ordered_connection_table_hash()</code>	Compute an ordered hash of the atoms and bonds in the molecule
<code>particle(index)</code>	Deprecated since version 0.11.0.
<code>particle_index(particle)</code>	Deprecated since version 0.11.0.
<code>perceive_residues([substructure_file_path, ...])</code>	Perceive a polymer's residues and permit iterating over them.
<code>remap(mapping_dict[, current_to_new, partial])</code>	Reorder the atoms in the molecule according to the given mapping dict.
<code>strip_atom_stereochemistry(smarts[, ...])</code>	Delete stereochemistry information for certain atoms, if it is present.
<code>to_bson()</code>	Return a BSON serialized representation.
<code>to_dict()</code>	Return a dictionary representation of the molecule.
<code>to_file(file_path, file_format[, ...])</code>	Write the current molecule to a file or file-like object
<code>to_hill_formula()</code>	Generate the Hill formula of this molecule.
<code>to_inchi([fixed_hydrogens, toolkit_registry])</code>	Create an InChI string for the molecule using the requested toolkit backend.
<code>to_inchikey([fixed_hydrogens, toolkit_registry])</code>	Create an InChIKey for the molecule using the requested toolkit backend.
<code>to_iupac([toolkit_registry])</code>	Generate IUPAC name from Molecule
<code>to_json([indent])</code>	Return a JSON serialized representation.

continues on next page



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<code>to_messagepack()</code>	Return a MessagePack representation.
<code>to_networkx()</code>	Generate a NetworkX undirected graph from the molecule.
<code>to_openeye([toolkit_registry, aromaticity_model])</code>	Create an OpenEye molecule
<code>to_pickle()</code>	Return a pickle serialized representation.
<code>to_qcschema([multiplicity, conformer, extras])</code>	Create a QCElemental Molecule.
<code>to_rdkit([aromaticity_model, toolkit_registry])</code>	Create an RDKit molecule
<code>to_smiles([isomeric, explicit_hydrogens, ...])</code>	Return a canonical isomeric SMILES representation of the current molecule.
<code>to_toml()</code>	Return a TOML serialized representation.
<code>to_topology()</code>	Return an OpenFF Topology representation containing one copy of this molecule
<code>to_xml([indent])</code>	Return an XML representation.
<code>to_yaml()</code>	Return a YAML serialized representation.
<code>update_hierarchy_schemes([iter_names])</code>	Infer a hierarchy from atom metadata according to the existing hierarchy schemes.
<code>visualize([backend, width, height, ...])</code>	Render a visualization of the molecule in Jupyter

## Attributes

<code>amber_impropers</code>	Iterate over all impropers with trivalent centers, reporting the central atom first.
<code>angles</code>	Get an iterator over all i-j-k angles.
<code>atoms</code>	Iterate over all Atom objects in the molecule.
<code>bonds</code>	Iterate over all Bond objects in the molecule.
<code>conformers</code>	Returns the list of conformers for this molecule.
<code>has_unique_atom_names</code>	True if the molecule has unique atom names, False otherwise.
<code>hierarchy_schemes</code>	The hierarchy schemes available on the molecule.
<code>hill_formula</code>	Get the Hill formula of the molecule
<code>impropers</code>	Iterate over all improper torsions in the molecule.
<code>n_angles</code>	Number of angles in the molecule.
<code>n_atoms</code>	The number of Atom objects.
<code>n_bonds</code>	The number of Bond objects in the molecule.
<code>n_conformers</code>	The number of conformers for this molecule.
<code>n_impropers</code>	Number of possible improper torsions in the molecule.
<code>n_particles</code>	Deprecated since version 0.11.0.
<code>n_propers</code>	Number of proper torsions in the molecule.
<code>name</code>	The name (or title) of the molecule
<code>partial_charges</code>	Returns the partial charges (if present) on the molecule.
<code>particles</code>	Deprecated since version 0.11.0.
<code>propers</code>	Iterate over all proper torsions in the molecule
<code>properties</code>	The properties dictionary of the molecule
<code>smirnoff_impropers</code>	Iterate over all impropers with trivalent centers, reporting the central atom second.
<code>torsions</code>	Get an iterator over all i-j-k-l torsions.
<code>total_charge</code>	Return the total charge on the molecule

**add\_atom**(*atomic\_number*: *int*, *formal\_charge*: *int*, *is\_aromatic*: *bool*, *stereochemistry*: *Optional[str]* = *None*, *name*: *Optional[str]* = *None*, *metadata*: *Optional[Dict[str, Union[int, str]]]* = *None*)  
→ *int*

Add an atom to the molecule.

### Parameters

- **atomic\_number** (*int*) – Atomic number of the atom
- **formal\_charge** (*int*) – Formal charge of the atom
- **is\_aromatic** (*bool*) – If True, atom is aromatic; if False, not aromatic
- **stereochemistry** (*str*, optional, default=None) – Either 'R' or 'S' for specified stereochemistry, or None if stereochemistry is irrelevant
- **name** (*str*, optional) – An optional name for the atom

- **metadata** (`dict[str: (int, str)]`, `default=None`) – An optional dictionary where keys are strings and values are strings or ints. This is intended to record atom-level information used to inform hierarchy definition and iteration, such as grouping atom by residue and chain.

**Returns** `index` (`int`) – The index of the atom in the molecule

### Examples

Define a methane molecule

```
>>> molecule = Molecule()
>>> molecule.name = 'methane'
>>> C = molecule.add_atom(6, 0, False)
>>> H1 = molecule.add_atom(1, 0, False)
>>> H2 = molecule.add_atom(1, 0, False)
>>> H3 = molecule.add_atom(1, 0, False)
>>> H4 = molecule.add_atom(1, 0, False)
>>> bond_idx = molecule.add_bond(C, H1, 1, False)
>>> bond_idx = molecule.add_bond(C, H2, 1, False)
>>> bond_idx = molecule.add_bond(C, H3, 1, False)
>>> bond_idx = molecule.add_bond(C, H4, 1, False)
>>> molecule.to_smiles(explicit_hydrogens=False)
'C'
```

**add\_bond**(`atom1: Union[int, Atom]`, `atom2: Union[int, Atom]`, `bond_order: int`, `is_aromatic: bool`, `stereochemistry: Optional[str] = None`, `fractional_bond_order: Optional[float] = None`)

Add a bond between two specified atom indices

#### Parameters

- **atom1** (`int` or `Atom`) – Index of first atom
- **atom2** (`int` or `Atom`) – Index of second atom
- **bond\_order** (`int`) – Integral bond order of Kekulized form
- **is\_aromatic** (`bool`) – True if this bond is aromatic, False otherwise
- **stereochemistry** (`str`, optional, `default=None`) – Either 'E' or 'Z' for specified stereochemistry, or None if stereochemistry is irrelevant
- **fractional\_bond\_order** (`float`, optional, `default=None`) – The fractional (eg. Wiberg) bond order

**Returns** `index` (`int`) – Index of the bond in this molecule

### Examples

For an example of use, see `add_atom()`.

**add\_conformer**(`coordinates`)

Add a conformation of the molecule

**Parameters** `coordinates` (unit-wrapped `np.array` with shape `(n_atoms, 3)` and dimension of distance) – Coordinates of the new conformer, with the first dimension of the array corresponding to the atom index in the molecule's indexing system.

**Returns** `index` (*int*) – The index of this conformer

**visualize**(*backend*='rdkit', *width*=None, *height*=None, *show\_all\_hydrogens*=True)

Render a visualization of the molecule in Jupyter

#### Parameters

- **backend** (*str*, optional, default='rdkit') – The visualization engine to use. Choose from:
  - "rdkit"
  - "openeye"
  - "nglview" (requires conformers)
- **width** (*int*, optional, default=500) – Width of the generated representation (only applicable to backend=openeye or backend=rdkit)
- **height** (*int*, optional, default=300) – Width of the generated representation (only applicable to backend=openeye or backend=rdkit)
- **show\_all\_hydrogens** (*bool*, optional, default=True) – Whether to explicitly depict all hydrogen atoms. (only applicable to backend=openeye or backend=rdkit)

#### Returns

*object* – Depending on the backend chosen:

- rdkit → IPython.display.SVG
- openeye → IPython.display.Image
- nglview → nglview.NGLWidget

**perceive\_residues**(*substructure\_file\_path*=None, *strict\_chirality*=True)

Perceive a polymer's residues and permit iterating over them.

Perceives residues by matching substructures in the current molecule with a substructure dictionary file, using SMARTS, and assigns residue names and numbers to atom metadata. It then constructs a residue hierarchy scheme to allow iterating over residues.

#### Parameters

- **substructure\_file\_path** (*str*, optional, default=None) – Path to substructure library file in JSON format. Defaults to using built-in substructure file.
- **strict\_chirality** (*bool*, optional, default=True) – Whether to use strict chirality symbols (stereomarks) for substructure matchings with SMARTS.

**add\_default\_hierarchy\_schemes**(*overwrite\_existing*=True)

Adds chain and residue hierarchy schemes.

The Open Force Field Toolkit has no native understanding of hierarchical atom organisation schemes common to other biomolecular software, such as “residues” or “chains” (see [Hierarchy data \(chains and residues\)](#)). Hierarchy schemes allow iteration over groups of atoms according to their metadata. For more information, see [HierarchyScheme](#).

If a Molecule with the default hierarchy schemes changes, [Molecule.update\\_hierarchy\\_schemes\(\)](#) must be called before the residues or chains are iterated over again or else the iteration may be incorrect.

**Parameters** **overwrite\_existing** (*bool*, default=True) – Whether to overwrite existing instances of the *residue* and *chain* hierarchy schemes. If this is False and either of the hierarchy schemes are already defined on this molecule, an exception will be raised.

**Raises** `HierarchySchemeWithIteratorNameAlreadyRegisteredException` – When `overwrite_existing=False` and either the chains or residues hierarchy scheme is already configured.

**See also:**

`HierarchyScheme`, `Molecule.add_hierarchy_scheme`, `Molecule.update_hierarchy_schemes`, `Molecule.perceive_residues`

**add\_hierarchy\_scheme**(*uniqueness\_criteria*, *iterator\_name*)

Use the molecule's metadata to facilitate iteration over its atoms.

This method will add an attribute with the name given by the `iterator_name` argument that provides an iterator over groups of atoms. Atoms are grouped by the values in their `atom.metadata` dictionary; any atoms with the same values for the keys given in the `uniqueness_criteria` argument will be in the same group. These groups have the type `HierarchyElement`.

Hierarchy schemes are not updated dynamically; if a `Molecule` with hierarchy schemes changes, `Molecule.update_hierarchy_schemes()` must be called before the scheme is iterated over again or else the grouping may be incorrect.

Hierarchy schemes allow iteration over groups of atoms according to their metadata. For more information, see `HierarchyScheme`.

#### Parameters

- **uniqueness\_criteria** (tuple of str) – The names of Atom metadata entries that define this scheme. An atom belongs to a `HierarchyElement` only if its metadata has the same values for these criteria as the other atoms in the `HierarchyElement`.
- **iterator\_name** (str) – Name of the iterator that will be exposed to access the hierarchy elements generated by this scheme.

**Returns** `new_hier_scheme` (`openff.toolkit.topology.HierarchyScheme`) – The newly created `HierarchyScheme`

**See also:**

`Molecule.add_default_hierarchy_schemes`, `Molecule.hierarchy_schemes`, `Molecule.delete_hierarchy_scheme`, `Molecule.update_hierarchy_schemes`, `HierarchyScheme`

**property** `amber_impropers`: `Set[Tuple[Atom, Atom, Atom, Atom]]`

Iterate over all impropers with trivalent centers, reporting the central atom first.

The central atom is reported first in each torsion. This method reports an improper for each trivalent atom in the molecule, whether or not any given force field would assign it improper torsion parameters.

Also note that this will return 6 possible atom orderings around each improper center. In current AMBER parameterization, one of these six orderings will be used for the actual assignment of the improper term and measurement of the angle. This method does not encode the logic to determine which of the six orderings AMBER would use.

**Returns** `impropers` (*set of tuple*) – An iterator of tuples, each containing the indices of atoms making up a possible improper torsion. The central atom is listed first in each tuple.

**See also:**

`impropers`, `smirnoff_impropers`

**property angles:** `Set[Tuple[Atom, Atom, Atom]]`

Get an iterator over all i-j-k angles.

**apply\_elf\_conformer\_selection**(percentage: *float* = 2.0, limit: *int* = 10, toolkit\_registry: *Optional[Union[ToolkitRegistry, ToolkitWrapper]]* = GLOBAL\_TOOLKIT\_REGISTRY, *\*\*kwargs*)

Select a set of diverse conformers from the molecule's conformers with ELF.

Applies the [Electrostatically Least-interacting Functional groups method](#) to select a set of diverse conformers which have minimal electrostatically strongly interacting functional groups from the molecule's conformers.

#### Parameters

- **toolkit\_registry** – The underlying toolkit to use to select the ELF conformers.
- **percentage** – The percentage of conformers with the lowest electrostatic interaction energies to greedily select from.
- **limit** – The maximum number of conformers to select.

#### Notes

- The input molecule should have a large set of conformers already generated to select the ELF conformers from.
- The selected conformers will be retained in the *conformers* list while unselected conformers will be discarded.

#### See also:

`openff.toolkit.utils.toolkits.OpenEyeToolkitWrapper.apply_elf_conformer_selection`,  
`openff.toolkit.utils.toolkits.RDKitToolkitWrapper.apply_elf_conformer_selection`

**static are\_isomorphic**(mol1: *Union[FrozenMolecule, Graph]*, mol2: *Union[FrozenMolecule, Graph]*, return\_atom\_map: *bool* = False, aromatic\_matching: *bool* = True, formal\_charge\_matching: *bool* = True, bond\_order\_matching: *bool* = True, atom\_stereochemistry\_matching: *bool* = True, bond\_stereochemistry\_matching: *bool* = True, strip\_pyramidal\_n\_atom\_stereo: *bool* = True, toolkit\_registry: *Union[ToolkitRegistry, ToolkitWrapper]* = GLOBAL\_TOOLKIT\_REGISTRY)

Determine if mol1 is isomorphic to mol2.

`are_isomorphic()` compares two molecule's graph representations and the chosen node/edge attributes. Connections and atomic numbers are always checked.

If `nx.Graphs()` are given they must at least have `atomic_number` attributes on nodes. Other attributes that `are_isomorphic()` can optionally check...

- ... in nodes are:
  - `is_aromatic`
  - `formal_charge`
  - `stereochemistry`
- ... in edges are:
  - `is_aromatic`

- `bond_order`
- `stereochemistry`

By default, all attributes are checked, but stereochemistry around pyrimidal nitrogen is ignored.

**Warning:** This API is experimental and subject to change.

### Parameters

- **mol1** (an `openff.toolkit.topology.molecule.FrozenMolecule` or `nx.Graph()`) – The first molecule to test for isomorphism.
- **mol2** (an `openff.toolkit.topology.molecule.FrozenMolecule` or `nx.Graph()`) – The second molecule to test for isomorphism.
- **return\_atom\_map** (*bool*, default=False, optional) – Return a dict containing the atomic mapping instead of a bool.
- **aromatic\_matching** (*bool*, default=True, optional) – If False, aromaticity of graph nodes and edges are ignored for the purpose of determining isomorphism.
- **formal\_charge\_matching** (*bool*, default=True, optional) – If False, formal charges of graph nodes are ignored for the purpose of determining isomorphism.
- **bond\_order\_matching** (*bool*, default=True, optional) – If False, bond orders of graph edges are ignored for the purpose of determining isomorphism.
- **atom\_stereochemistry\_matching** (*bool*, default=True, optional) – If False, atoms' stereochemistry is ignored for the purpose of determining isomorphism.
- **bond\_stereochemistry\_matching** (*bool*, default=True, optional) – If False, bonds' stereochemistry is ignored for the purpose of determining isomorphism.
- **strip\_pyrimidal\_n\_atom\_stereo** (*bool*, default=True, optional) – If True, any stereochemistry defined around pyrimidal nitrogen stereocenters will be disregarded in the isomorphism check.
- **toolkit\_registry** (*ToolkitRegistry*) – or `openff.toolkit.utils.toolkits.ToolkitWrapper`, optional, default=None *ToolkitRegistry* or *ToolkitWrapper* to use for removing stereochemistry from pyrimidal nitrogens.

### Returns

- **molecules\_are\_isomorphic** (*bool*)
- **atom\_map** (default=None, *Optional*,) – [Dict[int,int]] ordered by mol1 indexing {mol1\_index: mol2\_index} If molecules are not isomorphic given input arguments, will return None instead of dict.

```
assign_fractional_bond_orders(bond_order_model=None,
                             toolkit_registry=GLOBAL_TOOLKIT_REGISTRY,
                             use_conformers=None)
```

Update and store list of bond orders this molecule.

Bond orders are stored on each bond, in the `bond.fractional_bond_order` attribute.

**Warning:** This API is experimental and subject to change.

### Parameters

- **toolkit\_registry** (openff.toolkit.utils.toolkits.ToolkitRegistry or openff.toolkit.utils.toolkits.ToolkitWrapper, optional, default=None) – ToolkitRegistry or ToolkitWrapper to use for SMILES-to-molecule conversion
- **bond\_order\_model** (string, optional. Default=None) – The bond order model to use for fractional bond order calculation. If None, "am1-wiberg" is used.
- **use\_conformers** (iterable of openff.unit.Quantity(np.array) with shape (n\_atoms, 3) and dimension of distance,) – optional, default=None The conformers to use for fractional bond order calculation. If None, an appropriate number of conformers will be generated by an available ToolkitWrapper.

### Examples

```
>>> from openff.toolkit import Molecule
>>> molecule = Molecule.from_smiles('CCCCC')
>>> molecule.assign_fractional_bond_orders()
```

Raises **InvalidToolkitRegistryError** – If an invalid object is passed as the `toolkit_registry` parameter

```
assign_partial_charges(partial_charge_method: str, strict_n_conformers: bool = False,
                       use_conformers: Optional[List[Quantity]] = None, toolkit_registry:
                       Union[ToolkitRegistry, ToolkitWrapper] = GLOBAL_TOOLKIT_REGISTRY,
                       normalize_partial_charges: bool = True)
```

Calculate partial atomic charges and store them in the molecule.

`assign_partial_charges` computes charges using the specified toolkit and assigns the new values to the `partial_charges` attribute. Supported charge methods vary from toolkit to toolkit, but some supported methods are:

- "am1bcc"
- "am1bccelf10" (requires OpenEye Toolkits)
- "am1-mulliken"
- "mmff94"
- "gasteiger"

For more supported charge methods and details, see the corresponding methods in each toolkit wrapper:

- `OpenEyeToolkitWrapper.assign_partial_charges`
- `RDKitToolkitWrapper.assign_partial_charges`
- `AmberToolsToolkitWrapper.assign_partial_charges`
- `BuiltInToolkitWrapper.assign_partial_charges`

### Parameters

- **partial\_charge\_method** (string) – The partial charge calculation method to use for partial charge calculation.



- **strict\_n\_conformers** (`bool`, default=False) – Whether to raise an exception if an invalid number of conformers is provided for the given charge method. If this is False and an invalid number of conformers is found, a warning will be raised.
- **use\_conformers** (iterable of `openff.unit.Quantity`-wrapped numpy arrays, each with shape (n\_atoms, 3) and) – dimension of distance. Optional, default=None Coordinates to use for partial charge calculation. If None, an appropriate number of conformers will be generated.
- **toolkit\_registry** (`openff.toolkit.utils.toolkits.ToolkitRegistry` or) – `openff.toolkit.utils.toolkits.ToolkitWrapper`, optional, default=None `ToolkitRegistry` or `ToolkitWrapper` to use for the calculation.
- **normalize\_partial\_charges** (`bool`, default=True) – Whether to offset partial charges so that they sum to the total formal charge of the molecule. This is used to prevent accumulation of rounding errors when the partial charge assignment method returns values at limited precision.

### Examples

```
>>> molecule = Molecule.from_smiles('CCCCC')
>>> molecule.assign_partial_charges('am1-mulliken')
```

Raises `InvalidToolkitRegistryError` – If an invalid object is passed as the `toolkit_registry` parameter

See also:

```
openff.toolkit.utils.toolkits.OpenEyeToolkitWrapper.assign_partial_charges,
openff.toolkit.utils.toolkits.RDKitToolkitWrapper.assign_partial_charges,
openff.toolkit.utils.toolkits.AmberToolsToolkitWrapper.assign_partial_charges,
openff.toolkit.utils.toolkits.BuiltInToolkitWrapper.assign_partial_charges
```

**atom**(index: `int`) → `Atom`

Get the atom with the specified index.

**Parameters** `index` (`int`) –

**Returns** `atom` (`openff.toolkit.topology.Atom`)

**atom\_index**(atom: `Atom`) → `int`

Returns the index of the given atom in this molecule

**Parameters** `atom` (`Atom`) –

**Returns** `index` (`int`) – The index of the given atom in this molecule

**property atoms**

Iterate over all Atom objects in the molecule.

**bond**(index: `int`) → `Bond`

Get the bond with the specified index.

**Parameters** `index` (`int`) –

**Returns** `bond` (`openff.toolkit.topology.Bond`)

**property** `bonds`: `List[Bond]`

Iterate over all Bond objects in the molecule.

**canonical\_order\_atoms**(*toolkit\_registry*=`GLOBAL_TOOLKIT_REGISTRY`)

Produce a copy of the molecule with the atoms reordered canonically.

Each toolkit defines its own canonical ordering of atoms. The canonical order may change from toolkit version to toolkit version or between toolkits.

**Warning:** This API is experimental and subject to change.

**Parameters** `toolkit_registry` (`openff.toolkit.utils.toolkits.ToolkitRegistry` or) – `openff.toolkit.utils.toolkits.ToolkitWrapper`, optional `ToolkitRegistry` or `ToolkitWrapper` to use for SMILES-to-molecule conversion

**Returns** `molecule` (`openff.toolkit.topology.Molecule`) – An new OpenFF style molecule with atoms in the canonical order.

**chemical\_environment\_matches**(*query*: `str`, *unique*: `bool` = `False`,  
*toolkit\_registry*=`GLOBAL_TOOLKIT_REGISTRY`)

Find matches in the molecule for a SMARTS string

**Parameters**

- **query** (`str`) – SMARTS string (with one or more tagged atoms).
- **unique** (`bool`, default=`False`) –
- **toolkit\_registry** (`ToolkitRegistry`) – or `openff.toolkit.utils.toolkits.ToolkitWrapper`, optional, default=`GLOBAL_TOOLKIT_REGISTRY` `ToolkitRegistry` or `ToolkitWrapper` to use for chemical environment matches

**Returns** `matches` (*list of atom index tuples*) – A list of tuples, containing the indices of the matching atoms.

## Examples

Retrieve all the carbon-carbon bond matches in a molecule

```
>>> molecule = Molecule.from_iupac('imatinib')
>>> matches = molecule.chemical_environment_matches('[#6X3:1]~[#6X3:2]')
```

**property** `conformers`

Returns the list of conformers for this molecule.

Conformers are presented as a list of Quantity-wrapped NumPy arrays, of shape (3 x n\_atoms) and with dimensions of [Distance]. The return value is the actual list of conformers, and changes to the contents affect the original `FrozenMolecule`.

**delete\_hierarchy\_scheme**(*iter\_name*)

Remove an existing `HierarchyScheme` specified by its iterator name.

Hierarchy schemes allow iteration over groups of atoms according to their metadata. For more information, see [HierarchyScheme](#).

**Parameters** `iter_name` (`str`) –

See also:

`Molecule.add_hierarchy_scheme`, `Molecule.update_hierarchy_schemes`, `Molecule.hierarchy_schemes`, `HierarchyScheme`

**enumerate\_protomers**(*max\_states=10*)

Enumerate the formal charges of a molecule to generate different protomers.

**Parameters** *max\_states* (int optional, default=10,) – The maximum number of protomer states to be returned.

**Returns** *molecules* (*List[openff.toolkit.topology.Molecule]*,) – A list of the protomers of the input molecules not including the input.

**enumerate\_stereoisomers**(*undefined\_only=False*, *max\_isomers=20*, *rationalise=True*, *toolkit\_registry=GLOBAL\_TOOLKIT\_REGISTRY*)

Enumerate the stereocenters and bonds of the current molecule.

**Parameters**

- **undefined\_only** (bool optional, default=False) – If we should enumerate all stereocenters and bonds or only those with undefined stereochemistry
- **max\_isomers** (int optional, default=20) – The maximum amount of molecules that should be returned
- **rationalise** (bool optional, default=True) – If we should try to build and rationalise the molecule to ensure it can exist
- **toolkit\_registry** (*openff.toolkit.utils.toolkits.ToolkitRegistry* or *openff.toolkit.utils.toolkits.ToolkitWrapper*, default=*GLOBAL\_TOOLKIT\_REGISTRY* *ToolkitRegistry* or *ToolkitWrapper* to use to enumerate the stereoisomers.

**Returns** *molecules* (*List[openff.toolkit.topology.Molecule]*) – A list of *Molecule* instances not including the input molecule.

**enumerate\_tautomers**(*max\_states=20*, *toolkit\_registry=GLOBAL\_TOOLKIT\_REGISTRY*)

Enumerate the possible tautomers of the current molecule

**Parameters**

- **max\_states** (int optional, default=20) – The maximum amount of molecules that should be returned
- **toolkit\_registry** (*ToolkitRegistry*) – or *openff.toolkit.utils.toolkits.ToolkitWrapper*, default=*GLOBAL\_TOOLKIT\_REGISTRY* *ToolkitRegistry* or *ToolkitWrapper* to use to enumerate the tautomers.

**Returns** *molecules* (*List[openff.toolkit.topology.Molecule]*) – A list of *openff.toolkit.topology.Molecule* instances not including the input molecule.

**find\_rotatable\_bonds**(*ignore\_functional\_groups=None*, *toolkit\_registry=GLOBAL\_TOOLKIT\_REGISTRY*)

Find all bonds classed as rotatable ignoring any matched to the *ignore\_functional\_groups* list.

**Parameters**

- **ignore\_functional\_groups** (optional, *List[str]*, default=None,) – A list of bond SMARTS patterns to be ignored when finding rotatable bonds.

- **toolkit\_registry** (*ToolkitRegistry*) – or `openff.toolkit.utils.toolkits.ToolkitWrapper`, optional, default=None *ToolkitRegistry* or *ToolkitWrapper* to use for SMARTS matching

**Returns bonds** (*List[openff.toolkit.topology.molecule.Bond]*) – The list of `openff.toolkit.topology.molecule.Bond` instances which are rotatable.

**classmethod from\_bson**(*serialized*)

Instantiate an object from a BSON serialized representation.

Specification: <http://bsonspec.org/>

**Parameters serialized** (*bytes*) – A BSON serialized representation of the object

**Returns instance** (*cls*) – An instantiated object

**classmethod from\_dict**(*molecule\_dict: dict*)

Create a new Molecule from a dictionary representation

**Parameters molecule\_dict** (*dict*) – A dictionary representation of the molecule.

**Returns molecule** (*Molecule*) – A Molecule created from the dictionary representation

**classmethod from\_file**(*file\_path, file\_format=None, toolkit\_registry=<ToolkitRegistry containing The RDKit, AmberTools, Built-in Toolkit>, allow\_undefined\_stereo=False*)

Create one or more molecules from a file

**Parameters**

- **file\_path** (*str* or file-like object) – The path to the file or file-like object to stream one or more molecules from.
- **file\_format** (*str*, optional, default=None) – Format specifier, usually file suffix (eg. 'MOL2', 'SMI') Note that not all toolkits support all formats. Check `ToolkitWrapper.toolkit_file_read_formats` for your loaded toolkits for details.
- **toolkit\_registry** (`openff.toolkit.utils.toolkits.ToolkitRegistry` or) – `openff.toolkit.utils.toolkits.ToolkitWrapper`, optional, default=`GLOBAL_TOOLKIT_REGISTRY` *ToolkitRegistry* or *ToolkitWrapper* to use for file loading. If a Toolkit is passed, only the highest-precedence toolkit is used
- **allow\_undefined\_stereo** (*bool*, default=False) – If false, raises an exception if oemol contains undefined stereochemistry.

**Returns molecules** (*Molecule or list of Molecules*) – If there is a single molecule in the file, a Molecule is returned; otherwise, a list of Molecule objects is returned.

## Examples

```
>>> from openff.toolkit import Molecule
>>> from openff.toolkit.utils import get_data_file_path
>>> sdf_file_path = get_data_file_path("molecules/toluene.sdf")
>>> molecule = Molecule.from_file(sdf_file_path)
```

**classmethod from\_inchi**(*inchi: str, allow\_undefined\_stereo: bool = False, toolkit\_registry: ~typing.Union[~openff.toolkit.utils.toolkit\_registry.ToolkitRegistry, ~openff.toolkit.utils.base\_wrapper.ToolkitWrapper] = <ToolkitRegistry containing The RDKit, AmberTools, Built-in Toolkit>*)

Construct a Molecule from a InChI representation

#### Parameters

- **inchi** (*str*) – The InChI representation of the molecule.
- **allow\_undefined\_stereo** (*bool*, default=False) – Whether to accept InChI with undefined stereochemistry. If False, an exception will be raised if a InChI with undefined stereochemistry is passed into this function.
- **toolkit\_registry** (*openff.toolkit.utils.toolkits.ToolRegistry*) – or *openff.toolkit.utils.toolkits.ToolkitWrapper*, optional, default=None  
ToolkitRegistry or ToolkitWrapper to use for InChI-to-molecule conversion

**Returns** *molecule* (*openff.toolkit.topology.Molecule*)

#### Examples

Make cis-1,2-Dichloroethene:

```
>>> molecule = Molecule.from_inchi('InChI=1S/C2H2Cl2/c3-1-2-4/h1-2H/b2-1-')
```

```
classmethod from_iupac(iupac_name, toolkit_registry=<ToolkitRegistry containing The RDKit,  
AmberTools, Built-in Toolkit>, allow_undefined_stereo=False, **kwargs)
```

Generate a molecule from IUPAC or common name

---

**Note:** This method requires the OpenEye toolkit to be installed.

---

#### Parameters

- **iupac\_name** (*str*) – IUPAC name of molecule to be generated
- **toolkit\_registry** (*ToolkitRegistry*) – or *openff.toolkit.utils.toolkits.ToolkitWrapper*, optional, default=GLOBAL\_TOOLKIT\_REGISTRY  
ToolkitRegistry or ToolkitWrapper to use for chemical environment matches
- **allow\_undefined\_stereo** (*bool*, default=False) – If false, raises an exception if molecule contains undefined stereochemistry.

**Returns** *molecule* (*Molecule*) – The resulting molecule with position

#### Examples

Create a molecule from an IUPAC name

```
>>> molecule = Molecule.from_iupac('4-[(4-methylpiperazin-1-yl)methyl]-N-(4-methyl-  
↪3-[4-(pyridin-3-yl)pyrimidin-2-yl]amino}phenyl)benzamide') # noqa
```

Create a molecule from a common name

```
>>> molecule = Molecule.from_iupac('imatinib')
```

**classmethod** `from_json(serialized: str)`

Instantiate an object from a JSON serialized representation.

Specification: <https://www.json.org/>

**Parameters** `serialized (str)` – A JSON serialized representation of the object

**Returns** `instance (cls)` – An instantiated object

**classmethod** `from_mapped_smiles(mapped_smiles: str, toolkit_registry: ~typing.Union[~openff.toolkit.utils.toolkit_registry.ToolkitRegistry, ~openff.toolkit.utils.base_wrapper.ToolkitWrapper] = <ToolkitRegistry containing The RDKit, AmberTools, Built-in Toolkit>, allow_undefined_stereo: bool = False)`

Create a Molecule from a SMILES string, ordering atoms from mappings

SMILES strings support mapping integer indices to each atom by ending a bracketed atom declaration with a colon followed by a 1-indexed integer:

This method creates a Molecule from such a SMILES string whose atoms are ordered according to the mapping. Each atom must be mapped exactly once; any duplicate, missing, or out-of-range mappings will cause the method to fail.

**Warning:** This API is experimental and subject to change.

#### Parameters

- **mapped\_smiles (str)** – A mapped SMILES string with explicit hydrogens.
- **toolkit\_registry** – Cheminformatics toolkit to use for SMILES-to-molecule conversion
- **allow\_undefined\_stereo** – If false, raise an exception if the SMILES contains undefined stereochemistry.

**Returns** `offmol` – An OpenFF molecule instance.

#### Raises

- **SmilesParsingError** – If the given SMILES had no indexing picked up by the toolkits, or if the indexing is missing indices.
- **RemapIndexError** – If the mapping has duplicate or out-of-range indices.

#### Examples

Create a mapped chlorofluoriodomethane molecule and check the atoms are placed accordingly:

```
>>> molecule = Molecule.from_mapped_smiles(
...     "[C1:2][C@:1]([F:3])([I:4])[H:5]"
... )
>>> assert molecule.atom(0).symbol == "C"
>>> assert molecule.atom(1).symbol == "Cl"
>>> assert molecule.atom(2).symbol == "F"
>>> assert molecule.atom(3).symbol == "I"
>>> assert molecule.atom(4).symbol == "H"
```

See also:

`from_smiles`, `remap`

**classmethod** `from_messagepack(serialized)`

Instantiate an object from a MessagePack serialized representation.

Specification: <https://msgpack.org/index.html>

**Parameters** `serialized` (`bytes`) – A MessagePack-encoded bytes serialized representation

**Returns** `instance` (`cls`) – Instantiated object.

**classmethod** `from_openeye(oemol, allow_undefined_stereo=False)`

Create a Molecule from an OpenEye molecule.

Requires the OpenEye toolkit to be installed.

**Parameters**

- `oemol` (`openeye.oechem.OEMol`) – An OpenEye molecule
- `allow_undefined_stereo` (`bool`, default=False) – If False, raises an exception if oemol contains undefined stereochemistry.

**Returns** `molecule` (`openff.toolkit.topology.Molecule`) – An OpenFF molecule

## Examples

Create a Molecule from an OpenEye OEMol

```
>>> from openff.toolkit import Molecule
>>> from openeye import oechem
>>> oemol = oechem.OEMol()
>>> oechem.OESmilesToMol(oemol, '[H]C([H])([H])C([H])([H])O[H]')
True
>>> molecule = Molecule.from_openeye(oemol)
```

**classmethod** `from_pdb_and_smiles(file_path, smiles, allow_undefined_stereo=False)`

Create a Molecule from a pdb file and a SMILES string using RDKit.

Requires RDKit to be installed.

**Warning:** This API is experimental and subject to change.

The molecule is created and sanitised based on the SMILES string, we then find a mapping between this molecule and one from the PDB based only on atomic number and connections. The SMILES molecule is then reindexed to match the PDB, the conformer is attached, and the molecule returned.

Note that any stereochemistry in the molecule is set by the SMILES, and not the coordinates of the PDB.

**Parameters**

- `file_path` (`str`) – PDB file path

- **smiles** (*str*) – a valid smiles string for the pdb, used for stereochemistry, formal charges, and bond order
- **allow\_undefined\_stereo** (*bool*, default=False) – If false, raises an exception if SMILES contains undefined stereochemistry.

**Returns** *molecule* (*openff.toolkit.Molecule*) – An OFFMol instance with ordering the same as used in the PDB file.

**Raises** *InvalidConformerError* – If the SMILES and PDB molecules are not isomorphic.

**classmethod** *from\_pickle*(*serialized*)

Instantiate an object from a pickle serialized representation.

**Warning:** This is not recommended for safe, stable storage since the pickle specification may change between Python versions.

**Parameters** *serialized* (*str*) – A pickled representation of the object

**Returns** *instance* (*cls*) – An instantiated object

**classmethod** *from\_polymer\_pdb*(*file\_path*: *~typing.Union[str, ~typing.TextIO]*,  
*toolkit\_registry*=<ToolkitRegistry containing The RDKit, AmberTools,  
Built-in Toolkit>)

Loads a polymer from a PDB file.

Currently only supports proteins with canonical amino acids that are either uncapped or capped by ACE/NME groups, but may later be extended to handle other common polymers, or accept user-defined polymer templates. Only one polymer chain may be present in the PDB file, and it must be the only molecule present.

Connectivity and bond orders are assigned by matching SMARTS codes for the supported residues against atom names. The PDB file must include all atoms with the correct standard atom names described in the [PDB Chemical Component Dictionary](#). Residue names are used to assist troubleshooting failed assignments, but are not used in the actual assignment process.

Metadata such as residues, chains, and atom names are recorded in the *Atom.metadata* attribute, which is a dictionary mapping from strings like “residue\_name” to the appropriate value. *from\_polymer\_pdb* returns a molecule that can be iterated over with the *.residues* and *.chains* attributes, as well as the usual *.atoms*.

#### Parameters

- **file\_path** (*str* or *file* object) – PDB information to be passed to OpenMM PDBFile object for loading
- **None** (*toolkit\_registry* = *ToolkitWrapper* or *ToolkitRegistry*. Default =) – Either a *ToolkitRegistry*, *ToolkitWrapper*

**Returns** *molecule* (*openff.toolkit.topology.Molecule*)

#### Raises

- **UnassignedChemistryInPDBError** – If an atom or bond could not be assigned; the exception will provide a detailed diagnostic of what went wrong.
- **MultipleMoleculesInPDBError** – If all atoms and bonds could be assigned, but the PDB includes multiple chains or molecules.



**classmethod** `from_qcschema(qca_record, client=None, toolkit_registry=<ToolkitRegistry containing The RDKit, AmberTools, Built-in Toolkit>, allow_undefined_stereo=False)`

Create a Molecule from a QCArchive molecule record or dataset entry based on attached cmiles information.

For a molecule record, a conformer will be set from its geometry.

For a dataset entry, if a corresponding client instance is provided, the starting geometry for that entry will be used as a conformer.

A QCElemental Molecule produced from `Molecule.to_qcschema` can be round-tripped through this method to produce a new, valid Molecule.

#### Parameters

- **qca\_record** (`dict`) – A QCArchive molecule record or dataset entry.
- **client** (optional, default=None,) – A `qcportal.FractalClient` instance to use for fetching an initial geometry. Only used if `qca_record` is a dataset entry.
- **toolkit\_registry** (`openff.toolkit.utils.toolkits.ToolkitRegistry` or `openff.toolkit.utils.toolkits.ToolkitWrapper`, optional `ToolkitRegistry` or `ToolkitWrapper` to use for SMILES-to-molecule conversion
- **allow\_undefined\_stereo** (`bool`, default=False) – If false, raises an exception if `qca_record` contains undefined stereochemistry.

**Returns** `molecule` (`openff.toolkit.topology.Molecule`) – An OpenFF molecule instance.

#### Examples

Get Molecule from a QCArchive molecule record:

```
>>> from qcportal import FractalClient
>>> client = FractalClient()
>>> offmol = Molecule.from_qcschema(
...     client.query_molecules(molecular_formula="C16H20N3O5")[0]
... )
```

Get Molecule from a QCArchive optimization entry:

```
>>> from qcportal import FractalClient
>>> client = FractalClient()
>>> optds = client.get_collection(
...     "OptimizationDataset",
...     "SMIRNOFF Coverage Set 1"
... )
>>> offmol = Molecule.from_qcschema(optds.get_entry('coc(o)oc-0'))
```

Same as above, but with conformer(s) from initial molecule(s) by providing client to database:

```
>>> offmol = Molecule.from_qcschema(
...     optds.get_entry('coc(o)oc-0'),
...     client=client
... )
```

#### Raises

- **AttributeError** – If the record dict can not be made from `qca_record`, or if the provided client could not retrieve the initial molecule.
- **KeyError** – If the record does not contain the `canonical_isomeric_explicit_hydrogen_mapped_smiles`.
- **InvalidConformerError** – Silent error, if the conformer could not be attached.

**classmethod** `from_rdmol(rdmol, allow_undefined_stereo=False, hydrogens_are_explicit=False)`

Create a Molecule from an RDKit molecule.

Requires the RDKit to be installed.

#### Parameters

- **rdmol** (`rdkit.RDMol`) – An RDKit molecule
- **allow\_undefined\_stereo** (`bool`, default=`False`) – If `False`, raises an exception if `rdmol` contains undefined stereochemistry.
- **hydrogens\_are\_explicit** (`bool`, default=`False`) – If `False`, RDKit will perform hydrogen addition using `Chem.AddHs`

**Returns** **molecule** (`openff.toolkit.topology.Molecule`) – An OpenFF molecule

#### Examples

Create a molecule from an RDKit molecule

```
>>> from openff.toolkit import Molecule
>>> from rdkit import Chem
>>> rdmol = Chem.MolFromSmiles("CCO")
>>> molecule = Molecule.from_rdmol(rdmol)
```

**classmethod** `from_smiles(smiles: str, hydrogens_are_explicit: bool = False, toolkit_registry: ~typing.Union[~openff.toolkit.utils.toolkit_registry.ToolkitRegistry, ~openff.toolkit.utils.base_wrapper.ToolkitWrapper] = <ToolkitRegistry containing The RDKit, AmberTools, Built-in Toolkit>, allow_undefined_stereo: bool = False) → Molecule`

Construct a Molecule from a SMILES representation

The order of atoms in the Molecule is unspecified and may change from version to version or with different toolkits. SMILES atom indices (also known as atom maps) are not used to order atoms; instead, they are stored in the produced molecule's properties attribute, accessible via `molecule.properties["atom_map"]`. The atom map is stored as a dictionary mapping molecule atom indices to SMILES atom maps. To order atoms according to SMILES atom indices, see `Molecule.from_mapped_smiles()`, which helpfully raises an exception if any atom map is missing, duplicated, or out-of-range, or else `Molecule.remap()` for arbitrary remaps.

#### Parameters

- **smiles** – The SMILES representation of the molecule.
- **hydrogens\_are\_explicit** – If `True`, forbid the cheminformatics toolkit from inferring hydrogen atoms not explicitly specified in the SMILES.
- **toolkit\_registry** – The cheminformatics toolkit to use to interpret the SMILES.

- **allow\_undefined\_stereo** – Whether to accept SMILES with undefined stereochemistry. If False, an exception will be raised if a SMILES with undefined stereochemistry is passed into this function.

**Raises** `RadicalsNotSupportedError` – If any atoms in the input molecule contain radical electrons.

## Examples

Create a Molecule representing toluene from SMILES:

```
>>> molecule = Molecule.from_smiles('Cc1ccccc1')
```

Create a Molecule representing phenol from SMILES with the oxygen at atom index 0 (SMILES indices begin at 1):

```
>>> molecule = Molecule.from_smiles('c1ccccc1[OH:1]')
>>> molecule = molecule.remap(
...     {k: v - 1 for k, v in molecule.properties["atom_map"].items()},
...     partial=True,
... )
>>> assert molecule.atom(0).symbol == "O"
```

**See also:**

`from_mapped_smiles`, `remap`

**classmethod** `from_toml(serialized)`

Instantiate an object from a TOML serialized representation.

Specification: <https://github.com/toml-lang/toml>

**Parameters** `serialized (str)` – A TOML serialized representation of the object

**Returns** `instance (cls)` – An instantiated object

**classmethod** `from_topology(topology)`

Return a Molecule representation of an OpenFF Topology containing a single Molecule object.

**Parameters** `topology (Topology)` – The `Topology` object containing a single `Molecule` object. Note that OpenMM and MDTraj Topology objects are not supported.

**Returns** `molecule (openff.toolkit.topology.Molecule)` – The Molecule object in the topology

**Raises** `ValueError` – If the topology does not contain exactly one molecule.

## Examples

Create a molecule from a Topology object that contains exactly one molecule

```
>>> from openff.toolkit import Molecule, Topology
>>> topology = Topology.from_molecules(Molecule.from_smiles('[CH4]'))
>>> molecule = Molecule.from_topology(topology)
```

**classmethod** `from_xml(serialized)`

Instantiate an object from an XML serialized representation.

Specification: <https://www.w3.org/XML/>

**Parameters** `serialized (bytes)` – An XML serialized representation

**Returns** `instance (cls)` – Instantiated object.

**classmethod** `from_yaml(serialized)`

Instantiate from a YAML serialized representation.

Specification: <http://yaml.org/>

**Parameters** `serialized (str)` – A YAML serialized representation of the object

**Returns** `instance (cls)` – Instantiated object

**generate\_conformers**(`toolkit_registry: Union[ToolkitRegistry, ToolkitWrapper] = GLOBAL_TOOLKIT_REGISTRY`, `n_conformers: int = 10`, `rms_cutoff: Optional[Quantity] = None`, `clear_existing: bool = True`, `make_carboxylic_acids_cis: bool = True`)

Generate conformers for this molecule using an underlying toolkit.

If `n_conformers=0`, no toolkit wrapper will be called. If `n_conformers=0` and `clear_existing=True`, `molecule.conformers` will be set to `None`.

**Parameters**

- **toolkit\_registry** (`openff.toolkit.utils.toolkits.ToolkitRegistry` or) – `openff.toolkit.utils.toolkits.ToolkitWrapper`, optional, default=`None` `ToolkitRegistry` or `ToolkitWrapper` to use for SMILES-to-molecule conversion
- **n\_conformers** (`int`, default=1) – The maximum number of conformers to produce
- **rms\_cutoff** (`openff.unit.Quantity`-wrapped float, in units of distance, optional, default=`None`) – The minimum RMS value at which two conformers are considered redundant and one is deleted. Precise implementation of this cutoff may be toolkit-dependent. If `None`, the cutoff is set to be the default value for each `ToolkitWrapper` (generally 1 Angstrom).
- **clear\_existing** (`bool`, default=`True`) – Whether to overwrite existing conformers for the molecule
- **make\_carboxylic\_acids\_cis** (`bool`, default=`True`) – Guarantee all conformers have exclusively cis carboxylic acid groups (COOH) by rotating the proton in any trans carboxylic acids 180 degrees around the C-O bond. Works around a bug in conformer generation by the OpenEye toolkit where trans COOH is much more common than it should be.

## Examples

```
>>> molecule = Molecule.from_smiles('CCCCC')
>>> molecule.generate_conformers()
```

Raises `InvalidToolkitRegistryError` – If an invalid object is passed as the `toolkit_registry` parameter

### `generate_unique_atom_names()`

Generate unique atom names from the element symbol and count.

Names are generated from the elemental symbol and the number of times that element is found in the molecule. The character 'x' is appended to these generated names to reduce the odds that they clash with an atom name or type imported from another source. For example, generated atom names might begin 'C1x', 'H1x', 'O1x', 'C2x', etc.

`get_bond_between(i: Union[int, Atom], j: Union[int, Atom]) → Bond`

Returns the bond between two atoms

#### Parameters

- `i` (`int` or `Atom`) – Atoms or atom indices to check
- `j` (`int` or `Atom`) – Atoms or atom indices to check

Returns `bond` (`Bond`) – The bond between `i` and `j`.

property `has_unique_atom_names`: `bool`

True if the molecule has unique atom names, False otherwise.

property `hierarchy_schemes`: `Dict[str, HierarchyScheme]`

The hierarchy schemes available on the molecule.

Hierarchy schemes allow iteration over groups of atoms according to their metadata. For more information, see `HierarchyScheme`.

Returns A dict of the form `{str (HierarchyScheme)}` – The `HierarchySchemes` associated with the molecule.

#### See also:

`Molecule.add_hierarchy_scheme`, `Molecule.delete_hierarchy_scheme`, `Molecule.update_hierarchy_schemes`, `Topology.hierarchy_iterator`, `HierarchyScheme`

property `hill_formula`: `str`

Get the Hill formula of the molecule

property `impropers`: `Set[Tuple[Atom, Atom, Atom, Atom]]`

Iterate over all improper torsions in the molecule.

Returns `impropers` (*set of tuple*) – An iterator of tuples, each containing the atoms making up a possible improper torsion.

#### See also:

`smirnoff_impropers`, `amber_impropers`

**is\_isomorphic\_with**(*other*: *Union*[*FrozenMolecule*, *Graph*], *\*\*kwargs*)

Check if the molecule is isomorphic with the other molecule which can be an `openff.toolkit.topology.Molecule` or `nx.Graph()`. Full matching is done using the options described below.

**Warning:** This API is experimental and subject to change.

#### Parameters

- **other** (*Molecule* or `nx.Graph()`) –
- **aromatic\_matching** (*bool*, default=True, optional) –
- **atoms.** (compare the formal charges attributes of the) –
- **formal\_charge\_matching** (*bool*, default=True, optional) –
- **atoms.** –
- **bond\_order\_matching** (*bool*, default=True, optional) –
- **bonds.** (compare the bond order on attributes of the) –
- **atom\_stereochemistry\_matching** (*bool*, default=True, optional) – If False, atoms' stereochemistry is ignored for the purpose of determining equality.
- **bond\_stereochemistry\_matching** (*bool*, default=True, optional) – If False, bonds' stereochemistry is ignored for the purpose of determining equality.
- **strip\_pyrimidal\_n\_atom\_stereo** (*bool*, default=True, optional) – If True, any stereochemistry defined around pyrimidal nitrogen stereocenters will be disregarded in the isomorphism check.
- **toolkit\_registry** (*ToolkitRegistry*) – or `openff.toolkit.utils.toolkits.ToolkitWrapper`, optional, default=None *ToolkitRegistry* or *ToolkitWrapper* to use for removing stereochemistry from pyrimidal nitrogens.

Returns **isomorphic** (*bool*)

property **n\_angles**: *int*

Number of angles in the molecule.

property **n\_atoms**: *int*

The number of Atom objects.

property **n\_bonds**: *int*

The number of Bond objects in the molecule.

property **n\_conformers**: *int*

The number of conformers for this molecule.

property **n\_impropers**: *int*

Number of possible improper torsions in the molecule.

property **n\_particles**: *int*

Deprecated since version 0.11.0: This property has been deprecated and will soon be removed. Use `Molecule.n_atoms()` instead.

**property** `n_propers`: `int`

Number of proper torsions in the molecule.

**property** `name`: `str`

The name (or title) of the molecule

**nth\_degree\_neighbors**(`n_degrees`)

Return canonicalized pairs of atoms whose shortest separation is *exactly* `n` bonds. Only pairs with increasing atom indices are returned.

**Parameters** `n` (`int`) – The number of bonds separating atoms in each pair

**Returns** `neighbors` (*iterator of tuple of Atom*) – Tuples (len 2) of atom that are separated by `n` bonds.

## Notes

The criteria used here relies on minimum distances; when there are multiple valid paths between atoms, such as atoms in rings, the shortest path is considered. For example, two atoms in “meta” positions with respect to each other in a benzene are separated by two paths, one length 2 bonds and the other length 4 bonds. This function would consider them to be 2 apart and would not include them if `n=4` was passed.

**ordered\_connection\_table\_hash**()

Compute an ordered hash of the atoms and bonds in the molecule

**property** `partial_charges`

Returns the partial charges (if present) on the molecule.

**Returns** `partial_charges` (*a openff.unit.Quantity - wrapped numpy array [1 x n\_atoms] or None*) – The partial charges on the molecule’s atoms. Returns None if no charges have been specified.

**particle**(`index`: `int`) → `Atom`

Deprecated since version 0.11.0: This method has been deprecated and will soon be removed. Use `Molecule.atom()` instead.

**particle\_index**(`particle`: `Atom`) → `int`

Deprecated since version 0.11.0: This method has been deprecated and will soon be removed. Use `Molecule.atom_index()` instead.

**property** `particles`: `List[Atom]`

Deprecated since version 0.11.0: This property has been deprecated and will soon be removed. Use `Molecule.atoms()` instead.

**property** `probers`: `Set[Tuple[Atom, Atom, Atom, Atom]]`

Iterate over all proper torsions in the molecule

**property** `properties`: `Dict[str, Any]`

The properties dictionary of the molecule

**remap**(`mapping_dict`: `Dict[int, int]`, `current_to_new`: `bool` = `True`, `partial`: `bool` = `False`)

Reorder the atoms in the molecule according to the given mapping dict.

The mapping dict must be a dictionary mapping atom indices to atom indices. Each atom index must be an integer in the half-open interval `[0, n_atoms)`; ie, it must be a valid index into the `self.atoms` list. All atom indices in the molecule must be mapped from and to exactly once unless `partial=True` is given, in which case they must be mapped no more than once. Missing (unless

partial=True), out-of-range (including non-integer), or duplicate indices are not allowed in the mapping\_dict and will lead to an exception.

By default, the mapping dict's keys are the source indices and its values are destination indices, but this can be changed with the current\_to\_new argument.

The keys of the self.properties["atom\_map"] property are updated for the new ordering. Other values of the properties dictionary are transferred unchanged.

**Warning:** This API is experimental and subject to change.

#### Parameters

- **mapping\_dict** – A dictionary of the mapping between indices. The mapping should be indexed starting from 0 for both the source and destination; note that SMILES atom mapping is typically 1-based.
- **current\_to\_new** – If this is True, then mapping\_dict is of the form {current\_index: new\_index}; otherwise, it is of the form {new\_index: current\_index}.
- **partial** – If False (the default), an exception will be raised if any atom is lacking a destination in the atom map. Note that if this is True, atoms without entries in the mapping dict may be moved in addition to those in the dictionary. Note that partial maps must still be in-range and not include duplicates.

**Returns new\_molecule** (*openff.toolkit.topology.molecule.Molecule*) – A copy of the molecule in the new order.

**Raises RemapIndexError** – When an out-of-range, duplicate, or missing index is found in the mapping\_dict.

See also:

[from\\_mapped\\_smiles](#)

**property smirnoff\_impropers:** `Set[Tuple[Atom, Atom, Atom, Atom]]`

Iterate over all impropers with trivalent centers, reporting the central atom second.

The central atom is reported second in each torsion. This method reports an improper for each trivalent atom in the molecule, whether or not any given force field would assign it improper torsion parameters.

Also note that this will return 6 possible atom orderings around each improper center. In current SMIRNOFF parameterization, three of these six orderings will be used for the actual assignment of the improper term and measurement of the angles. These three orderings capture the three unique angles that could be calculated around the improper center, therefore the sum of these three terms will always return a consistent energy.

The exact three orderings that will be applied during parameterization can not be determined in this method, since it requires sorting the atom indices, and those indices may change when this molecule is added to a Topology.

For more details on the use of three-fold ('trefoil') impropers, see <https://openforcefield.github.io/standards/standards/smirnoff/#improPERTORSIONS>

**Returns impropers** (*set of tuple*) – An iterator of tuples, each containing the indices of atoms making up a possible improper torsion. The central atom is listed second in each tuple.



See also:

`impropers`, `amber_impropers`

**strip\_atom\_stereochemistry**(*smarts*: *str*, *toolkit\_registry*: *Union*[*ToolkitRegistry*, *ToolkitWrapper*] = *GLOBAL\_TOOLKIT\_REGISTRY*)

Delete stereochemistry information for certain atoms, if it is present. This method can be used to “normalize” molecules imported from different cheminformatics toolkits, which differ in which atom centers are considered stereogenic.

#### Parameters

- **smarts** (*str*) – Tagged SMARTS with a single atom with index 1. Any matches for this atom will have any assigned stereochemistry information removed.
- **toolkit\_registry** (a *ToolkitRegistry* or *ToolkitWrapper* object, optional,) – default=*GLOBAL\_TOOLKIT\_REGISTRY* *ToolkitRegistry* or *ToolkitWrapper* to use for I/O operations

**to\_bson()**

Return a BSON serialized representation.

Specification: <http://bsonspec.org/>

**Returns** *serialized* (*bytes*) – A BSON serialized representation of the object

**to\_dict()** → *dict*

Return a dictionary representation of the molecule.

**Returns** *molecule\_dict* (*dict*) – A dictionary representation of the molecule.

**to\_file**(*file\_path*, *file\_format*, *toolkit\_registry*=*GLOBAL\_TOOLKIT\_REGISTRY*)

Write the current molecule to a file or file-like object

#### Parameters

- **file\_path** (*str* or file-like object) – A file-like object or the path to the file to be written.
- **file\_format** (*str*) – Format specifier, one of ['MOL2', 'MOL2H', 'SDF', 'PDB', 'SMI', 'CAN', 'TDT'] Note that not all toolkits support all formats
- **toolkit\_registry** (*ToolkitRegistry*) – or `openff.toolkit.utils.toolkits.ToolkitWrapper`, optional, default=*GLOBAL\_TOOLKIT\_REGISTRY* *ToolkitRegistry* or *ToolkitWrapper* to use for file writing. If a *Toolkit* is passed, only the highest-precedence toolkit is used

**Raises** *ValueError* – If the requested *file\_format* is not supported by one of the installed cheminformatics toolkits

#### Examples

```
>>> molecule = Molecule.from_iupac('imatinib')
>>> molecule.to_file('imatinib.mol2', file_format='mol2')
>>> molecule.to_file('imatinib.sdf', file_format='sdf')
>>> molecule.to_file('imatinib.pdb', file_format='pdb')
```

**to\_hill\_formula()** → *str*

Generate the Hill formula of this molecule.

**Returns formula** (*the Hill formula of the molecule*)

:raises `NotImplementedError` : if the molecule is not of one of the specified types.:

**to\_inchi**(*fixed\_hydrogens*: `bool` = `False`, *toolkit\_registry*: `Union[ToolkitRegistry, ToolkitWrapper]` = `GLOBAL_TOOLKIT_REGISTRY`) → `str`

Create an InChI string for the molecule using the requested toolkit backend. InChI is a standardised representation that does not capture tautomers unless specified using the fixed hydrogen layer.

For information on InChi see here <https://iupac.org/who-we-are/divisions/division-details/inchi/>

#### Parameters

- **fixed\_hydrogens** (`bool`, default=`False`) – If a fixed hydrogen layer should be added to the InChI, if `True` this will produce a non standard specific InChI string of the molecule.
- **toolkit\_registry** (`openff.toolkit.utils.toolkits.ToolkitRegistry`) – or `openff.toolkit.utils.toolkits.ToolkitWrapper`, optional, default=`None` `ToolkitRegistry` or `ToolkitWrapper` to use for molecule-to-InChI conversion

**Returns inchi** (`str`) – The InChI string of the molecule.

**Raises `InvalidToolkitRegistryError`** – If an invalid object is passed as the `toolkit_registry` parameter

**to\_inchikey**(*fixed\_hydrogens*: `bool` = `False`, *toolkit\_registry*: `Union[ToolkitRegistry, ToolkitWrapper]` = `GLOBAL_TOOLKIT_REGISTRY`)

Create an InChIKey for the molecule using the requested toolkit backend. InChIKey is a standardised representation that does not capture tautomers unless specified using the fixed hydrogen layer.

For information on InChi see here <https://iupac.org/who-we-are/divisions/division-details/inchi/>

#### Parameters

- **fixed\_hydrogens** (`bool`, default=`False`) – If a fixed hydrogen layer should be added to the InChI, if `True` this will produce a non standard specific InChI string of the molecule.
- **toolkit\_registry** (`openff.toolkit.utils.toolkits.ToolkitRegistry`) – or `openff.toolkit.utils.toolkits.ToolkitWrapper`, optional, default=`None` `ToolkitRegistry` or `ToolkitWrapper` to use for molecule-to-InChIKey conversion

**Returns inchi\_key** (`str`) – The InChIKey representation of the molecule.

**Raises `InvalidToolkitRegistryError`** – If an invalid object is passed as the `toolkit_registry` parameter

**to\_iupac**(*toolkit\_registry*=`GLOBAL_TOOLKIT_REGISTRY`)

Generate IUPAC name from Molecule

#### Returns

- **iupac\_name** (`str`) – IUPAC name of the molecule
- .. note :: This method requires the `OpenEye` toolkit to be installed.

## Examples

```
>>> from openff.toolkit.utils import get_data_file_path
>>> sdf_filepath = get_data_file_path('molecules/ethanol.sdf')
>>> molecule = Molecule(sdf_filepath)
>>> iupac_name = molecule.to_iupac()
```

**to\_json**(*indent=None*) → *str*

Return a JSON serialized representation.

Specification: <https://www.json.org/>

**Parameters** *indent* (*int*, optional, default=None) – If not None, will pretty-print with specified number of spaces for indentation

**Returns** *serialized* (*str*) – A JSON serialized representation of the object

**to\_messagepack**()

Return a MessagePack representation.

Specification: <https://msgpack.org/index.html>

**Returns** *serialized* (*bytes*) – A MessagePack-encoded bytes serialized representation of the object

**to\_networkx**()

Generate a NetworkX undirected graph from the molecule.

Nodes are Atoms labeled with atom indices and atomic elements (via the element node attribute).

Edges denote chemical bonds between Atoms.

**Returns** *graph* (*networkx.Graph*) – The resulting graph, with nodes (atoms) labeled with atom indices, elements, stereochemistry and aromaticity flags and bonds with two atom indices, bond order, stereochemistry, and aromaticity flags

## Examples

Retrieve the bond graph for imatinib (OpenEye toolkit required)

```
>>> molecule = Molecule.from_iupac('imatinib')
>>> nxgraph = molecule.to_networkx()
```

**to\_openeye**(*toolkit\_registry=GLOBAL\_TOOLKIT\_REGISTRY*,  
*aromaticity\_model=DEFAULT\_AROMATICITY\_MODEL*)

Create an OpenEye molecule

Requires the OpenEye toolkit to be installed.

**Parameters** *aromaticity\_model* (*str*, optional, default="OEAroModel\_MDL") – The aromaticity model to use. Only OEAroModel\_MDL is supported.

**Returns** *oemol* (*openeye.ochem.OEMol*) – An OpenEye molecule

## Examples

Create an OpenEye molecule from a Molecule

```
>>> molecule = Molecule.from_smiles('CC')
>>> oemol = molecule.to_openeye()
```

### to\_pickle()

Return a pickle serialized representation.

**Warning:** This is not recommended for safe, stable storage since the pickle specification may change between Python versions.

**Returns** `serialized (str)` – A pickled representation of the object

### to\_qcschema(*multiplicity=1, conformer=0, extras=None*)

Create a QCElemental Molecule.

**Warning:** This API is experimental and subject to change.

### Parameters

- **multiplicity** (`int`, `default=1`,) – The multiplicity of the molecule; sets `molecular_multiplicity` field for QCElemental Molecule.
- **conformer** (`int`, `default=0`,) – The index of the conformer to use for the QCElemental Molecule geometry.
- **extras** (`dict`, `default=None`) – A dictionary that should be included in the `extras` field on the QCElemental Molecule. This can be used to include extra information, such as a smiles representation.

**Returns** `qcelemental.models.Molecule` – A validated QCElemental Molecule.

## Examples

Create a QCElemental Molecule:

```
>>> import qcelemental as qcel
>>> mol = Molecule.from_smiles('CC')
>>> mol.generate_conformers(n_conformers=1)
>>> qcemol = mol.to_qcschema()
```

### Raises

- **MissingOptionalDependencyError** – If qcelemental is not installed, the qcschema can not be validated.
- **InvalidConformerError** – No conformer found at the given index.

```
to_rdkit(aromaticity_model=DEFAULT_AROMATICITY_MODEL,
          toolkit_registry=GLOBAL_TOOLKIT_REGISTRY)
```

Create an RDKit molecule

Requires the RDKit to be installed.

**Parameters** **aromaticity\_model** (*str*, optional, default="OEAroModel\_MDL") – The aromaticity model to use. Only OEAroModel\_MDL is supported.

**Returns** **rdmol** (*rdkit.RDMol*) – An RDKit molecule

## Examples

Convert a molecule to RDKit

```
>>> from openff.toolkit.utils import get_data_file_path
>>> sdf_filepath = get_data_file_path('molecules/ethanol.sdf')
>>> molecule = Molecule(sdf_filepath)
>>> rdmol = molecule.to_rdkit()
```

```
to_smiles(isomeric: bool = True, explicit_hydrogens: bool = True, mapped: bool = False,
           toolkit_registry: Union[ToolkitRegistry, ToolkitWrapper] = GLOBAL_TOOLKIT_REGISTRY)
```

Return a canonical isomeric SMILES representation of the current molecule. A partially mapped smiles can also be generated for atoms of interest by supplying an *atom\_map* to the properties dictionary.

---

**Note:** RDKit and OpenEye versions will not necessarily return the same representation.

---

## Parameters

- **isomeric** (*bool* optional, default= True) – return an isomeric smiles
- **explicit\_hydrogens** (*bool* optional, default=True) – return a smiles string containing all hydrogens explicitly
- **mapped** (*bool* optional, default=False) – return a explicit hydrogen mapped smiles, the atoms to be mapped can be controlled by supplying an atom map into the properties dictionary. If no mapping is passed all atoms will be mapped in order, else an atom map dictionary from the current atom index to the map id should be supplied with no duplicates. The map ids (values) should start from 0 or 1.
- **toolkit\_registry** (*openff.toolkit.utils.toolkits.ToolkitRegistry* or *openff.toolkit.utils.toolkits.ToolkitWrapper*, optional, default=None) – ToolkitRegistry or ToolkitWrapper to use for SMILES conversion

**Returns** **smiles** (*str*) – Canonical isomeric explicit-hydrogen SMILES

## Examples

```
>>> from openff.toolkit.utils import get_data_file_path
>>> sdf_filepath = get_data_file_path('molecules/ethanol.sdf')
>>> molecule = Molecule(sdf_filepath)
>>> smiles = molecule.to_smiles()
```

### `to_toml()`

Return a TOML serialized representation.

Specification: <https://github.com/toml-lang/toml>

**Returns** `serialized` (*str*) – A TOML serialized representation of the object

### `to_topology()`

Return an OpenFF Topology representation containing one copy of this molecule

**Returns** `topology` (*openff.toolkit.topology.Topology*) – A Topology representation of this molecule

## Examples

```
>>> from openff.toolkit import Molecule
>>> molecule = Molecule.from_iupac('imatinib')
>>> topology = molecule.to_topology()
```

### `to_xml(indent=2)`

Return an XML representation.

Specification: <https://www.w3.org/XML/>

**Parameters** `indent` (*int*, optional, default=2) – If not None, will pretty-print with specified number of spaces for indentation

**Returns** `serialized` (*bytes*) – A MessagePack-encoded bytes serialized representation.

### `to_yaml()`

Return a YAML serialized representation.

Specification: <http://yaml.org/>

**Returns** `serialized` (*str*) – A YAML serialized representation of the object

### `property torsions: Set[Tuple[Atom, Atom, Atom, Atom]]`

Get an iterator over all i-j-k-l torsions. Note that i-j-k-i torsions (cycles) are excluded.

**Returns** `torsions` (*iterable of 4-Atom tuples*)

### `property total_charge`

Return the total charge on the molecule

### `update_hierarchy_schemes(iter_names=None)`

Infer a hierarchy from atom metadata according to the existing hierarchy schemes.

Hierarchy schemes allow iteration over groups of atoms according to their metadata. For more information, see [HierarchyScheme](#).

Parameters **iter\_names** (Iterable of str, Optional) – Only perceive hierarchy for HierarchySchemes that expose these iterator names. If not provided, all known hierarchies will be perceived, overwriting previous results if applicable.

See also:

`Molecule.add_hierarchy_scheme`, `Molecule.delete_hierarchy_schemes`, `Molecule.hierarchy_schemes`, `HierarchyScheme`

### 11.1.3 Topology

**class** `openff.toolkit.topology.Topology`(*other=None*)

A Topology is a chemical representation of a system containing one or more molecules appearing in a specified order.

**Warning:** This API is experimental and subject to change.

#### Examples

Import some utilities

```
>>> from openmm import app
>>> from openff.toolkit.tests.utils import get_data_file_path, get_packmol_pdb_file_path
>>> pdb_filepath = get_packmol_pdb_file_path('cyclohexane_ethanol_0.4_0.6')
>>> monomer_names = ('cyclohexane', 'ethanol')
```

Create a Topology object from a PDB file and sdf files defining the molecular contents

```
>>> from openff.toolkit import Molecule, Topology
>>> pdbfile = app.PDBFile(pdb_filepath)
>>> sdf_filepaths = [get_data_file_path(f'systems/monomers/{name}.sdf') for name in
↳ monomer_names]
>>> unique_molecules = [Molecule.from_file(sdf_filepath) for sdf_filepath in sdf_
↳ filepaths]
>>> topology = Topology.from_openmm(pdbfile.topology, unique_molecules=unique_molecules)
```

Create a Topology object from a PDB file and IUPAC names of the molecular contents

```
>>> pdbfile = app.PDBFile(pdb_filepath)
>>> unique_molecules = [Molecule.from_iupac(name) for name in monomer_names]
>>> topology = Topology.from_openmm(pdbfile.topology, unique_molecules=unique_molecules)
```

Create an empty Topology object and add a few copies of a single benzene molecule

```
>>> topology = Topology()
>>> molecule = Molecule.from_iupac('benzene')
>>> molecule_topology_indices = [topology.add_molecule(molecule) for index in range(10)]
```

**\_\_init\_\_**(*other=None*)

Create a new Topology.

**Parameters** **other** (optional, default=None) – If specified, attempt to construct a copy of the Topology from the specified object. This might be a Topology object, or a file that can be used to construct a Topology object or serialized Topology object.

## Methods

<code>__init__([other])</code>	Create a new Topology.
<code>add_constraint(iatom, jatom[, distance])</code>	Mark a pair of atoms as constrained.
<code>add_molecule(molecule)</code>	Add a copy of the molecule to the topology
<code>assert_bonded(atom1, atom2)</code>	Raise an exception if the specified atoms are not bonded in the topology.
<code>atom(atom_topology_index)</code>	Get the TopologyAtom at a given Topology atom index.
<code>atom_index(atom)</code>	Returns the index of a given atom in this topology
<code>bond(bond_topology_index)</code>	Get the TopologyBond at a given Topology bond index.
<code>chemical_environment_matches(query[, ...])</code>	Retrieve all matches for a given chemical environment query.
<code>copy_initializer(other)</code>	
<code>from_bson(serialized)</code>	Instantiate an object from a BSON serialized representation.
<code>from_dict(topology_dict)</code>	Create a new Topology from a dictionary representation
<code>from_json(serialized)</code>	Instantiate an object from a JSON serialized representation.
<code>from_mdtraj(mdtraj_topology[, ...])</code>	Construct an OpenFF Topology from an MDTraj Topology
<code>from_messagepack(serialized)</code>	Instantiate an object from a MessagePack serialized representation.
<code>from_molecules(molecules)</code>	Create a new Topology object containing one copy of each of the specified molecule(s).
<code>from_openmm(openmm_topology[, ...])</code>	Construct an OpenFF Topology object from an OpenMM Topology object.
<code>from_pickle(serialized)</code>	Instantiate an object from a pickle serialized representation.
<code>from_toml(serialized)</code>	Instantiate an object from a TOML serialized representation.
<code>from_xml(serialized)</code>	Instantiate an object from an XML serialized representation.
<code>from_yaml(serialized)</code>	Instantiate from a YAML serialized representation.
<code>get_bond_between(i, j)</code>	Returns the bond between two atoms
<code>get_positions()</code>	Copy the positions of the topology into a new array.
<code>hierarchy_iterator(iter_name)</code>	Iterate over all molecules with the given hierarchy scheme.
<code>is_bonded(i, j)</code>	Returns True if the two atoms are bonded
<code>is_constrained(iatom, jatom)</code>	Check if a pair of atoms are marked as constrained.

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Table 3 – continued from previous page

<code>molecule(index)</code>	Returns the molecule with a given index in this Topology.
<code>molecule_atom_start_index(molecule)</code>	Returns the index of a molecule's first atom in this topology
<code>molecule_index(molecule)</code>	Returns the index of a given molecule in this topology
<code>nth_degree_neighbors(n_degrees)</code>	Return canonicalized pairs of atoms whose shortest separation is <i>exactly</i> <i>n</i> bonds.
<code>particle_index(particle)</code>	Deprecated since version 0.11.0.
<code>set_positions(array)</code>	Set the positions in a topology by copying from a single $n \times 3$ array.
<code>to_bson()</code>	Return a BSON serialized representation.
<code>to_dict()</code>	
<code>to_file(file[, positions, file_format, ...])</code>	Save coordinates and topology to a PDB file.
<code>to_json([indent])</code>	Return a JSON serialized representation.
<code>to_messagepack()</code>	Return a MessagePack representation.
<code>to_openmm([ensure_unique_atom_names])</code>	Create an OpenMM Topology object.
<code>to_pickle()</code>	Return a pickle serialized representation.
<code>to_toml()</code>	Return a TOML serialized representation.
<code>to_xml([indent])</code>	Return an XML representation.
<code>to_yaml()</code>	Return a YAML serialized representation.

### Attributes

<code>amber_impropers</code>	Iterate over improper torsions in the molecule, but only those with trivalent centers, reporting the central atom first in each improper.
<code>angles</code>	iterator over the angles in this Topology.
<code>aromaticity_model</code>	Get the aromaticity model applied to all molecules in the topology.
<code>atoms</code>	Returns an iterator over the atoms in this Topology.
<code>bonds</code>	Returns an iterator over the bonds in this Topology
<code>box_vectors</code>	Return the box vectors of the topology, if specified
<code>constrained_atom_pairs</code>	Returns the constrained atom pairs of the Topology
<code>identical_molecule_groups</code>	Returns groups of chemically identical molecules, identified by index and atom map.
<code>impropers</code>	iterator over the possible improper torsions in this Topology.
<code>is_periodic</code>	Return whether or not this Topology is intended to be described with periodic boundary conditions.

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Table 4 – continued from previous page

<code>molecules</code>	Returns an iterator over all the Molecules in this Topology
<code>n_angles</code>	number of angles in this Topology.
<code>n_atoms</code>	Returns the number of atoms in in this Topology.
<code>n_bonds</code>	Returns the number of Bonds in in this Topology.
<code>n_impropers</code>	number of possible improper torsions in this Topology.
<code>n_molecules</code>	Returns the number of molecules in this Topology
<code>n_particles</code>	Deprecated since version 0.11.0.
<code>n_propers</code>	number of proper torsions in this Topology.
<code>n_reference_molecules</code>	Deprecated since version 0.11.0.
<code>n_topology_atoms</code>	Deprecated since version 0.11.0.
<code>n_topology_bonds</code>	Deprecated since version 0.11.0.
<code>n_topology_molecules</code>	Deprecated since version 0.11.0.
<code>n_topology_particles</code>	Deprecated since version 0.11.0.
<code>n_unique_molecules</code>	Returns the number of unique molecules in this Topology
<code>particles</code>	Deprecated since version 0.11.0.
<code>propers</code>	iterator over the proper torsions in this Topology.
<code>reference_molecules</code>	Deprecated since version 0.11.0.
<code>smirnoff_impropers</code>	Iterate over improper torsions in the molecule, but only those with trivalent centers, reporting the central atom second in each improper.
<code>topology_atoms</code>	Deprecated since version 0.11.0.
<code>topology_bonds</code>	Deprecated since version 0.11.0.
<code>topology_molecules</code>	Deprecated since version 0.11.0.

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Table 4 – continued from previous page

<code>topology_particles</code>	Deprecated since version 0.11.0.
<code>unique_molecules</code>	Get a list of chemically unique molecules in this Topology.
<p><b>property <code>unique_molecules</code>: <code>Iterator[Molecule]</code></b>          Get a list of chemically unique molecules in this Topology.</p> <p>Molecules are considered unique if they fail an isomorphism check with default values (see <code>Molecule.is_isomorphic_with()</code>). The order of molecules returned by this property is arbitrary.</p>	
<p><b>property <code>n_unique_molecules</code>: <code>int</code></b>          Returns the number of unique molecules in this Topology</p>	
<p><b>classmethod <code>from_molecules(molecules: Union[Molecule, List[Molecule]]) → Topology</code></b>          Create a new Topology object containing one copy of each of the specified molecule(s).</p> <p><b>Parameters</b> <code>molecules</code> (<code>Molecule</code> or iterable of <code>Molecules</code>) – One or more molecules to be added to the Topology</p> <p><b>Returns</b> <code>topology</code> (<code>Topology</code>) – The Topology created from the specified molecule(s)</p>	
<p><b>assert_bonded(atom1: Union[int, Atom], atom2: Union[int, Atom])</b>          Raise an exception if the specified atoms are not bonded in the topology.</p> <p><b>Parameters</b></p> <ul style="list-style-type: none"> <li>• <code>atom1</code> (<code>Atom</code> or <code>int</code>) – The atoms or atom topology indices to check to ensure they are bonded</li> <li>• <code>atom2</code> (<code>Atom</code> or <code>int</code>) – The atoms or atom topology indices to check to ensure they are bonded</li> </ul>	
<p><b>property <code>aromaticity_model</code>: <code>str</code></b>          Get the aromaticity model applied to all molecules in the topology.</p> <p><b>Returns</b> <code>aromaticity_model</code> (<code>str</code>) – Aromaticity model in use.</p>	
<p><b>property <code>box_vectors</code></b>          Return the box vectors of the topology, if specified</p> <p><b>Returns</b> <code>box_vectors</code> (<i>unit-wrapped numpy array of shape (3, 3)</i>) – The unit-wrapped box vectors of this topology</p>	
<p><b>property <code>is_periodic</code></b>          Return whether or not this Topology is intended to be described with periodic boundary conditions.</p>	
<p><b>property <code>constrained_atom_pairs</code>: <code>Dict[Tuple[int], Union[Quantity, bool]]</code></b>          Returns the constrained atom pairs of the Topology</p> <p><b>Returns</b> <code>constrained_atom_pairs</code> (<i>dict of <code>Tuple[int]: Union[unit.Quantity, bool]</code></i>) – dictionary of the form {(atom1_topology_index, atom2_topology_index): distance}</p>	
<p><b>property <code>n_molecules</code>: <code>int</code></b>          Returns the number of molecules in this Topology</p>	

**property** `molecules`: `Generator[Union[Molecule, openff.toolkit.topology._mm_molecule._SimpleMolecule], None, None]`

Returns an iterator over all the Molecules in this Topology

Returns `molecules` (*Iterable of Molecule*)

**molecule**(`index`)

Returns the molecule with a given index in this Topology.

Returns `molecule` (`openff.toolkit.topology.Molecule`)

**property** `n_atoms`: `int`

Returns the number of atoms in in this Topology.

Returns `n_atoms` (*int*)

**property** `atoms`: `Generator[Atom, None, None]`

Returns an iterator over the atoms in this Topology. These will be in ascending order of topology index.

Returns `atoms` (*Generator of TopologyAtom*)

**atom\_index**(`atom`: `Atom`) → `int`

Returns the index of a given atom in this topology

Parameters `atom` (`Atom`) –

Returns `index` (*int*) – The index of the given atom in this topology

Raises `AtomNotInTopologyError` – If the given atom is not in this topology

**molecule\_index**(`molecule`: `Molecule`) → `int`

Returns the index of a given molecule in this topology

Parameters `molecule` (`FrozenMolecule`) –

Returns `index` (*int*) – The index of the given molecule in this topology

Raises `MoleculeNotInTopologyError` – If the given atom is not in this topology

**molecule\_atom\_start\_index**(`molecule`: `Molecule`) → `int`

Returns the index of a molecule's first atom in this topology

Parameters `molecule` (`FrozenMolecule`) –

Returns `index` (*int*)

**property** `n_bonds`: `int`

Returns the number of Bonds in in this Topology.

Returns `n_bonds` (*int*)

**property** `bonds`: `Generator[Bond, None, None]`

Returns an iterator over the bonds in this Topology

Returns `bonds` (*Iterable of Bond*)

**property** `n_angles`: `int`

number of angles in this Topology.

Type *int*

**property angles:** `Generator[Tuple[Atom, ...], None, None]`

iterator over the angles in this Topology.

**Type** Iterable of `Tuple[Atom]`

**property n\_propers:** `int`

number of proper torsions in this Topology.

**Type** `int`

**property propers:** `Generator[Tuple[Atom, ...], None, None]`

iterator over the proper torsions in this Topology.

**Type** Iterable of `Tuple[TopologyAtom]`

**property n\_impropers:** `int`

number of possible improper torsions in this Topology.

**Type** `int`

**property impropers:** `Generator[Tuple[Atom, ...], None, None]`

iterator over the possible improper torsions in this Topology.

**Type** Iterable of `Tuple[TopologyAtom]`

**property smirnoff\_impropers:** `Generator[Tuple[Atom, ...], None, None]`

Iterate over improper torsions in the molecule, but only those with trivalent centers, reporting the central atom second in each improper.

Note that it's possible that a trivalent center will not have an improper assigned. This will depend on the force field that is used.

Also note that this will return 6 possible atom orderings around each improper center. In current SMIRNOFF parameterization, three of these six orderings will be used for the actual assignment of the improper term and measurement of the angles. These three orderings capture the three unique angles that could be calculated around the improper center, therefore the sum of these three terms will always return a consistent energy.

For more details on the use of three-fold ('trefoil') impropers, see <https://openforcefield.github.io/standards/standards/smirnoff/#impropertorsions>

**Returns impropers** (*set of tuple*) – An iterator of tuples, each containing the indices of atoms making up a possible improper torsion. The central atom is listed second in each tuple.

**See also:**

`impropers`, `amber_impropers`

**property amber\_impropers:** `Generator[Tuple[Atom, ...], None, None]`

Iterate over improper torsions in the molecule, but only those with trivalent centers, reporting the central atom first in each improper.

Note that it's possible that a trivalent center will not have an improper assigned. This will depend on the force field that is used.

Also note that this will return 6 possible atom orderings around each improper center. In current AMBER parameterization, one of these six orderings will be used for the actual assignment of the improper term and measurement of the angle. This method does not encode the logic to determine which of the six orderings AMBER would use.

**Returns** **impropers** (*set of tuple*) – An iterator of tuples, each containing the indices of atoms making up a possible improper torsion. The central atom is listed first in each tuple.

**See also:**

`impropers`, `smirnoff_impropers`

**nth\_degree\_neighbors**(*n\_degrees: int*)

Return canonicalized pairs of atoms whose shortest separation is *exactly* n bonds. Only pairs with increasing atom indices are returned.

**Parameters** **n** (*int*) – The number of bonds separating atoms in each pair

**Returns** **neighbors** (*iterator of tuple of Atom*) – Tuples (len 2) of atom that are separated by n bonds.

## Notes

The criteria used here relies on minimum distances; when there are multiple valid paths between atoms, such as atoms in rings, the shortest path is considered. For example, two atoms in “meta” positions with respect to each other in a benzene are separated by two paths, one length 2 bonds and the other length 4 bonds. This function would consider them to be 2 apart and would not include them if n=4 was passed.

**chemical\_environment\_matches**(*query: str, aromaticity\_model: str = 'MDL', unique: bool = False, toolkit\_registry: Union[ToolkitRegistry, ToolkitWrapper] = GLOBAL\_TOOLKIT\_REGISTRY*)

Retrieve all matches for a given chemical environment query.

TODO:

- Do we want to generalize this to other kinds of queries too, like mdtraj DSL, pymol selections, atom index slices, etc? We could just call it `topology.matches(query)`

## Parameters

- **query** (*str*) – SMARTS string (with one or more tagged atoms)
- **aromaticity\_model** (*str*) – Override the default aromaticity model for this topology and use the specified aromaticity model instead. Allowed values: ['MDL']

**Returns** **matches** (*list of Topology.ChemicalEnvironmentMatch*) – A list of tuples, containing the topology indices of the matching atoms.

**property identical\_molecule\_groups: Dict[int, List[Tuple[int, Dict[int, int]]]]**

Returns groups of chemically identical molecules, identified by index and atom map.

**Returns** *identical\_molecule\_groups* – A dict of the form {unique\_mol\_idx : [(topology\_mol\_idx, atom\_map), ...]}. Each key is the topology molecule index of the first instance of a unique chemical species. Iterating over the keys will yield all of the unique chemical species in the topology. Each value is a list of all instances of that chemical species in the topology. Each element of the list is a 2-tuple where the first element is the molecule index of the instance, and the second element maps the atom topology indices of the key molecule to the instance. The molecule instance corresponding to the key is included in the list, so the list is a complete list of all instances of that chemical species.

## Examples

```
>>> from openff.toolkit import Molecule, Topology
>>> # Create a water ordered as OHH
>>> water1 = Molecule()
>>> water1.add_atom(8, 0, False)
0
>>> water1.add_atom(1, 0, False)
1
>>> water1.add_atom(1, 0, False)
2
>>> _ = water1.add_bond(0, 1, 1, False)
>>> _ = water1.add_bond(0, 2, 1, False)
...
>>> # Create a different water ordered as HOH
>>> water2 = Molecule()
>>> water2.add_atom(1, 0, False)
0
>>> water2.add_atom(8, 0, False)
1
>>> water2.add_atom(1, 0, False)
2
>>> _ = water2.add_bond(0, 1, 1, False)
>>> _ = water2.add_bond(1, 2, 1, False)
...
>>> top = Topology.from_molecules([water1, water2])
>>> top.identical_molecule_groups
{0: [(0, {0: 0, 1: 1, 2: 2}), (1, {0: 1, 1: 0, 2: 2})]}
```

**classmethod** `from_dict(topology_dict: dict)`

Create a new Topology from a dictionary representation

**Parameters** `topology_dict` (dict) – A dictionary representation of the topology.

**Returns** `topology` (Topology) – A Topology created from the dictionary representation

**classmethod** `from_openmm(openmm_topology: openmm.app.Topology, unique_molecules: Optional[Iterable[FrozenMolecule]] = None, positions: Union[None, Quantity, OMMQuantity] = None) → Topology`

Construct an OpenFF Topology object from an OpenMM Topology object.

This method guarantees that the order of atoms in the input OpenMM Topology will be the same as the ordering of atoms in the output OpenFF Topology. However it does not guarantee the order of the bonds will be the same.

Hierarchy schemes are taken from the OpenMM topology, not from `unique_molecules`.

### Parameters

- **openmm\_topology** – The OpenMM Topology object to convert
- **unique\_molecules** – An iterable containing all the unique molecules in the topology. This is used to identify the molecules in the OpenMM topology and provide any missing chemical information. Each chemical species in the topology must be specified exactly once, though the topology may have any number of copies, including zero. The chemical elements of atoms and their bond connectivity will be

used to match these reference molecules to the molecules appearing in the topology. If bond orders are specified in the topology, these will be used in matching as well.

- **positions** – Positions for the atoms in the new topology.

**Returns** *topology* – An OpenFF Topology object, constructed from the molecules in *unique\_molecules*, with the same atom order as the input topology.

**Raises**

- **MissingUniqueMoleculesError** – If *unique\_molecules* is None
- **DuplicateUniqueMoleculeError** – If the same connectivity graph is represented by two different molecules in *unique\_molecules*
- **ValueError** – If a chemically impossible molecule is detected in the topology

**to\_openmm**(*ensure\_unique\_atom\_names*: *Union[str, bool]* = 'residues')

Create an OpenMM Topology object.

The atom metadata fields *residue\_name*, *residue\_number*, *insertion\_code*, and *chain\_id* are used to group atoms into OpenMM residues and chains.

Contiguously-indexed atoms with the same *residue\_name*, *residue\_number*, *insertion\_code*, and *chain\_id* will be put into the same OpenMM residue.

Contiguously-indexed residues with the same *chain\_id* will be put into the same OpenMM chain.

This method will never make an OpenMM chain or residue larger than the OpenFF Molecule that it came from. In other words, no chain or residue will span two OpenFF Molecules.

This method will **not** populate the OpenMM Topology with virtual sites.

**Parameters** *ensure\_unique\_atom\_names* – Whether to generate new atom names to ensure uniqueness within a molecule or hierarchy element.

- If the name of a *HierarchyScheme* is given as a string, new atom names will be generated so that each element of that scheme has unique atom names. Molecules without the given hierarchy scheme will be given unique atom names within that molecule.
- If True, new atom names will be generated so that atom names are unique within a molecule.
- If False, the existing atom names will be used.

**Returns** *openmm\_topology* (*openmm.app.Topology*) – An OpenMM Topology object

**to\_file**(*file*: *Union[Path, str, TextIO]*, *positions*: *Optional[Union[OMMQuantity, Quantity, ndarray[Any, dtype[ScalarType]]]]* = None, *file\_format*: *Literal['PDB']* = 'PDB', *keep\_ids*: *bool* = False, *ensure\_unique\_atom\_names*: *Union[str, bool]* = 'residues')

Save coordinates and topology to a PDB file.

Reference: <https://github.com/openforcefield/openff-toolkit/issues/502>

Notes:

1. Atom numbering may not remain same, for example if the atoms in water are numbered as 1001, 1002, 1003, they would change to 1, 2, 3. This doesn't affect the topology or coordinates or atom-ordering in any way.
2. Same issue with the amino acid names in the pdb file, they are not returned.



### Parameters

- **file** – A file-like object to write to, or a path to save the file to.
- **positions** (Array with shape (n\_atoms, 3) and dimensions of length) – May be a...
  - `openmm.unit.Quantity` object which has atomic positions as a list of unit-tagged `Vec3` objects
  - `openff.units.unit.Quantity` object which wraps a `numpy.ndarray` with dimensions of length
  - (unitless) 2D `numpy.ndarray`, in which it is assumed that the positions are in units of Angstroms.
  - None (the default), in which case the first conformer of each molecule in the topology will be used.
- **file\_format** – Output file format. Case insensitive. Currently only supported value is "PDB".
- **keep\_ids** – If True, keep the residue and chain IDs specified in the Topology rather than generating new ones.
- **ensure\_unique\_atom\_names** – Whether to generate new atom names to ensure uniqueness within a molecule or hierarchy element.
  - If the name of a [HierarchyScheme](#) is given as a string, new atom names will be generated so that each element of that scheme has unique atom names. Molecules without the given hierarchy scheme will be given unique atom names within that molecule.
  - If True, new atom names will be generated so that atom names are unique within a molecule.
  - If False, the existing atom names will be used.

Note that this option cannot guarantee name uniqueness for formats like PDB that truncate long atom names.

**get\_positions()** → [Optional\[Quantity\]](#)

Copy the positions of the topology into a new array.

Topology positions are stored as the first conformer of each molecule. If any molecule has no conformers, this method returns None. Note that modifying the returned array will not update the positions in the topology. To change the positions, use `Topology.set_positions()`.

See also:

[set\\_positions](#)

**set\_positions(array: [Quantity](#))**

Set the positions in a topology by copying from a single  $n \times 3$  array.

Note that modifying the original array will not update the positions in the topology; it must be passed again to `set_positions()`.

**Parameters array** – Positions for the topology. Should be a unit-wrapped array-like object with shape (n\_atoms, 3) and dimensions of length.

See also:

[get\\_positions](#)

```
classmethod from_mdtraj(mdtraj_topology: Topology, unique_molecules:
                        Optional[Iterable[FrozenMolecule]] = None, positions: Union[None,
                        OMMQuantity, Quantity] = None)
```

Construct an OpenFF Topology from an MDTraj Topology

This method guarantees that the order of atoms in the input MDTraj Topology will be the same as the ordering of atoms in the output OpenFF Topology. However it does not guarantee the order of the bonds will be the same.

Hierarchy schemes are taken from the MDTraj topology, not from unique\_molecules.

#### Parameters

- **mdtraj\_topology** – The MDTraj Topology object to convert
- **unique\_molecules** – An iterable containing all the unique molecules in the topology. This is used to identify the molecules in the MDTraj topology and provide any missing chemical information. Each chemical species in the topology must be specified exactly once, though the topology may have any number of copies, including zero. The chemical elements of atoms and their bond connectivity will be used to match these reference molecules to the molecules appearing in the topology. If bond orders are specified in the topology, these will be used in matching as well.
- **positions** – Positions for the atoms in the new topology.

**Returns** *topology* – An OpenFF Topology object, constructed from the molecules in unique\_molecules, with the same atom order as the input topology.

#### Raises

- **MissingUniqueMoleculesError** – If unique\_molecules is None
- **DuplicateUniqueMoleculeError** – If the same connectivity graph is represented by two different molecules in unique\_molecules
- **ValueError** – If a chemically impossible molecule is detected in the topology

```
get_bond_between(i, j)
```

Returns the bond between two atoms

#### Parameters

- **i** (*int* or *TopologyAtom*) – Atoms or atom indices to check
- **j** (*int* or *TopologyAtom*) – Atoms or atom indices to check

**Returns** **bond** (*TopologyBond*) – The bond between i and j.

```
is_bonded(i, j)
```

Returns True if the two atoms are bonded

#### Parameters

- **i** (*int* or *TopologyAtom*) – Atoms or atom indices to check
- **j** (*int* or *TopologyAtom*) – Atoms or atom indices to check

**Returns** **is\_bonded** (*bool*) – True if atoms are bonded, False otherwise.

```
atom(atom_topology_index)
```

Get the TopologyAtom at a given Topology atom index.

**Parameters** **atom\_topology\_index** (*int*) – The index of the TopologyAtom in this Topology

**Returns** *An `openff.toolkit.topology.TopologyAtom`*

**bond**(*bond\_topology\_index*)

Get the TopologyBond at a given Topology bond index.

**Parameters** **bond\_topology\_index** (*int*) – The index of the TopologyBond in this Topology

**Returns** *An `openff.toolkit.topology.TopologyBond`*

**Raises**

- **ValueError** if **bond\_topology\_index** is not an **int** –
- **BondNotInTopologyError** if **bond\_topology\_index** is not in the range **[0, self.n\_bonds)** –

**add\_molecule**(*molecule: Union[Molecule, SimpleMolecule]*) → *int*

Add a copy of the molecule to the topology

**add\_constraint**(*iatom, jatom, distance=True*)

Mark a pair of atoms as constrained.

Constraints between atoms that are not bonded (e.g., rigid waters) are permissible.

**Parameters**

- **iatom** (*Atom*) – Atoms to mark as constrained These atoms may be bonded or not in the Topology
- **jatom** (*Atom*) – Atoms to mark as constrained These atoms may be bonded or not in the Topology
- **distance** (*unit-wrapped float, optional, default=True*) – Constraint distance True if distance has yet to be determined False if constraint is to be removed

**is\_constrained**(*iatom, jatom*)

Check if a pair of atoms are marked as constrained.

**Parameters**

- **iatom** (*int*) – Indices of atoms to mark as constrained.
- **jatom** (*int*) – Indices of atoms to mark as constrained.

**Returns** **distance** (*unit-wrapped float or bool*) – True if constrained but constraints have not yet been applied Distance if constraint has already been added to Topology

**hierarchy\_iterator**(*iter\_name: str*) → *Iterator[HierarchyElement]*

Iterate over all molecules with the given hierarchy scheme.

Get an iterator over hierarchy elements from all of the molecules in this topology that provide the appropriately named iterator. This iterator will yield hierarchy elements sorted first by the order that molecules are listed in the Topology, and second by the specific sorting of hierarchy elements defined in each molecule. Molecules without the named iterator are not included.

**Parameters** **iter\_name** – The iterator name associated with the HierarchyScheme to retrieve (for example ‘residues’ or ‘chains’)

**Returns** iterator of *HierarchyElement*

**See also:**

*HierarchyScheme, HierarchyElement, Molecule.hierarchy\_schemes*

**property** `n_topology_atoms`: `int`

Deprecated since version 0.11.0: This property has been deprecated and will soon be removed.  
Use `Topology.n_atoms()` instead.

**property** `topology_atoms`

Deprecated since version 0.11.0: This property has been deprecated and will soon be removed.  
Use `Topology.atoms()` instead.

**property** `n_topology_bonds`: `int`

Deprecated since version 0.11.0: This property has been deprecated and will soon be removed.  
Use `Topology.n_bonds()` instead.

**property** `topology_bonds`

Deprecated since version 0.11.0: This property has been deprecated and will soon be removed.  
Use `Topology.bonds()` instead.

**property** `n_topology_particles`: `int`

Deprecated since version 0.11.0: This property has been deprecated and will soon be removed.  
Use `Topology.n_particles()` instead.

**property** `topology_particles`

Deprecated since version 0.11.0: This property has been deprecated and will soon be removed.  
Use `Topology.particles()` instead.

**property** `reference_molecules`: `Iterator[Molecule]`

Deprecated since version 0.11.0: This property has been deprecated and will soon be removed.  
Use `Topology.unique_molecules()` instead.

**property** `n_reference_molecules`: `int`

Deprecated since version 0.11.0: This property has been deprecated and will soon be removed.  
Use `Topology.n_unique_molecules()` instead.

**property** `n_topology_molecules`: `int`

Deprecated since version 0.11.0: This property has been deprecated and will soon be removed.  
Use `Topology.n_molecules()` instead.

**property** `topology_molecules`

Deprecated since version 0.11.0: This property has been deprecated and will soon be removed.  
Use `Topology.molecules()` instead.

**classmethod** `from_bson(serialized)`

Instantiate an object from a BSON serialized representation.

Specification: <http://bsonspec.org/>

**Parameters** `serialized` (`bytes`) – A BSON serialized representation of the object

**Returns** `instance` (`cls`) – An instantiated object

**classmethod** `from_json(serialized: str)`

Instantiate an object from a JSON serialized representation.

Specification: <https://www.json.org/>

**Parameters** `serialized` (`str`) – A JSON serialized representation of the object

**Returns** `instance` (`cls`) – An instantiated object

**classmethod** `from_messagepack(serialized)`

Instantiate an object from a MessagePack serialized representation.

Specification: <https://msgpack.org/index.html>

**Parameters** `serialized` (`bytes`) – A MessagePack-encoded bytes serialized representation

**Returns** `instance` (`cls`) – Instantiated object.

**classmethod** `from_pickle(serialized)`

Instantiate an object from a pickle serialized representation.

**Warning:** This is not recommended for safe, stable storage since the pickle specification may change between Python versions.

**Parameters** `serialized` (`str`) – A pickled representation of the object

**Returns** `instance` (`cls`) – An instantiated object

**classmethod** `from_toml(serialized)`

Instantiate an object from a TOML serialized representation.

Specification: <https://github.com/toml-lang/toml>

**Parameters** `serialized` (`str`) – A TOML serialized representation of the object

**Returns** `instance` (`cls`) – An instantiated object

**classmethod** `from_xml(serialized)`

Instantiate an object from an XML serialized representation.

Specification: <https://www.w3.org/XML/>

**Parameters** `serialized` (`bytes`) – An XML serialized representation

**Returns** `instance` (`cls`) – Instantiated object.

**classmethod** `from_yaml(serialized)`

Instantiate from a YAML serialized representation.

Specification: <http://yaml.org/>

**Parameters** `serialized` (`str`) – A YAML serialized representation of the object

**Returns** `instance` (`cls`) – Instantiated object

**property** `n_particles`: `int`

Deprecated since version 0.11.0: This property has been deprecated and will soon be removed. Use `Topology.n_atoms()` instead.

**to\_bson()**

Return a BSON serialized representation.

Specification: <http://bsonspec.org/>

**Returns** `serialized` (`bytes`) – A BSON serialized representation of the object

**to\_json**(*indent=None*) → *str*

Return a JSON serialized representation.

Specification: <https://www.json.org/>

**Parameters** *indent* (*int*, optional, default=None) – If not None, will pretty-print with specified number of spaces for indentation

**Returns** *serialized* (*str*) – A JSON serialized representation of the object

**to\_messagepack**()

Return a MessagePack representation.

Specification: <https://msgpack.org/index.html>

**Returns** *serialized* (*bytes*) – A MessagePack-encoded bytes serialized representation of the object

**to\_pickle**()

Return a pickle serialized representation.

**Warning:** This is not recommended for safe, stable storage since the pickle specification may change between Python versions.

**Returns** *serialized* (*str*) – A pickled representation of the object

**to\_toml**()

Return a TOML serialized representation.

Specification: <https://github.com/toml-lang/toml>

**Returns** *serialized* (*str*) – A TOML serialized representation of the object

**to\_xml**(*indent=2*)

Return an XML representation.

Specification: <https://www.w3.org/XML/>

**Parameters** *indent* (*int*, optional, default=2) – If not None, will pretty-print with specified number of spaces for indentation

**Returns** *serialized* (*bytes*) – A MessagePack-encoded bytes serialized representation.

**to\_yaml**()

Return a YAML serialized representation.

Specification: <http://yaml.org/>

**Returns** *serialized* (*str*) – A YAML serialized representation of the object

**property particles**

Deprecated since version 0.11.0: This property has been deprecated and will soon be removed.  
Use `Topology.atoms()` instead.

**particle\_index**(*particle*) → *int*

Deprecated since version 0.11.0: This method has been deprecated and will soon be removed.  
Use `Topology.atom_index()` instead.

## 11.2 Secondary objects

<a href="#">Particle</a>	Base class for all particles in a molecule.
<a href="#">Atom</a>	A chemical atom.
<a href="#">Bond</a>	Chemical bond representation.
<a href="#">ValenceDict</a>	Enforce uniqueness in atom indices.
<a href="#">ImproperDict</a>	Symmetrize improper torsions.
<a href="#">HierarchyScheme</a>	Perceives hierarchy elements from the metadata of atoms in a Molecule.
<a href="#">HierarchyElement</a>	An element in a metadata hierarchy scheme, such as a residue or chain.

### 11.2.1 Particle

**class** `openff.toolkit.topology.Particle`

Base class for all particles in a molecule.

A particle object could be an Atom or similar.

**Warning:** This API is experimental and subject to change.

`__init__()`

## Methods

<code>__init__()</code>	
<code>from_bson(serialized)</code>	Instantiate an object from a BSON serialized representation.
<code>from_dict(d)</code>	Static constructor from dictionary representation.
<code>from_json(serialized)</code>	Instantiate an object from a JSON serialized representation.
<code>from_messagepack(serialized)</code>	Instantiate an object from a MessagePack serialized representation.
<code>from_pickle(serialized)</code>	Instantiate an object from a pickle serialized representation.
<code>from_toml(serialized)</code>	Instantiate an object from a TOML serialized representation.
<code>from_xml(serialized)</code>	Instantiate an object from an XML serialized representation.
<code>from_yaml(serialized)</code>	Instantiate from a YAML serialized representation.
<code>to_bson()</code>	Return a BSON serialized representation.
<code>to_dict()</code>	Convert to dictionary representation.
<code>to_json([indent])</code>	Return a JSON serialized representation.
<code>to_messagepack()</code>	Return a MessagePack representation.
<code>to_pickle()</code>	Return a pickle serialized representation.
<code>to_toml()</code>	Return a TOML serialized representation.
<code>to_xml([indent])</code>	Return an XML representation.
<code>to_yaml()</code>	Return a YAML serialized representation.

## Attributes

<code>molecule</code>	The Molecule this particle is part of.
<code>molecule_particle_index</code>	Returns the index of this particle in its molecule
<code>name</code>	The name of the particle

**property molecule:** `FrozenMolecule`

The Molecule this particle is part of.

**property molecule\_particle\_index:** `int`

Returns the index of this particle in its molecule

**property name**

The name of the particle

**to\_dict()**

Convert to dictionary representation.

**classmethod from\_dict(d)**

Static constructor from dictionary representation.



**classmethod** `from_bson(serialized)`

Instantiate an object from a BSON serialized representation.

Specification: <http://bsonspec.org/>

**Parameters** `serialized` (`bytes`) – A BSON serialized representation of the object

**Returns** `instance` (`cls`) – An instantiated object

**classmethod** `from_json(serialized: str)`

Instantiate an object from a JSON serialized representation.

Specification: <https://www.json.org/>

**Parameters** `serialized` (`str`) – A JSON serialized representation of the object

**Returns** `instance` (`cls`) – An instantiated object

**classmethod** `from_messagepack(serialized)`

Instantiate an object from a MessagePack serialized representation.

Specification: <https://msgpack.org/index.html>

**Parameters** `serialized` (`bytes`) – A MessagePack-encoded bytes serialized representation

**Returns** `instance` (`cls`) – Instantiated object.

**classmethod** `from_pickle(serialized)`

Instantiate an object from a pickle serialized representation.

**Warning:** This is not recommended for safe, stable storage since the pickle specification may change between Python versions.

**Parameters** `serialized` (`str`) – A pickled representation of the object

**Returns** `instance` (`cls`) – An instantiated object

**classmethod** `from_toml(serialized)`

Instantiate an object from a TOML serialized representation.

Specification: <https://github.com/toml-lang/toml>

**Parameters** `serialized` (`str`) – A TOML serialized representation of the object

**Returns** `instance` (`cls`) – An instantiated object

**classmethod** `from_xml(serialized)`

Instantiate an object from an XML serialized representation.

Specification: <https://www.w3.org/XML/>

**Parameters** `serialized` (`bytes`) – An XML serialized representation

**Returns** `instance` (`cls`) – Instantiated object.

**classmethod** `from_yaml(serialized)`

Instantiate from a YAML serialized representation.

Specification: <http://yaml.org/>

**Parameters** `serialized` (`str`) – A YAML serialized representation of the object

**Returns instance** (*cls*) – Instantiated object

**to\_bson()**

Return a BSON serialized representation.

Specification: <http://bsonspec.org/>

**Returns serialized** (*bytes*) – A BSON serialized representation of the object

**to\_json(indent=None)** → *str*

Return a JSON serialized representation.

Specification: <https://www.json.org/>

**Parameters indent** (*int*, optional, default=None) – If not None, will pretty-print with specified number of spaces for indentation

**Returns serialized** (*str*) – A JSON serialized representation of the object

**to\_messagepack()**

Return a MessagePack representation.

Specification: <https://msgpack.org/index.html>

**Returns serialized** (*bytes*) – A MessagePack-encoded bytes serialized representation of the object

**to\_pickle()**

Return a pickle serialized representation.

**Warning:** This is not recommended for safe, stable storage since the pickle specification may change between Python versions.

**Returns serialized** (*str*) – A pickled representation of the object

**to\_toml()**

Return a TOML serialized representation.

Specification: <https://github.com/toml-lang/toml>

**Returns serialized** (*str*) – A TOML serialized representation of the object

**to\_xml(indent=2)**

Return an XML representation.

Specification: <https://www.w3.org/XML/>

**Parameters indent** (*int*, optional, default=2) – If not None, will pretty-print with specified number of spaces for indentation

**Returns serialized** (*bytes*) – A MessagePack-encoded bytes serialized representation.

**to\_yaml()**

Return a YAML serialized representation.

Specification: <http://yaml.org/>

**Returns serialized** (*str*) – A YAML serialized representation of the object

### 11.2.2 Atom

```
class openff.toolkit.topology.Atom(atomic_number, formal_charge, is_aromatic, name=None,  
                                  molecule=None, stereochemistry=None, metadata=None)
```

A chemical atom.

**Warning:** This API is experimental and subject to change.

```
__init__(atomic_number, formal_charge, is_aromatic, name=None, molecule=None,  
         stereochemistry=None, metadata=None)
```

Create an immutable Atom object.

Object is serializable and immutable.

#### Parameters

- **atomic\_number** (*int*) – Atomic number of the atom. Must be non-negative and non-zero.
- **formal\_charge** (*int* or *openff.units.unit.Quantity-wrapped int* with dimension "charge") – Formal charge of the atom
- **is\_aromatic** (*bool*) – If True, atom is aromatic; if False, not aromatic
- **stereochemistry** (*str*, optional, default=None) – Either 'R' or 'S' for specified stereochemistry, or None for ambiguous stereochemistry
- **name** (*str*, optional, default=None) – An optional name to be associated with the atom
- **metadata** (*dict[str: (int, str)]*, default=None) – An optional dictionary where keys are strings and values are strings or ints. This is intended to record atom-level information used to inform hierarchy definition and iteration, such as grouping atom by residue and chain.

#### Examples

Create a non-aromatic carbon atom

```
>>> atom = Atom(6, 0, False)
```

Create a chiral carbon atom

```
>>> atom = Atom(6, 0, False, stereochemistry='R', name='CT')
```

## Methods

<code>__init__(atomic_number, formal_charge, ...)</code>	Create an immutable Atom object.
<code>add_bond(bond)</code>	Adds a bond that this atom is involved in
<code>from_bson(serialized)</code>	Instantiate an object from a BSON serialized representation.
<code>from_dict(atom_dict)</code>	Create an Atom from a dict representation.
<code>from_json(serialized)</code>	Instantiate an object from a JSON serialized representation.
<code>from_messagepack(serialized)</code>	Instantiate an object from a MessagePack serialized representation.
<code>from_pickle(serialized)</code>	Instantiate an object from a pickle serialized representation.
<code>from_toml(serialized)</code>	Instantiate an object from a TOML serialized representation.
<code>from_xml(serialized)</code>	Instantiate an object from an XML serialized representation.
<code>from_yaml(serialized)</code>	Instantiate from a YAML serialized representation.
<code>is_bonded_to(atom2)</code>	Determine whether this atom is bound to another atom
<code>is_in_ring([toolkit_registry])</code>	Return whether or not this atom is in a ring(s) (of any size)
<code>to_bson()</code>	Return a BSON serialized representation.
<code>to_dict()</code>	Return a dict representation of the atom.
<code>to_json([indent])</code>	Return a JSON serialized representation.
<code>to_messagepack()</code>	Return a MessagePack representation.
<code>to_pickle()</code>	Return a pickle serialized representation.
<code>to_toml()</code>	Return a TOML serialized representation.
<code>to_xml([indent])</code>	Return an XML representation.
<code>to_yaml()</code>	Return a YAML serialized representation.

## Attributes

<code>atomic_number</code>	The integer atomic number of the atom.
<code>bonded_atoms</code>	The list of Atom objects this atom is involved in bonds with
<code>bonds</code>	The list of Bond objects this atom is involved in.
<code>formal_charge</code>	The atom's formal charge
<code>is_aromatic</code>	The atom's <code>is_aromatic</code> flag
<code>mass</code>	The standard atomic weight (abundance-weighted isotopic mass) of the atomic site.
<code>metadata</code>	The atom's metadata dictionary
<code>molecule</code>	The Molecule this particle is part of.
<code>molecule_atom_index</code>	The index of this Atom within the the list of atoms in the parent Molecule.
<code>molecule_particle_index</code>	Returns the index of this particle in its molecule
<code>name</code>	The name of this atom, if any
<code>partial_charge</code>	The partial charge of the atom, if any.
<code>stereochemistry</code>	The atom's stereochemistry (if defined, otherwise None)
<code>symbol</code>	Return the symbol implied by the atomic number of this atom

### `add_bond(bond)`

Adds a bond that this atom is involved in

**Parameters** `bond` (an `openff.toolkit.topology.molecule.Bond`) – A bond involving this atom

### `to_dict()` → `Dict[str, Union[str, int, bool, Dict[Any, Any]]]`

Return a dict representation of the atom.

### `classmethod from_dict(atom_dict)`

Create an Atom from a dict representation.

### **property** `metadata`

The atom's metadata dictionary

### **property** `formal_charge`

The atom's formal charge

### **property** `partial_charge`

The partial charge of the atom, if any.

**Returns** *unit-wrapped float with dimension of atomic charge, or None if no charge has been specified*

### **property** `is_aromatic`

The atom's `is_aromatic` flag

### **property** `stereochemistry`

The atom's stereochemistry (if defined, otherwise None)

### **property** `atomic_number`: `int`

The integer atomic number of the atom.

**property symbol:** `str`

Return the symbol implied by the atomic number of this atom

**property mass:** `Quantity`

The standard atomic weight (abundance-weighted isotopic mass) of the atomic site.

The mass is reported in units of Dalton.

**property name**

The name of this atom, if any

**property bonds**

The list of Bond objects this atom is involved in.

**property bonded\_atoms:** `Generator[Atom, None, None]`

The list of Atom objects this atom is involved in bonds with

**is\_bonded\_to**(*atom2*)

Determine whether this atom is bound to another atom

**Parameters** *atom2* (`Atom`) – a different atom in the same molecule

**Returns** `bool` – Whether this atom is bound to *atom2*

**is\_in\_ring**(*toolkit\_registry*=`GLOBAL_TOOLKIT_REGISTRY`) → `bool`

Return whether or not this atom is in a ring(s) (of any size)

This Atom is expected to be attached to a molecule (*Atom.molecule*).

**Parameters** *toolkit\_registry* (`ToolkitRegistry`, default=`GLOBAL_TOOLKIT_REGISTRY`)  
– `ToolkitRegistry` to use to enumerate the tautomers.

**property molecule\_atom\_index:** `int`

The index of this Atom within the the list of atoms in the parent Molecule.

**classmethod from\_bson**(*serialized*)

Instantiate an object from a BSON serialized representation.

Specification: <http://bsonspec.org/>

**Parameters** *serialized* (`bytes`) – A BSON serialized representation of the object

**Returns** `instance` (*cls*) – An instantiated object

**classmethod from\_json**(*serialized*: `str`)

Instantiate an object from a JSON serialized representation.

Specification: <https://www.json.org/>

**Parameters** *serialized* (`str`) – A JSON serialized representation of the object

**Returns** `instance` (*cls*) – An instantiated object

**classmethod from\_messagepack**(*serialized*)

Instantiate an object from a MessagePack serialized representation.

Specification: <https://msgpack.org/index.html>

**Parameters** *serialized* (`bytes`) – A MessagePack-encoded bytes serialized representation

**Returns** `instance` (*cls*) – Instantiated object.

**classmethod** `from_pickle(serialized)`

Instantiate an object from a pickle serialized representation.

**Warning:** This is not recommended for safe, stable storage since the pickle specification may change between Python versions.

**Parameters** `serialized (str)` – A pickled representation of the object

**Returns** `instance (cls)` – An instantiated object

**classmethod** `from_toml(serialized)`

Instantiate an object from a TOML serialized representation.

Specification: <https://github.com/toml-lang/toml>

**Parameters** `serialized (str)` – A TOML serialized representation of the object

**Returns** `instance (cls)` – An instantiated object

**classmethod** `from_xml(serialized)`

Instantiate an object from an XML serialized representation.

Specification: <https://www.w3.org/XML/>

**Parameters** `serialized (bytes)` – An XML serialized representation

**Returns** `instance (cls)` – Instantiated object.

**classmethod** `from_yaml(serialized)`

Instantiate from a YAML serialized representation.

Specification: <http://yaml.org/>

**Parameters** `serialized (str)` – A YAML serialized representation of the object

**Returns** `instance (cls)` – Instantiated object

**property** `molecule: FrozenMolecule`

The Molecule this particle is part of.

**property** `molecule_particle_index: int`

Returns the index of this particle in its molecule

**to\_bson()**

Return a BSON serialized representation.

Specification: <http://bsonspec.org/>

**Returns** `serialized (bytes)` – A BSON serialized representation of the object

**to\_json(indent=None) → str**

Return a JSON serialized representation.

Specification: <https://www.json.org/>

**Parameters** `indent (int, optional, default=None)` – If not None, will pretty-print with specified number of spaces for indentation

**Returns** `serialized (str)` – A JSON serialized representation of the object

**to\_messagepack()**

Return a MessagePack representation.

Specification: <https://msgpack.org/index.html>

**Returns serialized** (*bytes*) – A MessagePack-encoded bytes serialized representation of the object

**to\_pickle()**

Return a pickle serialized representation.

**Warning:** This is not recommended for safe, stable storage since the pickle specification may change between Python versions.

**Returns serialized** (*str*) – A pickled representation of the object

**to\_toml()**

Return a TOML serialized representation.

Specification: <https://github.com/toml-lang/toml>

**Returns serialized** (*str*) – A TOML serialized representation of the object

**to\_xml(indent=2)**

Return an XML representation.

Specification: <https://www.w3.org/XML/>

**Parameters indent** (*int*, optional, default=2) – If not None, will pretty-print with specified number of spaces for indentation

**Returns serialized** (*bytes*) – A MessagePack-encoded bytes serialized representation.

**to\_yaml()**

Return a YAML serialized representation.

Specification: <http://yaml.org/>

**Returns serialized** (*str*) – A YAML serialized representation of the object

### 11.2.3 Bond

```
class openff.toolkit.topology.Bond(atom1, atom2, bond_order, is_aromatic,
                                   fractional_bond_order=None, stereochemistry=None)
```

Chemical bond representation.

**Warning:** This API is experimental and subject to change.

#### Attributes

- **atom1, atom2** (*openff.toolkit.topology.Atom*) – Atoms involved in the bond
- **bond\_order** (*int*) – The (integer) bond order of this bond.
- **is\_aromatic** (*bool*) – Whether or not this bond is aromatic.



- **fractional\_bond\_order** (*float, optional*) – The fractional bond order, or partial bond order of this bond.
- **stereochemistry** (*str, optional, default=None*) – A string representing this stereochemistry of this bond.
- **.. warning :: This API is experimental and subject to change.**

`__init__(atom1, atom2, bond_order, is_aromatic, fractional_bond_order=None, stereochemistry=None)`

Create a new chemical bond.

## Methods

<code>__init__(atom1, atom2, bond_order, is_aromatic)</code>	Create a new chemical bond.
<code>from_bson(serialized)</code>	Instantiate an object from a BSON serialized representation.
<code>from_dict(molecule, d)</code>	Create a Bond from a dict representation.
<code>from_json(serialized)</code>	Instantiate an object from a JSON serialized representation.
<code>from_messagepack(serialized)</code>	Instantiate an object from a MessagePack serialized representation.
<code>from_pickle(serialized)</code>	Instantiate an object from a pickle serialized representation.
<code>from_toml(serialized)</code>	Instantiate an object from a TOML serialized representation.
<code>from_xml(serialized)</code>	Instantiate an object from an XML serialized representation.
<code>from_yaml(serialized)</code>	Instantiate from a YAML serialized representation.
<code>is_in_ring([toolkit_registry])</code>	Return whether or not this bond is in a ring(s) (of any size)
<code>to_bson()</code>	Return a BSON serialized representation.
<code>to_dict()</code>	Return a dict representation of the bond.
<code>to_json([indent])</code>	Return a JSON serialized representation.
<code>to_messagepack()</code>	Return a MessagePack representation.
<code>to_pickle()</code>	Return a pickle serialized representation.
<code>to_toml()</code>	Return a TOML serialized representation.
<code>to_xml([indent])</code>	Return an XML representation.
<code>to_yaml()</code>	Return a YAML serialized representation.

## Attributes

atom1	
atom1_index	
atom2	
atom2_index	
atoms	
bond_order	
fractional_bond_order	
is_aromatic	
molecule	
molecule_bond_index	The index of this Bond within the the list of bonds in Molecules.
stereochemistry	

**to\_dict()** → `Dict[str, Union[int, bool, str, float]]`

Return a dict representation of the bond.

**classmethod from\_dict**(*molecule*, *d*)

Create a Bond from a dict representation.

**property molecule\_bond\_index:** `int`

The index of this Bond within the the list of bonds in Molecules.

**is\_in\_ring**(*toolkit\_registry*=`GLOBAL_TOOLKIT_REGISTRY`) → `bool`

Return whether or not this bond is in a ring(s) (of any size)

This Bond is expected to be attached to a molecule (*Bond.molecule*).

**Note:** Bonds containing atoms that are only in separate rings, i.e. the central bond in a biphenyl, are not considered to be bonded by this criteria.

**Parameters** *toolkit\_registry* (`ToolkitRegistry`, default=`GLOBAL_TOOLKIT_REGISTRY`)

– `ToolkitRegistry` to use to enumerate the tautomers.

**Returns** *is\_in\_ring* (`bool`) – Whether or not this bond is in a ring.

**classmethod from\_bson**(*serialized*)

Instantiate an object from a BSON serialized representation.

Specification: <http://bsonspec.org/>

**Parameters** *serialized* (`bytes`) – A BSON serialized representation of the object

**Returns** *instance* (*cls*) – An instantiated object

**classmethod** `from_json(serialized: str)`

Instantiate an object from a JSON serialized representation.

Specification: <https://www.json.org/>

**Parameters** `serialized (str)` – A JSON serialized representation of the object

**Returns** `instance (cls)` – An instantiated object

**classmethod** `from_messagepack(serialized)`

Instantiate an object from a MessagePack serialized representation.

Specification: <https://msgpack.org/index.html>

**Parameters** `serialized (bytes)` – A MessagePack-encoded bytes serialized representation

**Returns** `instance (cls)` – Instantiated object.

**classmethod** `from_pickle(serialized)`

Instantiate an object from a pickle serialized representation.

**Warning:** This is not recommended for safe, stable storage since the pickle specification may change between Python versions.

**Parameters** `serialized (str)` – A pickled representation of the object

**Returns** `instance (cls)` – An instantiated object

**classmethod** `from_toml(serialized)`

Instantiate an object from a TOML serialized representation.

Specification: <https://github.com/toml-lang/toml>

**Parameters** `serialized (str)` – A TOML serialized representation of the object

**Returns** `instance (cls)` – An instantiated object

**classmethod** `from_xml(serialized)`

Instantiate an object from an XML serialized representation.

Specification: <https://www.w3.org/XML/>

**Parameters** `serialized (bytes)` – An XML serialized representation

**Returns** `instance (cls)` – Instantiated object.

**classmethod** `from_yaml(serialized)`

Instantiate from a YAML serialized representation.

Specification: <http://yaml.org/>

**Parameters** `serialized (str)` – A YAML serialized representation of the object

**Returns** `instance (cls)` – Instantiated object

**to\_bson()**

Return a BSON serialized representation.

Specification: <http://bsonspec.org/>

**Returns** `serialized (bytes)` – A BSON serialized representation of the object

**to\_json**(*indent=None*) → *str*

Return a JSON serialized representation.

Specification: <https://www.json.org/>

**Parameters** **indent** (*int*, optional, default=None) – If not None, will pretty-print with specified number of spaces for indentation

**Returns** **serialized** (*str*) – A JSON serialized representation of the object

**to\_messagepack**()

Return a MessagePack representation.

Specification: <https://msgpack.org/index.html>

**Returns** **serialized** (*bytes*) – A MessagePack-encoded bytes serialized representation of the object

**to\_pickle**()

Return a pickle serialized representation.

**Warning:** This is not recommended for safe, stable storage since the pickle specification may change between Python versions.

**Returns** **serialized** (*str*) – A pickled representation of the object

**to\_toml**()

Return a TOML serialized representation.

Specification: <https://github.com/toml-lang/toml>

**Returns** **serialized** (*str*) – A TOML serialized representation of the object

**to\_xml**(*indent=2*)

Return an XML representation.

Specification: <https://www.w3.org/XML/>

**Parameters** **indent** (*int*, optional, default=2) – If not None, will pretty-print with specified number of spaces for indentation

**Returns** **serialized** (*bytes*) – A MessagePack-encoded bytes serialized representation.

**to\_yaml**()

Return a YAML serialized representation.

Specification: <http://yaml.org/>

**Returns** **serialized** (*str*) – A YAML serialized representation of the object

### 11.2.4 ValenceDict

**class** openff.toolkit.topology.ValenceDict(\*args, \*\*kwargs)

Enforce uniqueness in atom indices.

**\_\_init\_\_**(\*args, \*\*kwargs)

#### Methods

<code>__init__(*args, **kwargs)</code>	
<code>clear()</code>	
<code>get(k[,d])</code>	
<code>index_of(key[, possible])</code>	Generates a canonical ordering of the equivalent permutations of key (equivalent rearrangements of indices) and identifies which of those possible orderings this particular ordering is.
<code>items()</code>	
<code>key_transform(key)</code>	Reverse tuple if first element is larger than last element.
<code>keys()</code>	
<code>pop(k[,d])</code>	If key is not found, d is returned if given, otherwise KeyError is raised.
<code>popitem()</code>	as a 2-tuple; but raise KeyError if D is empty.
<code>setdefault(k[,d])</code>	
<code>update([E, ]**F)</code>	If E present and has a .keys() method, does: for k in E: D[k] = E[k] If E present and lacks .keys() method, does: for (k, v) in E: D[k] = v In either case, this is followed by: for k, v in F.items(): D[k] = v
<code>values()</code>	

**static key\_transform(key)**

Reverse tuple if first element is larger than last element.

**classmethod index\_of(key, possible=None)**

Generates a canonical ordering of the equivalent permutations of key (equivalent rearrangements of indices) and identifies which of those possible orderings this particular ordering is. This method is useful when multiple SMARTS patterns might match the same atoms, but local molecular symmetry or the use of wildcards in the SMARTS could make the matches occur in arbitrary order.

This method can be restricted to a subset of the canonical orderings, by providing the optional possible keyword argument. If provided, the index returned by this method will be the index of the element in possible after undergoing the same canonical sorting as above.

#### Parameters

- **key** (iterable of int) – A valid key for ValenceDict
- **possible** (iterable of iterable of int, optional. default=```None```) – A subset of the possible orderings that this match might take.

**Returns** `index` (*int*)

**clear**() → None. Remove all items from D.

**get**(*k*, *d*) → D[*k*] if *k* in D, else *d*. *d* defaults to None.

**items**() → a set-like object providing a view on D's items

**keys**() → a set-like object providing a view on D's keys

**pop**(*k*, *d*) → *v*, remove specified key and return the corresponding value.

If key is not found, *d* is returned if given, otherwise `KeyError` is raised.

**popitem**() → (*k*, *v*), remove and return some (key, value) pair

as a 2-tuple; but raise `KeyError` if D is empty.

**setdefault**(*k*, *d*) → D.get(*k*,*d*), also set D[*k*]=*d* if *k* not in D

**update**(*E*, *\*\*F*) → None. Update D from mapping/iterable *E* and *F*.

If *E* present and has a `.keys()` method, does: for *k* in *E*: D[*k*] = *E*[*k*] If *E* present and lacks `.keys()` method, does: for (*k*, *v*) in *E*: D[*k*] = *v* In either case, this is followed by: for *k*, *v* in *F*.items(): D[*k*] = *v*

**values**() → an object providing a view on D's values

### 11.2.5 ImproperDict

**class** openff.toolkit.topology.ImproperDict(\*args, \*\*kwargs)

Symmetrize improper torsions.

**\_\_init\_\_**(\*args, \*\*kwargs)

## Methods

<code>__init__(*args, **kwargs)</code>	
<code>clear()</code>	
<code>get(k[,d])</code>	
<code>index_of(key[, possible])</code>	Generates a canonical ordering of the equivalent permutations of key (equivalent rearrangements of indices) and identifies which of those possible orderings this particular ordering is.
<code>items()</code>	
<code>key_transform(key)</code>	Reorder tuple in numerical order except for element[1] which is the central atom; it retains its position.
<code>keys()</code>	
<code>pop(k[,d])</code>	If key is not found, d is returned if given, otherwise KeyError is raised.
<code>popitem()</code>	as a 2-tuple; but raise KeyError if D is empty.
<code>setdefault(k[,d])</code>	
<code>update([E, ]**F)</code>	If E present and has a .keys() method, does: for k in E: D[k] = E[k] If E present and lacks .keys() method, does: for (k, v) in E: D[k] = v In either case, this is followed by: for k, v in F.items(): D[k] = v
<code>values()</code>	

### **static** `key_transform(key)`

Reorder tuple in numerical order except for element[1] which is the central atom; it retains its position.

### **classmethod** `index_of(key, possible=None)`

Generates a canonical ordering of the equivalent permutations of key (equivalent rearrangements of indices) and identifies which of those possible orderings this particular ordering is. This method is useful when multiple SMARTS patterns might match the same atoms, but local molecular symmetry or the use of wildcards in the SMARTS could make the matches occur in arbitrary order.

This method can be restricted to a subset of the canonical orderings, by providing the optional possible keyword argument. If provided, the index returned by this method will be the index of the element in possible after undergoing the same canonical sorting as above.

#### **Parameters**

- **key** (iterable of int) – A valid key for ValenceDict
- **possible** (iterable of iterable of int, optional. default=`None`) – A subset of the possible orderings that this match might take.

#### **Returns** `index (int)`

**clear()** → None. Remove all items from D.

**get**(*k*[, *d*]) → D[*k*] if *k* in D, else *d*. *d* defaults to None.

**items()** → a set-like object providing a view on D's items

**keys()** → a set-like object providing a view on D's keys

**pop**(*k*[, *d*]) → *v*, remove specified key and return the corresponding value.

If key is not found, *d* is returned if given, otherwise `KeyError` is raised.

**popitem()** → (*k*, *v*), remove and return some (key, value) pair  
as a 2-tuple; but raise `KeyError` if D is empty.

**setdefault**(*k*[, *d*]) → D.get(*k*,*d*), also set D[*k*]=*d* if *k* not in D

**update**([*E*], *\*\*F*) → None. Update D from mapping/iterable *E* and *F*.

If *E* present and has a `.keys()` method, does: for *k* in *E*: D[*k*] = *E*[*k*] If *E* present and lacks `.keys()` method, does: for (*k*, *v*) in *E*: D[*k*] = *v* In either case, this is followed by: for *k*, *v* in *F*.items(): D[*k*] = *v*

**values()** → an object providing a view on D's values

## 11.2.6 HierarchyScheme

```
class openff.toolkit.topology.HierarchyScheme(parent: FrozenMolecule, uniqueness_criteria:  
Union[Tuple[str], List[str]], iterator_name: str)
```

Perceives hierarchy elements from the metadata of atoms in a Molecule.

The Open Force Field Toolkit has no native understanding of hierarchical atom organisation schemes common to other biomolecular software, such as “residues” or “chains” (see [Hierarchy data \(chains and residues\)](#)). To facilitate iterating over groups of atoms, a `HierarchyScheme` can be used to collect atoms into `HierarchyElements`, groups of atoms that share the same values for certain metadata elements. Metadata elements are stored in the `Atom.properties` attribute.

Hierarchy schemes are not updated dynamically; if a `Molecule` with hierarchy schemes changes, `Molecule.update_hierarchy_schemes()` must be called before the scheme is iterated over again or else the grouping may be incorrect.

A `HierarchyScheme` contains the information needed to perceive `HierarchyElement` objects from a `Molecule` containing atoms with metadata.

**See also:**

`Molecule.add_default_hierarchy_schemes`, `Molecule.add_hierarchy_scheme`, `Molecule.hierarchy_schemes`, `Molecule.delete_hierarchy_scheme`, `Molecule.update_hierarchy_schemes`, `Molecule.perceive_residues`, `Topology.hierarchy_iterator`, `HierarchyElement`

```
__init__(parent: FrozenMolecule, uniqueness_criteria: Union[Tuple[str], List[str]], iterator_name:  
str)
```

Create a new hierarchy scheme for iterating over groups of atoms.

**Parameters**

- **parent** – The `Molecule` to which this scheme belongs.



- **uniqueness\_criteria** – The names of Atom metadata entries that define this scheme. An atom belongs to a `HierarchyElement` only if its metadata has the same values for these criteria as the other atoms in the `HierarchyElement`.
- **iterator\_name** – The name of the iterator that will be exposed to access the hierarchy elements generated by this scheme

## Methods

<code>__init__(parent, uniqueness_criteria, ...)</code>	Create a new hierarchy scheme for iterating over groups of atoms.
<code>add_hierarchy_element(identifier, atom_indices)</code>	Instantiate a new <code>HierarchyElement</code> belonging to this <code>HierarchyScheme</code> .
<code>perceive_hierarchy()</code>	Prepare the parent <code>Molecule</code> for iteration according to this scheme.
<code>sort_hierarchy_elements()</code>	Semantically sort the <code>HierarchyElements</code> belonging to this object, according to their identifiers.
<code>to_dict()</code>	Serialize this object to a basic dict of strings, ints, and floats

### `to_dict()`

Serialize this object to a basic dict of strings, ints, and floats

### `perceive_hierarchy()`

Prepare the parent `Molecule` for iteration according to this scheme.

Groups the atoms of the parent of this `HierarchyScheme` according to their metadata, and creates `HierarchyElement` objects suitable for iteration over the parent. Atoms missing the metadata fields in this object's `uniqueness_criteria` tuple will have those spots populated with the string `'None'`.

This method overwrites the scheme's `hierarchy_elements` attribute in place. Each `HierarchyElement` in the scheme's `hierarchy_elements` attribute is *static* — that is, it is updated only when `perceive_hierarchy()` is called, and *not* on-the-fly when atom metadata is modified.

### `add_hierarchy_element(identifier: Tuple[Union[str, int]], atom_indices: Sequence[int])`

Instantiate a new `HierarchyElement` belonging to this `HierarchyScheme`.

This is the main way to instantiate new `HierarchyElements`.

#### Parameters

- **identifier** (tuple of str and int) – Tuple of metadata values (not keys) that define the uniqueness criteria for this element
- **atom\_indices** (sequence of int) – The indices of atoms in `scheme.parent` that are in this element

### `sort_hierarchy_elements()`

Semantically sort the `HierarchyElements` belonging to this object, according to their identifiers.

## 11.2.7 HierarchyElement

**class** openff.toolkit.topology.HierarchyElement(scheme: HierarchyScheme, identifier: Tuple[Union[str, int]], atom\_indices: Sequence[int])

An element in a metadata hierarchy scheme, such as a residue or chain.

**\_\_init\_\_**(scheme: HierarchyScheme, identifier: Tuple[Union[str, int]], atom\_indices: Sequence[int])

Create a new hierarchy element.

### Parameters

- **scheme** (HierarchyScheme) – The scheme to which this HierarchyElement belongs
- **identifier** (tuple of str and int) – Tuple of metadata values (not keys) that define the uniqueness criteria for this element
- **atom\_indices** (sequence of int) – The indices of particles in scheme.parent that are in this element

### Methods

<code>__init__(scheme, identifier, atom_indices)</code>	Create a new hierarchy element.
<code>atom(index)</code>	Get the atom with the specified index.
<code>generate_unique_atom_names()</code>	Generate unique atom names from the element symbol and count.
<code>to_dict()</code>	Serialize this object to a basic dict of strings and lists of ints.

### Attributes

<code>atoms</code>	Iterator over the atoms in this hierarchy element.
<code>has_unique_atom_names</code>	True if the element has unique atom names, False otherwise.
<code>n_atoms</code>	The number of atoms in this hierarchy element.
<code>parent</code>	The parent molecule for this hierarchy element

**to\_dict()** → Dict[str, Union[Tuple[Union[str, int]], Sequence[int]]]

Serialize this object to a basic dict of strings and lists of ints.

**property n\_atoms:** int

The number of atoms in this hierarchy element.

**property atoms:** Generator[Atom, None, None]

Iterator over the atoms in this hierarchy element.

**atom(index: int)** → Atom

Get the atom with the specified index.

**property parent:** FrozenMolecule

The parent molecule for this hierarchy element

**property** `has_unique_atom_names`: `bool`

True if the element has unique atom names, False otherwise.

**generate\_unique\_atom\_names()**

Generate unique atom names from the element symbol and count.

Names are generated from the elemental symbol and the number of times that element is found in the hierarchy element. The character 'x' is appended to these generated names to reduce the odds that they clash with an atom name or type imported from another source. For example, generated atom names might begin 'C1x', 'H1x', 'O1x', 'C2x', etc.



## FORCE FIELD TYPING TOOLS

## 12.1 Chemical environments

Tools for representing and operating on chemical environments

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<code>ChemicalEnvironment</code>	Chemical environment abstract base class used for validating SMIRKS
----------------------------------	---

---

### 12.1.1 `ChemicalEnvironment`

```
class openff.toolkit.typing.chemistry.ChemicalEnvironment(smirks=None, label=None,
                                                         validate_parsable=True,
                                                         validate_valence_type=True,
                                                         toolkit_registry=None)
```

Chemical environment abstract base class used for validating SMIRKS

```
__init__(smirks=None, label=None, validate_parsable=True, validate_valence_type=True,
         toolkit_registry=None)
```

Initialize a chemical environment abstract base class.

**smirks = string, optional** if smirks is not None, a chemical environment is built from the provided SMIRKS string

**label = anything, optional** intended to be used to label this chemical environment could be a string, int, or float, or anything

**validate\_parsable: bool, optional, default=True** If specified, ensure the provided smirks is parsable

**validate\_valence\_type** [bool, optional, default=True] If specified, ensure the tagged atoms are appropriate to the specified valence type

**toolkit\_registry = string or ToolkitWrapper or ToolkitRegistry. Default = None** Either a ToolkitRegistry, ToolkitWrapper, or the strings 'openeye' or 'rdkit', indicating the backend to use for validating the correct connectivity of the SMIRKS during initialization. If None, this function will use the GLOBAL\_TOOLKIT\_REGISTRY

#### Raises

- **SMIRKSParsingError** – if smirks was unparsable
- **SMIRKSMismatchError** – if smirks did not have expected connectivity between tagged atoms and validate\_valence\_type=True

## Methods

<code>__init__([smirks, label, validate_parsable, ...])</code>	Initialize a chemical environment abstract base class.
<code>get_type([toolkit_registry])</code>	Return the valence type implied by the connectivity of the bound atoms in this ChemicalEnvironment.
<code>validate([validate_valence_type, ...])</code>	Returns True if the underlying smirks is the correct valence type, False otherwise.
<code>validate_smirks(smirks[, validate_parsable, ...])</code>	Check the provided SMIRKS string is valid, and if requested, tags atoms appropriate to the specified valence type.

**validate**(*validate\_valence\_type*=True, *toolkit\_registry*=None)

Returns True if the underlying smirks is the correct valence type, False otherwise. If the expected type is None, this method always returns True.

**validate\_valence\_type** [bool, optional, default=True] If specified, ensure the tagged atoms are appropriate to the specified valence type

**toolkit\_registry** = **ToolkitWrapper** or **ToolkitRegistry**. **Default = None** Either a **ToolkitRegistry** or **ToolkitWrapper**, indicating the backend to use for validating the correct connectivity of the SMIRKS during initialization. If None, this function will use the **GLOBAL\_TOOLKIT\_REGISTRY**

### Raises

- **SMIRKSParsingError** – if smirks was unparsable
- **SMIRKSMismatchError** – if smirks did not have expected connectivity between tagged atoms and *validate\_valence\_type*=True

**classmethod validate\_smirks**(*smirks*, *validate\_parsable*=True, *validate\_valence\_type*=True, *toolkit\_registry*=None)

Check the provided SMIRKS string is valid, and if requested, tags atoms appropriate to the specified valence type.

### Parameters

- **smirks** (*str*) – The SMIRKS expression to validate
- **validate\_parsable** (*bool*, optional, default=True) – If specified, ensure the provided smirks is parsable
- **validate\_valence\_type** (*bool*, optional, default=True) – If specified, ensure the tagged atoms are appropriate to the specified valence type
- **None** (*toolkit\_registry* = *string* or **ToolkitWrapper** or **ToolkitRegistry**. **Default =** ) – Either a **ToolkitRegistry**, **ToolkitWrapper**, or the strings ‘openeye’ or ‘rdkit’, indicating the backend to use for validating the correct connectivity of the SMIRKS during initialization. If None, this function will use the **GLOBAL\_TOOLKIT\_REGISTRY**

### Raises

- **SMIRKSParsingError** – if smirks was unparsable

- **SMIRKSMismatchError** – if smirks did not have expected connectivity between tagged atoms and `validate_valence_type=True`

**get\_type**(*toolkit\_registry=None*)

Return the valence type implied by the connectivity of the bound atoms in this ChemicalEnvironment.

**Parameters** **toolkit\_registry** (openff.toolkit.utils.ToolkitRegistry or openff.toolkit.utils.ToolkitWrapper) – The cheminformatics toolkit to use for parsing the smirks

**Returns** **valence\_type** (*str*) – One of “Atom”, “Bond”, “Angle”, “ProperTorsion”, “ImproperTorsion”, or None. If tagged atoms are not connected in a known pattern this method will return None.

**Raises** **SMIRKSParsingError** – if smirks was unparsable

## 12.2 Force field typing engines

Engines for applying parameters to chemical systems

### 12.2.1 The SMIRks-Native Open Force Field (SMIRNOFF)

A reference implementation of the SMIRNOFF specification for parameterizing biomolecular systems

#### ForceField

The ForceField class is a primary part of the top-level toolkit API. ForceField objects are initialized from SMIRNOFF data sources (e.g. an OFFXML file). For a basic example of OpenMM System creation using a ForceField, see `examples/SMIRNOFF_simulation`.

<code>ForceField</code>	A factory that assigns SMIRNOFF parameters to a molecular system
<code>get_available_force_fields</code>	Get the filenames of all available .offxml force field files.

#### ForceField

```
class openff.toolkit.typing.engines.smirnoff.ForceField(*sources, aromaticity_model=DEFAULT_AROMATICITY_MODEL,
parameter_handler_classes=None,
parameter_io_handler_classes=None,
disable_version_check=False,
allow_cosmetic_attributes=False,
load_plugins=False)
```

A factory that assigns SMIRNOFF parameters to a molecular system

`ForceField` is a factory that constructs an OpenMM `openmm.System` object from a `openff.toolkit.topology.Topology` object defining a (bio)molecular system containing one or more molecules.

When a `ForceField` object is created from one or more specified SMIRNOFF serialized representations, all `ParameterHandler` subclasses currently imported are identified and registered to handle different sections of the SMIRNOFF force field definition file(s).

All `ParameterIOHandler` subclasses currently imported are identified and registered to handle different serialization formats (such as XML).

The force field definition is processed by these handlers to populate the `ForceField` object model data structures that can easily be manipulated via the API:

Processing a `Topology` object defining a chemical system will then call all `ParameterHandler` objects in an order guaranteed to satisfy the declared processing order constraints of each `ParameterHandler`.

## Examples

Create a new `ForceField` object from the distributed OpenFF 2.0 (“Sage”) file:

```
>>> from openff.toolkit import ForceField
>>> force_field = ForceField('openff-2.0.0.offxml')
```

Create an OpenMM system from a `openff.toolkit.topology.Topology` object:

```
>>> from openff.toolkit import Molecule, Topology
>>> ethanol = Molecule.from_smiles('CCO')
>>> topology = Topology.from_molecules(molecules=[ethanol])
>>> system = force_field.create_openmm_system(topology)
```

Modify the long-range electrostatics method:

```
>>> force_field.get_parameter_handler('Electrostatics').periodic_potential = 'PME'
```

Inspect the first few vdW parameters:

```
>>> low_precedence_parameters = force_field.get_parameter_handler('vdW').parameters[0:3]
```

Retrieve the vdW parameters by SMIRKS string and manipulate it:

```
>>> from openff.units import unit
>>> parameter = force_field.get_parameter_handler('vdW').parameters['[#1:1]-[#7]']
>>> parameter.rmin_half += 0.1 * unit.angstroms
>>> parameter.epsilon *= 1.02
```

Make a child vdW type more specific (checking modified SMIRKS for validity):

```
>>> force_field.get_parameter_handler('vdW').parameters[-1].smirks += '~[#53]'
```

**Warning:** While we check whether the modified SMIRKS is still valid and has the appropriate valence type, we currently don’t check whether the typing remains hierarchical, which could result in some types no longer being assignable because more general types now come *below* them and preferentially match.

Delete a parameter:



```
>>> del force_field.get_parameter_handler('vdW').parameters['[#1:1]-[#6X4]']
```

Insert a parameter at a specific point in the parameter tree:

```
>>> from openff.toolkit.typing.engines.smirnoff import vdWHandler
>>> new_parameter = vdWHandler.vdWType(
...     smirks='[*:1]',
...     epsilon=0.0157*unit.kilocalories_per_mole,
...     rmin_half=0.6000*unit.angstroms,
... )
>>> force_field.get_parameter_handler('vdW').parameters.insert(0, new_parameter)
```

**Warning:** We currently don't check whether removing a parameter could accidentally remove the root type, so it's possible to no longer type all molecules this way.

```
__init__(*sources, aromaticity_model=DEFAULT_AROMATICITY_MODEL,
         parameter_handler_classes=None, parameter_io_handler_classes=None,
         disable_version_check=False, allow_cosmetic_attributes=False, load_plugins=False)
```

Create a new `ForceField` object from one or more SMIRNOFF parameter definition files.

#### Parameters

- **sources** (string or file-like object or open file handle or URL (or iterable of these)) – A list of files defining the SMIRNOFF force field to be loaded. Currently, only the SMIRNOFF XML format is supported. Each entry may be an absolute file path, a path relative to the current working directory, a path relative to this module's data subdirectory (for built in force fields), or an open file-like object with a `read()` method from which the force field XML data can be loaded. If multiple files are specified, any top-level tags that are repeated will be merged if they are compatible, with files appearing later in the sequence resulting in parameters that have higher precedence. Support for multiple files is primarily intended to allow solvent parameters to be specified by listing them last in the sequence.
- **aromaticity\_model** (`str`, optional, default="OEAroModel\_MDL") – The aromaticity model to use. Only OEAroModel\_MDL is supported.
- **parameter\_handler\_classes** (iterable of `ParameterHandler` classes, optional, default=None) – If not None, the specified set of `ParameterHandler` classes will be instantiated to create the parameter object model. By default, all imported subclasses of `ParameterHandler` not loaded as plugins are automatically registered.
- **parameter\_io\_handler\_classes** (iterable of `ParameterIOHandler` classes) – If not None, the specified set of `ParameterIOHandler` classes will be used to parse/generate serialized parameter sets. By default, all imported subclasses of `ParameterIOHandler` are automatically registered.
- **disable\_version\_check** (`bool`, optional, default=False) – If True, will disable checks against the current highest supported force field version. This option is primarily intended for force field development.
- **allow\_cosmetic\_attributes** (`bool`, optional. Default = False) – Whether to retain non-spec kwargs from data sources.

- **load\_plugins** (*bool*, optional. Default = False) – Whether to load ParameterHandler classes which have been registered by installed plugins.

### Examples

Load one SMIRNOFF parameter set in XML format (searching the package data directory by default, which includes some standard parameter sets):

```
>>> forcefield = ForceField('openff-2.0.0.offxml')
```

Load multiple SMIRNOFF parameter sets:

```
>>> from openff.toolkit.tests.utils import get_data_file_path
>>> forcefield = ForceField('openff-2.0.0.offxml', get_data_file_path('test_
↳ forcefields/tip3p.offxml'))
```

Load a parameter set from a string:

```
>>> offxml = '<SMIRNOFF version="0.2" aromaticity_model="OEAroModel_MDL"/>'
>>> forcefield = ForceField(offxml)
```

## Methods

<code>__init__(*sources[, aromaticity_model, ...])</code>	Create a new <code>ForceField</code> object from one or more SMIRNOFF parameter definition files.
<code>create_interchange(topology[, ...])</code>	Create an Interchange object from a ForceField, Topology, and (optionally) box vectors.
<code>create_openmm_system(topology, *[, ...])</code>	Create an OpenMM System from this ForceField and a Topology.
<code>deregister_parameter_handler(handler)</code>	Deregister a parameter handler specified by tag name, class, or instance.
<code>get_parameter_handler(tagname[, ...])</code>	Retrieve the parameter handlers associated with the provided tagname.
<code>get_parameter_io_handler(io_format)</code>	Retrieve the parameter handlers associated with the provided tagname.
<code>get_partial_charges(molecule, **kwargs)</code>	Generate the partial charges for the given molecule in this force field.
<code>label_molecules(topology)</code>	Return labels for a list of molecules corresponding to parameters from this force field.
<code>parse_smirnoff_from_source(source)</code>	Reads a SMIRNOFF data structure from a source, which can be one of many types.
<code>parse_sources(sources[, ...])</code>	Parse a SMIRNOFF force field definition.
<code>register_parameter_handler(parameter_handler)</code>	Register a new ParameterHandler for a specific tag, making it available for lookup in the ForceField.
<code>register_parameter_io_handler(...)</code>	Register a new ParameterIOHandler, making it available for lookup in the ForceField.
<code>to_file(filename[, io_format, ...])</code>	Write this Forcefield and all its associated parameters to a string in a given format which complies with the SMIRNOFF spec.
<code>to_string([io_format, ...])</code>	Write this Forcefield and all its associated parameters to a string in a given format which complies with the SMIRNOFF spec.

## Attributes

<code>aromaticity_model</code>	Returns the aromaticity model for this ForceField object.
<code>author</code>	Returns the author data for this ForceField object.
<code>date</code>	Returns the date data for this ForceField object.
<code>registered_parameter_handlers</code>	Return the list of registered parameter handlers by name

### property aromaticity\_model

Returns the aromaticity model for this ForceField object.

**Returns** `aromaticity_model` – The aromaticity model for this force field.

### property author

Returns the author data for this ForceField object. If not defined in any loaded files, this will be `None`.

**Returns** **author** (*str*) – The author data for this force field.

**property date**

Returns the date data for this ForceField object. If not defined in any loaded files, this will be None.

**Returns** **date** (*str*) – The date data for this force field.

**register\_parameter\_handler**(*parameter\_handler*)

Register a new ParameterHandler for a specific tag, making it available for lookup in the ForceField.

**Warning:** This API is experimental and subject to change.

**Parameters** **parameter\_handler** (A `ParameterHandler` object) – The `ParameterHandler` to register. The `TAGNAME` attribute of this object will be used as the key for registration.

**register\_parameter\_io\_handler**(*parameter\_io\_handler*)

Register a new ParameterIOHandler, making it available for lookup in the ForceField.

**Warning:** This API is experimental and subject to change.

**Parameters** **parameter\_io\_handler** (A `ParameterIOHandler` object) – The `ParameterIOHandler` to register. The `FORMAT` attribute of this object will be used to associate it to a file format/suffix.

**property registered\_parameter\_handlers: List[str]**

Return the list of registered parameter handlers by name

**Warning:** This API is experimental and subject to change.

**Returns** **registered\_parameter\_handlers** (*iterable of names of ParameterHandler objects in this ForceField*)

**get\_parameter\_handler**(*tagname*, *handler\_kwargs=None*, *allow\_cosmetic\_attributes=False*)

Retrieve the parameter handlers associated with the provided tagname.

If the parameter handler has not yet been instantiated, it will be created and returned. If a parameter handler object already exists, it will be checked for compatibility and an `Exception` raised if it is incompatible with the provided `kwargs`. If compatible, the existing `ParameterHandler` will be returned.

**Parameters**

- **tagname** (*str*) – The name of the parameter to be handled.
- **handler\_kwargs** (*dict*, optional. Default = None) – Dict to be passed to the handler for construction or checking compatibility. If this is None and no existing `ParameterHandler` exists for the desired tag, a handler will be initialized with all default values. If this is None and a handler for the desired tag exists, the existing `ParameterHandler` will be returned.

- **allow\_cosmetic\_attributes** (*bool*, optional. Default = False) – Whether to permit non-spec kwargs in `smirnoff_data`.

**Returns handler** (*An `openff.toolkit.engines.typing.smirnoff.ParameterHandler`*)

**Raises `KeyError`** – If there is no `ParameterHandler` for the given tagname

**get\_parameter\_io\_handler**(*io\_format*)

Retrieve the parameter handlers associated with the provided tagname. If the parameter IO handler has not yet been instantiated, it will be created.

**Parameters io\_format** (*str*) – The name of the io format to be handled.

**Returns io\_handler** (*An `openff.toolkit.engines.typing.smirnoff.ParameterIOHandler`*)

**Raises `KeyError`** – If there is no `ParameterIOHandler` for the given tagname

**deregister\_parameter\_handler**(*handler*)

Deregister a parameter handler specified by tag name, class, or instance.

**Parameters handler** (*str, `openff.toolkit.typing.engines.smirnoff.ParameterHandler`-derived type or `object`*) – The handler to deregister.

**parse\_sources**(*sources, allow\_cosmetic\_attributes=True*)

Parse a SMIRNOFF force field definition.

**Parameters**

- **sources** (string or file-like object or open file handle or URL (or iterable of these)) – A list of files defining the SMIRNOFF force field to be loaded. Currently, only the `SMIRNOFF XML format` is supported. Each entry may be an absolute file path, a path relative to the current working directory, a path relative to this module's data subdirectory (for built in force fields), or an open file-like object with a `read()` method from which the force field XML data can be loaded. If multiple files are specified, any top-level tags that are repeated will be merged if they are compatible, with files appearing later in the sequence resulting in parameters that have higher precedence. Support for multiple files is primarily intended to allow solvent parameters to be specified by listing them last in the sequence.
- **allow\_cosmetic\_attributes** (*bool*, optional. Default = False) – Whether to permit non-spec kwargs present in the source.

## Notes

- New SMIRNOFF sections are handled independently, as if they were specified in the same file.
- If a SMIRNOFF section that has already been read appears again, its definitions are appended to the end of the previously-read definitions if the sections are configured with compatible attributes; otherwise, an `IncompatibleTagException` is raised.

**parse\_smirnoff\_from\_source**(*source*) → *dict*

Reads a SMIRNOFF data structure from a source, which can be one of many types.

**Parameters source** (*str or bytes or file-like object*) – File defining the SMIRNOFF force field to be loaded. Currently, only the `SMIRNOFF XML format` is supported. The file may be an absolute file path, a path relative to the current working directory, a path relative to this module's data subdirectory (for built in force fields), or an open file-like object with a `read()` method from which the force field XML data can be loaded.

**Returns** `smirnoff_data` (*dict*) – A representation of a SMIRNOFF-format data structure. Begins at top-level ‘SMIRNOFF’ key.

**to\_string**(*io\_format*='XML', *discard\_cosmetic\_attributes*=False)

Write this Forcefield and all its associated parameters to a string in a given format which complies with the SMIRNOFF spec.

**Parameters**

- **io\_format** (*str* or `ParameterIOHandler`, optional. Default='XML') – The serialization format to write to
- **discard\_cosmetic\_attributes** (*bool*, default=False) – Whether to discard any non-spec attributes stored in the ForceField.

**Returns** `forcefield_string` (*str*) – The string representation of the serialized force field

**to\_file**(*filename*, *io\_format*=None, *discard\_cosmetic\_attributes*=False)

Write this Forcefield and all its associated parameters to a string in a given format which complies with the SMIRNOFF spec.

**Parameters**

- **filename** (*str*) – The filename to write to
- **io\_format** (*str* or `ParameterIOHandler`, optional. Default=None) – The serialization format to write out. If None, will attempt to be inferred from the filename.
- **discard\_cosmetic\_attributes** (*bool*, default=False) – Whether to discard any non-spec attributes stored in the ForceField.

**Returns** `forcefield_string` (*str*) – The string representation of the serialized force field

**create\_openmm\_system**(*topology*: `Topology`, \*, *return\_topology*: *bool* = False, *toolkit\_registry*: *Optional*[*Union*[`ToolkitRegistry`, `ToolkitWrapper`]] = None, *charge\_from\_molecules*: *Optional*[*List*[`Molecule`]] = None, *partial\_bond\_orders\_from\_molecules*: *Optional*[*List*[`Molecule`]] = None, *allow\_nonintegral\_charges*: *bool* = False) → *Union*[`openmm.System`, *Tuple*[`openmm.System`, `Topology`]]

Create an OpenMM System from this ForceField and a Topology.

**Parameters**

- **topology** – The Topology which is to be parameterized with this ForceField.
- **toolkit\_registry** – The toolkit registry to use for parametrization (eg, for calculating partial charges and partial bond orders)
- **charge\_from\_molecules** – Take partial charges from the input topology rather than calculating them. This may be useful for avoiding recalculating charges, but take care to ensure that your charges are appropriate for the force field.
- **partial\_bond\_orders\_from\_molecules** – Take partial bond orders from the input topology rather than calculating them. This may be useful for avoiding recalculating PBOs, but take to ensure that they are appropriate for the force field.
- **allow\_nonintegral\_charges** – Allow charges that do not sum to an integer.
- **return\_topology** – Deprecated since version 0.11.0: The *return\_topology* argument has been deprecated and will be removed in v0.12.0. Call `ForceField.create_interchange()` and take the topology from *interchange.topology* instead.

Return the Topology with any modifications needed to parametrize it in a tuple along with the OpenMM system.

```
create_interchange(topology: Topology, toolkit_registry: Optional[Union[ToolkitRegistry,  

ToolkitWrapper]] = None, charge_from_molecules: Optional[List[Molecule]] =  

None, partial_bond_orders_from_molecules: Optional[List[Molecule]] = None,  

allow_nonintegral_charges: bool = False)
```

Create an Interchange object from a ForceField, Topology, and (optionally) box vectors.

WARNING: This API and functionality are experimental and not suitable for production.

#### Parameters

- **topology** ([Topology](#)) – The topology to create this *Interchange* object from.
- **toolkit\_registry** – The toolkit registry to use for parametrization (eg, for calculating partial charges and partial bond orders)
- **charge\_from\_molecules** – Take charges from the input topology rather than calculating them. This may be useful for avoiding recalculating charges, but take care to ensure that your charges are appropriate for the force field.
- **partial\_bond\_orders\_from\_molecules** – Take partial bond orders from the input topology rather than calculating them. This may be useful for avoiding recalculating PBOs, but take to ensure that they are appropriate for the force field.
- **allow\_nonintegral\_charges** – Allow charges that do not sum to an integer.

**Returns** *interchange* (*openff.interchange.Interchange*) – An *Interchange* object resulting from applying this *ForceField* to a *Topology*.

```
label_molecules(topology)
```

Return labels for a list of molecules corresponding to parameters from this force field. For each molecule, a dictionary of force types is returned, and for each force type, each force term is provided with the atoms involved, the parameter id assigned, and the corresponding SMIRKS.

**Parameters** **topology** ([Topology](#)) – A *Topology* object containing one or more unique molecules to be labeled

#### Returns

- **molecule\_labels** (*list*) – List of labels for unique molecules. Each entry in the list corresponds to one unique molecule in the *Topology* and is a dictionary keyed by force type, i.e., `molecule_labels[0]['HarmonicBondForce']` gives details for the harmonic bond parameters for the first molecule. Each element is a list of the form: `[ ( [ atom1, ..., atomN], parameter_id, SMIRKS), ... ]`.
- *.. todo ::* – What is the most useful API for this method? Should we instead accept *Molecule* objects as input and individually return labels? Should we attach the labels to the *Molecule* object? Or should we label all interactions in a *Topology* instead of just labeling its

unique\_molecules?

```
get_partial_charges(molecule: Molecule, **kwargs) → unit.Quantity
```

Generate the partial charges for the given molecule in this force field.

#### Parameters

- **molecule** (*openff.toolkit.topology.Molecule*) – The *Molecule* corresponding to the system to be parameterized

- **toolkit\_registry** (`openff.toolkit.utils.toolkits.ToolkitRegistry`, default=`GLOBAL_TOOLKIT_REGISTRY`) – The toolkit registry to use for operations like conformer generation and partial charge assignment.

**Returns** **charges** (`openmm.unit.Quantity` with shape `(n_atoms,)` and dimensions of charge) – The partial charges of the provided molecule in this force field.

**Raises**

- **PartialChargeVirtualSitesError** – If the ForceField applies virtual sites to the Molecule. `get_partial_charges` cannot identify which virtual site charges may belong to which atoms in this case.
- **Other exceptions** – As any ParameterHandler may in principle modify charges, the entire force field must be applied to the molecule to produce the charges. Calls to this method from incorrectly or incompletely specified ForceField objects thus may raise an exception.

### Examples

```
>>> from openff.toolkit import ForceField, Molecule
>>> ethanol = Molecule.from_smiles('CCO')
>>> force_field = ForceField('openff-2.0.0.offxml')
```

Assign partial charges to the molecule according to the force field:

```
>>> ethanol.partial_charges = force_field.get_partial_charges(ethanol)
```

Use the assigned partial charges when creating an OpenMM System:

```
>>> topology = ethanol.to_topology()
>>> system = force_field.create_openmm_system(
...     topology,
...     charge_from_molecules=[ethanol]
... )
```

This is especially useful when you want to create multiple systems with the same molecule or molecules, as it allows the expensive charge calculation to be cached.

### `get_available_force_fields`

`openff.toolkit.typing.engines.smirnoff.get_available_force_fields(full_paths=False)`

Get the filenames of all available `.offxml` force field files.

Availability is determined by what is discovered through the `openforcefield.smirnoff_forcefield_directory` entry point. If the `openff-forcefields` package is installed, this should include several `.offxml` files such as `openff-1.0.0.offxml`.

**Parameters** **full\_paths** (`bool`, default=`False`) – If `False`, return the name of each available `*.offxml` file. If `True`, return the full path to each available `*.offxml` file.

**Returns** **available\_force\_fields** (`List[str]`) – List of available force field files



## Parameter Type

ParameterType objects are representations of individual SMIRKS-based SMIRNOFF parameters. These are usually initialized during ForceField creation, and can be inspected and modified by users via the Python API. For more information, see `examples/forcefield_modification`.

---

ParameterType

Base class for SMIRNOFF parameter types.

---

### ParameterType

```
class openff.toolkit.typing.engines.smirnoff.ParameterType(smirks, allow_cosmetic_attributes=False,
                                                         **kwargs)
```

Base class for SMIRNOFF parameter types.

This base class provides utilities to create new parameter types. See the below for examples of how to do this.

**Warning:** This API is experimental and subject to change.

#### Attributes

- **smirks** (*str*) – The SMIRKS pattern that this parameter matches.
- **id** (*str or None*) – An optional identifier for the parameter.
- **parent\_id** (*str or None*) – Optionally, the identifier of the parameter of which this parameter is a specialization.

#### See also:

ParameterAttribute, IndexedParameterAttribute

### Examples

This class allows to define new parameter types by just listing its attributes. In the example below, `_ELEMENT_NAME` is used to describe the SMIRNOFF parameter being defined, and is used during automatic serialization/deserialization into a dict.

```
>>> class MyBondParameter(ParameterType):
...     _ELEMENT_NAME = 'Bond'
...     length = ParameterAttribute(unit=unit.angstrom)
...     k = ParameterAttribute(unit=unit.kilocalorie / unit.mole / unit.angstrom**2)
... 
```

The parameter automatically inherits the required `smirks` attribute from `ParameterType`. Associating a unit to a `ParameterAttribute` cause the attribute to accept only values in compatible units and to parse string expressions.

```
>>> my_par = MyBondParameter(
...     smirks='[*:1]-[*:2]',
...     length='1.01 * angstrom',
...     k=5 * unit.kilocalorie / unit.mole / unit.angstrom**2
... )
```

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```

... )
>>> my_par.length
<Quantity(1.01, 'angstrom')>
>>> my_par.k = 3.0 * unit.gram
Traceback (most recent call last):
...
openff.toolkit.utils.exceptions.IncompatibleUnitError:
k=3.0 gram should have units of kilocalorie / angstrom ** 2 / mole

```

Each attribute can be made optional by specifying a default value, and you can attach a converter function by passing a callable as an argument or through the decorator syntax.

```

>>> class MyParameterType(ParameterType):
...     _ELEMENT_NAME = 'Atom'
...
...     attr_optional = ParameterAttribute(default=2)
...     attr_all_to_float = ParameterAttribute(converter=float)
...     attr_int_to_float = ParameterAttribute()
...
...     @attr_int_to_float.converter
...     def attr_int_to_float(self, attr, value):
...         # This converter converts only integers to floats
...         # and raise an exception for the other types.
...         if isinstance(value, int):
...             return float(value)
...         elif not isinstance(value, float):
...             raise TypeError(f"Cannot convert '{value}' to float")
...         return value
...
>>> my_par = MyParameterType(smirks='[*:1]', attr_all_to_float='3.0', attr_int_to_
↪float=1)
>>> my_par.attr_optional
2
>>> my_par.attr_all_to_float
3.0
>>> my_par.attr_int_to_float
1.0

```

The float() function can convert strings to integers, but our custom converter forbids it

```

>>> my_par.attr_all_to_float = '2.0'
>>> my_par.attr_int_to_float = '4.0'
Traceback (most recent call last):
...
TypeError: Cannot convert '4.0' to float

```

Parameter attributes that can be indexed can be handled with the IndexedParameterAttribute. These support unit validation and converters exactly as ParameterAttributes, but the validation/conversion is performed for each indexed attribute.

```

>>> class MyTorsionType(ParameterType):
...     _ELEMENT_NAME = 'Proper'
...     periodicity = IndexedParameterAttribute(converter=int)

```

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```

...     k = IndexedParameterAttribute(unit=unit.kilocalorie / unit.mole)
...
>>> my_par = MyTorsionType(
...     smirks='[*:1]-[*:2]-[*:3]-[*:4]',
...     periodicity1=2,
...     k1=5 * unit.kilocalorie / unit.mole,
...     periodicity2='3',
...     k2=6 * unit.kilocalorie / unit.mole,
... )
>>> my_par.periodicity
[2, 3]

```

Indexed attributes, can be accessed both as a list or as their indexed parameter name.

```

>>> my_par.periodicity2 = 6
>>> my_par.periodicity[0] = 1
>>> my_par.periodicity
[1, 6]

```

**\_\_init\_\_**(*smirks*, *allow\_cosmetic\_attributes*=False, *\*\*kwargs*)

Create a ParameterType.

#### Parameters

- **smirks** (*str*) – The SMIRKS match for the provided parameter type.
- **allow\_cosmetic\_attributes** (bool optional. Default = False) – Whether to permit non-spec kwargs (“cosmetic attributes”). If True, non-spec kwargs will be stored as an attribute of this parameter which can be accessed and written out. Otherwise an exception will be raised.

#### Methods

<code>__init__(smirks[, allow_cosmetic_attributes])</code>	Create a ParameterType.
<code>add_cosmetic_attribute(attr_name, attr_value)</code>	Add a cosmetic attribute to this object.
<code>attribute_is_cosmetic(attr_name)</code>	Determine whether an attribute of this object is cosmetic.
<code>delete_cosmetic_attribute(attr_name)</code>	Delete a cosmetic attribute from this object.
<code>to_dict([discard_cosmetic_attributes, ...])</code>	Convert this object to dict format.

#### Attributes

<code>id</code>
<code>parent_id</code>
<code>smirks</code>

**add\_cosmetic\_attribute**(*attr\_name*, *attr\_value*)

Add a cosmetic attribute to this object.

This attribute will not have a functional effect on the object in the OpenFF Toolkit, but can be written out during output.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters**

- **attr\_name** (*str*) – Name of the attribute to define for this object.
- **attr\_value** (*str*) – The value of the attribute to define for this object.

**attribute\_is\_cosmetic**(*attr\_name*)

Determine whether an attribute of this object is cosmetic.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** **attr\_name** (*str*) – The attribute name to check

**Returns** **is\_cosmetic** (*bool*) – Returns True if the attribute is defined and is cosmetic.  
Returns False otherwise.

**delete\_cosmetic\_attribute**(*attr\_name*)

Delete a cosmetic attribute from this object.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** **attr\_name** (*str*) – Name of the cosmetic attribute to delete.

**to\_dict**(*discard\_cosmetic\_attributes=False*, *duplicate\_attributes=None*)

Convert this object to dict format.

The returning dictionary contains all the ParameterAttribute and IndexedParameterAttribute as well as cosmetic attributes if `discard_cosmetic_attributes` is False.

**Parameters**

- **discard\_cosmetic\_attributes** (*bool*, optional. Default = False) – Whether to discard non-spec attributes of this object
- **duplicate\_attributes** (list of string, optional. Default = None) – A list of names of attributes that redundantly describe data and should be discarded during serialization

**Returns** **smirnoff\_dict** (*dict*) – The SMIRNOFF-compliant dict representation of this object.

## Parameter Handlers

Each ForceField primarily consists of several ParameterHandler objects, which each contain the machinery to add one energy component to an OpenMM System. During System creation, each ParameterHandler registered to a ForceField has its `assign_parameters()` function called.

<code>ParameterList</code>	Parameter list that also supports accessing items by SMARTS string.
<code>ParameterHandler</code>	Base class for parameter handlers.
<code>ConstraintHandler</code>	Handle SMIRNOFF <Constraints> tags
<code>BondHandler</code>	Handle SMIRNOFF <Bonds> tags
<code>AngleHandler</code>	Handle SMIRNOFF <AngleForce> tags
<code>ProperTorsionHandler</code>	Handle SMIRNOFF <ProperTorsionForce> tags
<code>ImproperTorsionHandler</code>	Handle SMIRNOFF <ImproperTorsionForce> tags
<code>vdWHandler</code>	Handle SMIRNOFF <vdW> tags
<code>ElectrostaticsHandler</code>	Handles SMIRNOFF <Electrostatics> tags.
<code>LibraryChargeHandler</code>	Handle SMIRNOFF <LibraryCharges> tags
<code>ToolkitAM1BCCHandler</code>	Handle SMIRNOFF <ToolkitAM1BCC> tags
<code>GBSAHandler</code>	Handle SMIRNOFF <GBSA> tags
<code>ChargeIncrementModelHandler</code>	Handle SMIRNOFF <ChargeIncrementModel> tags
<code>VirtualSiteHandler</code>	Handle SMIRNOFF <VirtualSites> tags TODO: Add example usage/documentation .

## ParameterList

**class** `openff.toolkit.typing.engines.smirnoff.parameters.ParameterList(input_parameter_list=None)`  
Parameter list that also supports accessing items by SMARTS string.

**Warning:** This API is experimental and subject to change.

**\_\_init\_\_**(`input_parameter_list=None`)

Initialize a new ParameterList, optionally providing a list of ParameterType objects to initially populate it.

**Parameters** `input_parameter_list` (`list[ParameterType]`, `default=None`) – A pre-existing list of ParameterType-based objects. If None, this ParameterList will be initialized empty.

## Methods

<code>__init__([input_parameter_list])</code>	Initialize a new <code>ParameterList</code> , optionally providing a list of <code>ParameterType</code> objects to initially populate it.
<code>append(parameter)</code>	Add a <code>ParameterType</code> object to the end of the <code>ParameterList</code>
<code>clear()</code>	Remove all items from list.
<code>copy()</code>	Return a shallow copy of the list.
<code>count(value, /)</code>	Return number of occurrences of value.
<code>extend(other)</code>	Add a <code>ParameterList</code> object to the end of the <code>ParameterList</code>
<code>index(item)</code>	Get the numerical index of a <code>ParameterType</code> object or SMIRKS in this <code>ParameterList</code> .
<code>insert(index, parameter)</code>	Add a <code>ParameterType</code> object as if this were a list
<code>pop([index])</code>	Remove and return item at index (default last).
<code>remove(value, /)</code>	Remove first occurrence of value.
<code>reverse()</code>	Reverse <i>IN PLACE</i> .
<code>sort(*[, key, reverse])</code>	Sort the list in ascending order and return None.
<code>to_list([discard_cosmetic_attributes])</code>	Render this <code>ParameterList</code> to a normal list, serializing each <code>ParameterType</code> object in it to dict.

### `append(parameter)`

Add a `ParameterType` object to the end of the `ParameterList`

**Parameters** `parameter` (a `ParameterType` object) –

### `extend(other)`

Add a `ParameterList` object to the end of the `ParameterList`

**Parameters** `other` (a `ParameterList`) –

### `index(item)`

Get the numerical index of a `ParameterType` object or SMIRKS in this `ParameterList`. Raises `ParameterLookupError` if the item is not found.

**Parameters** `item` (`ParameterType` object or `str`) – The parameter or SMIRKS to look up in this `ParameterList`

**Returns** `index` (`int`) – The index of the found item

**Raises** `ParameterLookupError` if SMIRKS pattern is passed in but not found –

### `insert(index, parameter)`

Add a `ParameterType` object as if this were a list

**Parameters**

- `index` (`int`) – The numerical position to insert the parameter at
- `parameter` (a `ParameterType` object) – The parameter to insert

### `to_list(discard_cosmetic_attributes=True)`

Render this `ParameterList` to a normal list, serializing each `ParameterType` object in it to dict.

**Parameters** `discard_cosmetic_attributes` (`bool`, optional. Default = `True`) – Whether to discard non-spec attributes of each `ParameterType` object.

**Returns** `parameter_list` (`List[dict]`) – A serialized representation of a `ParameterList`, with each `ParameterType` it contains converted to dict.

**clear()**

Remove all items from list.

**copy()**

Return a shallow copy of the list.

**count**(`value`, /)

Return number of occurrences of value.

**pop**(`index=- 1`, /)

Remove and return item at index (default last).

Raises `IndexError` if list is empty or index is out of range.

**remove**(`value`, /)

Remove first occurrence of value.

Raises `ValueError` if the value is not present.

**reverse()**

Reverse *IN PLACE*.

**sort**(`*`, `key=None`, `reverse=False`)

Sort the list in ascending order and return `None`.

The sort is in-place (i.e. the list itself is modified) and stable (i.e. the order of two equal elements is maintained).

If a key function is given, apply it once to each list item and sort them, ascending or descending, according to their function values.

The reverse flag can be set to sort in descending order.

## ParameterHandler

```
class openff.toolkit.typing.engines.smirnoff.parameters.ParameterHandler(allow_cosmetic_attributes=False,
                                                                           skip_version_check=False,
                                                                           **kwargs)
```

Base class for parameter handlers.

Parameter handlers are configured with some global parameters for a given section. They may also contain a `ParameterList` populated with `ParameterType` objects if they are responsible for assigning SMIRKS-based parameters.

**Warning:** This API is experimental and subject to change.

**\_\_init\_\_**(`allow_cosmetic_attributes=False`, `skip_version_check=False`, `**kwargs`)

Initialize a `ParameterHandler`, optionally with a list of parameters and other kwargs.

### Parameters

- **allow\_cosmetic\_attributes** (`bool`, optional. Default = `False`) – Whether to permit non-spec kwargs. If `True`, non-spec kwargs will be stored as attributes of this

object and can be accessed and modified. Otherwise an exception will be raised if a non-spec kwarg is encountered.

- **skip\_version\_check** (*bool*, optional. Default = False) – If False, the SMIRNOFF section version will not be checked, and the ParameterHandler will be initialized with version set to `_MAX_SUPPORTED_SECTION_VERSION`.
- **\*\*kwargs** (*dict*) – The dict representation of the SMIRNOFF data source

## Methods

<code>__init__([allow_cosmetic_attributes, ...])</code>	Initialize a ParameterHandler, optionally with a list of parameters and other kwargs.
<code>add_cosmetic_attribute(attr_name, attr_value)</code>	Add a cosmetic attribute to this object.
<code>add_parameter([parameter_kwargs, parameter, ...])</code>	Add a parameter to the force field, ensuring all parameters are valid.
<code>attribute_is_cosmetic(attr_name)</code>	Determine whether an attribute of this object is cosmetic.
<code>check_handler_compatibility(handler_kwargs)</code>	Checks if a set of kwargs used to create a ParameterHandler are compatible with this ParameterHandler.
<code>create_force(*args, **kwargs)</code>	Deprecated since version 0.11.0.
<code>delete_cosmetic_attribute(attr_name)</code>	Delete a cosmetic attribute from this object.
<code>find_matches(entity[, unique])</code>	Find the elements of the topology/molecule matched by a parameter type.
<code>get_parameter(parameter_attrs)</code>	Return the parameters in this ParameterHandler that match the <code>parameter_attrs</code> argument.
<code>to_dict([discard_cosmetic_attributes])</code>	Convert this ParameterHandler to a dict, compliant with the SMIRNOFF data spec.

## Attributes

<code>TAGNAME</code>	The name of this ParameterHandler corresponding to the SMIRNOFF tag name
<code>known_kwargs</code>	List of kwargs that can be parsed by the function.
<code>parameters</code>	The ParameterList that holds this ParameterHandler's parameter objects
<code>version</code>	

### property parameters

The ParameterList that holds this ParameterHandler's parameter objects

### property TAGNAME

The name of this ParameterHandler corresponding to the SMIRNOFF tag name

Returns **handler\_name** (*str*) – The name of this parameter handler



**property known\_kwargs**

List of kwargs that can be parsed by the function.

**check\_handler\_compatibility(handler\_kwargs)**

Checks if a set of kwargs used to create a ParameterHandler are compatible with this ParameterHandler. This is called if a second handler is attempted to be initialized for the same tag.

**Parameters** *handler\_kwargs* (*dict*) – The kwargs that would be used to construct

**Raises** *IncompatibleParameterError* if *handler\_kwargs* are incompatible with existing parameters. –

**add\_parameter(parameter\_kwargs=None, parameter=None, after=None, before=None)**

Add a parameter to the force field, ensuring all parameters are valid.

**Parameters**

- **parameter\_kwargs** (*dict*, optional) – The kwargs to pass to the ParameterHandler.INFO\_TYPE (a ParameterType) constructor
- **parameter** (*ParameterType*, optional) – A ParameterType to add to the ParameterHandler
- **after** (*str* or *int*, optional) – The SMIRKS pattern (if *str*) or index (if *int*) of the parameter directly before where the new parameter will be added
- **before** (*str*, optional) – The SMIRKS pattern (if *str*) or index (if *int*) of the parameter directly after where the new parameter will be added
- **behavior** (Note the following) –
  - Either *parameter\_kwargs* or *parameter* must be specified.
  - When *before* and *after* are both *None*, the new parameter will be appended to the **END** of the parameter list.
  - When *before* and *after* are both specified, the new parameter will be added immediately after the parameter matching the *after* pattern or index.
  - The order of parameters in a parameter list can have significant impacts on parameter assignment. For details, see the SMIRNOFF specification: <https://openforcefield.github.io/standards/standards/smirnoff/#smirnoff-parameter-specification-is-hierarchical>

**Examples**

Add a ParameterType to an existing ParameterList at a specified position.

Given an existing parameter handler and a new parameter to add to it:

```
>>> from openff.units import unit
>>> bh = BondHandler(skip_version_check=True)
>>> length = 1.5 * unit.angstrom
>>> k = 100 * unit.kilocalorie / unit.mole / unit.angstrom ** 2
>>> bh.add_parameter({'smirks': '[*:1]-[:2]', 'length': length, 'k': k, 'id': 'b1'})
↳
>>> bh.add_parameter({'smirks': '[*:1]=[:2]', 'length': length, 'k': k, 'id': 'b2'})
↳
>>> bh.add_parameter({'smirks': '[*:1]#[:2]', 'length': length, 'k': k, 'id': 'b3'})
↳
```

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```
>>> [p.id for p in bh.parameters]
['b1', 'b2', 'b3']
```

```
>>> param = {'smirks': '[*:1]-[*:2]', 'length': length, 'k': k, 'id': 'b4'}
```

Add a new parameter immediately after the parameter with the smirks `[:1]=[:2]`

```
>>> bh.add_parameter(param, after='[*:1]=[*:2]')
>>> [p.id for p in bh.parameters]
['b1', 'b2', 'b4', 'b3']
```

### `get_parameter(parameter_attrs)`

Return the parameters in this ParameterHandler that match the `parameter_attrs` argument. When multiple attrs are passed, parameters that have any (not all) matching attributes are returned.

**Parameters** `parameter_attrs` (dict of {attr: value}) – The attrs mapped to desired values (for example {"smirks": "[\*:1]~[#16:2]=,[:#6:3]~[:4]", "id": "t105"})

**Returns** `params` (list of *ParameterType* objects) – A list of matching *ParameterType* objects

## Examples

Create a parameter handler and populate it with some data.

```
>>> from openff.units import unit
>>> handler = BondHandler(skip_version_check=True)
>>> handler.add_parameter(
...     {
...         'smirks': '[*:1]-[*:2]',
...         'length': 1*unit.angstrom,
...         'k': 10*unit.kilocalorie / unit.mole/unit.angstrom**2,
...     }
... )
```

Look up, from this handler, all parameters matching some SMIRKS pattern

```
>>> handler.get_parameter({'smirks': '[*:1]-[*:2]'})
[<BondType with smirks: [*:1]-[*:2] length: 1 angstrom k: 10.0 kilocalorie /
↳ angstrom ** 2 / mole >]
```

### `find_matches(entity, unique=False)`

Find the elements of the topology/molecule matched by a parameter type.

#### Parameters

- **entity** (*Topology*) – Topology to search.
- **unique** (*bool*, default=False) – If False, SMARTS matching will enumerate every valid permutation of matching atoms. If True, only one order of each unique match will be returned.

**Returns** `matches` (*ValenceDict[Tuple[int], ParameterHandler.Match]*) – `matches[atom_indices]` is the *ParameterType* object matching the tuple of atom indices in `entity`.

**create\_force**(\*args, \*\*kwargs)

Deprecated since version 0.11.0: This method was deprecated in v0.11.0, no longer has any functionality, and will soon be removed. Use the [OpenFF Interchange](#) package instead.

**to\_dict**(discard\_cosmetic\_attributes=False)

Convert this ParameterHandler to a dict, compliant with the SMIRNOFF data spec.

**Parameters** **discard\_cosmetic\_attributes** (*bool*, optional. Default = False.) – Whether to discard non-spec parameter and header attributes in this ParameterHandler.

**Returns** **smirnoff\_data** (*dict*) – SMIRNOFF-spec compliant representation of this ParameterHandler and its internal ParameterList.

**add\_cosmetic\_attribute**(attr\_name, attr\_value)

Add a cosmetic attribute to this object.

This attribute will not have a functional effect on the object in the OpenFF Toolkit, but can be written out during output.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

#### Parameters

- **attr\_name** (*str*) – Name of the attribute to define for this object.
- **attr\_value** (*str*) – The value of the attribute to define for this object.

**attribute\_is\_cosmetic**(attr\_name)

Determine whether an attribute of this object is cosmetic.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** **attr\_name** (*str*) – The attribute name to check

**Returns** **is\_cosmetic** (*bool*) – Returns True if the attribute is defined and is cosmetic. Returns False otherwise.

**delete\_cosmetic\_attribute**(attr\_name)

Delete a cosmetic attribute from this object.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** **attr\_name** (*str*) – Name of the cosmetic attribute to delete.

## ConstraintHandler

```
class openff.toolkit.typing.engines.smirnoff.parameters.ConstraintHandler(allow_cosmetic_attributes=False,
                                                                    skip_version_check=False,
                                                                    **kwargs)
```

Handle SMIRNOFF <Constraints> tags

ConstraintHandler must be applied before BondHandler and AngleHandler, since those classes add constraints for which equilibrium geometries are needed from those tags.

**Warning:** This API is experimental and subject to change.

```
__init__(allow_cosmetic_attributes=False, skip_version_check=False, **kwargs)
```

Initialize a ParameterHandler, optionally with a list of parameters and other kwargs.

### Parameters

- **allow\_cosmetic\_attributes** (*bool*, optional. Default = False) – Whether to permit non-spec kwargs. If True, non-spec kwargs will be stored as attributes of this object and can be accessed and modified. Otherwise an exception will be raised if a non-spec kwarg is encountered.
- **skip\_version\_check** (*bool*, optional. Default = False) – If False, the SMIRNOFF section version will not be checked, and the ParameterHandler will be initialized with version set to `_MAX_SUPPORTED_SECTION_VERSION`.
- **\*\*kwargs** (*dict*) – The dict representation of the SMIRNOFF data source

### Methods

<code>__init__([allow_cosmetic_attributes, ...])</code>	Initialize a ParameterHandler, optionally with a list of parameters and other kwargs.
<code>add_cosmetic_attribute(attr_name, attr_value)</code>	Add a cosmetic attribute to this object.
<code>add_parameter([parameter_kwargs, parameter, ...])</code>	Add a parameter to the force field, ensuring all parameters are valid.
<code>attribute_is_cosmetic(attr_name)</code>	Determine whether an attribute of this object is cosmetic.
<code>check_handler_compatibility(handler_kwargs)</code>	Checks if a set of kwargs used to create a ParameterHandler are compatible with this ParameterHandler.
<code>create_force(*args, **kwargs)</code>	Deprecated since version 0.11.0.
<code>delete_cosmetic_attribute(attr_name)</code>	Delete a cosmetic attribute from this object.
<code>find_matches(entity[, unique])</code>	Find the elements of the topology/molecule matched by a parameter type.
<code>get_parameter(parameter_attrs)</code>	Return the parameters in this ParameterHandler that match the <code>parameter_attrs</code> argument.
<code>to_dict([discard_cosmetic_attributes])</code>	Convert this ParameterHandler to a dict, compliant with the SMIRNOFF data spec.

## Attributes

<code>TAGNAME</code>	The name of this ParameterHandler corresponding to the SMIRNOFF tag name
<code>known_kwargs</code>	List of kwargs that can be parsed by the function.
<code>parameters</code>	The ParameterList that holds this ParameterHandler's parameter objects
<code>version</code>	

**class** `ConstraintType`(*smirks*, *allow\_cosmetic\_attributes=False*, *\*\*kwargs*)

A SMIRNOFF constraint type

**Warning:** This API is experimental and subject to change.

**add\_cosmetic\_attribute**(*attr\_name*, *attr\_value*)

Add a cosmetic attribute to this object.

This attribute will not have a functional effect on the object in the OpenFF Toolkit, but can be written out during output.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

### Parameters

- **attr\_name** (*str*) – Name of the attribute to define for this object.
- **attr\_value** (*str*) – The value of the attribute to define for this object.

**attribute\_is\_cosmetic**(*attr\_name*)

Determine whether an attribute of this object is cosmetic.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** **attr\_name** (*str*) – The attribute name to check

**Returns** **is\_cosmetic** (*bool*) – Returns True if the attribute is defined and is cosmetic.  
Returns False otherwise.

**delete\_cosmetic\_attribute**(*attr\_name*)

Delete a cosmetic attribute from this object.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** **attr\_name** (*str*) – Name of the cosmetic attribute to delete.

**to\_dict**(*discard\_cosmetic\_attributes=False*, *duplicate\_attributes=None*)

Convert this object to dict format.

The returning dictionary contains all the `ParameterAttribute` and `IndexedParameterAttribute` as well as cosmetic attributes if `discard_cosmetic_attributes` is `False`.

**Parameters**

- **`discard_cosmetic_attributes`** (`bool`, optional. Default = `False`) – Whether to discard non-spec attributes of this object
- **`duplicate_attributes`** (list of string, optional. Default = `None`) – A list of names of attributes that redundantly describe data and should be discarded during serialization

**Returns** `smirnoff_dict` (`dict`) – The SMIRNOFF-compliant dict representation of this object.

**property** `TAGNAME`

The name of this `ParameterHandler` corresponding to the SMIRNOFF tag name

**Returns** `handler_name` (`str`) – The name of this parameter handler

**add\_cosmetic\_attribute**(`attr_name`, `attr_value`)

Add a cosmetic attribute to this object.

This attribute will not have a functional effect on the object in the OpenFF Toolkit, but can be written out during output.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters**

- **`attr_name`** (`str`) – Name of the attribute to define for this object.
- **`attr_value`** (`str`) – The value of the attribute to define for this object.

**add\_parameter**(`parameter_kwargs=None`, `parameter=None`, `after=None`, `before=None`)

Add a parameter to the force field, ensuring all parameters are valid.

**Parameters**

- **`parameter_kwargs`** (`dict`, optional) – The kwargs to pass to the `ParameterHandler.INFO_TYPE` (a `ParameterType`) constructor
- **`parameter`** (`ParameterType`, optional) – A `ParameterType` to add to the `ParameterHandler`
- **`after`** (`str` or `int`, optional) – The SMIRKS pattern (if `str`) or index (if `int`) of the parameter directly before where the new parameter will be added
- **`before`** (`str`, optional) – The SMIRKS pattern (if `str`) or index (if `int`) of the parameter directly after where the new parameter will be added
- **`behavior`** (Note the following) –
  - Either `parameter_kwargs` or `parameter` must be specified.
  - When `before` and `after` are both `None`, the new parameter will be appended to the **END** of the parameter list.
  - When `before` and `after` are both specified, the new parameter will be added immediately after the parameter matching the `after` pattern or index.

- The order of parameters in a parameter list can have significant impacts on parameter assignment. For details, see the SMIRNOFF specification: <https://openforcefield.github.io/standards/standards/smirnoff/#smirnoff-parameter-specification-is-hierarchical>

## Examples

Add a `ParameterType` to an existing `ParameterList` at a specified position.

Given an existing parameter handler and a new parameter to add to it:

```
>>> from openff.units import unit
>>> bh = BondHandler(skip_version_check=True)
>>> length = 1.5 * unit.angstrom
>>> k = 100 * unit.kilocalorie / unit.mole / unit.angstrom ** 2
>>> bh.add_parameter({'smirks': '[*:1]-[:2]', 'length': length, 'k': k, 'id': 'b1'})
↪
>>> bh.add_parameter({'smirks': '[*:1]=[:2]', 'length': length, 'k': k, 'id': 'b2'})
↪
>>> bh.add_parameter({'smirks': '[*:1]#[:2]', 'length': length, 'k': k, 'id': 'b3'})
↪
>>> [p.id for p in bh.parameters]
['b1', 'b2', 'b3']
```

```
>>> param = {'smirks': '[#1:1]-[#6:2]', 'length': length, 'k': k, 'id': 'b4'}
```

Add a new parameter immediately after the parameter with the smirks `[:1]=[:2]`

```
>>> bh.add_parameter(param, after='[:1]=[:2]')
>>> [p.id for p in bh.parameters]
['b1', 'b2', 'b4', 'b3']
```

**attribute\_is\_cosmetic(attr\_name)**

Determine whether an attribute of this object is cosmetic.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** `attr_name` (`str`) – The attribute name to check

**Returns** `is_cosmetic` (`bool`) – Returns True if the attribute is defined and is cosmetic.  
Returns False otherwise.

**check\_handler\_compatibility(handler\_kwargs)**

Checks if a set of kwargs used to create a `ParameterHandler` are compatible with this `ParameterHandler`. This is called if a second handler is attempted to be initialized for the same tag.

**Parameters** `handler_kwargs` (`dict`) – The kwargs that would be used to construct

**Raises** `IncompatibleParameterError` if `handler_kwargs` are incompatible with existing parameters. –

**create\_force**(\*args, \*\*kwargs)

Deprecated since version 0.11.0: This method was deprecated in v0.11.0, no longer has any functionality, and will soon be removed. Use the [OpenFF Interchange](#) package instead.

**delete\_cosmetic\_attribute**(attr\_name)

Delete a cosmetic attribute from this object.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** **attr\_name** (*str*) – Name of the cosmetic attribute to delete.

**find\_matches**(entity, unique=False)

Find the elements of the topology/molecule matched by a parameter type.

**Parameters**

- **entity** (*Topology*) – Topology to search.
- **unique** (*bool*, default=False) – If False, SMARTS matching will enumerate every valid permutation of matching atoms. If True, only one order of each unique match will be returned.

**Returns** **matches** (*ValenceDict[Tuple[int], ParameterHandler.Match]*) – matches[atom\_indices] is the ParameterType object matching the tuple of atom indices in entity.

**get\_parameter**(parameter\_attrs)

Return the parameters in this ParameterHandler that match the parameter\_attrs argument. When multiple attrs are passed, parameters that have any (not all) matching attributes are returned.

**Parameters** **parameter\_attrs** (dict of {attr: value}) – The attrs mapped to desired values (for example {"smirks": "[\*:1]~[#16:2]=,[#6:3]~[:4]", "id": "t105"})

**Returns** **params** (*list of ParameterType objects*) – A list of matching ParameterType objects

## Examples

Create a parameter handler and populate it with some data.

```
>>> from openff.units import unit
>>> handler = BondHandler(skip_version_check=True)
>>> handler.add_parameter(
...     {
...         'smirks': '[*:1]-[:2]',
...         'length': 1*unit.angstrom,
...         'k': 10*unit.kilocalorie / unit.mole/unit.angstrom**2,
...     }
... )
```

Look up, from this handler, all parameters matching some SMIRKS pattern

```
>>> handler.get_parameter({'smirks': '[*:1]-[:2]'})
<BondType with smirks: [*:1]-[:2] length: 1 angstrom k: 10.0 kilocalorie /
↳ angstrom ** 2 / mole >]
```

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**property known\_kwargs**

List of kwargs that can be parsed by the function.

**property parameters**

The ParameterList that holds this ParameterHandler's parameter objects

**to\_dict**(discard\_cosmetic\_attributes=False)

Convert this ParameterHandler to a dict, compliant with the SMIRNOFF data spec.

**Parameters** **discard\_cosmetic\_attributes** (*bool*, optional. Default = False.) – Whether to discard non-spec parameter and header attributes in this ParameterHandler.

**Returns** **smirnoff\_data** (*dict*) – SMIRNOFF-spec compliant representation of this ParameterHandler and its internal ParameterList.

**BondHandler**

**class** openff.toolkit.typing.engines.smirnoff.parameters.**BondHandler**(\*\*kwargs)

Handle SMIRNOFF <Bonds> tags

**Warning:** This API is experimental and subject to change.

**\_\_init\_\_**(\*\*kwargs)

Initialize a ParameterHandler, optionally with a list of parameters and other kwargs.

**Parameters**

- **allow\_cosmetic\_attributes** (*bool*, optional. Default = False) – Whether to permit non-spec kwargs. If True, non-spec kwargs will be stored as attributes of this object and can be accessed and modified. Otherwise an exception will be raised if a non-spec kwarg is encountered.
- **skip\_version\_check** (*bool*, optional. Default = False) – If False, the SMIRNOFF section version will not be checked, and the ParameterHandler will be initialized with version set to `_MAX_SUPPORTED_SECTION_VERSION`.
- **\*\*kwargs** (*dict*) – The dict representation of the SMIRNOFF data source

## Methods

<code>__init__(**kwargs)</code>	Initialize a ParameterHandler, optionally with a list of parameters and other kwargs.
<code>add_cosmetic_attribute(attr_name, attr_value)</code>	Add a cosmetic attribute to this object.
<code>add_parameter([parameter_kwargs, parameter, ...])</code>	Add a parameter to the force field, ensuring all parameters are valid.
<code>attribute_is_cosmetic(attr_name)</code>	Determine whether an attribute of this object is cosmetic.
<code>check_handler_compatibility(other_handler)</code>	Checks whether this ParameterHandler encodes compatible physics as another ParameterHandler.
<code>create_force(*args, **kwargs)</code>	Deprecated since version 0.11.0.
<code>delete_cosmetic_attribute(attr_name)</code>	Delete a cosmetic attribute from this object.
<code>find_matches(entity[, unique])</code>	Find the elements of the topology/molecule matched by a parameter type.
<code>get_parameter(parameter_attrs)</code>	Return the parameters in this ParameterHandler that match the parameter_attrs argument.
<code>to_dict([discard_cosmetic_attributes])</code>	Convert this ParameterHandler to a dict, compliant with the SMIRNOFF data spec.

## Attributes

<code>TAGNAME</code>	The name of this ParameterHandler corresponding to the SMIRNOFF tag name
<code>fractional_bondorder_interpolation</code>	
<code>fractional_bondorder_method</code>	
<code>known_kwargs</code>	List of kwargs that can be parsed by the function.
<code>parameters</code>	The ParameterList that holds this ParameterHandler's parameter objects
<code>potential</code>	
<code>version</code>	

**class** `BondType(**kwargs)`  
 A SMIRNOFF bond type

**Warning:** This API is experimental and subject to change.

**add\_cosmetic\_attribute(attr\_name, attr\_value)**  
 Add a cosmetic attribute to this object.

This attribute will not have a functional effect on the object in the OpenFF Toolkit, but can be written out during output.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters**

- **attr\_name** (*str*) – Name of the attribute to define for this object.
- **attr\_value** (*str*) – The value of the attribute to define for this object.

**attribute\_is\_cosmetic**(*attr\_name*)

Determine whether an attribute of this object is cosmetic.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** **attr\_name** (*str*) – The attribute name to check

**Returns** **is\_cosmetic** (*bool*) – Returns True if the attribute is defined and is cosmetic. Returns False otherwise.

**delete\_cosmetic\_attribute**(*attr\_name*)

Delete a cosmetic attribute from this object.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** **attr\_name** (*str*) – Name of the cosmetic attribute to delete.

**to\_dict**(*discard\_cosmetic\_attributes=False, duplicate\_attributes=None*)

Convert this object to dict format.

The returning dictionary contains all the `ParameterAttribute` and `IndexedParameterAttribute` as well as cosmetic attributes if `discard_cosmetic_attributes` is False.

**Parameters**

- **discard\_cosmetic\_attributes** (*bool*, optional. Default = False) – Whether to discard non-spec attributes of this object
- **duplicate\_attributes** (list of string, optional. Default = None) – A list of names of attributes that redundantly describe data and should be discarded during serializaiton

**Returns** **smirnoff\_dict** (*dict*) – The SMIRNOFF-compliant dict representation of this object.

**check\_handler\_compatibility**(*other\_handler*)

Checks whether this `ParameterHandler` encodes compatible physics as another `ParameterHandler`. This is called if a second handler is attempted to be initialized for the same tag.

**Parameters** **other\_handler** (a `ParameterHandler` object) – The handler to compare to.

**Raises** `IncompatibleParameterError` if **handler\_kwargs** are incompatible with existing parameters. –

**property** **TAGNAME**

The name of this `ParameterHandler` corresponding to the SMIRNOFF tag name

**Returns** **handler\_name** (*str*) – The name of this parameter handler

`add_cosmetic_attribute(attr_name, attr_value)`

Add a cosmetic attribute to this object.

This attribute will not have a functional effect on the object in the OpenFF Toolkit, but can be written out during output.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

#### Parameters

- **attr\_name** (`str`) – Name of the attribute to define for this object.
- **attr\_value** (`str`) – The value of the attribute to define for this object.

`add_parameter(parameter_kwarg=None, parameter=None, after=None, before=None)`

Add a parameter to the force field, ensuring all parameters are valid.

#### Parameters

- **parameter\_kwarg** (`dict`, optional) – The kwargs to pass to the `ParameterHandler.INFO_TYPE` (a `ParameterType`) constructor
- **parameter** (`ParameterType`, optional) – A `ParameterType` to add to the `ParameterHandler`
- **after** (`str` or `int`, optional) – The SMIRKS pattern (if `str`) or index (if `int`) of the parameter directly before where the new parameter will be added
- **before** (`str`, optional) – The SMIRKS pattern (if `str`) or index (if `int`) of the parameter directly after where the new parameter will be added
- **behavior** (Note the following) –
  - Either `parameter_kwarg` or `parameter` must be specified.
  - When `before` and `after` are both `None`, the new parameter will be appended to the **END** of the parameter list.
  - When `before` and `after` are both specified, the new parameter will be added immediately after the parameter matching the `after` pattern or index.
  - The order of parameters in a parameter list can have significant impacts on parameter assignment. For details, see the SMIRNOFF specification: <https://openforcefield.github.io/standards/standards/smirnoff/#smirnoff-parameter-specification-is-hierarchical>

#### Examples

Add a `ParameterType` to an existing `ParameterList` at a specified position.

Given an existing parameter handler and a new parameter to add to it:

```
>>> from openff.units import unit
>>> bh = BondHandler(skip_version_check=True)
>>> length = 1.5 * unit.angstrom
>>> k = 100 * unit.kilocalorie / unit.mole / unit.angstrom ** 2
>>> bh.add_parameter({'smirks': '[*:1]-[:2]', 'length': length, 'k': k, 'id': 'b1'})
```

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```
>>> bh.add_parameter({'smirks': '[*:1]=[*:2]', 'length': length, 'k': k, 'id': 'b2'})
↵
>>> bh.add_parameter({'smirks': '[*:1]#[*:2]', 'length': length, 'k': k, 'id': 'b3'})
↵
>>> [p.id for p in bh.parameters]
['b1', 'b2', 'b3']
```

```
>>> param = {'smirks': '[#1:1]-[#6:2]', 'length': length, 'k': k, 'id': 'b4'}
```

Add a new parameter immediately after the parameter with the smirks `[:1]=[:2]`

```
>>> bh.add_parameter(param, after='[:1]=[*:2]')
>>> [p.id for p in bh.parameters]
['b1', 'b2', 'b4', 'b3']
```

**attribute\_is\_cosmetic**(*attr\_name*)

Determine whether an attribute of this object is cosmetic.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** *attr\_name* (*str*) – The attribute name to check

**Returns** *is\_cosmetic* (*bool*) – Returns True if the attribute is defined and is cosmetic.  
Returns False otherwise.

**create\_force**(\*args, \*\*kwargs)

Deprecated since version 0.11.0: This method was deprecated in v0.11.0, no longer has any functionality, and will soon be removed. Use the [OpenFF Interchange](#) package instead.

**delete\_cosmetic\_attribute**(*attr\_name*)

Delete a cosmetic attribute from this object.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** *attr\_name* (*str*) – Name of the cosmetic attribute to delete.

**find\_matches**(*entity*, *unique=False*)

Find the elements of the topology/molecule matched by a parameter type.

**Parameters**

- **entity** (*Topology*) – Topology to search.
- **unique** (*bool*, default=False) – If False, SMARTS matching will enumerate every valid permutation of matching atoms. If True, only one order of each unique match will be returned.

**Returns** *matches* (*ValenceDict[Tuple[int], ParameterHandler.Match]*) –  
*matches*[*atom\_indices*] is the *ParameterType* object matching the tuple of atom indices in *entity*.

**get\_parameter**(*parameter\_attrs*)

Return the parameters in this ParameterHandler that match the *parameter\_attrs* argument. When multiple *attrs* are passed, parameters that have any (not all) matching attributes are returned.

**Parameters** *parameter\_attrs* (dict of {attr: value}) – The *attrs* mapped to desired values (for example {"smirks": "[\*:1]~[#16:2]=,:[#6:3]~[:4]", "id": "t105"})

**Returns** *params* (list of ParameterType objects) – A list of matching ParameterType objects

## Examples

Create a parameter handler and populate it with some data.

```
>>> from openff.units import unit
>>> handler = BondHandler(skip_version_check=True)
>>> handler.add_parameter(
...     {
...         'smirks': '[*:1]-[:2]',
...         'length': 1*unit.angstrom,
...         'k': 10*unit.kilocalorie / unit.mole/unit.angstrom**2,
...     }
... )
```

Look up, from this handler, all parameters matching some SMIRKS pattern

```
>>> handler.get_parameter({'smirks': '[*:1]-[:2]'})
[<BondType with smirks: [*:1]-[:2] length: 1 angstrom k: 10.0 kilocalorie /
↳ angstrom ** 2 / mole >]
```

**property known\_kwargs**

List of kwargs that can be parsed by the function.

**property parameters**

The ParameterList that holds this ParameterHandler's parameter objects

**to\_dict**(*discard\_cosmetic\_attributes=False*)

Convert this ParameterHandler to a dict, compliant with the SMIRNOFF data spec.

**Parameters** *discard\_cosmetic\_attributes* (bool, optional. Default = False.) – Whether to discard non-spec parameter and header attributes in this ParameterHandler.

**Returns** *smirnoff\_data* (dict) – SMIRNOFF-spec compliant representation of this ParameterHandler and its internal ParameterList.

## AngleHandler

```
class openff.toolkit.typing.engines.smirnoff.parameters.AngleHandler(allow_cosmetic_attributes=False,
                                                                    skip_version_check=False,
                                                                    **kwargs)
```

Handle SMIRNOFF <AngleForce> tags

**Warning:** This API is experimental and subject to change.

```
__init__(allow_cosmetic_attributes=False, skip_version_check=False, **kwargs)
```

Initialize a ParameterHandler, optionally with a list of parameters and other kwargs.

### Parameters

- **allow\_cosmetic\_attributes** (*bool*, optional. Default = `False`) – Whether to permit non-spec kwargs. If `True`, non-spec kwargs will be stored as attributes of this object and can be accessed and modified. Otherwise an exception will be raised if a non-spec kwarg is encountered.
- **skip\_version\_check** (*bool*, optional. Default = `False`) – If `False`, the SMIRNOFF section version will not be checked, and the ParameterHandler will be initialized with version set to `_MAX_SUPPORTED_SECTION_VERSION`.
- **\*\*kwargs** (*dict*) – The dict representation of the SMIRNOFF data source

## Methods

<code>__init__([allow_cosmetic_attributes, ...])</code>	Initialize a ParameterHandler, optionally with a list of parameters and other kwargs.
<code>add_cosmetic_attribute(attr_name, attr_value)</code>	Add a cosmetic attribute to this object.
<code>add_parameter([parameter_kwargs, parameter, ...])</code>	Add a parameter to the force field, ensuring all parameters are valid.
<code>attribute_is_cosmetic(attr_name)</code>	Determine whether an attribute of this object is cosmetic.
<code>check_handler_compatibility(other_handler)</code>	Checks whether this ParameterHandler encodes compatible physics as another ParameterHandler.
<code>create_force(*args, **kwargs)</code>	Deprecated since version 0.11.0.
<code>delete_cosmetic_attribute(attr_name)</code>	Delete a cosmetic attribute from this object.
<code>find_matches(entity[, unique])</code>	Find the elements of the topology/molecule matched by a parameter type.
<code>get_parameter(parameter_attrs)</code>	Return the parameters in this ParameterHandler that match the <code>parameter_attrs</code> argument.
<code>to_dict([discard_cosmetic_attributes])</code>	Convert this ParameterHandler to a dict, compliant with the SMIRNOFF data spec.

## Attributes

<code>TAGNAME</code>	The name of this ParameterHandler corresponding to the SMIRNOFF tag name
<code>known_kwargs</code>	List of kwargs that can be parsed by the function.
<code>parameters</code>	The ParameterList that holds this ParameterHandler's parameter objects
<code>potential</code>	
<code>version</code>	

**class** `AngleType`(*smirks*, *allow\_cosmetic\_attributes*=False, *\*\*kwargs*)

A SMIRNOFF angle type.

**Warning:** This API is experimental and subject to change.

**add\_cosmetic\_attribute**(*attr\_name*, *attr\_value*)

Add a cosmetic attribute to this object.

This attribute will not have a functional effect on the object in the OpenFF Toolkit, but can be written out during output.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

### Parameters

- **attr\_name** (*str*) – Name of the attribute to define for this object.
- **attr\_value** (*str*) – The value of the attribute to define for this object.

**attribute\_is\_cosmetic**(*attr\_name*)

Determine whether an attribute of this object is cosmetic.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** **attr\_name** (*str*) – The attribute name to check

**Returns** **is\_cosmetic** (*bool*) – Returns True if the attribute is defined and is cosmetic.  
Returns False otherwise.

**delete\_cosmetic\_attribute**(*attr\_name*)

Delete a cosmetic attribute from this object.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** **attr\_name** (*str*) – Name of the cosmetic attribute to delete.



**to\_dict**(*discard\_cosmetic\_attributes=False, duplicate\_attributes=None*)

Convert this object to dict format.

The returning dictionary contains all the `ParameterAttribute` and `IndexedParameterAttribute` as well as cosmetic attributes if `discard_cosmetic_attributes` is `False`.

**Parameters**

- **discard\_cosmetic\_attributes** (`bool`, optional. Default = `False`) – Whether to discard non-spec attributes of this object
- **duplicate\_attributes** (list of `string`, optional. Default = `None`) – A list of names of attributes that redundantly describe data and should be discarded during serialization

**Returns** `smirnoff_dict` (`dict`) – The SMIRNOFF-compliant dict representation of this object.

**check\_handler\_compatibility**(*other\_handler*)

Checks whether this `ParameterHandler` encodes compatible physics as another `ParameterHandler`. This is called if a second handler is attempted to be initialized for the same tag.

**Parameters** *other\_handler* (a `ParameterHandler` object) – The handler to compare to.

**Raises** `IncompatibleParameterError` if `handler_kwargs` are incompatible with existing parameters. –

**property** `TAGNAME`

The name of this `ParameterHandler` corresponding to the SMIRNOFF tag name

**Returns** `handler_name` (`str`) – The name of this parameter handler

**add\_cosmetic\_attribute**(*attr\_name, attr\_value*)

Add a cosmetic attribute to this object.

This attribute will not have a functional effect on the object in the OpenFF Toolkit, but can be written out during output.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters**

- **attr\_name** (`str`) – Name of the attribute to define for this object.
- **attr\_value** (`str`) – The value of the attribute to define for this object.

**add\_parameter**(*parameter\_kwargs=None, parameter=None, after=None, before=None*)

Add a parameter to the force field, ensuring all parameters are valid.

**Parameters**

- **parameter\_kwargs** (`dict`, optional) – The kwargs to pass to the `ParameterHandler.INFOType` (a `ParameterType`) constructor
- **parameter** (`ParameterType`, optional) – A `ParameterType` to add to the `ParameterHandler`
- **after** (`str` or `int`, optional) – The SMIRKS pattern (if `str`) or index (if `int`) of the parameter directly before where the new parameter will be added

- **before** (*str*, optional) – The SMIRKS pattern (if *str*) or index (if *int*) of the parameter directly after where the new parameter will be added
- **behavior** (Note the following) –
  - Either *parameter\_kwargs* or *parameter* must be specified.
  - When *before* and *after* are both *None*, the new parameter will be appended to the **END** of the parameter list.
  - When *before* and *after* are both specified, the new parameter will be added immediately after the parameter matching the *after* pattern or index.
  - The order of parameters in a parameter list can have significant impacts on parameter assignment. For details, see the SMIRNOFF specification: <https://openforcefield.github.io/standards/standards/smirnoff/#smirnoff-parameter-specification-is-hierarchical>

## Examples

Add a ParameterType to an existing ParameterList at a specified position.

Given an existing parameter handler and a new parameter to add to it:

```
>>> from openff.units import unit
>>> bh = BondHandler(skip_version_check=True)
>>> length = 1.5 * unit.angstrom
>>> k = 100 * unit.kilocalorie / unit.mole / unit.angstrom ** 2
>>> bh.add_parameter({'smirks': '[*:1]-[:2]', 'length': length, 'k': k, 'id': 'b1'})
↳
>>> bh.add_parameter({'smirks': '[*:1]=[:2]', 'length': length, 'k': k, 'id': 'b2'})
↳
>>> bh.add_parameter({'smirks': '[*:1]#[:2]', 'length': length, 'k': k, 'id': 'b3'})
↳
>>> [p.id for p in bh.parameters]
['b1', 'b2', 'b3']
```

```
>>> param = {'smirks': '[#1:1]-[#6:2]', 'length': length, 'k': k, 'id': 'b4'}
```

Add a new parameter immediately after the parameter with the smirks `[:1]=[:2]`

```
>>> bh.add_parameter(param, after='[:1]=[:2]')
>>> [p.id for p in bh.parameters]
['b1', 'b2', 'b4', 'b3']
```

**attribute\_is\_cosmetic**(*attr\_name*)

Determine whether an attribute of this object is cosmetic.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** *attr\_name* (*str*) – The attribute name to check

**Returns** *is\_cosmetic* (*bool*) – Returns True if the attribute is defined and is cosmetic.  
Returns False otherwise.

**create\_force**(\*args, \*\*kwargs)

Deprecated since version 0.11.0: This method was deprecated in v0.11.0, no longer has any functionality, and will soon be removed. Use the [OpenFF Interchange](#) package instead.

**delete\_cosmetic\_attribute**(attr\_name)

Delete a cosmetic attribute from this object.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** **attr\_name** (*str*) – Name of the cosmetic attribute to delete.

**find\_matches**(entity, unique=False)

Find the elements of the topology/molecule matched by a parameter type.

**Parameters**

- **entity** (*Topology*) – Topology to search.
- **unique** (*bool*, default=False) – If False, SMARTS matching will enumerate every valid permutation of matching atoms. If True, only one order of each unique match will be returned.

**Returns** **matches** (*ValenceDict[Tuple[int], ParameterHandler.Match]*) – matches[atom\_indices] is the *ParameterType* object matching the tuple of atom indices in entity.

**get\_parameter**(parameter\_attrs)

Return the parameters in this *ParameterHandler* that match the *parameter\_attrs* argument. When multiple attrs are passed, parameters that have any (not all) matching attributes are returned.

**Parameters** **parameter\_attrs** (dict of {attr: value}) – The attrs mapped to desired values (for example {"smirks": "[\*:1]~[#16:2]=,[#6:3]~[:4]", "id": "t105"})

**Returns** **params** (*list of ParameterType objects*) – A list of matching *ParameterType* objects

## Examples

Create a parameter handler and populate it with some data.

```
>>> from openff.units import unit
>>> handler = BondHandler(skip_version_check=True)
>>> handler.add_parameter(
...     {
...         'smirks': '[*:1]-[:2]',
...         'length': 1*unit.angstrom,
...         'k': 10*unit.kilocalorie / unit.mole/unit.angstrom**2,
...     }
... )
```

Look up, from this handler, all parameters matching some SMIRKS pattern

```
>>> handler.get_parameter({'smirks': '[*:1]-[:2]'})
<BondType with smirks: [*:1]-[:2] length: 1 angstrom k: 10.0 kilocalorie /
↳ angstrom ** 2 / mole >]
```

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**property known\_kwargs**

List of kwargs that can be parsed by the function.

**property parameters**

The ParameterList that holds this ParameterHandler's parameter objects

**to\_dict**(discard\_cosmetic\_attributes=False)

Convert this ParameterHandler to a dict, compliant with the SMIRNOFF data spec.

**Parameters** **discard\_cosmetic\_attributes** (*bool*, optional. Default = False.) – Whether to discard non-spec parameter and header attributes in this ParameterHandler.

**Returns** **smirnoff\_data** (*dict*) – SMIRNOFF-spec compliant representation of this ParameterHandler and its internal ParameterList.

**ProperTorsionHandler**

```
class openff.toolkit.typing.engines.smirnoff.parameters.ProperTorsionHandler(allow_cosmetic_attributes=False,
                                                                           skip_version_check=False,
                                                                           **kwargs)
```

Handle SMIRNOFF <ProperTorsionForce> tags

**Warning:** This API is experimental and subject to change.

```
__init__(allow_cosmetic_attributes=False, skip_version_check=False, **kwargs)
```

Initialize a ParameterHandler, optionally with a list of parameters and other kwargs.

**Parameters**

- **allow\_cosmetic\_attributes** (*bool*, optional. Default = False) – Whether to permit non-spec kwargs. If True, non-spec kwargs will be stored as attributes of this object and can be accessed and modified. Otherwise an exception will be raised if a non-spec kwarg is encountered.
- **skip\_version\_check** (*bool*, optional. Default = False) – If False, the SMIRNOFF section version will not be checked, and the ParameterHandler will be initialized with version set to `_MAX_SUPPORTED_SECTION_VERSION`.
- **\*\*kwargs** (*dict*) – The dict representation of the SMIRNOFF data source

## Methods

<code>__init__([allow_cosmetic_attributes, ...])</code>	Initialize a ParameterHandler, optionally with a list of parameters and other kwargs.
<code>add_cosmetic_attribute(attr_name, attr_value)</code>	Add a cosmetic attribute to this object.
<code>add_parameter([parameter_kwargs, parameter, ...])</code>	Add a parameter to the force field, ensuring all parameters are valid.
<code>attribute_is_cosmetic(attr_name)</code>	Determine whether an attribute of this object is cosmetic.
<code>check_handler_compatibility(other_handler)</code>	Checks whether this ParameterHandler encodes compatible physics as another ParameterHandler.
<code>create_force(*args, **kwargs)</code>	Deprecated since version 0.11.0.
<code>delete_cosmetic_attribute(attr_name)</code>	Delete a cosmetic attribute from this object.
<code>find_matches(entity[, unique])</code>	Find the elements of the topology/molecule matched by a parameter type.
<code>get_parameter(parameter_attrs)</code>	Return the parameters in this ParameterHandler that match the parameter_attrs argument.
<code>to_dict([discard_cosmetic_attributes])</code>	Convert this ParameterHandler to a dict, compliant with the SMIRNOFF data spec.

## Attributes

<code>TAGNAME</code>	The name of this ParameterHandler corresponding to the SMIRNOFF tag name
<code>default_idivf</code>	
<code>fractional_bondorder_interpolation</code>	
<code>fractional_bondorder_method</code>	
<code>known_kwargs</code>	List of kwargs that can be parsed by the function.
<code>parameters</code>	The ParameterList that holds this ParameterHandler's parameter objects
<code>potential</code>	
<code>version</code>	

**class ProperTorsionType**(*smirks*, *allow\_cosmetic\_attributes=False*, *\*\*kwargs*)

A SMIRNOFF torsion type for proper torsions.

**Warning:** This API is experimental and subject to change.

**add\_cosmetic\_attribute**(*attr\_name*, *attr\_value*)

Add a cosmetic attribute to this object.

This attribute will not have a functional effect on the object in the OpenFF Toolkit, but can be written out during output.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters**

- **attr\_name** (*str*) – Name of the attribute to define for this object.
- **attr\_value** (*str*) – The value of the attribute to define for this object.

**attribute\_is\_cosmetic**(*attr\_name*)

Determine whether an attribute of this object is cosmetic.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** **attr\_name** (*str*) – The attribute name to check

**Returns** **is\_cosmetic** (*bool*) – Returns True if the attribute is defined and is cosmetic.

Returns False otherwise.

**delete\_cosmetic\_attribute**(*attr\_name*)

Delete a cosmetic attribute from this object.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** **attr\_name** (*str*) – Name of the cosmetic attribute to delete.

**to\_dict**(*discard\_cosmetic\_attributes=False, duplicate\_attributes=None*)

Convert this object to dict format.

The returning dictionary contains all the `ParameterAttribute` and `IndexedParameterAttribute` as well as cosmetic attributes if `discard_cosmetic_attributes` is False.

**Parameters**

- **discard\_cosmetic\_attributes** (*bool*, optional. Default = False) – Whether to discard non-spec attributes of this object
- **duplicate\_attributes** (list of string, optional. Default = None) – A list of names of attributes that redundantly describe data and should be discarded during serializaiton

**Returns** **smirnoff\_dict** (*dict*) – The SMIRNOFF-compliant dict representation of this object.

**check\_handler\_compatibility**(*other\_handler*)

Checks whether this `ParameterHandler` encodes compatible physics as another `ParameterHandler`. This is called if a second handler is attempted to be initialized for the same tag.

**Parameters** **other\_handler** (a `ParameterHandler` object) – The handler to compare to.

**Raises** `IncompatibleParameterError` if **handler\_kwargs** are incompatible with existing parameters. –

**property** **TAGNAME**

The name of this `ParameterHandler` corresponding to the SMIRNOFF tag name

Returns **handler\_name** (*str*) – The name of this parameter handler

**add\_cosmetic\_attribute**(*attr\_name*, *attr\_value*)

Add a cosmetic attribute to this object.

This attribute will not have a functional effect on the object in the OpenFF Toolkit, but can be written out during output.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

#### Parameters

- **attr\_name** (*str*) – Name of the attribute to define for this object.
- **attr\_value** (*str*) – The value of the attribute to define for this object.

**add\_parameter**(*parameter\_kwargs*=None, *parameter*=None, *after*=None, *before*=None)

Add a parameter to the force field, ensuring all parameters are valid.

#### Parameters

- **parameter\_kwargs** (*dict*, optional) – The kwargs to pass to the ParameterHandler.INFO\_TYPE (a ParameterType) constructor
- **parameter** (*ParameterType*, optional) – A ParameterType to add to the ParameterHandler
- **after** (*str* or *int*, optional) – The SMIRKS pattern (if *str*) or index (if *int*) of the parameter directly before where the new parameter will be added
- **before** (*str*, optional) – The SMIRKS pattern (if *str*) or index (if *int*) of the parameter directly after where the new parameter will be added
- **behavior** (Note the following) –
  - Either *parameter\_kwargs* or *parameter* must be specified.
  - When *before* and *after* are both None, the new parameter will be appended to the **END** of the parameter list.
  - When *before* and *after* are both specified, the new parameter will be added immediately after the parameter matching the *after* pattern or index.
  - The order of parameters in a parameter list can have significant impacts on parameter assignment. For details, see the SMIRNOFF specification: <https://openforcefield.github.io/standards/standards/smirnoff/#smirnoff-parameter-specification-is-hierarchical>

## Examples

Add a ParameterType to an existing ParameterList at a specified position.

Given an existing parameter handler and a new parameter to add to it:

```
>>> from openff.units import unit
>>> bh = BondHandler(skip_version_check=True)
>>> length = 1.5 * unit.angstrom
>>> k = 100 * unit.kilocalorie / unit.mole / unit.angstrom ** 2
>>> bh.add_parameter({'smirks': '[*:1]-[:2]', 'length': length, 'k': k, 'id': 'b1'})
↵
>>> bh.add_parameter({'smirks': '[*:1]=[*:2]', 'length': length, 'k': k, 'id': 'b2'})
↵
>>> bh.add_parameter({'smirks': '[*:1]#[:2]', 'length': length, 'k': k, 'id': 'b3'})
↵
>>> [p.id for p in bh.parameters]
['b1', 'b2', 'b3']
```

```
>>> param = {'smirks': '[#1:1]-[#6:2]', 'length': length, 'k': k, 'id': 'b4'}
```

Add a new parameter immediately after the parameter with the smirks `[:1]=[:2]`

```
>>> bh.add_parameter(param, after='[:1]=[*:2]')
>>> [p.id for p in bh.parameters]
['b1', 'b2', 'b4', 'b3']
```

**attribute\_is\_cosmetic(attr\_name)**

Determine whether an attribute of this object is cosmetic.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** `attr_name` (`str`) – The attribute name to check

**Returns** `is_cosmetic` (`bool`) – Returns True if the attribute is defined and is cosmetic.  
Returns False otherwise.

**create\_force(\*args, \*\*kwargs)**

Deprecated since version 0.11.0: This method was deprecated in v0.11.0, no longer has any functionality, and will soon be removed. Use the [OpenFF Interchange](#) package instead.

**delete\_cosmetic\_attribute(attr\_name)**

Delete a cosmetic attribute from this object.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** `attr_name` (`str`) – Name of the cosmetic attribute to delete.



**find\_matches**(entity, unique=False)

Find the elements of the topology/molecule matched by a parameter type.

**Parameters**

- **entity** (*Topology*) – Topology to search.
- **unique** (*bool*, default=False) – If False, SMARTS matching will enumerate every valid permutation of matching atoms. If True, only one order of each unique match will be returned.

**Returns matches** (*ValenceDict[Tuple[int], ParameterHandler.Match]*) – matches[atom\_indices] is the ParameterType object matching the tuple of atom indices in entity.

**get\_parameter**(parameter\_attrs)

Return the parameters in this ParameterHandler that match the parameter\_attrs argument. When multiple attrs are passed, parameters that have any (not all) matching attributes are returned.

**Parameters parameter\_attrs** (dict of {attr: value}) – The attrs mapped to desired values (for example {"smirks": "[\*:1]~[#16:2]=,[#6:3]~[:4]", "id": "t105"})

**Returns params** (list of ParameterType objects) – A list of matching ParameterType objects

## Examples

Create a parameter handler and populate it with some data.

```
>>> from openff.units import unit
>>> handler = BondHandler(skip_version_check=True)
>>> handler.add_parameter(
...     {
...         'smirks': '[*:1]-[:2]',
...         'length': 1*unit.angstrom,
...         'k': 10*unit.kilocalorie / unit.mole/unit.angstrom**2,
...     }
... )
```

Look up, from this handler, all parameters matching some SMIRKS pattern

```
>>> handler.get_parameter({'smirks': '[*:1]-[:2]'})
[<BondType with smirks: [*:1]-[:2] length: 1 angstrom k: 10.0 kilocalorie /
↳ angstrom ** 2 / mole >]
```

**property known\_kwargs**

List of kwargs that can be parsed by the function.

**property parameters**

The ParameterList that holds this ParameterHandler's parameter objects

**to\_dict**(discard\_cosmetic\_attributes=False)

Convert this ParameterHandler to a dict, compliant with the SMIRNOFF data spec.

**Parameters discard\_cosmetic\_attributes** (*bool*, optional. Default = False.) – Whether to discard non-spec parameter and header attributes in this ParameterHandler.

**Returns** `smirnoff_data` (*dict*) – SMIRNOFF-spec compliant representation of this ParameterHandler and its internal ParameterList.

### ImproperTorsionHandler

**class** `openff.toolkit.typing.engines.smirnoff.parameters.ImproperTorsionHandler`(*allow\_cosmetic\_attributes=False*, *skip\_version\_check=False*, *\*\*kwargs*)

Handle SMIRNOFF <ImproperTorsionForce> tags

**Warning:** This API is experimental and subject to change.

`__init__`(*allow\_cosmetic\_attributes=False*, *skip\_version\_check=False*, *\*\*kwargs*)

Initialize a ParameterHandler, optionally with a list of parameters and other kwargs.

#### Parameters

- **allow\_cosmetic\_attributes** (*bool*, optional. Default = False) – Whether to permit non-spec kwargs. If True, non-spec kwargs will be stored as attributes of this object and can be accessed and modified. Otherwise an exception will be raised if a non-spec kwarg is encountered.
- **skip\_version\_check** (*bool*, optional. Default = False) – If False, the SMIRNOFF section version will not be checked, and the ParameterHandler will be initialized with version set to `_MAX_SUPPORTED_SECTION_VERSION`.
- **\*\*kwargs** (*dict*) – The dict representation of the SMIRNOFF data source

### Methods

<code>__init__</code> ([ <i>allow_cosmetic_attributes</i> , ...])	Initialize a ParameterHandler, optionally with a list of parameters and other kwargs.
<code>add_cosmetic_attribute</code> ( <i>attr_name</i> , <i>attr_value</i> )	Add a cosmetic attribute to this object.
<code>add_parameter</code> ([ <i>parameter_kwargs</i> , <i>parameter</i> , ...])	Add a parameter to the force field, ensuring all parameters are valid.
<code>attribute_is_cosmetic</code> ( <i>attr_name</i> )	Determine whether an attribute of this object is cosmetic.
<code>check_handler_compatibility</code> ( <i>other_handler</i> )	Checks whether this ParameterHandler encodes compatible physics as another ParameterHandler.
<code>create_force</code> (*args, <i>**kwargs</i> )	Deprecated since version 0.11.0.
<code>delete_cosmetic_attribute</code> ( <i>attr_name</i> )	Delete a cosmetic attribute from this object.
<code>find_matches</code> ( <i>entity</i> [, <i>unique</i> ])	Find the improper torsions in the topology/molecule matched by a parameter type.
<code>get_parameter</code> ( <i>parameter_attrs</i> )	Return the parameters in this ParameterHandler that match the <i>parameter_attrs</i> argument.
<code>to_dict</code> ([ <i>discard_cosmetic_attributes</i> ])	Convert this ParameterHandler to a dict, compliant with the SMIRNOFF data spec.

## Attributes

<code>TAGNAME</code>	The name of this ParameterHandler corresponding to the SMIRNOFF tag name
<code>default_idivf</code>	
<code>known_kwargs</code>	List of kwargs that can be parsed by the function.
<code>parameters</code>	The ParameterList that holds this ParameterHandler's parameter objects
<code>potential</code>	
<code>version</code>	

**class** `ImproperTorsionType`(*smirks*, *allow\_cosmetic\_attributes=False*, *\*\*kwargs*)

A SMIRNOFF torsion type for improper torsions.

**Warning:** This API is experimental and subject to change.

**add\_cosmetic\_attribute**(*attr\_name*, *attr\_value*)

Add a cosmetic attribute to this object.

This attribute will not have a functional effect on the object in the OpenFF Toolkit, but can be written out during output.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

### Parameters

- **attr\_name** (*str*) – Name of the attribute to define for this object.
- **attr\_value** (*str*) – The value of the attribute to define for this object.

**attribute\_is\_cosmetic**(*attr\_name*)

Determine whether an attribute of this object is cosmetic.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** *attr\_name* (*str*) – The attribute name to check

**Returns** *is\_cosmetic* (*bool*) – Returns True if the attribute is defined and is cosmetic. Returns False otherwise.

**delete\_cosmetic\_attribute**(*attr\_name*)

Delete a cosmetic attribute from this object.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** *attr\_name* (*str*) – Name of the cosmetic attribute to delete.

**to\_dict**(*discard\_cosmetic\_attributes=False, duplicate\_attributes=None*)

Convert this object to dict format.

The returning dictionary contains all the `ParameterAttribute` and `IndexedParameterAttribute` as well as cosmetic attributes if `discard_cosmetic_attributes` is `False`.

**Parameters**

- **discard\_cosmetic\_attributes** (`bool`, optional. Default = `False`) – Whether to discard non-spec attributes of this object
- **duplicate\_attributes** (list of string, optional. Default = `None`) – A list of names of attributes that redundantly describe data and should be discarded during serialization

**Returns** `smirnoff_dict` (`dict`) – The SMIRNOFF-compliant dict representation of this object.

**check\_handler\_compatibility**(*other\_handler*)

Checks whether this `ParameterHandler` encodes compatible physics as another `ParameterHandler`. This is called if a second handler is attempted to be initialized for the same tag.

**Parameters** *other\_handler* (a `ParameterHandler` object) – The handler to compare to.

**Raises** `IncompatibleParameterError` if `handler_kwargs` are incompatible with existing parameters. –

**find\_matches**(*entity, unique=False*)

Find the improper torsions in the topology/molecule matched by a parameter type.

**Parameters** *entity* (`Topology`) – Topology to search.

**Returns** `matches` (`ImproperDict[Tuple[int], ParameterHandler.Match]`) – `matches[atom_indices]` is the `ParameterType` object matching the 4-tuple of atom indices in *entity*.

**property** `TAGNAME`

The name of this `ParameterHandler` corresponding to the SMIRNOFF tag name

**Returns** `handler_name` (`str`) – The name of this parameter handler

**add\_cosmetic\_attribute**(*attr\_name, attr\_value*)

Add a cosmetic attribute to this object.

This attribute will not have a functional effect on the object in the OpenFF Toolkit, but can be written out during output.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters**

- **attr\_name** (`str`) – Name of the attribute to define for this object.
- **attr\_value** (`str`) – The value of the attribute to define for this object.

**add\_parameter**(*parameter\_kwargs=None, parameter=None, after=None, before=None*)

Add a parameter to the force field, ensuring all parameters are valid.

**Parameters**

- **parameter\_kwargs** (`dict`, optional) – The kwargs to pass to the `ParameterHandler.INFO_TYPE` (a `ParameterType`) constructor
- **parameter** (`ParameterType`, optional) – A `ParameterType` to add to the `ParameterHandler`
- **after** (`str` or `int`, optional) – The SMIRKS pattern (if `str`) or index (if `int`) of the parameter directly before where the new parameter will be added
- **before** (`str`, optional) – The SMIRKS pattern (if `str`) or index (if `int`) of the parameter directly after where the new parameter will be added
- **behavior** (Note the following) –
  - Either `parameter_kwargs` or `parameter` must be specified.
  - When `before` and `after` are both `None`, the new parameter will be appended to the **END** of the parameter list.
  - When `before` and `after` are both specified, the new parameter will be added immediately after the parameter matching the `after` pattern or index.
  - The order of parameters in a parameter list can have significant impacts on parameter assignment. For details, see the SMIRNOFF specification: <https://openforcefield.github.io/standards/standards/smirnoff/#smirnoff-parameter-specification-is-hierarchical>

## Examples

Add a `ParameterType` to an existing `ParameterList` at a specified position.

Given an existing parameter handler and a new parameter to add to it:

```
>>> from openff.units import unit
>>> bh = BondHandler(skip_version_check=True)
>>> length = 1.5 * unit.angstrom
>>> k = 100 * unit.kilocalorie / unit.mole / unit.angstrom ** 2
>>> bh.add_parameter({'smirks': '[*:1]-[:2]', 'length': length, 'k': k, 'id': 'b1'})
↳
>>> bh.add_parameter({'smirks': '[*:1]=[:2]', 'length': length, 'k': k, 'id': 'b2'})
↳
>>> bh.add_parameter({'smirks': '[*:1]#[:2]', 'length': length, 'k': k, 'id': 'b3'})
↳
>>> [p.id for p in bh.parameters]
['b1', 'b2', 'b3']
```

```
>>> param = {'smirks': '[#1:1]-[#6:2]', 'length': length, 'k': k, 'id': 'b4'}
```

Add a new parameter immediately after the parameter with the smirks `[:1]=[:2]`

```
>>> bh.add_parameter(param, after='[:1]=[:2]')
>>> [p.id for p in bh.parameters]
['b1', 'b2', 'b4', 'b3']
```

**attribute\_is\_cosmetic**(*attr\_name*)

Determine whether an attribute of this object is cosmetic.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** `attr_name` (`str`) – The attribute name to check

**Returns** `is_cosmetic` (`bool`) – Returns True if the attribute is defined and is cosmetic. Returns False otherwise.

**create\_force**(*\*args, \*\*kwargs*)

Deprecated since version 0.11.0: This method was deprecated in v0.11.0, no longer has any functionality, and will soon be removed. Use the [OpenFF Interchange](#) package instead.

**delete\_cosmetic\_attribute**(*attr\_name*)

Delete a cosmetic attribute from this object.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** `attr_name` (`str`) – Name of the cosmetic attribute to delete.

**get\_parameter**(*parameter\_attrs*)

Return the parameters in this ParameterHandler that match the `parameter_attrs` argument. When multiple attrs are passed, parameters that have any (not all) matching attributes are returned.

**Parameters** `parameter_attrs` (dict of {attr: value}) – The attrs mapped to desired values (for example {"smirks": "[\*:1]~[#16:2]=,:[#6:3]~[:4]", "id": "t105"})

**Returns** `params` (list of *ParameterType* objects) – A list of matching *ParameterType* objects

## Examples

Create a parameter handler and populate it with some data.

```
>>> from openff.units import unit
>>> handler = BondHandler(skip_version_check=True)
>>> handler.add_parameter(
...     {
...         'smirks': '[*:1]-[:2]',
...         'length': 1*unit.angstrom,
...         'k': 10*unit.kilocalorie / unit.mole/unit.angstrom**2,
...     }
... )
```

Look up, from this handler, all parameters matching some SMIRKS pattern

```
>>> handler.get_parameter({'smirks': '[*:1]-[:2]'})
[<BondType with smirks: [*:1]-[:2] length: 1 angstrom k: 10.0 kilocalorie /
↳ angstrom ** 2 / mole >]
```

**property known\_kwargs**

List of kwargs that can be parsed by the function.

**property parameters**

The ParameterList that holds this ParameterHandler's parameter objects

**to\_dict**(*discard\_cosmetic\_attributes=False*)

Convert this ParameterHandler to a dict, compliant with the SMIRNOFF data spec.

**Parameters** **discard\_cosmetic\_attributes** (*bool*, optional. Default = False.) – Whether to discard non-spec parameter and header attributes in this ParameterHandler.

**Returns** **smirnoff\_data** (*dict*) – SMIRNOFF-spec compliant representation of this ParameterHandler and its internal ParameterList.

**vdwHandler**

```
class openff.toolkit.typing.engines.smirnoff.parameters.vdwHandler(allow_cosmetic_attributes=False,  
                                                                skip_version_check=False,  
                                                                **kwargs)
```

Handle SMIRNOFF <vdw> tags

**Warning:** This API is experimental and subject to change.

```
__init__(allow_cosmetic_attributes=False, skip_version_check=False, **kwargs)
```

Initialize a ParameterHandler, optionally with a list of parameters and other kwargs.

**Parameters**

- **allow\_cosmetic\_attributes** (*bool*, optional. Default = False) – Whether to permit non-spec kwargs. If True, non-spec kwargs will be stored as attributes of this object and can be accessed and modified. Otherwise an exception will be raised if a non-spec kwarg is encountered.
- **skip\_version\_check** (*bool*, optional. Default = False) – If False, the SMIRNOFF section version will not be checked, and the ParameterHandler will be initialized with version set to `_MAX_SUPPORTED_SECTION_VERSION`.
- **\*\*kwargs** (*dict*) – The dict representation of the SMIRNOFF data source

## Methods

<code>__init__([allow_cosmetic_attributes, ...])</code>	Initialize a ParameterHandler, optionally with a list of parameters and other kwargs.
<code>add_cosmetic_attribute(attr_name, attr_value)</code>	Add a cosmetic attribute to this object.
<code>add_parameter([parameter_kwargs, parameter, ...])</code>	Add a parameter to the force field, ensuring all parameters are valid.
<code>attribute_is_cosmetic(attr_name)</code>	Determine whether an attribute of this object is cosmetic.
<code>check_handler_compatibility(other_handler)</code>	Checks whether this ParameterHandler encodes compatible physics as another ParameterHandler.
<code>create_force(*args, **kwargs)</code>	Deprecated since version 0.11.0.
<code>delete_cosmetic_attribute(attr_name)</code>	Delete a cosmetic attribute from this object.
<code>find_matches(entity[, unique])</code>	Find the elements of the topology/molecule matched by a parameter type.
<code>get_parameter(parameter_attrs)</code>	Return the parameters in this ParameterHandler that match the parameter_attrs argument.
<code>to_dict([discard_cosmetic_attributes])</code>	Convert this ParameterHandler to a dict, compliant with the SMIRNOFF data spec.

## Attributes

<code>TAGNAME</code>	The name of this ParameterHandler corresponding to the SMIRNOFF tag name
<code>combining_rules</code>	
<code>cutoff</code>	
<code>known_kwargs</code>	List of kwargs that can be parsed by the function.
<code>method</code>	
<code>parameters</code>	The ParameterList that holds this ParameterHandler's parameter objects
<code>potential</code>	
<code>scale12</code>	
<code>scale13</code>	
<code>scale14</code>	
<code>scale15</code>	
<code>switch_width</code>	
<code>version</code>	



```
class vdWType(**kwargs)
```

A SMIRNOFF vdWForce type.

**Warning:** This API is experimental and subject to change.

```
to_dict(discard_cosmetic_attributes=False, duplicate_attributes=None)
```

Convert this object to dict format.

The returning dictionary contains all the ParameterAttribute and IndexedParameterAttribute as well as cosmetic attributes if discard\_cosmetic\_attributes is False.

**Parameters**

- **discard\_cosmetic\_attributes** (*bool*, optional. Default = False) – Whether to discard non-spec attributes of this object
- **duplicate\_attributes** (list of string, optional. Default = None) – A list of names of attributes that redundantly describe data and should be discarded during serialization

**Returns** **smirnoff\_dict** (*dict*) – The SMIRNOFF-compliant dict representation of this object.

```
add_cosmetic_attribute(attr_name, attr_value)
```

Add a cosmetic attribute to this object.

This attribute will not have a functional effect on the object in the OpenFF Toolkit, but can be written out during output.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters**

- **attr\_name** (*str*) – Name of the attribute to define for this object.
- **attr\_value** (*str*) – The value of the attribute to define for this object.

```
attribute_is_cosmetic(attr_name)
```

Determine whether an attribute of this object is cosmetic.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** **attr\_name** (*str*) – The attribute name to check

**Returns** **is\_cosmetic** (*bool*) – Returns True if the attribute is defined and is cosmetic. Returns False otherwise.

```
delete_cosmetic_attribute(attr_name)
```

Delete a cosmetic attribute from this object.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** **attr\_name** (*str*) – Name of the cosmetic attribute to delete.

**check\_handler\_compatibility**(*other\_handler*)

Checks whether this ParameterHandler encodes compatible physics as another ParameterHandler. This is called if a second handler is attempted to be initialized for the same tag.

**Parameters** *other\_handler* (a ParameterHandler object) – The handler to compare to.

**Raises** `IncompatibleParameterError` if `handler_kwargs` are incompatible with existing parameters. –

**property** `TAGNAME`

The name of this ParameterHandler corresponding to the SMIRNOFF tag name

**Returns** `handler_name` (*str*) – The name of this parameter handler

**add\_cosmetic\_attribute**(*attr\_name*, *attr\_value*)

Add a cosmetic attribute to this object.

This attribute will not have a functional effect on the object in the OpenFF Toolkit, but can be written out during output.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

#### Parameters

- **attr\_name** (*str*) – Name of the attribute to define for this object.
- **attr\_value** (*str*) – The value of the attribute to define for this object.

**add\_parameter**(*parameter\_kwargs=None*, *parameter=None*, *after=None*, *before=None*)

Add a parameter to the force field, ensuring all parameters are valid.

#### Parameters

- **parameter\_kwargs** (*dict*, optional) – The kwargs to pass to the `ParameterHandler.INFO_TYPE` (a `ParameterType`) constructor
- **parameter** (*ParameterType*, optional) – A `ParameterType` to add to the `ParameterHandler`
- **after** (*str* or *int*, optional) – The SMIRKS pattern (if *str*) or index (if *int*) of the parameter directly before where the new parameter will be added
- **before** (*str*, optional) – The SMIRKS pattern (if *str*) or index (if *int*) of the parameter directly after where the new parameter will be added
- **behavior** (Note the following) –
  - Either *parameter\_kwargs* or *parameter* must be specified.
  - When *before* and *after* are both *None*, the new parameter will be appended to the **END** of the parameter list.
  - When *before* and *after* are both specified, the new parameter will be added immediately after the parameter matching the *after* pattern or index.
  - The order of parameters in a parameter list can have significant impacts on parameter assignment. For details, see the SMIRNOFF specification: <https://openforcefield.github.io/standards/standards/smirnoff/#smirnoff-parameter-specification-is-hierarchical>

## Examples

Add a ParameterType to an existing ParameterList at a specified position.

Given an existing parameter handler and a new parameter to add to it:

```
>>> from openff.units import unit
>>> bh = BondHandler(skip_version_check=True)
>>> length = 1.5 * unit.angstrom
>>> k = 100 * unit.kilocalorie / unit.mole / unit.angstrom ** 2
>>> bh.add_parameter({'smirks': '[*:1]-[:2]', 'length': length, 'k': k, 'id': 'b1'})
↳
>>> bh.add_parameter({'smirks': '[*:1]=[*:2]', 'length': length, 'k': k, 'id': 'b2'})
↳
>>> bh.add_parameter({'smirks': '[*:1]#[:2]', 'length': length, 'k': k, 'id': 'b3'})
↳
>>> [p.id for p in bh.parameters]
['b1', 'b2', 'b3']
```

```
>>> param = {'smirks': '[#1:1]-[#6:2]', 'length': length, 'k': k, 'id': 'b4'}
```

Add a new parameter immediately after the parameter with the smirks `[:1]=[:2]`

```
>>> bh.add_parameter(param, after='[:1]=[:2]')
>>> [p.id for p in bh.parameters]
['b1', 'b2', 'b4', 'b3']
```

**attribute\_is\_cosmetic**(*attr\_name*)

Determine whether an attribute of this object is cosmetic.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** *attr\_name* (*str*) – The attribute name to check

**Returns** *is\_cosmetic* (*bool*) – Returns True if the attribute is defined and is cosmetic.  
Returns False otherwise.

**create\_force**(\*args, \*\*kwargs)

Deprecated since version 0.11.0: This method was deprecated in v0.11.0, no longer has any functionality, and will soon be removed. Use the [OpenFF Interchange](#) package instead.

**delete\_cosmetic\_attribute**(*attr\_name*)

Delete a cosmetic attribute from this object.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** *attr\_name* (*str*) – Name of the cosmetic attribute to delete.

**find\_matches**(entity, unique=False)

Find the elements of the topology/molecule matched by a parameter type.

**Parameters**

- **entity** (*Topology*) – Topology to search.
- **unique** (*bool*, default=False) – If False, SMARTS matching will enumerate every valid permutation of matching atoms. If True, only one order of each unique match will be returned.

**Returns matches** (*ValenceDict[Tuple[int], ParameterHandler.Match]*) – matches[atom\_indices] is the *ParameterType* object matching the tuple of atom indices in entity.

**get\_parameter**(parameter\_attrs)

Return the parameters in this *ParameterHandler* that match the *parameter\_attrs* argument. When multiple attrs are passed, parameters that have any (not all) matching attributes are returned.

**Parameters parameter\_attrs** (dict of {attr: value}) – The attrs mapped to desired values (for example {"smirks": "[\*:1]~[#16:2]=,[#6:3]~[:4]", "id": "t105"})

**Returns params** (*list of ParameterType objects*) – A list of matching *ParameterType* objects

## Examples

Create a parameter handler and populate it with some data.

```
>>> from openff.units import unit
>>> handler = BondHandler(skip_version_check=True)
>>> handler.add_parameter(
...     {
...         'smirks': '[*:1]-[:2]',
...         'length': 1*unit.angstrom,
...         'k': 10*unit.kilocalorie / unit.mole/unit.angstrom**2,
...     }
... )
```

Look up, from this handler, all parameters matching some SMIRKS pattern

```
>>> handler.get_parameter({'smirks': '[*:1]-[:2]'})
[<BondType with smirks: [*:1]-[:2] length: 1 angstrom k: 10.0 kilocalorie /
↳ angstrom ** 2 / mole >]
```

## property known\_kwargs

List of kwargs that can be parsed by the function.

## property parameters

The *ParameterList* that holds this *ParameterHandler*'s parameter objects

**to\_dict**(discard\_cosmetic\_attributes=False)

Convert this *ParameterHandler* to a dict, compliant with the SMIRNOFF data spec.

**Parameters discard\_cosmetic\_attributes** (*bool*, optional. Default = False.) – Whether to discard non-spec parameter and header attributes in this *ParameterHandler*.

Returns **smirnoff\_data** (*dict*) – SMIRNOFF-spec compliant representation of this ParameterHandler and its internal ParameterList.

## ElectrostaticsHandler

**class** openff.toolkit.typing.engines.smirnoff.parameters.**ElectrostaticsHandler**(*\*\*kwargs*)

Handles SMIRNOFF <Electrostatics> tags.

**Warning:** This API is experimental and subject to change.

**\_\_init\_\_**(*\*\*kwargs*)

Initialize a ParameterHandler, optionally with a list of parameters and other kwargs.

### Parameters

- **allow\_cosmetic\_attributes** (*bool*, optional. Default = False) – Whether to permit non-spec kwargs. If True, non-spec kwargs will be stored as attributes of this object and can be accessed and modified. Otherwise an exception will be raised if a non-spec kwarg is encountered.
- **skip\_version\_check** (*bool*, optional. Default = False) – If False, the SMIRNOFF section version will not be checked, and the ParameterHandler will be initialized with version set to `_MAX_SUPPORTED_SECTION_VERSION`.
- **\*\*kwargs** (*dict*) – The dict representation of the SMIRNOFF data source

## Methods

<code>__init__</code> ( <i>**kwargs</i> )	Initialize a ParameterHandler, optionally with a list of parameters and other kwargs.
<code>add_cosmetic_attribute</code> ( <i>attr_name</i> , <i>attr_value</i> )	Add a cosmetic attribute to this object.
<code>add_parameter</code> ([ <i>parameter_kwargs</i> , <i>parameter</i> , ...])	Add a parameter to the force field, ensuring all parameters are valid.
<code>attribute_is_cosmetic</code> ( <i>attr_name</i> )	Determine whether an attribute of this object is cosmetic.
<code>check_handler_compatibility</code> ( <i>other_handler</i> )	Checks whether this ParameterHandler encodes compatible physics as another ParameterHandler.
<code>create_force</code> ( <i>*args</i> , <i>**kwargs</i> )	Deprecated since version 0.11.0.
<code>delete_cosmetic_attribute</code> ( <i>attr_name</i> )	Delete a cosmetic attribute from this object.
<code>find_matches</code> ( <i>entity</i> [, <i>unique</i> ])	Find the elements of the topology/molecule matched by a parameter type.
<code>get_parameter</code> ( <i>parameter_attrs</i> )	Return the parameters in this ParameterHandler that match the <i>parameter_attrs</i> argument.
<code>to_dict</code> ([ <i>discard_cosmetic_attributes</i> ])	Convert this ParameterHandler to a dict, compliant with the SMIRNOFF data spec.

## Attributes

<code>TAGNAME</code>	The name of this ParameterHandler corresponding to the SMIRNOFF tag name
<code>cutoff</code>	
<code>exception_potential</code>	
<code>known_kwargs</code>	List of kwargs that can be parsed by the function.
<code>nonperiodic_potential</code>	
<code>parameters</code>	The ParameterList that holds this ParameterHandler's parameter objects
<code>periodic_potential</code>	
<code>scale12</code>	
<code>scale13</code>	
<code>scale14</code>	
<code>scale15</code>	
<code>solvent_dielectric</code>	
<code>switch_width</code>	
<code>version</code>	

### `check_handler_compatibility(other_handler)`

Checks whether this ParameterHandler encodes compatible physics as another ParameterHandler. This is called if a second handler is attempted to be initialized for the same tag.

**Parameters** `other_handler` (a ParameterHandler object) – The handler to compare to.

**Raises** `IncompatibleParameterError` if `handler_kwargs` are incompatible with existing parameters. –

### `property TAGNAME`

The name of this ParameterHandler corresponding to the SMIRNOFF tag name

**Returns** `handler_name` (*str*) – The name of this parameter handler

### `add_cosmetic_attribute(attr_name, attr_value)`

Add a cosmetic attribute to this object.

This attribute will not have a functional effect on the object in the OpenFF Toolkit, but can be written out during output.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

## Parameters

- **attr\_name** (*str*) – Name of the attribute to define for this object.
- **attr\_value** (*str*) – The value of the attribute to define for this object.

**add\_parameter**(*parameter\_kwargs=None, parameter=None, after=None, before=None*)

Add a parameter to the force field, ensuring all parameters are valid.

#### Parameters

- **parameter\_kwargs** (*dict*, optional) – The kwargs to pass to the ParameterHandler.INFO\_TYPE (a ParameterType) constructor
- **parameter** (*ParameterType*, optional) – A ParameterType to add to the ParameterHandler
- **after** (*str* or *int*, optional) – The SMIRKS pattern (if *str*) or index (if *int*) of the parameter directly before where the new parameter will be added
- **before** (*str*, optional) – The SMIRKS pattern (if *str*) or index (if *int*) of the parameter directly after where the new parameter will be added
- **behavior** (Note the following) –
  - Either *parameter\_kwargs* or *parameter* must be specified.
  - When *before* and *after* are both *None*, the new parameter will be appended to the END of the parameter list.
  - When *before* and *after* are both specified, the new parameter will be added immediately after the parameter matching the *after* pattern or index.
  - The order of parameters in a parameter list can have significant impacts on parameter assignment. For details, see the SMIRNOFF specification: <https://openforcefield.github.io/standards/standards/smirnoff/#smirnoff-parameter-specification-is-hierarchical>

#### Examples

Add a ParameterType to an existing ParameterList at a specified position.

Given an existing parameter handler and a new parameter to add to it:

```
>>> from openff.units import unit
>>> bh = BondHandler(skip_version_check=True)
>>> length = 1.5 * unit.angstrom
>>> k = 100 * unit.kilocalorie / unit.mole / unit.angstrom ** 2
>>> bh.add_parameter({'smirks': '[*:1]-[*:2]', 'length': length, 'k': k, 'id': 'b1'})
↪
>>> bh.add_parameter({'smirks': '[*:1]=[*:2]', 'length': length, 'k': k, 'id': 'b2'})
↪
>>> bh.add_parameter({'smirks': '[*:1]#[*:2]', 'length': length, 'k': k, 'id': 'b3'})
↪
>>> [p.id for p in bh.parameters]
['b1', 'b2', 'b3']
```

```
>>> param = {'smirks': '[#1:1]-[#6:2]', 'length': length, 'k': k, 'id': 'b4'}
```

Add a new parameter immediately after the parameter with the smirks `[*:1]=[*:2]`

```
>>> bh.add_parameter(param, after='[*:1]=[*:2]')
>>> [p.id for p in bh.parameters]
['b1', 'b2', 'b4', 'b3']
```

**attribute\_is\_cosmetic**(*attr\_name*)

Determine whether an attribute of this object is cosmetic.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** *attr\_name* (*str*) – The attribute name to check

**Returns** *is\_cosmetic* (*bool*) – Returns True if the attribute is defined and is cosmetic.  
Returns False otherwise.

**create\_force**(\**args*, \*\**kwargs*)

Deprecated since version 0.11.0: This method was deprecated in v0.11.0, no longer has any functionality, and will soon be removed. Use the [OpenFF Interchange](#) package instead.

**delete\_cosmetic\_attribute**(*attr\_name*)

Delete a cosmetic attribute from this object.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** *attr\_name* (*str*) – Name of the cosmetic attribute to delete.

**find\_matches**(*entity*, *unique=False*)

Find the elements of the topology/molecule matched by a parameter type.

**Parameters**

- **entity** (*Topology*) – Topology to search.
- **unique** (*bool*, default=False) – If False, SMARTS matching will enumerate every valid permutation of matching atoms. If True, only one order of each unique match will be returned.

**Returns** *matches* (*ValenceDict[Tuple[int], ParameterHandler.\_Match]*) –  
*matches[atom\_indices]* is the *ParameterType* object matching the tuple of atom indices in *entity*.

**get\_parameter**(*parameter\_attrs*)

Return the parameters in this *ParameterHandler* that match the *parameter\_attrs* argument. When multiple attrs are passed, parameters that have any (not all) matching attributes are returned.

**Parameters** *parameter\_attrs* (dict of {attr: value}) – The attrs mapped to desired values (for example {"smirks": "[\*:1]~[#16:2]=,:[#6:3]~[:4]", "id": "t105"})

**Returns** *params* (*list of ParameterType objects*) – A list of matching *ParameterType* objects



## Examples

Create a parameter handler and populate it with some data.

```
>>> from openff.units import unit
>>> handler = BondHandler(skip_version_check=True)
>>> handler.add_parameter(
...     {
...         'smirks': '[*:1]-[:2]',
...         'length': 1*unit.angstrom,
...         'k': 10*unit.kilocalorie / unit.mole/unit.angstrom**2,
...     }
... )
```

Look up, from this handler, all parameters matching some SMIRKS pattern

```
>>> handler.get_parameter({'smirks': '[*:1]-[:2]'})
[<BondType with smirks: [*:1]-[:2] length: 1 angstrom k: 10.0 kilocalorie / _
↳ angstrom ** 2 / mole >]
```

### property known\_kwargs

List of kwargs that can be parsed by the function.

### property parameters

The ParameterList that holds this ParameterHandler's parameter objects

### to\_dict(discard\_cosmetic\_attributes=False)

Convert this ParameterHandler to a dict, compliant with the SMIRNOFF data spec.

**Parameters** `discard_cosmetic_attributes` (`bool`, optional. Default = `False`.) – Whether to discard non-spec parameter and header attributes in this ParameterHandler.

**Returns** `smirnoff_data` (`dict`) – SMIRNOFF-spec compliant representation of this ParameterHandler and its internal ParameterList.

## LibraryChargeHandler

```
class openff.toolkit.typing.engines.smirnoff.parameters.LibraryChargeHandler(allow_cosmetic_attributes=False,
                                                                              skip_version_check=False,
                                                                              **kwargs)
```

Handle SMIRNOFF <LibraryCharges> tags

**Warning:** This API is experimental and subject to change.

```
__init__(allow_cosmetic_attributes=False, skip_version_check=False, **kwargs)
```

Initialize a ParameterHandler, optionally with a list of parameters and other kwargs.

### Parameters

- **allow\_cosmetic\_attributes** (`bool`, optional. Default = `False`) – Whether to permit non-spec kwargs. If `True`, non-spec kwargs will be stored as attributes of this object and can be accessed and modified. Otherwise an exception will be raised if a non-spec kwarg is encountered.

- **skip\_version\_check** (`bool`, optional. Default = `False`) – If `False`, the SMIRNOFF section version will not be checked, and the `ParameterHandler` will be initialized with version set to `_MAX_SUPPORTED_SECTION_VERSION`.
- **\*\*kwargs** (`dict`) – The dict representation of the SMIRNOFF data source

## Methods

<code>__init__([allow_cosmetic_attributes, ...])</code>	Initialize a <code>ParameterHandler</code> , optionally with a list of parameters and other kwargs.
<code>add_cosmetic_attribute(attr_name, attr_value)</code>	Add a cosmetic attribute to this object.
<code>add_parameter([parameter_kwargs, parameter, ...])</code>	Add a parameter to the force field, ensuring all parameters are valid.
<code>attribute_is_cosmetic(attr_name)</code>	Determine whether an attribute of this object is cosmetic.
<code>check_handler_compatibility(handler_kwargs)</code>	Checks if a set of kwargs used to create a <code>ParameterHandler</code> are compatible with this <code>ParameterHandler</code> .
<code>create_force(*args, **kwargs)</code>	Deprecated since version 0.11.0.
<code>delete_cosmetic_attribute(attr_name)</code>	Delete a cosmetic attribute from this object.
<code>find_matches(entity[, unique])</code>	Find the elements of the topology/molecule matched by a parameter type.
<code>get_parameter(parameter_attrs)</code>	Return the parameters in this <code>ParameterHandler</code> that match the <code>parameter_attrs</code> argument.
<code>to_dict([discard_cosmetic_attributes])</code>	Convert this <code>ParameterHandler</code> to a dict, compliant with the SMIRNOFF data spec.

## Attributes

<code>TAGNAME</code>	The name of this <code>ParameterHandler</code> corresponding to the SMIRNOFF tag name
<code>known_kwargs</code>	List of kwargs that can be parsed by the function.
<code>parameters</code>	The <code>ParameterList</code> that holds this <code>ParameterHandler</code> 's parameter objects
<code>version</code>	

**class** `LibraryChargeType(**kwargs)`  
 A SMIRNOFF Library Charge type.

**Warning:** This API is experimental and subject to change.

**classmethod** `from_molecule(molecule: Molecule)`

Construct a `LibraryChargeType` from a molecule with existing partial charges.

**Parameters** `molecule` (`Molecule`) – The molecule to create the `LibraryChargeType` from. The molecule must have partial charges.

**Returns** `library_charge_type` (*LibraryChargeType*) – A *LibraryChargeType* that is expected to match this molecule and its partial charges.  
 :raises `MissingPartialChargesError` : If the input molecule does not have partial charges.:

**add\_cosmetic\_attribute**(*attr\_name*, *attr\_value*)

Add a cosmetic attribute to this object.

This attribute will not have a functional effect on the object in the OpenFF Toolkit, but can be written out during output.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters**

- **attr\_name** (*str*) – Name of the attribute to define for this object.
- **attr\_value** (*str*) – The value of the attribute to define for this object.

**attribute\_is\_cosmetic**(*attr\_name*)

Determine whether an attribute of this object is cosmetic.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** *attr\_name* (*str*) – The attribute name to check

**Returns** *is\_cosmetic* (*bool*) – Returns True if the attribute is defined and is cosmetic.  
 Returns False otherwise.

**delete\_cosmetic\_attribute**(*attr\_name*)

Delete a cosmetic attribute from this object.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** *attr\_name* (*str*) – Name of the cosmetic attribute to delete.

**to\_dict**(*discard\_cosmetic\_attributes=False*, *duplicate\_attributes=None*)

Convert this object to dict format.

The returning dictionary contains all the `ParameterAttribute` and `IndexedParameterAttribute` as well as cosmetic attributes if `discard_cosmetic_attributes` is False.

**Parameters**

- **discard\_cosmetic\_attributes** (*bool*, optional. Default = False) – Whether to discard non-spec attributes of this object
- **duplicate\_attributes** (list of string, optional. Default = None) – A list of names of attributes that redundantly describe data and should be discarded during serializaiton

**Returns** *smirnoff\_dict* (*dict*) – The SMIRNOFF-compliant dict representation of this object.

**find\_matches**(*entity*, *unique=False*)

Find the elements of the topology/molecule matched by a parameter type.

**Parameters** *entity* (*Topology*) – Topology to search.

**Returns matches** (*ValenceDict[Tuple[int], ParameterHandler.Match]*) – matches[atom\_indices] is the ParameterType object matching the tuple of atom indices in entity.

**property TAGNAME**

The name of this ParameterHandler corresponding to the SMIRNOFF tag name

**Returns handler\_name** (*str*) – The name of this parameter handler

**add\_cosmetic\_attribute**(*attr\_name, attr\_value*)

Add a cosmetic attribute to this object.

This attribute will not have a functional effect on the object in the OpenFF Toolkit, but can be written out during output.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

#### Parameters

- **attr\_name** (*str*) – Name of the attribute to define for this object.
- **attr\_value** (*str*) – The value of the attribute to define for this object.

**add\_parameter**(*parameter\_kwargs=None, parameter=None, after=None, before=None*)

Add a parameter to the force field, ensuring all parameters are valid.

#### Parameters

- **parameter\_kwargs** (*dict*, optional) – The kwargs to pass to the ParameterHandler.INFO\_TYPE (a ParameterType) constructor
- **parameter** (*ParameterType*, optional) – A ParameterType to add to the ParameterHandler
- **after** (*str* or *int*, optional) – The SMIRKS pattern (if str) or index (if int) of the parameter directly before where the new parameter will be added
- **before** (*str*, optional) – The SMIRKS pattern (if str) or index (if int) of the parameter directly after where the new parameter will be added
- **behavior** (Note the following) –
  - Either *parameter\_kwargs* or *parameter* must be specified.
  - When *before* and *after* are both *None*, the new parameter will be appended to the **END** of the parameter list.
  - When *before* and *after* are both specified, the new parameter will be added immediately after the parameter matching the *after* pattern or index.
  - The order of parameters in a parameter list can have significant impacts on parameter assignment. For details, see the SMIRNOFF specification: <https://openforcefield.github.io/standards/standards/smirnoff/#smirnoff-parameter-specification-is-hierarchical>

## Examples

Add a ParameterType to an existing ParameterList at a specified position.

Given an existing parameter handler and a new parameter to add to it:

```
>>> from openff.units import unit
>>> bh = BondHandler(skip_version_check=True)
>>> length = 1.5 * unit.angstrom
>>> k = 100 * unit.kilocalorie / unit.mole / unit.angstrom ** 2
>>> bh.add_parameter({'smirks': '[*:1]-[:2]', 'length': length, 'k': k, 'id': 'b1'})
↳
>>> bh.add_parameter({'smirks': '[*:1]=[*:2]', 'length': length, 'k': k, 'id': 'b2'})
↳
>>> bh.add_parameter({'smirks': '[*:1]#[:2]', 'length': length, 'k': k, 'id': 'b3'})
↳
>>> [p.id for p in bh.parameters]
['b1', 'b2', 'b3']
```

```
>>> param = {'smirks': '[#1:1]-[#6:2]', 'length': length, 'k': k, 'id': 'b4'}
```

Add a new parameter immediately after the parameter with the smirks `[:1]=[:2]`

```
>>> bh.add_parameter(param, after='[:1]=[:2]')
>>> [p.id for p in bh.parameters]
['b1', 'b2', 'b4', 'b3']
```

**attribute\_is\_cosmetic(attr\_name)**

Determine whether an attribute of this object is cosmetic.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** *attr\_name* (*str*) – The attribute name to check

**Returns** *is\_cosmetic* (*bool*) – Returns True if the attribute is defined and is cosmetic.  
Returns False otherwise.

**check\_handler\_compatibility(handler\_kwargs)**

Checks if a set of kwargs used to create a ParameterHandler are compatible with this ParameterHandler. This is called if a second handler is attempted to be initialized for the same tag.

**Parameters** *handler\_kwargs* (*dict*) – The kwargs that would be used to construct

**Raises** *IncompatibleParameterError* if *handler\_kwargs* are incompatible with existing parameters. –

**create\_force(\*args, \*\*kwargs)**

Deprecated since version 0.11.0: This method was deprecated in v0.11.0, no longer has any functionality, and will soon be removed. Use the [OpenFF Interchange](#) package instead.

**delete\_cosmetic\_attribute(attr\_name)**

Delete a cosmetic attribute from this object.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** `attr_name` (`str`) – Name of the cosmetic attribute to delete.

**get\_parameter**(`parameter_attrs`)

Return the parameters in this `ParameterHandler` that match the `parameter_attrs` argument. When multiple attrs are passed, parameters that have any (not all) matching attributes are returned.

**Parameters** `parameter_attrs` (dict of {attr: value}) – The attrs mapped to desired values (for example {"smirks": "[\*:1]~[#16:2]=,:[#6:3]~[:4]", "id": "t105"})

**Returns** `params` (list of `ParameterType` objects) – A list of matching `ParameterType` objects

## Examples

Create a parameter handler and populate it with some data.

```
>>> from openff.units import unit
>>> handler = BondHandler(skip_version_check=True)
>>> handler.add_parameter(
...     {
...         'smirks': '[*:1]-[:2]',
...         'length': 1*unit.angstrom,
...         'k': 10*unit.kilocalorie / unit.mole/unit.angstrom**2,
...     }
... )
```

Look up, from this handler, all parameters matching some SMIRKS pattern

```
>>> handler.get_parameter({'smirks': '[*:1]-[:2]'})
[<BondType with smirks: [*:1]-[:2] length: 1 angstrom k: 10.0 kilocalorie /
↳ angstrom ** 2 / mole >]
```

**property** `known_kwargs`

List of kwargs that can be parsed by the function.

**property** `parameters`

The `ParameterList` that holds this `ParameterHandler`'s parameter objects

**to\_dict**(`discard_cosmetic_attributes=False`)

Convert this `ParameterHandler` to a dict, compliant with the SMIRNOFF data spec.

**Parameters** `discard_cosmetic_attributes` (`bool`, optional. Default = `False`.) – Whether to discard non-spec parameter and header attributes in this `ParameterHandler`.

**Returns** `smirnoff_data` (`dict`) – SMIRNOFF-spec compliant representation of this `ParameterHandler` and its internal `ParameterList`.

## ToolkitAM1BCHandler

```
class openff.toolkit.typing.engines.smirnoff.parameters.ToolkitAM1BCHandler(allow_cosmetic_attributes=False,
                                                                    skip_version_check=False,
                                                                    **kwargs)
```

Handle SMIRNOFF <ToolkitAM1BCC> tags

**Warning:** This API is experimental and subject to change.

```
__init__(allow_cosmetic_attributes=False, skip_version_check=False, **kwargs)
```

Initialize a ParameterHandler, optionally with a list of parameters and other kwargs.

### Parameters

- **allow\_cosmetic\_attributes** (*bool*, optional. Default = `False`) – Whether to permit non-spec kwargs. If `True`, non-spec kwargs will be stored as attributes of this object and can be accessed and modified. Otherwise an exception will be raised if a non-spec kwarg is encountered.
- **skip\_version\_check** (*bool*, optional. Default = `False`) – If `False`, the SMIRNOFF section version will not be checked, and the ParameterHandler will be initialized with version set to `_MAX_SUPPORTED_SECTION_VERSION`.
- **\*\*kwargs** (*dict*) – The dict representation of the SMIRNOFF data source

### Methods

<code>__init__([allow_cosmetic_attributes, ...])</code>	Initialize a ParameterHandler, optionally with a list of parameters and other kwargs.
<code>add_cosmetic_attribute(attr_name, attr_value)</code>	Add a cosmetic attribute to this object.
<code>add_parameter([parameter_kwargs, parameter, ...])</code>	Add a parameter to the force field, ensuring all parameters are valid.
<code>attribute_is_cosmetic(attr_name)</code>	Determine whether an attribute of this object is cosmetic.
<code>check_handler_compatibility(other_handler[, ...])</code>	Checks whether this ParameterHandler encodes compatible physics as another ParameterHandler.
<code>create_force(*args, **kwargs)</code>	Deprecated since version 0.11.0.
<code>delete_cosmetic_attribute(attr_name)</code>	Delete a cosmetic attribute from this object.
<code>find_matches(entity[, unique])</code>	Find the elements of the topology/molecule matched by a parameter type.
<code>get_parameter(parameter_attrs)</code>	Return the parameters in this ParameterHandler that match the <code>parameter_attrs</code> argument.
<code>to_dict([discard_cosmetic_attributes])</code>	Convert this ParameterHandler to a dict, compliant with the SMIRNOFF data spec.

## Attributes

<code>TAGNAME</code>	The name of this ParameterHandler corresponding to the SMIRNOFF tag name
<code>known_kwargs</code>	List of kwargs that can be parsed by the function.
<code>parameters</code>	The ParameterList that holds this ParameterHandler's parameter objects
<code>version</code>	

**check\_handler\_compatibility**(*other\_handler*, *assume\_missing\_is\_default=True*)

Checks whether this ParameterHandler encodes compatible physics as another ParameterHandler. This is called if a second handler is attempted to be initialized for the same tag.

**Parameters** *other\_handler* (a ParameterHandler object) – The handler to compare to.

**Raises** `IncompatibleParameterError` if `handler_kwargs` are incompatible with existing parameters. –

**property** `TAGNAME`

The name of this ParameterHandler corresponding to the SMIRNOFF tag name

**Returns** `handler_name` (*str*) – The name of this parameter handler

**add\_cosmetic\_attribute**(*attr\_name*, *attr\_value*)

Add a cosmetic attribute to this object.

This attribute will not have a functional effect on the object in the OpenFF Toolkit, but can be written out during output.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

### Parameters

- **attr\_name** (*str*) – Name of the attribute to define for this object.
- **attr\_value** (*str*) – The value of the attribute to define for this object.

**add\_parameter**(*parameter\_kwargs=None*, *parameter=None*, *after=None*, *before=None*)

Add a parameter to the force field, ensuring all parameters are valid.

### Parameters

- **parameter\_kwargs** (*dict*, optional) – The kwargs to pass to the ParameterHandler.INFO\_TYPE (a ParameterType) constructor
- **parameter** (*ParameterType*, optional) – A ParameterType to add to the ParameterHandler
- **after** (*str* or *int*, optional) – The SMIRKS pattern (if *str*) or index (if *int*) of the parameter directly before where the new parameter will be added
- **before** (*str*, optional) – The SMIRKS pattern (if *str*) or index (if *int*) of the parameter directly after where the new parameter will be added
- **behavior** (Note the following) –



- Either *parameter\_kwargs* or *parameter* must be specified.
- When *before* and *after* are both *None*, the new parameter will be appended to the **END** of the parameter list.
- When *before* and *after* are both specified, the new parameter will be added immediately after the parameter matching the *after* pattern or index.
- The order of parameters in a parameter list can have significant impacts on parameter assignment. For details, see the SMIRNOFF specification: <https://openforcefield.github.io/standards/standards/smirnoff/#smirnoff-parameter-specification-is-hierarchical>

## Examples

Add a ParameterType to an existing ParameterList at a specified position.

Given an existing parameter handler and a new parameter to add to it:

```
>>> from openff.units import unit
>>> bh = BondHandler(skip_version_check=True)
>>> length = 1.5 * unit.angstrom
>>> k = 100 * unit.kilocalorie / unit.mole / unit.angstrom ** 2
>>> bh.add_parameter({'smirks': '[*:1]-[*:2]', 'length': length, 'k': k, 'id': 'b1'})
↪
>>> bh.add_parameter({'smirks': '[*:1]=[*:2]', 'length': length, 'k': k, 'id': 'b2'})
↪
>>> bh.add_parameter({'smirks': '[*:1]#[*:2]', 'length': length, 'k': k, 'id': 'b3'})
↪
>>> [p.id for p in bh.parameters]
['b1', 'b2', 'b3']
```

```
>>> param = {'smirks': '[#1:1]-[#6:2]', 'length': length, 'k': k, 'id': 'b4'}
```

Add a new parameter immediately after the parameter with the smirks `[:1]=[:2]`

```
>>> bh.add_parameter(param, after='[:1]=[:2]')
>>> [p.id for p in bh.parameters]
['b1', 'b2', 'b4', 'b3']
```

**attribute\_is\_cosmetic**(*attr\_name*)

Determine whether an attribute of this object is cosmetic.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** *attr\_name* (*str*) – The attribute name to check

**Returns** *is\_cosmetic* (*bool*) – Returns True if the attribute is defined and is cosmetic.  
Returns False otherwise.

**create\_force**(\*args, \*\*kwargs)

Deprecated since version 0.11.0: This method was deprecated in v0.11.0, no longer has any functionality, and will soon be removed. Use the [OpenFF Interchange](#) package instead.

**delete\_cosmetic\_attribute**(*attr\_name*)

Delete a cosmetic attribute from this object.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** *attr\_name* (*str*) – Name of the cosmetic attribute to delete.

**find\_matches**(*entity*, *unique=False*)

Find the elements of the topology/molecule matched by a parameter type.

**Parameters**

- **entity** (*Topology*) – Topology to search.
- **unique** (*bool*, default=False) – If False, SMARTS matching will enumerate every valid permutation of matching atoms. If True, only one order of each unique match will be returned.

**Returns** *matches* (*ValenceDict[Tuple[int], ParameterHandler.\_Match]*) – *matches[atom\_indices]* is the *ParameterType* object matching the tuple of atom indices in *entity*.

**get\_parameter**(*parameter\_attrs*)

Return the parameters in this *ParameterHandler* that match the *parameter\_attrs* argument. When multiple attrs are passed, parameters that have any (not all) matching attributes are returned.

**Parameters** *parameter\_attrs* (dict of {attr: value}) – The attrs mapped to desired values (for example {"smirks": "[\*:1]~[#16:2]=,:[#6:3]~[:4]", "id": "t105"})

**Returns** *params* (list of *ParameterType* objects) – A list of matching *ParameterType* objects

## Examples

Create a parameter handler and populate it with some data.

```
>>> from openff.units import unit
>>> handler = BondHandler(skip_version_check=True)
>>> handler.add_parameter(
...     {
...         'smirks': '[*:1]-[:2]',
...         'length': 1*unit.angstrom,
...         'k': 10*unit.kilocalorie / unit.mole/unit.angstrom**2,
...     }
... )
```

Look up, from this handler, all parameters matching some SMIRKS pattern

```
>>> handler.get_parameter({'smirks': '[*:1]-[:2]'})
[<BondType with smirks: [*:1]-[:2] length: 1 angstrom k: 10.0 kilocalorie /
↳ angstrom ** 2 / mole >]
```

**property** `known_kwargs`

List of kwargs that can be parsed by the function.

**property** `parameters`

The ParameterList that holds this ParameterHandler's parameter objects

**to\_dict**(*discard\_cosmetic\_attributes=False*)

Convert this ParameterHandler to a dict, compliant with the SMIRNOFF data spec.

**Parameters** `discard_cosmetic_attributes` (*bool*, optional. Default = `False`.) – Whether to discard non-spec parameter and header attributes in this ParameterHandler.

**Returns** `smirnoff_data` (*dict*) – SMIRNOFF-spec compliant representation of this ParameterHandler and its internal ParameterList.

**GBSAHandler**

```
class openff.toolkit.typing.engines.smirnoff.parameters.GBSAHandler(allow_cosmetic_attributes=False,  
                                                                skip_version_check=False,  
                                                                **kwargs)
```

Handle SMIRNOFF <GBSA> tags

**Warning:** This API is experimental and subject to change.

```
__init__(allow_cosmetic_attributes=False, skip_version_check=False, **kwargs)
```

Initialize a ParameterHandler, optionally with a list of parameters and other kwargs.

**Parameters**

- **`allow_cosmetic_attributes`** (*bool*, optional. Default = `False`) – Whether to permit non-spec kwargs. If `True`, non-spec kwargs will be stored as attributes of this object and can be accessed and modified. Otherwise an exception will be raised if a non-spec kwarg is encountered.
- **`skip_version_check`** (*bool*, optional. Default = `False`) – If `False`, the SMIRNOFF section version will not be checked, and the ParameterHandler will be initialized with version set to `_MAX_SUPPORTED_SECTION_VERSION`.
- **`**kwargs`** (*dict*) – The dict representation of the SMIRNOFF data source

## Methods

<code>__init__([allow_cosmetic_attributes, ...])</code>	Initialize a <code>ParameterHandler</code> , optionally with a list of parameters and other kwargs.
<code>add_cosmetic_attribute(attr_name, attr_value)</code>	Add a cosmetic attribute to this object.
<code>add_parameter([parameter_kwargs, parameter, ...])</code>	Add a parameter to the force field, ensuring all parameters are valid.
<code>attribute_is_cosmetic(attr_name)</code>	Determine whether an attribute of this object is cosmetic.
<code>check_handler_compatibility(other_handler)</code>	Checks whether this <code>ParameterHandler</code> encodes compatible physics as another <code>ParameterHandler</code> .
<code>create_force(*args, **kwargs)</code>	Deprecated since version 0.11.0.
<code>delete_cosmetic_attribute(attr_name)</code>	Delete a cosmetic attribute from this object.
<code>find_matches(entity[, unique])</code>	Find the elements of the topology/molecule matched by a parameter type.
<code>get_parameter(parameter_attrs)</code>	Return the parameters in this <code>ParameterHandler</code> that match the <code>parameter_attrs</code> argument.
<code>to_dict([discard_cosmetic_attributes])</code>	Convert this <code>ParameterHandler</code> to a dict, compliant with the SMIRNOFF data spec.

## Attributes

<code>TAGNAME</code>	The name of this <code>ParameterHandler</code> corresponding to the SMIRNOFF tag name
<code>gb_model</code>	
<code>known_kwargs</code>	List of kwargs that can be parsed by the function.
<code>parameters</code>	The <code>ParameterList</code> that holds this <code>ParameterHandler</code> 's parameter objects
<code>sa_model</code>	
<code>solute_dielectric</code>	
<code>solvent_dielectric</code>	
<code>solvent_radius</code>	
<code>surface_area_penalty</code>	
<code>version</code>	

**class** `GBSAType(smirks, allow_cosmetic_attributes=False, **kwargs)`

A SMIRNOFF GBSA type.

**Warning:** This API is experimental and subject to change.

**add\_cosmetic\_attribute**(*attr\_name*, *attr\_value*)

Add a cosmetic attribute to this object.

This attribute will not have a functional effect on the object in the OpenFF Toolkit, but can be written out during output.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters**

- **attr\_name** (*str*) – Name of the attribute to define for this object.
- **attr\_value** (*str*) – The value of the attribute to define for this object.

**attribute\_is\_cosmetic**(*attr\_name*)

Determine whether an attribute of this object is cosmetic.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** **attr\_name** (*str*) – The attribute name to check

**Returns** **is\_cosmetic** (*bool*) – Returns True if the attribute is defined and is cosmetic.  
Returns False otherwise.

**delete\_cosmetic\_attribute**(*attr\_name*)

Delete a cosmetic attribute from this object.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** **attr\_name** (*str*) – Name of the cosmetic attribute to delete.

**to\_dict**(*discard\_cosmetic\_attributes=False*, *duplicate\_attributes=None*)

Convert this object to dict format.

The returning dictionary contains all the `ParameterAttribute` and `IndexedParameterAttribute` as well as cosmetic attributes if `discard_cosmetic_attributes` is False.

**Parameters**

- **discard\_cosmetic\_attributes** (*bool*, optional. Default = False) – Whether to discard non-spec attributes of this object
- **duplicate\_attributes** (list of string, optional. Default = None) – A list of names of attributes that redundantly describe data and should be discarded during serializaiton

**Returns** **smirnoff\_dict** (*dict*) – The SMIRNOFF-compliant dict representation of this object.

**check\_handler\_compatibility**(*other\_handler*)

Checks whether this `ParameterHandler` encodes compatible physics as another `ParameterHandler`. This is called if a second handler is attempted to be initialized for the same tag.

**Parameters** `other_handler` (a `ParameterHandler` object) – The handler to compare to.

**Raises** `IncompatibleParameterError` if `handler_kwargs` are incompatible with existing parameters. –

**property** `TAGNAME`

The name of this `ParameterHandler` corresponding to the SMIRNOFF tag name

**Returns** `handler_name` (*str*) – The name of this parameter handler

**add\_cosmetic\_attribute**(*attr\_name*, *attr\_value*)

Add a cosmetic attribute to this object.

This attribute will not have a functional effect on the object in the OpenFF Toolkit, but can be written out during output.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

#### Parameters

- **attr\_name** (*str*) – Name of the attribute to define for this object.
- **attr\_value** (*str*) – The value of the attribute to define for this object.

**add\_parameter**(*parameter\_kwargs*=None, *parameter*=None, *after*=None, *before*=None)

Add a parameter to the force field, ensuring all parameters are valid.

#### Parameters

- **parameter\_kwargs** (*dict*, optional) – The kwargs to pass to the `ParameterHandler.INFOType` (a `ParameterType`) constructor
- **parameter** (*ParameterType*, optional) – A `ParameterType` to add to the `ParameterHandler`
- **after** (*str* or *int*, optional) – The SMIRKS pattern (if *str*) or index (if *int*) of the parameter directly before where the new parameter will be added
- **before** (*str*, optional) – The SMIRKS pattern (if *str*) or index (if *int*) of the parameter directly after where the new parameter will be added
- **behavior** (Note the following) –
  - Either *parameter\_kwargs* or *parameter* must be specified.
  - When *before* and *after* are both *None*, the new parameter will be appended to the **END** of the parameter list.
  - When *before* and *after* are both specified, the new parameter will be added immediately after the parameter matching the *after* pattern or index.
  - The order of parameters in a parameter list can have significant impacts on parameter assignment. For details, see the SMIRNOFF specification: <https://openforcefield.github.io/standards/standards/smirnoff/#smirnoff-parameter-specification-is-hierarchical>

## Examples

Add a ParameterType to an existing ParameterList at a specified position.

Given an existing parameter handler and a new parameter to add to it:

```
>>> from openff.units import unit
>>> bh = BondHandler(skip_version_check=True)
>>> length = 1.5 * unit.angstrom
>>> k = 100 * unit.kilocalorie / unit.mole / unit.angstrom ** 2
>>> bh.add_parameter({'smirks': '[*:1]-[:2]', 'length': length, 'k': k, 'id': 'b1'})
↳
>>> bh.add_parameter({'smirks': '[*:1]=[:2]', 'length': length, 'k': k, 'id': 'b2'})
↳
>>> bh.add_parameter({'smirks': '[*:1]#[:2]', 'length': length, 'k': k, 'id': 'b3'})
↳
>>> [p.id for p in bh.parameters]
['b1', 'b2', 'b3']
```

```
>>> param = {'smirks': '[#1:1]-[#6:2]', 'length': length, 'k': k, 'id': 'b4'}
```

Add a new parameter immediately after the parameter with the smirks `[:1]=[:2]`

```
>>> bh.add_parameter(param, after='[:1]=[:2]')
>>> [p.id for p in bh.parameters]
['b1', 'b2', 'b4', 'b3']
```

**attribute\_is\_cosmetic(attr\_name)**

Determine whether an attribute of this object is cosmetic.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** `attr_name` (`str`) – The attribute name to check

**Returns** `is_cosmetic` (`bool`) – Returns True if the attribute is defined and is cosmetic.  
Returns False otherwise.

**create\_force(\*args, \*\*kwargs)**

Deprecated since version 0.11.0: This method was deprecated in v0.11.0, no longer has any functionality, and will soon be removed. Use the [OpenFF Interchange](#) package instead.

**delete\_cosmetic\_attribute(attr\_name)**

Delete a cosmetic attribute from this object.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** `attr_name` (`str`) – Name of the cosmetic attribute to delete.

**find\_matches**(entity, unique=False)

Find the elements of the topology/molecule matched by a parameter type.

#### Parameters

- **entity** (*Topology*) – Topology to search.
- **unique** (*bool*, default=False) – If False, SMARTS matching will enumerate every valid permutation of matching atoms. If True, only one order of each unique match will be returned.

**Returns matches** (*ValenceDict[Tuple[int], ParameterHandler.Match]*) – matches[atom\_indices] is the *ParameterType* object matching the tuple of atom indices in entity.

**get\_parameter**(parameter\_attrs)

Return the parameters in this *ParameterHandler* that match the *parameter\_attrs* argument. When multiple attrs are passed, parameters that have any (not all) matching attributes are returned.

**Parameters parameter\_attrs** (dict of {attr: value}) – The attrs mapped to desired values (for example {"smirks": "[\*:1]~[#16:2]=,[#6:3]~[:4]", "id": "t105"})

**Returns params** (*list of ParameterType objects*) – A list of matching *ParameterType* objects

## Examples

Create a parameter handler and populate it with some data.

```
>>> from openff.units import unit
>>> handler = BondHandler(skip_version_check=True)
>>> handler.add_parameter(
...     {
...         'smirks': '[*:1]-[:2]',
...         'length': 1*unit.angstrom,
...         'k': 10*unit.kilocalorie / unit.mole/unit.angstrom**2,
...     }
... )
```

Look up, from this handler, all parameters matching some SMIRKS pattern

```
>>> handler.get_parameter({'smirks': '[*:1]-[:2]'})
[<BondType with smirks: [*:1]-[:2] length: 1 angstrom k: 10.0 kilocalorie /
↳ angstrom ** 2 / mole >]
```

#### property known\_kwargs

List of kwargs that can be parsed by the function.

#### property parameters

The *ParameterList* that holds this *ParameterHandler*'s parameter objects

**to\_dict**(discard\_cosmetic\_attributes=False)

Convert this *ParameterHandler* to a dict, compliant with the SMIRNOFF data spec.

**Parameters discard\_cosmetic\_attributes** (*bool*, optional. Default = False.) – Whether to discard non-spec parameter and header attributes in this *ParameterHandler*.



Returns **smirnoff\_data** (*dict*) – SMIRNOFF-spec compliant representation of this ParameterHandler and its internal ParameterList.

### ChargeIncrementModelHandler

```
class openff.toolkit.typing.engines.smirnoff.parameters.ChargeIncrementModelHandler(allow_cosmetic_attributes=False,  
                                                                                   skip_version_check=False,  
                                                                                   **kwargs)
```

Handle SMIRNOFF <ChargeIncrementModel> tags

**Warning:** This API is experimental and subject to change.

```
__init__(allow_cosmetic_attributes=False, skip_version_check=False, **kwargs)
```

Initialize a ParameterHandler, optionally with a list of parameters and other kwargs.

#### Parameters

- **allow\_cosmetic\_attributes** (*bool*, optional. Default = False) – Whether to permit non-spec kwargs. If True, non-spec kwargs will be stored as attributes of this object and can be accessed and modified. Otherwise an exception will be raised if a non-spec kwarg is encountered.
- **skip\_version\_check** (*bool*, optional. Default = False) – If False, the SMIRNOFF section version will not be checked, and the ParameterHandler will be initialized with version set to `_MAX_SUPPORTED_SECTION_VERSION`.
- **\*\*kwargs** (*dict*) – The dict representation of the SMIRNOFF data source

### Methods

<code>__init__([allow_cosmetic_attributes, ...])</code>	Initialize a ParameterHandler, optionally with a list of parameters and other kwargs.
<code>add_cosmetic_attribute(attr_name, attr_value)</code>	Add a cosmetic attribute to this object.
<code>add_parameter([parameter_kwargs, parameter, ...])</code>	Add a parameter to the force field, ensuring all parameters are valid.
<code>attribute_is_cosmetic(attr_name)</code>	Determine whether an attribute of this object is cosmetic.
<code>check_handler_compatibility(other_handler[, ...])</code>	Checks whether this ParameterHandler encodes compatible physics as another ParameterHandler.
<code>create_force(*args, **kwargs)</code>	Deprecated since version 0.11.0.
<code>delete_cosmetic_attribute(attr_name)</code>	Delete a cosmetic attribute from this object.
<code>find_matches(entity[, unique])</code>	Find the elements of the topology/molecule matched by a parameter type.
<code>get_parameter(parameter_attrs)</code>	Return the parameters in this ParameterHandler that match the parameter_attrs argument.
<code>to_dict([discard_cosmetic_attributes])</code>	Convert this ParameterHandler to a dict, compliant with the SMIRNOFF data spec.

## Attributes

<code>TAGNAME</code>	The name of this ParameterHandler corresponding to the SMIRNOFF tag name
<code>known_kwargs</code>	List of kwargs that can be parsed by the function.
<code>number_of_conformers</code>	
<code>parameters</code>	The ParameterList that holds this ParameterHandler's parameter objects
<code>partial_charge_method</code>	
<code>version</code>	

**class** `ChargeIncrementType(**kwargs)`

A SMIRNOFF bond charge correction type.

**Warning:** This API is experimental and subject to change.

**add\_cosmetic\_attribute**(*attr\_name*, *attr\_value*)

Add a cosmetic attribute to this object.

This attribute will not have a functional effect on the object in the OpenFF Toolkit, but can be written out during output.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

### Parameters

- **attr\_name** (*str*) – Name of the attribute to define for this object.
- **attr\_value** (*str*) – The value of the attribute to define for this object.

**attribute\_is\_cosmetic**(*attr\_name*)

Determine whether an attribute of this object is cosmetic.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** *attr\_name* (*str*) – The attribute name to check

**Returns** *is\_cosmetic* (*bool*) – Returns True if the attribute is defined and is cosmetic.  
Returns False otherwise.

**delete\_cosmetic\_attribute**(*attr\_name*)

Delete a cosmetic attribute from this object.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** *attr\_name* (*str*) – Name of the cosmetic attribute to delete.

**to\_dict**(*discard\_cosmetic\_attributes=False, duplicate\_attributes=None*)

Convert this object to dict format.

The returning dictionary contains all the `ParameterAttribute` and `IndexedParameterAttribute` as well as cosmetic attributes if `discard_cosmetic_attributes` is `False`.

**Parameters**

- **discard\_cosmetic\_attributes** (`bool`, optional. Default = `False`) – Whether to discard non-spec attributes of this object
- **duplicate\_attributes** (list of string, optional. Default = `None`) – A list of names of attributes that redundantly describe data and should be discarded during serialization

**Returns** `smirnoff_dict` (`dict`) – The SMIRNOFF-compliant dict representation of this object.

**check\_handler\_compatibility**(*other\_handler, assume\_missing\_is\_default=True*)

Checks whether this `ParameterHandler` encodes compatible physics as another `ParameterHandler`. This is called if a second handler is attempted to be initialized for the same tag.

**Parameters** `other_handler` (a `ParameterHandler` object) – The handler to compare to.

**Raises** `IncompatibleParameterError` if `handler_kwargs` are incompatible with existing parameters. –

**find\_matches**(*entity, unique=False*)

Find the elements of the topology/molecule matched by a parameter type.

**Parameters** `entity` (`Topology`) – Topology to search.

**Returns** `matches` (`ValenceDict[Tuple[int], ParameterHandler.Match]`) – `matches[atom_indices]` is the `ParameterType` object matching the tuple of atom indices in `entity`.

**property** `TAGNAME`

The name of this `ParameterHandler` corresponding to the SMIRNOFF tag name

**Returns** `handler_name` (`str`) – The name of this parameter handler

**add\_cosmetic\_attribute**(*attr\_name, attr\_value*)

Add a cosmetic attribute to this object.

This attribute will not have a functional effect on the object in the OpenFF Toolkit, but can be written out during output.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters**

- **attr\_name** (`str`) – Name of the attribute to define for this object.
- **attr\_value** (`str`) – The value of the attribute to define for this object.

**add\_parameter**(*parameter\_kwargs=None, parameter=None, after=None, before=None*)

Add a parameter to the force field, ensuring all parameters are valid.

**Parameters**

- **parameter\_kwargs** (`dict`, optional) – The kwargs to pass to the `ParameterHandler.INFO_TYPE` (a `ParameterType`) constructor
- **parameter** (`ParameterType`, optional) – A `ParameterType` to add to the `ParameterHandler`
- **after** (`str` or `int`, optional) – The SMIRKS pattern (if `str`) or index (if `int`) of the parameter directly before where the new parameter will be added
- **before** (`str`, optional) – The SMIRKS pattern (if `str`) or index (if `int`) of the parameter directly after where the new parameter will be added
- **behavior** (Note the following) –
  - Either `parameter_kwargs` or `parameter` must be specified.
  - When `before` and `after` are both `None`, the new parameter will be appended to the **END** of the parameter list.
  - When `before` and `after` are both specified, the new parameter will be added immediately after the parameter matching the `after` pattern or index.
  - The order of parameters in a parameter list can have significant impacts on parameter assignment. For details, see the SMIRNOFF specification: <https://openforcefield.github.io/standards/standards/smirnoff/#smirnoff-parameter-specification-is-hierarchical>

## Examples

Add a `ParameterType` to an existing `ParameterList` at a specified position.

Given an existing parameter handler and a new parameter to add to it:

```
>>> from openff.units import unit
>>> bh = BondHandler(skip_version_check=True)
>>> length = 1.5 * unit.angstrom
>>> k = 100 * unit.kilocalorie / unit.mole / unit.angstrom ** 2
>>> bh.add_parameter({'smirks': '[*:1]-[:2]', 'length': length, 'k': k, 'id': 'b1'})
↳
>>> bh.add_parameter({'smirks': '[*:1]=[:2]', 'length': length, 'k': k, 'id': 'b2'})
↳
>>> bh.add_parameter({'smirks': '[*:1]#[:2]', 'length': length, 'k': k, 'id': 'b3'})
↳
>>> [p.id for p in bh.parameters]
['b1', 'b2', 'b3']
```

```
>>> param = {'smirks': '[#1:1]-[#6:2]', 'length': length, 'k': k, 'id': 'b4'}
```

Add a new parameter immediately after the parameter with the smirks `[:1]=[:2]`

```
>>> bh.add_parameter(param, after='[:1]=[:2]')
>>> [p.id for p in bh.parameters]
['b1', 'b2', 'b4', 'b3']
```

**attribute\_is\_cosmetic**(*attr\_name*)

Determine whether an attribute of this object is cosmetic.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** `attr_name` (`str`) – The attribute name to check

**Returns** `is_cosmetic` (`bool`) – Returns True if the attribute is defined and is cosmetic. Returns False otherwise.

**create\_force**(*\*args, \*\*kwargs*)

Deprecated since version 0.11.0: This method was deprecated in v0.11.0, no longer has any functionality, and will soon be removed. Use the [OpenFF Interchange](#) package instead.

**delete\_cosmetic\_attribute**(*attr\_name*)

Delete a cosmetic attribute from this object.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** `attr_name` (`str`) – Name of the cosmetic attribute to delete.

**get\_parameter**(*parameter\_attrs*)

Return the parameters in this ParameterHandler that match the `parameter_attrs` argument. When multiple attrs are passed, parameters that have any (not all) matching attributes are returned.

**Parameters** `parameter_attrs` (dict of {attr: value}) – The attrs mapped to desired values (for example {"smirks": "[\*:1]~[#16:2]=,:[#6:3]~[:4]", "id": "t105"})

**Returns** `params` (list of *ParameterType* objects) – A list of matching *ParameterType* objects

## Examples

Create a parameter handler and populate it with some data.

```
>>> from openff.units import unit
>>> handler = BondHandler(skip_version_check=True)
>>> handler.add_parameter(
...     {
...         'smirks': '[*:1]-[:2]',
...         'length': 1*unit.angstrom,
...         'k': 10*unit.kilocalorie / unit.mole/unit.angstrom**2,
...     }
... )
```

Look up, from this handler, all parameters matching some SMIRKS pattern

```
>>> handler.get_parameter({'smirks': '[*:1]-[:2]'})
[<BondType with smirks: [*:1]-[:2] length: 1 angstrom k: 10.0 kilocalorie /
↳ angstrom ** 2 / mole >]
```

**property known\_kwargs**

List of kwargs that can be parsed by the function.

**property parameters**

The ParameterList that holds this ParameterHandler's parameter objects

**to\_dict**(*discard\_cosmetic\_attributes=False*)

Convert this ParameterHandler to a dict, compliant with the SMIRNOFF data spec.

**Parameters** **discard\_cosmetic\_attributes** (*bool*, optional. Default = False.) – Whether to discard non-spec parameter and header attributes in this ParameterHandler.

**Returns** **smirnoff\_data** (*dict*) – SMIRNOFF-spec compliant representation of this ParameterHandler and its internal ParameterList.

**VirtualSiteHandler**

```
class openff.toolkit.typing.engines.smirnoff.parameters.VirtualSiteHandler(allow_cosmetic_attributes=False,  
                                                                           skip_version_check=False,  
                                                                           **kwargs)
```

Handle SMIRNOFF <VirtualSites> tags TODO: Add example usage/documentation .. warning :: This API is experimental and subject to change.

```
__init__(allow_cosmetic_attributes=False, skip_version_check=False, **kwargs)
```

Initialize a ParameterHandler, optionally with a list of parameters and other kwargs.

**Parameters**

- **allow\_cosmetic\_attributes** (*bool*, optional. Default = False) – Whether to permit non-spec kwargs. If True, non-spec kwargs will be stored as attributes of this object and can be accessed and modified. Otherwise an exception will be raised if a non-spec kwarg is encountered.
- **skip\_version\_check** (*bool*, optional. Default = False) – If False, the SMIRNOFF section version will not be checked, and the ParameterHandler will be initialized with version set to `_MAX_SUPPORTED_SECTION_VERSION`.
- **\*\*kwargs** (*dict*) – The dict representation of the SMIRNOFF data source

## Methods

<code>__init__([allow_cosmetic_attributes, ...])</code>	Initialize a <code>ParameterHandler</code> , optionally with a list of parameters and other kwargs.
<code>add_cosmetic_attribute(attr_name, attr_value)</code>	Add a cosmetic attribute to this object.
<code>add_parameter([parameter_kwargs, parameter, ...])</code>	Add a parameter to the force field, ensuring all parameters are valid.
<code>attribute_is_cosmetic(attr_name)</code>	Determine whether an attribute of this object is cosmetic.
<code>check_handler_compatibility(other_handler)</code>	Checks if a set of kwargs used to create a <code>ParameterHandler</code> are compatible with this <code>ParameterHandler</code> .
<code>create_force(*args, **kwargs)</code>	Deprecated since version 0.11.0.
<code>delete_cosmetic_attribute(attr_name)</code>	Delete a cosmetic attribute from this object.
<code>find_matches(entity[, unique])</code>	Find the elements of the topology/molecule matched by a parameter type.
<code>get_parameter(parameter_attrs)</code>	Return the parameters in this <code>ParameterHandler</code> that match the <code>parameter_attrs</code> argument.
<code>to_dict([discard_cosmetic_attributes])</code>	Convert this <code>ParameterHandler</code> to a dict, compliant with the SMIRNOFF data spec.

## Attributes

<code>TAGNAME</code>	The name of this <code>ParameterHandler</code> corresponding to the SMIRNOFF tag name
<code>exclusion_policy</code>	
<code>known_kwargs</code>	List of kwargs that can be parsed by the function.
<code>parameters</code>	The <code>ParameterList</code> that holds this <code>ParameterHandler</code> 's parameter objects
<code>version</code>	

**class** `VirtualSiteType(**kwargs)`

**property** `parent_index: int`

Returns the index of the atom matched by the SMIRKS pattern that should be considered the 'parent' to the virtual site. A value of 0 corresponds to the atom matched by the :1 selector in the SMIRKS pattern, a value 2 the atom matched by :2 and so on.

**classmethod** `type_to_parent_index(type_: Literal['BondCharge', 'MonovalentLonePair', 'DivalentLonePair', 'TrivalentLonePair']) → int`

Returns the index of the atom matched by the SMIRKS pattern that should be considered the 'parent' to a given type of virtual site. A value of 0 corresponds to the atom matched by the :1 selector in the SMIRKS pattern, a value 2 the atom matched by :2 and so on.

**add\_cosmetic\_attribute**(`attr_name`, `attr_value`)

Add a cosmetic attribute to this object.

This attribute will not have a functional effect on the object in the OpenFF Toolkit, but can be written out during output.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters**

- **attr\_name** (*str*) – Name of the attribute to define for this object.
- **attr\_value** (*str*) – The value of the attribute to define for this object.

**attribute\_is\_cosmetic**(*attr\_name*)

Determine whether an attribute of this object is cosmetic.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** **attr\_name** (*str*) – The attribute name to check

**Returns** **is\_cosmetic** (*bool*) – Returns True if the attribute is defined and is cosmetic.

Returns False otherwise.

**delete\_cosmetic\_attribute**(*attr\_name*)

Delete a cosmetic attribute from this object.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** **attr\_name** (*str*) – Name of the cosmetic attribute to delete.

**to\_dict**(*discard\_cosmetic\_attributes=False, duplicate\_attributes=None*)

Convert this object to dict format.

The returning dictionary contains all the `ParameterAttribute` and `IndexedParameterAttribute` as well as cosmetic attributes if `discard_cosmetic_attributes` is False.

**Parameters**

- **discard\_cosmetic\_attributes** (*bool*, optional. Default = False) – Whether to discard non-spec attributes of this object
- **duplicate\_attributes** (list of string, optional. Default = None) – A list of names of attributes that redundantly describe data and should be discarded during serializaiton

**Returns** **smirnoff\_dict** (*dict*) – The SMIRNOFF-compliant dict representation of this object.

**property** **TAGNAME**

The name of this `ParameterHandler` corresponding to the SMIRNOFF tag name

**Returns** **handler\_name** (*str*) – The name of this parameter handler

**add\_cosmetic\_attribute**(*attr\_name, attr\_value*)

Add a cosmetic attribute to this object.

This attribute will not have a functional effect on the object in the OpenFF Toolkit, but can be written out during output.



**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

### Parameters

- **attr\_name** (*str*) – Name of the attribute to define for this object.
- **attr\_value** (*str*) – The value of the attribute to define for this object.

**add\_parameter**(*parameter\_kwargs=None, parameter=None, after=None, before=None*)

Add a parameter to the force field, ensuring all parameters are valid.

### Parameters

- **parameter\_kwargs** (*dict*, optional) – The kwargs to pass to the ParameterHandler.INFO\_TYPE (a ParameterType) constructor
- **parameter** (*ParameterType*, optional) – A ParameterType to add to the ParameterHandler
- **after** (*str* or *int*, optional) – The SMIRKS pattern (if *str*) or index (if *int*) of the parameter directly before where the new parameter will be added
- **before** (*str*, optional) – The SMIRKS pattern (if *str*) or index (if *int*) of the parameter directly after where the new parameter will be added
- **behavior** (Note the following) –
  - Either *parameter\_kwargs* or *parameter* must be specified.
  - When *before* and *after* are both *None*, the new parameter will be appended to the **END** of the parameter list.
  - When *before* and *after* are both specified, the new parameter will be added immediately after the parameter matching the *after* pattern or index.
  - The order of parameters in a parameter list can have significant impacts on parameter assignment. For details, see the SMIRNOFF specification: <https://openforcefield.github.io/standards/standards/smirnoff/#smirnoff-parameter-specification-is-hierarchical>

### Examples

Add a ParameterType to an existing ParameterList at a specified position.

Given an existing parameter handler and a new parameter to add to it:

```
>>> from openff.units import unit
>>> bh = BondHandler(skip_version_check=True)
>>> length = 1.5 * unit.angstrom
>>> k = 100 * unit.kilocalorie / unit.mole / unit.angstrom ** 2
>>> bh.add_parameter({'smirks': '[*:1]-[:2]', 'length': length, 'k': k, 'id': 'b1'})
↪
>>> bh.add_parameter({'smirks': '[*:1]=[:2]', 'length': length, 'k': k, 'id': 'b2'})
↪
>>> bh.add_parameter({'smirks': '[*:1]#[:2]', 'length': length, 'k': k, 'id': 'b3'})
↪
```

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```
>>> [p.id for p in bh.parameters]
['b1', 'b2', 'b3']
```

```
>>> param = {'smirks': '[#1:1]-[#6:2]', 'length': length, 'k': k, 'id': 'b4'}
```

Add a new parameter immediately after the parameter with the smirks `[:1]=[:2]`

```
>>> bh.add_parameter(param, after='[*:1]=[*:2]')
>>> [p.id for p in bh.parameters]
['b1', 'b2', 'b4', 'b3']
```

**attribute\_is\_cosmetic**(*attr\_name*)

Determine whether an attribute of this object is cosmetic.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** *attr\_name* (*str*) – The attribute name to check

**Returns** *is\_cosmetic* (*bool*) – Returns True if the attribute is defined and is cosmetic.  
Returns False otherwise.

**create\_force**(\*args, \*\*kwargs)

Deprecated since version 0.11.0: This method was deprecated in v0.11.0, no longer has any functionality, and will soon be removed. Use the [OpenFF Interchange](#) package instead.

**delete\_cosmetic\_attribute**(*attr\_name*)

Delete a cosmetic attribute from this object.

**Warning:** The API for modifying cosmetic attributes is experimental and may change in the future (see issue #338).

**Parameters** *attr\_name* (*str*) – Name of the cosmetic attribute to delete.

**find\_matches**(*entity*, *unique=False*)

Find the elements of the topology/molecule matched by a parameter type.

**Parameters**

- **entity** (*Topology*) – Topology to search.
- **unique** (*bool*, default=False) – If False, SMARTS matching will enumerate every valid permutation of matching atoms. If True, only one order of each unique match will be returned.

**Returns** *matches* (*ValenceDict[Tuple[int], ParameterHandler.Match]*) –  
*matches*[*atom\_indices*] is the *ParameterType* object matching the tuple of atom indices in *entity*.

**get\_parameter**(*parameter\_attrs*)

Return the parameters in this *ParameterHandler* that match the *parameter\_attrs* argument. When multiple attrs are passed, parameters that have any (not all) matching attributes are returned.

**Parameters** `parameter_attrs` (dict of {attr: value}) – The attrs mapped to desired values (for example {"smirks": "[\*:1]~[#16:2]=,:[#6:3]~[:4]", "id": "t105"} )

**Returns** `params` (list of `ParameterType` objects) – A list of matching `ParameterType` objects

## Examples

Create a parameter handler and populate it with some data.

```
>>> from openff.units import unit
>>> handler = BondHandler(skip_version_check=True)
>>> handler.add_parameter(
...     {
...         'smirks': '[*:1]-[:2]',
...         'length': 1*unit.angstrom,
...         'k': 10*unit.kilocalorie / unit.mole/unit.angstrom**2,
...     }
... )
```

Look up, from this handler, all parameters matching some SMIRKS pattern

```
>>> handler.get_parameter({'smirks': '[*:1]-[:2]'})
[<BondType with smirks: [*:1]-[:2] length: 1 angstrom k: 10.0 kilocalorie /
↳ angstrom ** 2 / mole >]
```

### property `known_kwargs`

List of kwargs that can be parsed by the function.

### property `parameters`

The `ParameterList` that holds this `ParameterHandler`'s parameter objects

### `to_dict(discard_cosmetic_attributes=False)`

Convert this `ParameterHandler` to a dict, compliant with the SMIRNOFF data spec.

**Parameters** `discard_cosmetic_attributes` (`bool`, optional. Default = `False`.) – Whether to discard non-spec parameter and header attributes in this `ParameterHandler`.

**Returns** `smirnoff_data` (`dict`) – SMIRNOFF-spec compliant representation of this `ParameterHandler` and its internal `ParameterList`.

### `check_handler_compatibility(other_handler)`

Checks if a set of kwargs used to create a `ParameterHandler` are compatible with this `ParameterHandler`. This is called if a second handler is attempted to be initialized for the same tag.

**Parameters** `handler_kwargs` (`dict`) – The kwargs that would be used to construct

Raises `IncompatibleParameterError` if `handler_kwargs` are incompatible with existing parameters. –

## Parameter I/O Handlers

ParameterIOHandler objects handle reading and writing of serialized SMIRNOFF data sources.

<code>ParameterIOHandler</code>	Base class for handling serialization/deserialization of SMIRNOFF ForceField objects
<code>XMLParameterIOHandler</code>	Handles serialization/deserialization of SMIRNOFF ForceField objects from OFFXML format.

### ParameterIOHandler

**class** `openff.toolkit.typing.engines.smirnoff.io.ParameterIOHandler`

Base class for handling serialization/deserialization of SMIRNOFF ForceField objects

`__init__()`

Create a new ParameterIOHandler.

#### Methods

<code>__init__()</code>	Create a new ParameterIOHandler.
<code>parse_file(file_path)</code>	<b>param</b> <code>file_path</code>
<code>parse_string(data)</code>	Parse a SMIRNOFF force field definition in a serialized format
<code>to_file(file_path, smirnoff_data)</code>	Write the current force field parameter set to a file.
<code>to_string(smirnoff_data)</code>	Render the force field parameter set to a string

`parse_file(file_path)`

**Parameters** `file_path` –

`parse_string(data)`

Parse a SMIRNOFF force field definition in a serialized format

**Parameters** `data` –

`to_file(file_path, smirnoff_data)`

Write the current force field parameter set to a file.

**Parameters**

- `file_path` (`str`) – The path to the file to write to.
- `smirnoff_data` (`dict`) – A dictionary structured in compliance with the SMIRNOFF spec

`to_string(smirnoff_data)`

Render the force field parameter set to a string

**Parameters** `smirnoff_data` (`dict`) – A dictionary structured in compliance with the SMIRNOFF spec

**Returns** `str`

## XMLParameterIOHandler

**class** openff.toolkit.typing.engines.smirnoff.io.XMLParameterIOHandler

Handles serialization/deserialization of SMIRNOFF ForceField objects from OFFXML format.

**\_\_init\_\_()**

Create a new ParameterIOHandler.

## Methods

<code>__init__()</code>	Create a new ParameterIOHandler.
<code>parse_file(source)</code>	Parse a SMIRNOFF force field definition in XML format, read from a file.
<code>parse_string(data)</code>	Parse a SMIRNOFF force field definition in XML format.
<code>to_file(file_path, smirnoff_data)</code>	Write the current force field parameter set to a file.
<code>to_string(smirnoff_data)</code>	Write the current force field parameter set to an XML string.

**parse\_file(source)**

Parse a SMIRNOFF force field definition in XML format, read from a file.

**Parameters** **source** (*str* or *RawIOBase*) – File path of file-like object implementing a `read()` method specifying a SMIRNOFF force field definition in the SMIRNOFF XML format.

### Raises

- **SMIRNOFFParseError** – If the XML cannot be processed.
- **FileNotFoundError** – If the file could not found.

**parse\_string(data)**

Parse a SMIRNOFF force field definition in XML format.

A SMIRNOFFParseError is raised if the XML cannot be processed.

**Parameters** **data** (*str*) – A SMIRNOFF force field definition in the SMIRNOFF XML format.

**to\_file(file\_path, smirnoff\_data)**

Write the current force field parameter set to a file.

### Parameters

- **file\_path** (*str*) – The path to the file to be written. The *.offxml* or *.xml* file extension must be present.
- **smirnoff\_data** (*dict*) – A dict structured in compliance with the SMIRNOFF data spec.

**to\_string(smirnoff\_data)**

Write the current force field parameter set to an XML string.

**Parameters** **smirnoff\_data** (*dict*) – A dictionary structured in compliance with the SMIRNOFF spec

Returns `serialized_forcefield` (*str*) – XML String representation of this force field.

## Parameter Attributes

`ParameterAttribute` and `IndexedParameterAttribute` provide a standard backend for `ParameterHandler` and Parameter attributes, while also enforcing validation of types and units.

<code>ParameterAttribute</code>	A descriptor for <code>ParameterType</code> attributes.
<code>IndexedParameterAttribute</code>	The attribute of a parameter with an unspecified number of terms.
<code>MappedParameterAttribute</code>	The attribute of a parameter in which each term is a mapping.
<code>IndexedMappedParameterAttribute</code>	The attribute of a parameter with an unspecified number of terms, where each term is a mapping.

## ParameterAttribute

```
class openff.toolkit.typing.engines.smirnoff.parameters.ParameterAttribute(default: Any =  
                                UNDEFINED, unit:  
                                Optional[Unit] =  
                                None, converter:  
                                Optional[Callable] =  
                                None, docstring: str =  
                                "")
```

A descriptor for `ParameterType` attributes.

The descriptors allows associating to the parameter a default value, which makes the attribute optional, a unit, and a custom converter.

Because we may want to have `None` as a default value, required attributes have the default set to the special type `UNDEFINED`.

Converters can be both static or instance functions/methods with respective signatures:

```
converter(value): -> converted_value  
converter(instance, parameter_attribute, value): -> converted_value
```

A decorator syntax is available (see example below).

### Parameters

- **default** (`object`, optional) – When specified, the descriptor makes this attribute optional by attaching a default value to it.
- **unit** (`Quantity`, optional) – When specified, only quantities with compatible units are allowed to be set, and string expressions are automatically parsed into a `Quantity`.
- **converter** (callable, optional) – An optional function that can be used to convert values before setting the attribute.

See also:

**`IndexedParameterAttribute`** A parameter attribute with multiple terms.

## Examples

Create a parameter type with an optional and a required attribute.

```
>>> class MyParameter:
...     attr_required = ParameterAttribute()
...     attr_optional = ParameterAttribute(default=2)
...
>>> my_par = MyParameter()
```

Even without explicit assignment, the default value is returned.

```
>>> my_par.attr_optional
2
```

If you try to access an attribute without setting it first, an exception is raised.

```
>>> my_par.attr_required
Traceback (most recent call last):
...
AttributeError: 'MyParameter' object has no attribute '_attr_required'
```

The attribute allow automatic conversion and validation of units.

```
>>> from openff.units import unit
>>> class MyParameter:
...     attr_quantity = ParameterAttribute(unit=unit.angstrom)
...
>>> my_par = MyParameter()
>>> my_par.attr_quantity = '1.0 * nanometer'
>>> my_par.attr_quantity
<Quantity(1.0, 'nanometer')>
>>> my_par.attr_quantity = 3.0
Traceback (most recent call last):
...
openff.toolkit.utils.exceptions.IncompatibleUnitError:
attr_quantity=3.0 dimensionless should have units of angstrom
```

You can attach a custom converter to an attribute.

```
>>> class MyParameter:
...     # Both strings and integers convert nicely to floats with float().
...     attr_all_to_float = ParameterAttribute(converter=float)
...     attr_int_to_float = ParameterAttribute()
...     @attr_int_to_float.converter
...     def attr_int_to_float(self, attr, value):
...         # This converter converts only integers to float
...         # and raise an exception for the other types.
...         if isinstance(value, int):
...             return float(value)
...         elif not isinstance(value, float):
...             raise TypeError(f"Cannot convert '{value}' to float")
...         return value
...
>>> my_par = MyParameter()
```

`attr_all_to_float` accepts and convert to float both strings and integers

```
>>> my_par.attr_all_to_float = 1
>>> my_par.attr_all_to_float
1.0
>>> my_par.attr_all_to_float = '2.0'
>>> my_par.attr_all_to_float
2.0
```

The custom converter associated to `attr_int_to_float` converts only integers instead.

```
>>> my_par.attr_int_to_float = 3
>>> my_par.attr_int_to_float
3.0
>>> my_par.attr_int_to_float = '4.0'
Traceback (most recent call last):
...
TypeError: Cannot convert '4.0' to float
```

```
__init__(default: Any = UNDEFINED, unit: Optional[Unit] = None, converter: Optional[Callable] = None, docstring: str = "")
```

## Methods

---

`__init__`([default, unit, converter, docstring])

---

<code>converter</code> (converter)	Create a new <code>ParameterAttribute</code> with an associated converter.
------------------------------------	--

---

## Attributes

---

`name`

---

### **class** `UNDEFINED`

Custom type used by `ParameterAttribute` to differentiate between `None` and undeclared default.

### **converter**(converter)

Create a new `ParameterAttribute` with an associated converter.

This is meant to be used as a decorator (see main examples).



## IndexedParameterAttribute

```
class openff.toolkit.typing.engines.smirnoff.parameters.IndexedParameterAttribute(default: Any
=
    UNDEFINED,
    unit: Optional[Unit]
    = None,
    converter:
    Optional[Callable]
    = None,
    docstring: str
    = ")
```

The attribute of a parameter with an unspecified number of terms.

Some parameters can be associated to multiple terms, For example, torsions have parameters such as  $k_1$ ,  $k_2$ , ..., and `IndexedParameterAttribute` can be used to encapsulate the sequence of terms.

The only substantial difference with `ParameterAttribute` is that only sequences are supported as values and converters and units are checked on each element of the sequence.

Currently, the descriptor makes the sequence immutable. This is to avoid that an element of the sequence could be set without being properly validated. In the future, the data could be wrapped in a safe list that would safely allow mutability.

### Parameters

- **default** (`object`, optional) – When specified, the descriptor makes this attribute optional by attaching a default value to it.
- **unit** (`Quantity`, optional) – When specified, only sequences of quantities with compatible units are allowed to be set.
- **converter** (callable, optional) – An optional function that can be used to validate and cast each element of the sequence before setting the attribute.

See also:

**ParameterAttribute** A simple parameter attribute.

**MappedParameterAttribute** A parameter attribute representing a mapping.

**IndexedMappedParameterAttribute** A parameter attribute representing a sequence, each term of which is a mapping.

### Examples

Create an optional indexed attribute with unit of angstrom.

```
>>> from openff.units import unit
>>> class MyParameter:
...     length = IndexedParameterAttribute(default=None, unit=unit.angstrom)
...
>>> my_par = MyParameter()
>>> my_par.length is None
True
```

Strings are parsed into Quantity objects.

```
>>> my_par.length = ['1 * angstrom', 0.5 * unit.nanometer]
>>> my_par.length[0]
<Quantity(1, 'angstrom')>
```

Similarly, custom converters work as with ParameterAttribute, but they are used to validate each value in the sequence.

```
>>> class MyParameter:
...     attr_indexed = IndexedParameterAttribute(converter=float)
...
>>> my_par = MyParameter()
>>> my_par.attr_indexed = [1, '1.0', '1e-2', 4.0]
>>> my_par.attr_indexed
[1.0, 1.0, 0.01, 4.0]
```

```
__init__(default: Any = UNDEFINED, unit: Optional[Unit] = None, converter: Optional[Callable] =
        None, docstring: str = ")
```

## Methods

---

```
__init__([default, unit, converter, docstring])
```

---

<code>converter</code> (converter)	Create a new ParameterAttribute with an associated converter.
------------------------------------	---

---

## Attributes

---

```
name
```

---

### class UNDEFINED

Custom type used by ParameterAttribute to differentiate between None and undeclared default.

### converter(converter)

Create a new ParameterAttribute with an associated converter.

This is meant to be used as a decorator (see main examples).

## MappedParameterAttribute

```
class openff.toolkit.typing.engines.smirnoff.parameters.MappedParameterAttribute(default: Any =
                                                                    UNDEFINED,
                                                                    unit:
                                                                    Optional[Unit]
                                                                    = None,
                                                                    converter: Op-
                                                                    tional[Callable]
                                                                    = None,
                                                                    docstring: str
                                                                    = ")")
```

The attribute of a parameter in which each term is a mapping.

The substantial difference with `IndexedParameterAttribute` is that, unlike indexing, the mapping can be based on arbitrary references, like indices but can starting at non-zero values and include non-adjacent keys.

### Parameters

- **default** (`object`, optional) – When specified, the descriptor makes this attribute optional by attaching a default value to it.
- **unit** (`Quantity`, optional) – When specified, only sequences of mappings where values are quantities with compatible units are allowed to be set.
- **converter** (`callable`, optional) – An optional function that can be used to validate and cast each component of each element of the sequence before setting the attribute.

See also:

**IndexedParameterAttribute** A parameter attribute representing a sequence.

**IndexedMappedParameterAttribute** A parameter attribute representing a sequence, each term of which is a mapping.

### Examples

Create an optional indexed attribute with unit of angstrom.

```
>>> from openff.units import unit
>>> class MyParameter:
...     length = MappedParameterAttribute(default=None, unit=unit.angstrom)
...
>>> my_par = MyParameter()
>>> my_par.length is None
True
```

Like other `ParameterAttribute` objects, strings are parsed into `Quantity` objects.

```
>>> my_par.length = {1: '1.5 * angstrom', 2: '1.4 * angstrom'}
>>> my_par.length[1]
<Quantity(1.5, 'angstrom')>
```

Unlike other `ParameterAttribute` objects, the reference points can do not need ot be zero-indexed, non-adjacent, such as interpolating defining a bond parameter for interpolation by defining references values and bond orders 2 and 3:

```
>>> my_par.length = {2: '1.42 * angstrom', 3: '1.35 * angstrom'}
>>> my_par.length[2]
<Quantity(1.42, 'angstrom')>
```

```
__init__(default: Any = UNDEFINED, unit: Optional[Unit] = None, converter: Optional[Callable] =
        None, docstring: str = "")
```

## Methods

---

```
__init__([default, unit, converter, docstring])
```

---

<code>converter</code> (converter)	Create a new ParameterAttribute with an associated converter.
------------------------------------	---

---

## Attributes

---

```
name
```

---

### class UNDEFINED

Custom type used by ParameterAttribute to differentiate between None and undeclared default.

### converter(converter)

Create a new ParameterAttribute with an associated converter.

This is meant to be used as a decorator (see main examples).

## IndexedMappedParameterAttribute

```
class openff.toolkit.typing.engines.smirnoff.parameters.IndexedMappedParameterAttribute(default:
                                                                                          Any =
                                                                                          UNDE-
                                                                                          FINED,
                                                                                          unit:
                                                                                          Op-
                                                                                          tional[Unit]
                                                                                          =
                                                                                          None,
                                                                                          con-
                                                                                          verter:
                                                                                          Op-
                                                                                          tional[Callable]
                                                                                          =
                                                                                          None,
                                                                                          doc-
                                                                                          string:
                                                                                          str =
                                                                                          "")
```

The attribute of a parameter with an unspecified number of terms, where each term is a mapping.

Some parameters can be associated to multiple terms, where those terms have multiple components. For example, torsions with fractional bond orders have parameters such as `k1_bondorder1`, `k1_bondorder2`, `k2_bondorder1`, `k2_bondorder2`, ..., and `IndexedMappedParameterAttribute` can be used to encapsulate the sequence of terms as mappings (typically, dicts) of their components.

The only substantial difference with `IndexedParameterAttribute` is that only sequences of mappings are supported as values and converters and units are checked on each component of each element in the sequence.

Currently, the descriptor makes the sequence immutable. This is to avoid that an element of the sequence could be set without being properly validated. In the future, the data could be wrapped in a safe list that would safely allow mutability.

### Parameters

- **default** (`object`, optional) – When specified, the descriptor makes this attribute optional by attaching a default value to it.
- **unit** (`Quantity`, optional) – When specified, only sequences of mappings where values are quantities with compatible units are allowed to be set.
- **converter** (callable, optional) – An optional function that can be used to validate and cast each component of each element of the sequence before setting the attribute.

See also:

**`IndexedParameterAttribute`** A parameter attribute representing a sequence.

**`MappedParameterAttribute`** A parameter attribute representing a mapping.

### Examples

Create an optional indexed attribute with unit of angstrom.

```
>>> from openff.units import unit
>>> class MyParameter:
...     length = IndexedMappedParameterAttribute(default=None, unit=unit.angstrom)
...
>>> my_par = MyParameter()
>>> my_par.length is None
True
```

Strings are parsed into `Quantity` objects.

```
>>> my_par.length = [{1: '1 * angstrom'}, {1: 0.5 * unit.nanometer}]
>>> my_par.length[0]
{1: <Quantity(1, 'angstrom')>}
```

Similarly, custom converters work as with `ParameterAttribute`, but they are used to validate each value in the sequence.

```
>>> class MyParameter:
...     attr_indexed = IndexedMappedParameterAttribute(converter=float)
```

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```

...
>>> my_par = MyParameter()
>>> my_par.attr_indexed = [{1: 1}, {2: '1.0', 3: '1e-2'}, {4: 4.0}]
>>> my_par.attr_indexed
[{1: 1.0}, {2: 1.0, 3: 0.01}, {4: 4.0}]

```

```

__init__(default: Any = UNDEFINED, unit: Optional[Unit] = None, converter: Optional[Callable] =
        None, docstring: str = ")

```

## Methods

---

```
__init__([default, unit, converter, docstring])
```

---

```
converter(converter)
```

---

Create a new ParameterAttribute with an associated converter.

---

## Attributes

---

```
name
```

---

### class UNDEFINED

Custom type used by ParameterAttribute to differentiate between None and undeclared default.

### converter(converter)

Create a new ParameterAttribute with an associated converter.

This is meant to be used as a decorator (see main examples).

## UTILITIES

### 13.1 Toolkit wrappers

The toolkit wrappers provide a simple uniform API for accessing minimal functionality of cheminformatics toolkits.

These toolkit wrappers are generally used through a ToolkitRegistry, which can be constructed with a desired precedence of toolkits:

```
>>> from openff.toolkit.utils.toolkits import ToolkitRegistry, OpenEyeToolkitWrapper, \
↳ RDKitToolkitWrapper, AmberToolsToolkitWrapper
>>> toolkit_registry = ToolkitRegistry()
>>> toolkit_precedence = [OpenEyeToolkitWrapper, RDKitToolkitWrapper, \
↳ AmberToolsToolkitWrapper]
>>> [ toolkit_registry.register_toolkit(toolkit) for toolkit in toolkit_precedence if \
↳ toolkit.is_available() ]
[None, None, None]
```

The toolkit wrappers can then be accessed through the registry:

```
>>> from openff.toolkit.utils.toolkits import GLOBAL_TOOLKIT_REGISTRY as toolkit_registry
>>> from openff.toolkit import Molecule
>>> molecule = Molecule.from_smiles('Cc1ccccc1')
>>> smiles = toolkit_registry.call('to_smiles', molecule)
```

The order of toolkits, as specified in `toolkit_precedence` above, determines the order in which the called method is resolved, i.e. if the toolkit with highest precedence has a `to_smiles` method, that is the toolkit that will be called. If the toolkit with highest precedence does not have such a method, it is attempted with other toolkits until one is found. By default, if a toolkit with an appropriately-named method raises an exception of any type, then iteration over the registered toolkits stops and that exception is raised. To continue iteration if specific exceptions are encountered, customize this behavior using the optional `raise_exception_types` keyword argument to `ToolkitRegistry.call`. If no registered toolkits have the method, a `ValueError` is raised, containing a message listing the registered toolkits and exceptions (if any) that were ignored.

Alternatively, the global toolkit registry (which will attempt to register any available toolkits) can be used:

```
>>> from openff.toolkit.utils.toolkits import GLOBAL_TOOLKIT_REGISTRY as toolkit_registry
>>> len(toolkit_registry.registered_toolkits)
4
```

Individual toolkits can be registered or deregistered to control the backend that `ToolkitRegistry` calls resolve to. This can be useful for debugging and exploring subtly different behavior between toolkit wrappers.

```

from openff.toolkit.utils.toolkits import OpenEyeToolkitWrapper, BuiltInToolkitWrapper
from openff.toolkit.utils.toolkits import GLOBAL_TOOLKIT_REGISTRY as toolkit_registry
toolkit_registry.deregister_toolkit(OpenEyeToolkitWrapper)
toolkit_registry.register_toolkit(BuiltInToolkitWrapper)
toolkit_registry.registered_toolkits

```

For example, differences in `to_smiles` functionality between OpenEye toolkits and The RDKit can be explored by selecting which toolkit(s) are and are not registered.

```

>>> from openff.toolkit.utils.toolkits import OpenEyeToolkitWrapper, GLOBAL_TOOLKIT_REGISTRY_
↳as toolkit_registry
>>> from openff.toolkit import Molecule
>>> molecule = Molecule.from_smiles('Cc1ccccc1')
>>> smiles_via_openeye = toolkit_registry.call('to_smiles', molecule)
>>> print(smiles_via_openeye)
[H]c1c(c(c(c(c1[H])[H])C([H])([H])[H])[H])[H]

>>> toolkit_registry.deregister_toolkit(OpenEyeToolkitWrapper)
>>> smiles_via_rdkit = toolkit_registry.call('to_smiles', molecule)
>>> print(smiles_via_rdkit)
[H][c]1[c]([H])[c]([H])[c]([C]([H])([H])[H])[c]([H])[c]1[H]

```

<code>ToolkitRegistry</code>	Registry for <code>ToolkitWrapper</code> objects
<code>ToolkitWrapper</code>	Toolkit wrapper base class.
<code>OpenEyeToolkitWrapper</code>	OpenEye toolkit wrapper
<code>RDKitToolkitWrapper</code>	RDKit toolkit wrapper
<code>AmberToolsToolkitWrapper</code>	AmberTools toolkit wrapper
<code>BuiltInToolkitWrapper</code>	Built-in <code>ToolkitWrapper</code> for very basic functionality.

### 13.1.1 ToolkitRegistry

```

class openff.toolkit.utils.toolkits.ToolkitRegistry(toolkit_precedence=None,
                                                    exception_if_unavailable=True,
                                                    _register_imported_toolkit_wrappers=False)

```

Registry for `ToolkitWrapper` objects

#### Examples

Register toolkits in a specified order, skipping if unavailable

```

>>> from openff.toolkit.utils.toolkits import ToolkitRegistry
>>> toolkit_precedence = [OpenEyeToolkitWrapper, RDKitToolkitWrapper,
↳AmberToolsToolkitWrapper]
>>> toolkit_registry = ToolkitRegistry(toolkit_precedence)
>>> toolkit_registry
<ToolkitRegistry containing OpenEye Toolkit, The RDKit, AmberTools>

```

Register all available toolkits (in the order OpenEye, RDKit, AmberTools, built-in)



```
>>> toolkits = [OpenEyeToolkitWrapper, RDKitToolkitWrapper, AmberToolsToolkitWrapper,
↳ BuiltInToolkitWrapper]
>>> toolkit_registry = ToolkitRegistry(toolkit_precedence=toolkits)
>>> toolkit_registry
<ToolkitRegistry containing OpenEye Toolkit, The RDKit, AmberTools, Built-in Toolkit>
```

Retrieve the global singleton toolkit registry, which is created when this module is imported from all available toolkits:

```
>>> from openff.toolkit.utils.toolkits import GLOBAL_TOOLKIT_REGISTRY as toolkit_
↳ registry
>>> toolkit_registry
<ToolkitRegistry containing OpenEye Toolkit, The RDKit, AmberTools, Built-in Toolkit>
```

Note that this will contain different ToolkitWrapper objects based on what toolkits are currently installed.

**Warning:** This API is experimental and subject to change.

```
__init__(toolkit_precedence=None, exception_if_unavailable=True,
         _register_imported_toolkit_wrappers=False)
```

Create an empty toolkit registry.

#### Parameters

- **toolkit\_precedence** (`list`, optional, default=None) – List of toolkit wrapper classes, in order of desired precedence when performing molecule operations. If None, no toolkits will be registered.
- **exception\_if\_unavailable** (`bool`, optional, default=True) – If True, an exception will be raised if the toolkit is unavailable
- **\_register\_imported\_toolkit\_wrappers** (`bool`, optional, default=False) – If True, will attempt to register all imported ToolkitWrapper subclasses that can be found in the order of toolkit\_precedence, if specified. If toolkit\_precedence is not specified, the default order is [OpenEyeToolkitWrapper, RDKitToolkitWrapper, AmberToolsToolkitWrapper, BuiltInToolkitWrapper].

#### Methods

<code>__init__([toolkit_precedence, ...])</code>	Create an empty toolkit registry.
<code>add_toolkit(toolkit_wrapper)</code>	Append a ToolkitWrapper onto the list of toolkits in this ToolkitRegistry
<code>call(method_name, *args[, raise_exception_types])</code>	Execute the requested method by attempting to use all registered toolkits in order of precedence.
<code>deregister_toolkit(toolkit_wrapper)</code>	Remove a ToolkitWrapper from the list of toolkits in this ToolkitRegistry
<code>register_toolkit(toolkit_wrapper[, ...])</code>	Register the provided toolkit wrapper class, instantiating an object of it.
<code>resolve(method_name)</code>	Resolve the requested method name by checking all registered toolkits in order of precedence for one that provides the requested method.

## Attributes

<code>registered_toolkit_versions</code>	Return a dict containing the version of each registered toolkit.
<code>registered_toolkits</code>	List registered toolkits.

### property `registered_toolkits`

List registered toolkits.

**Warning:** This API is experimental and subject to change.

**Returns** `toolkits` (*iterable of toolkit objects*)

### property `registered_toolkit_versions`

Return a dict containing the version of each registered toolkit.

**Warning:** This API is experimental and subject to change.

**Returns** `toolkit_versions` (*dict[str, str]*) – A dictionary mapping names and versions of wrapped toolkits

### `register_toolkit(toolkit_wrapper, exception_if_unavailable=True)`

Register the provided toolkit wrapper class, instantiating an object of it.

**Warning:** This API is experimental and subject to change.

#### Parameters

- **`toolkit_wrapper`** (instance or subclass of `ToolkitWrapper`) – The toolkit wrapper to register or its class.
- **`exception_if_unavailable`** (`bool`, optional, default=`True`) – If `True`, an exception will be raised if the toolkit is unavailable

### `deregister_toolkit(toolkit_wrapper)`

Remove a `ToolkitWrapper` from the list of toolkits in this `ToolkitRegistry`

**Warning:** This API is experimental and subject to change.

**Parameters** **`toolkit_wrapper`** (instance or subclass of `ToolkitWrapper`) – The toolkit wrapper to remove from the registry

#### Raises

- **`InvalidToolkitError`** – If `toolkit_wrapper` is not a `ToolkitWrapper` or subclass
- **`ToolkitUnavailableException`** – If `toolkit_wrapper` is not found in the registry

**add\_toolkit**(*toolkit\_wrapper*)

Append a ToolkitWrapper onto the list of toolkits in this ToolkitRegistry

**Warning:** This API is experimental and subject to change.

**Parameters** *toolkit\_wrapper* (openff.toolkit.utils.ToolkitWrapper) – The ToolkitWrapper object to add to the list of registered toolkits

**Raises** `InvalidToolkitError` – If *toolkit\_wrapper* is not a ToolkitWrapper or subclass

**resolve**(*method\_name*)

Resolve the requested method name by checking all registered toolkits in order of precedence for one that provides the requested method.

**Parameters** *method\_name* (*str*) – The name of the method to resolve

**Returns** *method* – The method of the first registered toolkit that provides the requested method name

**Raises** `NotImplementedError` if the requested method cannot be found among the registered toolkits –

## Examples

Create a molecule, and call the toolkit `to_smiles()` method directly

```
>>> from openff.toolkit import Molecule
>>> molecule = Molecule.from_smiles('Cc1ccccc1')
>>> toolkit_registry = ToolkitRegistry([OpenEyeToolkitWrapper, RDKitToolkitWrapper,
↳ AmberToolsToolkitWrapper])
>>> method = toolkit_registry.resolve('to_smiles')
>>> smiles = method(molecule)
```

**call**(*method\_name*, \*args, raise\_exception\_types=None, \*\*kwargs)

Execute the requested method by attempting to use all registered toolkits in order of precedence.

\*args and \*\*kwargs are passed to the desired method, and return values of the method are returned

This is a convenient shorthand for `toolkit_registry.resolve_method(method_name)(*args, **kwargs)`

### Parameters

- **method\_name** (*str*) – The name of the method to execute
- **raise\_exception\_types** (list of Exception subclasses, default=None) – A list of exception-derived types to catch and raise immediately. If None, this will be set to `[Exception]`, which will raise an error immediately if the first ToolkitWrapper in the registry fails. To try each ToolkitWrapper that provides a suitably-named method, set this to the empty list (`[]`). If all ToolkitWrappers run without raising any exceptions in this list, a single `ValueError` will be raised containing the each ToolkitWrapper that was tried and the exception it raised.

### Raises

- `NotImplementedError` if the requested method cannot be found among the registered toolkits –
- `ValueError` if no exceptions in the `raise_exception_types` list were raised by `ToolkitWrappers`, and –
- all `ToolkitWrappers` in the `ToolkitRegistry` were tried. –
- Other forms of exceptions are possible if `raise_exception_types` is specified. –
- These are defined by the `ToolkitWrapper` method being called. –

### Examples

Create a molecule, and call the toolkit `to_smiles()` method directly

```
>>> from openff.toolkit import Molecule
>>> molecule = Molecule.from_smiles('Cc1ccccc1')
>>> toolkit_registry = ToolkitRegistry([OpenEyeToolkitWrapper, RDKitToolkitWrapper])
>>> smiles = toolkit_registry.call('to_smiles', molecule)
```

## 13.1.2 ToolkitWrapper

**class** `openff.toolkit.utils.toolkits.ToolkitWrapper`

Toolkit wrapper base class.

**Warning:** This API is experimental and subject to change.

`__init__()`

### Methods

<code>__init__()</code>	
<code>from_file(file_path, file_format[, ...])</code>	Return an <code>openff.toolkit.topology.Molecule</code> from a file using this toolkit.
<code>from_file_obj(file_obj, file_format[, ...])</code>	Return an <code>openff.toolkit.topology.Molecule</code> from a file-like object (an object with a <code>".read()"</code> method using this toolkit.
<code>is_available()</code>	Check whether the corresponding toolkit can be imported
<code>requires_toolkit()</code>	

## Attributes

<code>toolkit_file_read_formats</code>	List of file formats that this toolkit can read.
<code>toolkit_file_write_formats</code>	List of file formats that this toolkit can write.
<code>toolkit_installation_instructions</code>	Instructions on how to install the wrapped toolkit.
<code>toolkit_name</code>	Return the name of the toolkit wrapped by this class as a str
<code>toolkit_version</code>	Return the version of the wrapped toolkit as a str

### property `toolkit_name`

Return the name of the toolkit wrapped by this class as a str

**Warning:** This API is experimental and subject to change.

**Returns** `toolkit_name` (*str*) – The name of the wrapped toolkit

### property `toolkit_installation_instructions`

Instructions on how to install the wrapped toolkit.

### property `toolkit_file_read_formats`

List of file formats that this toolkit can read.

### property `toolkit_file_write_formats`

List of file formats that this toolkit can write.

### classmethod `is_available()`

Check whether the corresponding toolkit can be imported

**Returns** `is_installed` (*bool*) – True if corresponding toolkit is installed, False otherwise.

### property `toolkit_version`

Return the version of the wrapped toolkit as a str

**Warning:** This API is experimental and subject to change.

**Returns** `toolkit_version` (*str*) – The version of the wrapped toolkit

### `from_file(file_path, file_format, allow_undefined_stereo=False)`

Return an `openff.toolkit.topology.Molecule` from a file using this toolkit.

#### Parameters

- **file\_path** (*str*) – The file to read the molecule from
- **file\_format** (*str*) – Format specifier, usually file suffix (eg. ‘MOL2’, ‘SMI’) Note that not all toolkits support all formats. Check `ToolkitWrapper.toolkit_file_read_formats` for details.
- **allow\_undefined\_stereo** (*bool*, default=False) – If false, raises an exception if any molecules contain undefined stereochemistry.

- **\_cls** (class) – Molecule constructor

**Returns** **molecules** (*Molecule or list of Molecules*) – a list of Molecule objects is returned.

**from\_file\_obj**(*file\_obj*, *file\_format*, *allow\_undefined\_stereo=False*, *\_cls=None*)

Return an openff.toolkit.topology.Molecule from a file-like object (an object with a “.read()” method using this toolkit).

**Parameters**

- **file\_obj** (file-like object) – The file-like object to read the molecule from
- **file\_format** (*str*) – Format specifier, usually file suffix (eg. ‘MOL2’, ‘SMI’) Note that not all toolkits support all formats. Check ToolkitWrapper.toolkit\_file\_read\_formats for details.
- **allow\_undefined\_stereo** (*bool*, default=False) – If false, raises an exception if any molecules contain undefined stereochemistry. If false, the function skips loading the molecule.
- **\_cls** (class) – Molecule constructor

**Returns** **molecules** (*Molecule or list of Molecules*) – a list of Molecule objects is returned.

### 13.1.3 OpenEyeToolkitWrapper

**class** openff.toolkit.utils.toolkits.**OpenEyeToolkitWrapper**

OpenEye toolkit wrapper

**Warning:** This API is experimental and subject to change.

**\_\_init\_\_**()



## Methods

<code>__init__()</code>	
<code>apply_elf_conformer_selection(molecule[, ...])</code>	Applies the <a href="#">ELF method</a> to select a set of diverse conformers which have minimal electrostatically strongly interacting functional groups from a molecules conformers.
<code>assign_fractional_bond_orders(molecule[, ...])</code>	Update and store list of bond orders this molecule.
<code>assign_partial_charges(molecule[, ...])</code>	Compute partial charges with OpenEye quacpac, and assign the new values to the <code>partial_charges</code> attribute.
<code>atom_is_in_ring(atom)</code>	Return whether or not an atom is in a ring.
<code>bond_is_in_ring(bond)</code>	Return whether or not a bond is in a ring.
<code>canonical_order_atoms(molecule)</code>	Canonical order the atoms in the molecule using the OpenEye toolkit.
<code>enumerate_protomers(molecule[, max_states])</code>	Enumerate the formal charges of a molecule to generate different protomoers.
<code>enumerate_stereoisomers(molecule[, ...])</code>	Enumerate the stereocenters and bonds of the current molecule.
<code>enumerate_tautomers(molecule[, max_states])</code>	Enumerate the possible tautomers of the current molecule
<code>find_smarts_matches(molecule, smarts[, ...])</code>	Find all SMARTS matches for the specified molecule, using the specified aromaticity model.
<code>from_file(file_path, file_format[, ...])</code>	Return an <code>openff.toolkit.topology.Molecule</code> from a file using this toolkit.
<code>from_file_obj(file_obj, file_format[, ...])</code>	Return an <code>openff.toolkit.topology.Molecule</code> from a file-like object (an object with a <code>".read()"</code> method using this toolkit.
<code>from_inchi(inchi[, allow_undefined_stereo, _cls])</code>	Construct a Molecule from a InChI representation
<code>from_iupac(iupac_name[, ...])</code>	Construct a Molecule from an IUPAC name
<code>from_object(obj[, allow_undefined_stereo, _cls])</code>	Convert an OEMol (or OEMol-derived object) into an <code>openff.toolkit.topology.molecule</code>
<code>from_openeye(oemol[, ...])</code>	Create a Molecule from an OpenEye molecule.
<code>from_smiles(smiles[, ...])</code>	Create a Molecule from a SMILES string using the OpenEye toolkit.
<code>generate_conformers(molecule[, ...])</code>	Generate molecule conformers using OpenEye Omega.
<code>get_tagged_smarts_connectivity(smarts)</code>	Returns a tuple of tuples indicating connectivity between tagged atoms in a SMARTS string.
<code>is_available()</code>	Check if the given OpenEye toolkit components are available.
<code>requires_toolkit()</code>	
<code>to_file(molecule, file_path, file_format)</code>	Writes an OpenFF Molecule to a file-like object
<code>to_file_obj(molecule, file_obj, file_format)</code>	Writes an OpenFF Molecule to a file-like object
<code>to_inchi(molecule[, fixed_hydrogens])</code>	Create an InChI string for the molecule using the RDKit Toolkit.
<code>to_inchikey(molecule[, fixed_hydrogens])</code>	Create an InChIKey for the molecule using the RDKit Toolkit.
<code>to_iupac(molecule)</code>	Generate IUPAC name from Molecule
<code>to_openeye(molecule[, aromaticity_model])</code>	Create an OpenEye molecule using the specified aromaticity model
<code>to_smiles(molecule[, isomeric, ...])</code>	Uses the OpenEye toolkit to convert a Molecule into a SMILES string.



## Attributes

<code>to_openeye_cache</code>	
<code>toolkit_file_read_formats</code>	List of file formats that this toolkit can read.
<code>toolkit_file_write_formats</code>	List of file formats that this toolkit can write.
<code>toolkit_installation_instructions</code>	Instructions on how to install the wrapped toolkit.
<code>toolkit_name</code>	Return the name of the toolkit wrapped by this class as a str
<code>toolkit_version</code>	Return the version of the wrapped toolkit as a str

**classmethod** `is_available()` → `bool`

Check if the given OpenEye toolkit components are available.

If the OpenEye toolkit is not installed or no license is found for at least one the required toolkits, False is returned.

**Returns** `all_installed` (`bool`) – True if all required OpenEye tools are installed and licensed, False otherwise

**from\_object**(*obj*, *allow\_undefined\_stereo*: `bool` = False, *\_cls*=None) → `Molecule`

Convert an OEMol (or OEMol-derived object) into an `openff.toolkit.topology.molecule`

### Parameters

- **obj** (A molecule-like object) – An object to be type-checked.
- **allow\_undefined\_stereo** (`bool`, default=False) – Whether to accept molecules with undefined stereocenters. If False, an exception will be raised if a molecule with undefined stereochemistry is passed into this function.
- **\_cls** (class) – Molecule constructor

**Returns** `Molecule` – An `openff.toolkit.topology.molecule` `Molecule`.

**Raises** `NotImplementedError` – If the object could not be converted into a `Molecule`.

**from\_file**(*file\_path*: `str`, *file\_format*: `str`, *allow\_undefined\_stereo*: `bool` = False, *\_cls*=None) → `List[Molecule]`

Return an `openff.toolkit.topology.Molecule` from a file using this toolkit.

### Parameters

- **file\_path** (`str`) – The file to read the molecule from
- **file\_format** (`str`) – Format specifier, usually file suffix (eg. 'MOL2', 'SMI') Note that not all toolkits support all formats. Check `ToolkitWrapper.toolkit_file_read_formats` for details.
- **allow\_undefined\_stereo** (`bool`, default=False) – If false, raises an exception if oemol contains undefined stereochemistry.
- **\_cls** (class) – Molecule constructor

**Returns** `molecules` (`List[Molecule]`) – The list of `Molecule` objects in the file.

**Raises** `GAFFAtomTypeWarning` – If the loaded mol2 file possibly uses GAFF atom types, which are not supported.

## Examples

Load a mol2 file into an OpenFF Molecule object.

```
>>> from openff.toolkit.utils import get_data_file_path
>>> mol2_file_path = get_data_file_path('molecules/cyclohexane.mol2')
>>> toolkit = OpenEyeToolkitWrapper()
>>> molecule = toolkit.from_file(mol2_file_path, file_format='mol2')
```

**from\_file\_obj**(*file\_obj*, *file\_format*: *str*, *allow\_undefined\_stereo*: *bool* = *False*, *\_cls*=*None*) → *List*[*Molecule*]

Return an openff.toolkit.topology.Molecule from a file-like object (an object with a “.read()” method using this toolkit.

### Parameters

- **file\_obj** (file-like object) – The file-like object to read the molecule from
- **file\_format** (*str*) – Format specifier, usually file suffix (eg. ‘MOL2’, ‘SMI’) Note that not all toolkits support all formats. Check `ToolkitWrapper.toolkit_file_read_formats` for details.
- **allow\_undefined\_stereo** (*bool*, default=*False*) – If false, raises an exception if oemol contains undefined stereochemistry.
- **\_cls** (*class*) – Molecule constructor

**Returns** *molecules* (*List*[*Molecule*]) – The list of Molecule objects in the file object.

**Raises** *GAFFAtomTypeWarning* – If the loaded mol2 file possibly uses GAFF atom types, which are not supported.

**to\_file\_obj**(*molecule*: *Molecule*, *file\_obj*, *file\_format*: *str*)

Writes an OpenFF Molecule to a file-like object

### Parameters

- **molecule** (an OpenFF Molecule) – The molecule to write
- **file\_obj** – The file-like object to write to
- **file\_format** – The format for writing the molecule data

**to\_file**(*molecule*: *Molecule*, *file\_path*: *str*, *file\_format*: *str*)

Writes an OpenFF Molecule to a file-like object

### Parameters

- **molecule** (an OpenFF Molecule) – The molecule to write
- **file\_path** – The file path to write to.
- **file\_format** – The format for writing the molecule data

**enumerate\_protomers**(*molecule*: *Molecule*, *max\_states*: *int* = *10*) → *List*[*Molecule*]

Enumerate the formal charges of a molecule to generate different protomoers.

### Parameters

- **molecule** (*Molecule*) – The molecule whose state we should enumerate
- **max\_states** (*int* optional, default=*10*,) – The maximum number of protomer states to be returned.

**Returns molecules** (*List[openff.toolkit.topology.Molecule]*,) – A list of the protomers of the input molecules not including the input.

**enumerate\_stereoisomers**(*molecule: Molecule, undefined\_only: bool = False, max\_isomers: int = 20, rationalise: bool = True*) → *List[Molecule]*

Enumerate the stereocenters and bonds of the current molecule.

#### Parameters

- **molecule** (*Molecule*) – The molecule whose state we should enumerate
- **undefined\_only** (*bool* optional, *default=False*) – If we should enumerate all stereocenters and bonds or only those with undefined stereochemistry
- **max\_isomers** (*int* optional, *default=20*) – The maximum amount of molecules that should be returned
- **rationalise** (*bool* optional, *default=True*) – If we should try to build and rationalise the molecule to ensure it can exist

**Returns molecules** (*List[openff.toolkit.topology.Molecule]*) – A list of *openff.toolkit.topology.Molecule* instances

**enumerate\_tautomers**(*molecule: Molecule, max\_states: int = 20*) → *List[Molecule]*

Enumerate the possible tautomers of the current molecule

#### Parameters

- **molecule** (*Molecule*) – The molecule whose state we should enumerate
- **max\_states** (*int* optional, *default=20*) – The maximum amount of molecules that should be returned

**Returns molecules** (*List[openff.toolkit.topology.Molecule]*) – A list of *openff.toolkit.topology.Molecule* instances excluding the input molecule.

**static from\_openeye**(*oemol, allow\_undefined\_stereo: bool = False, \_cls=None*) → *Molecule*

Create a *Molecule* from an OpenEye molecule. If the OpenEye molecule has implicit hydrogens, this function will make them explicit.

*OEOAtom*s have a different set of allowed value for partial charges than *openff.toolkit.topology.Molecule*s. In the OpenEye toolkits, partial charges are stored on individual *OEOAtom*s, and their values are initialized to 0.0. In the Open Force Field Toolkit, an *openff.toolkit.topology.Molecule*'s *partial\_charges* attribute is initialized to *None* and can be set to a unit-wrapped numpy array with units of elementary charge. The Open Force Field Toolkit considers an *OEMol* where every *OEOAtom* has a partial charge of *float('nan')* to be equivalent to an Open Force Field Toolkit *Molecule*'s *partial\_charges = None*. This assumption is made in both *to\_openeye* and *from\_openeye*.

**Warning:** This API is experimental and subject to change.

#### Parameters

- **oemol** (*openeye.ochem.OEMol*) – An OpenEye molecule
- **allow\_undefined\_stereo** (*bool*, *default=False*) – If false, raises an exception if *oemol* contains undefined stereochemistry.
- **\_cls** (*class*) – *Molecule* constructor

**Returns molecule** (*openff.toolkit.topology.Molecule*) – An OpenFF molecule

## Examples

Create a Molecule from an OpenEye OEMol

```
>>> from openeye import oechem
>>> from openff.toolkit.tests.utils import get_data_file_path
>>> ifs = oechem.oemolistream(get_data_file_path('systems/monomers/ethanol.mol2'))
>>> oemols = list(ifs.GetOEGraphMols())
```

```
>>> toolkit_wrapper = OpenEyeToolkitWrapper()
>>> molecule = toolkit_wrapper.from_openeye(oemols[0])
```

**to\_openeye**(*molecule*: [Molecule](#), *aromaticity\_model*: *str* = `DEFAULT_AROMATICITY_MODEL`)

Create an OpenEye molecule using the specified aromaticity model

OEAtom s have a different set of allowed value for partial charges than `openff.toolkit.topology.Molecules`. In the OpenEye toolkits, partial charges are stored on individual OEAtoms, and their values are initialized to 0.0. In the Open Force Field Toolkit, an `openff.toolkit.topology.Molecule`'s `partial_charges` attribute is initialized to None and can be set to a unit-wrapped numpy array with units of elementary charge. The Open Force Field Toolkit considers an OEMol where every OEAtom has a partial charge of `float('nan')` to be equivalent to an Open Force Field Toolkit Molecule's `partial_charges = None`. This assumption is made in both `to_openeye` and `from_openeye`.

**Warning:** This API is experimental and subject to change.

### Parameters

- **molecule** (`openff.toolkit.topology.molecule.Molecule` object) – The molecule to convert to an OEMol
- **aromaticity\_model** (*str*, optional, default=`DEFAULT_AROMATICITY_MODEL`) – The aromaticity model to use

**Returns** *oemol* (`openeye.oechem.OEMol`) – An OpenEye molecule

## Examples

Create an OpenEye molecule from a Molecule

```
>>> from openff.toolkit import Molecule
>>> toolkit_wrapper = OpenEyeToolkitWrapper()
>>> molecule = Molecule.from_smiles('CC')
>>> oemol = toolkit_wrapper.to_openeye(molecule)
```

**atom\_is\_in\_ring**(*atom*: [Atom](#)) → *bool*

Return whether or not an atom is in a ring.

It is assumed that this atom is in molecule.

**Parameters** *atom* ([Atom](#)) – The molecule containing the atom of interest

**Returns** *is\_in\_ring* (*bool*) – Whether or not the atom is in a ring.

**Raises** [NotAttachedToMoleculeError](#) –

**bond\_is\_in\_ring**(*bond*: [Bond](#)) → *bool*

Return whether or not a bond is in a ring.

It is assumed that this atom is in molecule.

**Parameters** *bond* ([Bond](#)) – The molecule containing the atom of interest

**Returns** *is\_in\_ring* (*bool*) – Whether or not the bond of index *bond\_index* is in a ring

**Raises** [NotAttachedToMoleculeError](#) –

**to\_smiles**(*molecule*: [Molecule](#), *isomeric*: *bool* = *True*, *explicit\_hydrogens*: *bool* = *True*, *mapped*: *bool* = *False*) → *str*

Uses the OpenEye toolkit to convert a Molecule into a SMILES string. A partially mapped smiles can also be generated for atoms of interest by supplying an *atom\_map* to the properties dictionary.

#### Parameters

- **molecule** (An `openff.toolkit.topology.Molecule`) – The molecule to convert into a SMILES.
- **isomeric** (*bool* optional, default= *True*) – return an isomeric smiles
- **explicit\_hydrogens** (*bool* optional, default=*True*) – return a smiles string containing all hydrogens explicitly
- **mapped** (*bool* optional, default=*False*) – return a explicit hydrogen mapped smiles, the atoms to be mapped can be controlled by supplying an atom map into the properties dictionary. If no mapping is passed all atoms will be mapped in order, else an atom map dictionary from the current atom index to the map id should be supplied with no duplicates. The map ids (values) should start from 0 or 1.

**Returns** *smiles* (*str*) – The SMILES of the input molecule.

**to\_inchi**(*molecule*: [Molecule](#), *fixed\_hydrogens*: *bool* = *False*) → *str*

Create an InChI string for the molecule using the RDKit Toolkit. InChI is a standardised representation that does not capture tautomers unless specified using the fixed hydrogen layer.

For information on InChi see here <https://iupac.org/who-we-are/divisions/division-details/inchi/>

#### Parameters

- **molecule** (An `openff.toolkit.topology.Molecule`) – The molecule to convert into a SMILES.
- **fixed\_hydrogens** (*bool*, default=*False*) – If a fixed hydrogen layer should be added to the InChI, if *True* this will produce a non standard specific InChI string of the molecule.

**Returns** *inchi* (*str*) – The InChI string of the molecule.

**to\_inchikey**(*molecule*: [Molecule](#), *fixed\_hydrogens*: *bool* = *False*) → *str*

Create an InChIKey for the molecule using the RDKit Toolkit. InChIKey is a standardised representation that does not capture tautomers unless specified using the fixed hydrogen layer.

For information on InChi see here <https://iupac.org/who-we-are/divisions/division-details/inchi/>

#### Parameters

- **molecule** (An `openff.toolkit.topology.Molecule`) – The molecule to convert into a SMILES.
- **fixed\_hydrogens** (`bool`, default=False) – If a fixed hydrogen layer should be added to the InChI, if `True` this will produce a non standard specific InChI string of the molecule.

**Returns** `inchi_key` (`str`) – The InChIKey representation of the molecule.

**to\_iupac**(*molecule*: `Molecule`) → `str`

Generate IUPAC name from Molecule

**Parameters** **molecule** (An `openff.toolkit.topology.Molecule`) – The molecule to convert into a SMILES.

**Returns** `iupac_name` (`str`) – IUPAC name of the molecule

### Examples

```
>>> from openff.toolkit import Molecule
>>> from openff.toolkit.utils import get_data_file_path
>>> sdf_filepath = get_data_file_path('molecules/ethanol.sdf')
>>> molecule = Molecule(sdf_filepath)
>>> toolkit = OpenEyeToolkitWrapper()
>>> iupac_name = toolkit.to_iupac(molecule)
```

**canonical\_order\_atoms**(*molecule*: `Molecule`) → `Molecule`

Canonical order the atoms in the molecule using the OpenEye toolkit.

#### Parameters

- **molecule** (`Molecule`) – The input molecule

Returns

- `-----` \_
- **molecule** – The input molecule, with canonically-indexed atoms and bonds.

**from\_smiles**(*smiles*: `str`, *hydrogens\_are\_explicit*: `bool` = `False`, *allow\_undefined\_stereo*: `bool` = `False`, *\_cls*=None) → `Molecule`

Create a Molecule from a SMILES string using the OpenEye toolkit.

**Warning:** This API is experimental and subject to change.

#### Parameters

- **smiles** (`str`) – The SMILES string to turn into a molecule
- **hydrogens\_are\_explicit** (`bool`, default = `False`) – If `False`, OE will perform hydrogen addition using `OEAddExplicitHydrogens`
- **allow\_undefined\_stereo** (`bool`, default=False) – Whether to accept SMILES with undefined stereochemistry. If `False`, an exception will be raised if a SMILES with undefined stereochemistry is passed into this function.
- **\_cls** (`class`) – Molecule constructor

**Returns** **molecule** (`openff.toolkit.topology.Molecule`) – An OpenFF style molecule.

:raises RadicalsNotSupportedError : If any atoms in the OpenEye molecule contain radical electrons.:

**from\_inchi**(*inchi*: *str*, *allow\_undefined\_stereo*: *bool* = False, *\_cls*=None) → *Molecule*

Construct a Molecule from a InChI representation

#### Parameters

- **inchi** (*str*) – The InChI representation of the molecule.
- **allow\_undefined\_stereo** (*bool*, default=False) – Whether to accept InChI with undefined stereochemistry. If False, an exception will be raised if a InChI with undefined stereochemistry is passed into this function.
- **\_cls** (*class*) – Molecule constructor

**Returns** *molecule* (*openff.toolkit.topology.Molecule*)

**from\_iupac**(*iupac\_name*: *str*, *allow\_undefined\_stereo*: *bool* = False, *\_cls*=None, *\*\*kwargs*) → *Molecule*

Construct a Molecule from an IUPAC name

#### Parameters

- **iupac\_name** (*str*) – The IUPAC or common name of the molecule.
- **allow\_undefined\_stereo** (*bool*, default=False) – Whether to accept a molecule name with undefined stereochemistry. If False, an exception will be raised if a molecule name with undefined stereochemistry is passed into this function.
- **\_cls** (*class*) – Molecule constructor

**Returns** *molecule* (*openff.toolkit.topology.Molecule*)

**generate\_conformers**(*molecule*: *Molecule*, *n\_conformers*: *int* = 1, *rms\_cutoff*: *Optional[Quantity]* = None, *clear\_existing*: *bool* = True, *make\_carboxylic\_acids\_cis*: *bool* = False)

Generate molecule conformers using OpenEye Omega.

**Warning:** This API is experimental and subject to change.

#### Parameters

- **molecule** (a *Molecule*) – The molecule to generate conformers for.
- **n\_conformers** (*int*, default=1) – The maximum number of conformers to generate.
- **rms\_cutoff** (unit-wrapped float, in units of distance, optional, default=None) – The minimum RMS value at which two conformers are considered redundant and one is deleted. If None, the cutoff is set to 1 Angstrom
- **clear\_existing** (*bool*, default=True) – Whether to overwrite existing conformers for the molecule
- **make\_carboxylic\_acids\_cis** (*bool*, default=False) – Guarantee all conformers have exclusively cis carboxylic acid groups (COOH) by rotating the proton in any trans carboxylic acids 180 degrees around the C-O bond.

**apply\_elf\_conformer\_selection**(*molecule*: *Molecule*, *percentage*: *float* = 2.0, *limit*: *int* = 10)

Applies the [ELF method](#) to select a set of diverse conformers which have minimal electrostatically strongly interacting functional groups from a molecules conformers.

## Notes

- The input molecule should have a large set of conformers already generated to select the ELF conformers from.
- The selected conformers will be retained in the `molecule.conformers` list while unselected conformers will be discarded.
- Conformers generated with the OpenEye toolkit often include trans carboxylic acids (COOH). These are unphysical and will be rejected by `apply_elf_conformer_selection`. If no conformers are selected, try re-running `generate_conformers` with the `make_carboxylic_acids_cis` argument set to `True`

## See also:

`RDKitToolkitWrapper.apply_elf_conformer_selection`

## Parameters

- **molecule** – The molecule which contains the set of conformers to select from.
- **percentage** – The percentage of conformers with the lowest electrostatic interaction energies to greedily select from.
- **limit** – The maximum number of conformers to select.

`assign_partial_charges(molecule: Molecule, partial_charge_method: Optional[str] = None, use_conformers: Optional[List[Quantity]] = None, strict_n_conformers: bool = False, normalize_partial_charges: bool = True, _cls=None)`

Compute partial charges with OpenEye quacpac, and assign the new values to the `partial_charges` attribute.

**Warning:** This API is experimental and subject to change.

## Parameters

- **molecule** (`Molecule`) – Molecule for which partial charges are to be computed
- **partial\_charge\_method** (`str`, optional, default=None) – The charge model to use. One of ['amberff94', 'mmff', 'mmff94', 'am1-mulliken', 'am1bcc', 'am1bccnosymspt', 'am1bccelf10', 'gasteiger'] If None, 'am1-mulliken' will be used.
- **use\_conformers** (iterable of unit-wrapped numpy arrays, each with) – shape (n\_atoms, 3) and dimension of distance. Optional, default = None Coordinates to use for partial charge calculation. If None, an appropriate number of conformers will be generated.
- **strict\_n\_conformers** (`bool`, default=False) – Whether to raise an exception if an invalid number of conformers is provided for the given charge method. If this is False and an invalid number of conformers is found, a warning will be raised.
- **normalize\_partial\_charges** (`bool`, default=True) – Whether to offset partial charges so that they sum to the total formal charge of the molecule. This is used to prevent accumulation of rounding errors when the partial charge generation method has low precision.
- **\_cls** (`class`) – Molecule constructor

## Raises



- `ChargeMethodUnavailableError` if the requested charge method can not be handled by this toolkit –
- `ChargeCalculationError` if the charge method is supported by this toolkit, but fails –

`assign_fractional_bond_orders(molecule: Molecule, bond_order_model: Optional[str] = None, use_conformers: Optional[List[Quantity]] = None, _cls=None)`

Update and store list of bond orders this molecule. Bond orders are stored on each bond, in the `bond.fractional_bond_order` attribute.

**Warning:** This API is experimental and subject to change.

#### Parameters

- **molecule** (`openff.toolkit.topology.molecule Molecule`) – The molecule to assign wiberg bond orders to
- **bond\_order\_model** (`str`, optional, default=None) – The charge model to use. One of ['am1-wiberg', 'am1-wiberg-elf10', 'pm3-wiberg', 'pm3-wiberg-elf10']. If None, 'am1-wiberg' will be used.
- **use\_conformers** (iterable of unit-wrapped `np.array` with shape (n\_atoms, 3) and) – dimension of distance, optional, default=None The conformers to use for fractional bond order calculation. If None, an appropriate number of conformers will be generated by an available ToolkitWrapper. If the chosen `bond_order_model` is an ELF variant, the ELF conformer selection method will be applied to the provided conformers.
- **\_cls** (class) – Molecule constructor

`get_tagged_smarts_connectivity(smarts: str) → Tuple[Tuple[Tuple[Any, ...], ...], ...]`

Returns a tuple of tuples indicating connectivity between tagged atoms in a SMARTS string. Does not return bond order.

**Parameters** **smarts** (`str`) – The tagged SMARTS to analyze

#### Returns

- **unique\_tags** (*tuple of int*) – A sorted tuple of all unique tagged atom map indices.
- **tagged\_atom\_connectivity** (*tuple of tuples of int, shape n\_tagged\_bonds x 2*) – A tuple of tuples, where each inner tuple is a pair of tagged atoms (`tag_idx_1`, `tag_idx_2`) which are bonded. The inner tuples are ordered smallest-to-largest, and the tuple of tuples is ordered lexically. The return value for an improper torsion would be ((1, 2), (2, 3), (2, 4)).

**Raises** `SMIRKSParsingError` – If OpenEye toolkit was unable to parse the provided smirks/tagged smarts

`find_smarts_matches(molecule: Molecule, smarts: str, aromaticity_model=DEFAULT_AROMATICITY_MODEL, unique=False) → List[Tuple[int, ...]]`

Find all SMARTS matches for the specified molecule, using the specified aromaticity model.

**Warning:** This API is experimental and subject to change.

#### Parameters

- **molecule** ([Molecule](#)) – The molecule for which all specified SMARTS matches are to be located
- **smarts** ([str](#)) – SMARTS string with optional SMIRKS-style atom tagging
- **aromaticity\_model** ([str](#), optional, default="OEAroModel\_MDL") – The aromaticity model to use. Only OEAroModel\_MDL is supported.
- **unique** ([bool](#), default=False) – If True, only return unique matches. If False, return all matches.
- **:** ([.. note](#)) – Currently:
- **OEAroModel\_MDL** (the only supported aromaticity\_model is) –

#### property toolkit\_file\_read\_formats

List of file formats that this toolkit can read.

#### property toolkit\_file\_write\_formats

List of file formats that this toolkit can write.

#### property toolkit\_installation\_instructions

Instructions on how to install the wrapped toolkit.

#### property toolkit\_name

Return the name of the toolkit wrapped by this class as a str

**Warning:** This API is experimental and subject to change.

**Returns** **toolkit\_name** (*str*) – The name of the wrapped toolkit

#### property toolkit\_version

Return the version of the wrapped toolkit as a str

**Warning:** This API is experimental and subject to change.

**Returns** **toolkit\_version** (*str*) – The version of the wrapped toolkit

### 13.1.4 RDKitToolkitWrapper

**class** openff.toolkit.utils.toolkits.RDKitToolkitWrapper

RDKit toolkit wrapper

**Warning:** This API is experimental and subject to change.

**\_\_init\_\_**()

## Methods

<code>__init__()</code>	
<code>apply_elf_conformer_selection(molecule[, ...])</code>	Applies the <a href="#">ELF method</a> to select a set of diverse conformers which have minimal electrostatically strongly interacting functional groups from a molecules conformers.
<code>assign_partial_charges(molecule[, ...])</code>	Compute partial charges with RDKit, and assign the new values to the <code>partial_charges</code> attribute.
<code>atom_is_in_ring(atom)</code>	Return whether or not an atom is in a ring.
<code>bond_is_in_ring(bond)</code>	Return whether or not a bond is in a ring.
<code>canonical_order_atoms(molecule)</code>	Canonical order the atoms in the molecule using the RDKit.
<code>enumerate_stereoisomers(molecule[, ...])</code>	Enumerate the stereocenters and bonds of the current molecule.
<code>enumerate_tautomers(molecule[, max_states])</code>	Enumerate the possible tautomers of the current molecule.
<code>find_smarts_matches(molecule, smarts[, ...])</code>	Find all SMARTS matches for the specified molecule, using the specified aromaticity model.
<code>from_file(file_path, file_format[, ...])</code>	Create an <code>openff.toolkit.topology.Molecule</code> from a file using this toolkit.
<code>from_file_obj(file_obj, file_format[, ...])</code>	Return an <code>openff.toolkit.topology.Molecule</code> from a file-like object using this toolkit.
<code>from_inchi(inchi[, allow_undefined_stereo, _cls])</code>	Construct a <code>Molecule</code> from a InChI representation
<code>from_object(obj[, allow_undefined_stereo, _cls])</code>	If given an <code>rdchem.Mol</code> (or <code>rdchem.Mol</code> -derived object), this function will load it into an <code>openff.toolkit.topology.molecule</code> .
<code>from_pdb_and_smiles(file_path, smiles[, ...])</code>	Create a <code>Molecule</code> from a <code>pdb</code> file and a SMILES string using RDKit.
<code>from_rdkit(rdmol[, allow_undefined_stereo, ...])</code>	Create a <code>Molecule</code> from an RDKit molecule.
<code>from_smiles(smiles[, ...])</code>	Create a <code>Molecule</code> from a SMILES string using the RDKit toolkit.
<code>generate_conformers(molecule[, ...])</code>	Generate molecule conformers using RDKit.
<code>get_tagged_smarts_connectivity(smarts)</code>	Returns a tuple of tuples indicating connectivity between tagged atoms in a SMARTS string.
<code>is_available()</code>	Check whether the RDKit toolkit can be imported
<code>requires_toolkit()</code>	
<code>to_file(molecule, file_path, file_format)</code>	Writes an OpenFF <code>Molecule</code> to a file-like object
<code>to_file_obj(molecule, file_obj, file_format)</code>	Writes an OpenFF <code>Molecule</code> to a file-like object
<code>to_inchi(molecule[, fixed_hydrogens])</code>	Create an InChI string for the molecule using the RDKit Toolkit.
<code>to_inchikey(molecule[, fixed_hydrogens])</code>	Create an InChIKey for the molecule using the RDKit Toolkit.
<code>to_rdkit(molecule[, aromaticity_model])</code>	Create an RDKit molecule Requires the RDKit to be installed.
<code>to_smiles(molecule[, isomeric, ...])</code>	Uses the RDKit toolkit to convert a <code>Molecule</code> into a SMILES string.

## Attributes

<code>to_rdkit_cache</code>	
<code>toolkit_file_read_formats</code>	List of file formats that this toolkit can read.
<code>toolkit_file_write_formats</code>	List of file formats that this toolkit can write.
<code>toolkit_installation_instructions</code>	Instructions on how to install the wrapped toolkit.
<code>toolkit_name</code>	Return the name of the toolkit wrapped by this class as a str
<code>toolkit_version</code>	Return the version of the wrapped toolkit as a str

**property** `toolkit_file_write_formats: List[str]`

List of file formats that this toolkit can write.

**classmethod** `is_available() → bool`

Check whether the RDKit toolkit can be imported

**Returns** `is_installed (bool)` – True if RDKit is installed, False otherwise.

**from\_object**(*obj*, *allow\_undefined\_stereo: bool = False*, *\_cls=None*)

If given an `rdchem.Mol` (or `rdchem.Mol`-derived object), this function will load it into an `openff.toolkit.topology.molecule`. Otherwise, it will return False.

### Parameters

- **obj** (A `rdchem.Mol`-derived object) – An object to be type-checked and converted into a `Molecule`, if possible.
- **allow\_undefined\_stereo** (`bool`, `default=False`) – Whether to accept molecules with undefined stereocenters. If False, an exception will be raised if a molecule with undefined stereochemistry is passed into this function.
- **\_cls** (`class`) – `Molecule` constructor

**Returns** *Molecule or False* – An `openff.toolkit.topology.molecule` `Molecule`.

**Raises** `NotImplementedError` – If the object could not be converted into a `Molecule`.

**from\_pdb\_and\_smiles**(*file\_path: str*, *smiles: str*, *allow\_undefined\_stereo: bool = False*, *\_cls=None*)

Create a `Molecule` from a `pdb` file and a `SMILES` string using `RDKit`.

Requires `RDKit` to be installed.

The molecule is created and sanitised based on the `SMILES` string, we then find a mapping between this molecule and one from the `PDB` based only on atomic number and connections. The `SMILES` molecule is then reindexed to match the `PDB`, the conformer is attached, and the molecule returned.

Note that any stereochemistry in the molecule is set by the `SMILES`, and not the coordinates of the `PDB`.

### Parameters

- **file\_path** (`str`) – `PDB` file path
- **smiles** (`str`) – a valid smiles string for the `pdb`, used for stereochemistry, formal charges, and bond order

- **allow\_undefined\_stereo** (*bool*, default=False) – If false, raises an exception if SMILES contains undefined stereochemistry.
- **\_cls** (*class*) – Molecule constructor

**Returns** *molecule* (*openff.toolkit.Molecule* (or *\_cls()* type)) – An OFFMol instance with ordering the same as used in the PDB file.

:raises InvalidConformerError : if the SMILES and PDB molecules are not isomorphic.:

**from\_file**(*file\_path*: *str*, *file\_format*: *str*, *allow\_undefined\_stereo*: *bool* = False, *\_cls*=None)

Create an openff.toolkit.topology.Molecule from a file using this toolkit.

#### Parameters

- **file\_path** (*str*) – The file to read the molecule from
- **file\_format** (*str*) – Format specifier, usually file suffix (eg. ‘MOL2’, ‘SMI’) Note that not all toolkits support all formats. Check ToolkitWrapper.toolkit\_file\_read\_formats for details.
- **allow\_undefined\_stereo** (*bool*, default=False) – If false, raises an exception if oemol contains undefined stereochemistry.
- **\_cls** (*class*) – Molecule constructor

**Returns** *molecules* (*iterable of Molecules*) – a list of Molecule objects is returned.

**from\_file\_obj**(*file\_obj*, *file\_format*: *str*, *allow\_undefined\_stereo*: *bool* = False, *\_cls*=None)

Return an openff.toolkit.topology.Molecule from a file-like object using this toolkit.

A file-like object is an object with a “.read()” method.

**Warning:** This API is experimental and subject to change.

#### Parameters

- **file\_obj** (*file-like object*) – The file-like object to read the molecule from
- **file\_format** (*str*) – Format specifier, usually file suffix (eg. ‘MOL2’, ‘SMI’) Note that not all toolkits support all formats. Check ToolkitWrapper.toolkit\_file\_read\_formats for details.
- **allow\_undefined\_stereo** (*bool*, default=False) – If false, raises an exception if oemol contains undefined stereochemistry.
- **\_cls** (*class*) – Molecule constructor

**Returns** *molecules* (*Molecule or list of Molecules*) – a list of Molecule objects is returned.

**to\_file\_obj**(*molecule*: *Molecule*, *file\_obj*, *file\_format*: *str*)

Writes an OpenFF Molecule to a file-like object

#### Parameters

- **molecule** (an OpenFF Molecule) – The molecule to write
- **file\_obj** – The file-like object to write to
- **file\_format** – The format for writing the molecule data

**to\_file**(*molecule*: [Molecule](#), *file\_path*: *str*, *file\_format*: *str*)

Writes an OpenFF Molecule to a file-like object

**Parameters**

- **molecule** (an OpenFF Molecule) – The molecule to write
- **file\_path** – The file path to write to
- **file\_format** – The format for writing the molecule data

**enumerate\_stereoisomers**(*molecule*: [Molecule](#), *undefined\_only*: *bool* = *False*, *max\_isomers*: *int* = 20, *rationalise*: *bool* = *True*) → [List](#)[[Molecule](#)]

Enumerate the stereocenters and bonds of the current molecule.

**Parameters**

- **molecule** ([Molecule](#)) – The molecule whose state we should enumerate
- **undefined\_only** (*bool* optional, default=*False*) – If we should enumerate all stereocenters and bonds or only those with undefined stereochemistry
- **max\_isomers** (*int* optional, default=20) – The maximum amount of molecules that should be returned
- **rationalise** (*bool* optional, default=*True*) – If we should try to build and rationalise the molecule to ensure it can exist

**Returns molecules** ([List](#)[[openff.toolkit.topology.Molecule](#)]) – A list of [openff.toolkit.topology.Molecule](#) instances

**enumerate\_tautomers**(*molecule*: [Molecule](#), *max\_states*: *int* = 20) → [List](#)[[Molecule](#)]

Enumerate the possible tautomers of the current molecule.

**Parameters**

- **molecule** ([Molecule](#)) – The molecule whose state we should enumerate
- **max\_states** (*int* optional, default=20) – The maximum amount of molecules that should be returned

**Returns molecules** ([List](#)[[openff.toolkit.topology.Molecule](#)]) – A list of [openff.toolkit.topology.Molecule](#) instances not including the input molecule.

**canonical\_order\_atoms**(*molecule*: [Molecule](#)) → [Molecule](#)

Canonical order the atoms in the molecule using the RDKit.

**Parameters**

- **molecule** ([Molecule](#)) – The input molecule

Returns

- ----- \_
- **molecule** – The input molecule, with canonically-indexed atoms and bonds.

**to\_smiles**(*molecule*: [Molecule](#), *isomeric*: *bool* = *True*, *explicit\_hydrogens*: *bool* = *True*, *mapped*: *bool* = *False*)

Uses the RDKit toolkit to convert a Molecule into a SMILES string. A partially mapped smiles can also be generated for atoms of interest by supplying an *atom\_map* to the properties dictionary.

**Parameters**

- **molecule** (An `openff.toolkit.topology.Molecule`) – The molecule to convert into a SMILES.
- **isomeric** (bool optional, default= True) – return an isomeric smiles
- **explicit\_hydrogens** (bool optional, default=True) – return a smiles string containing all hydrogens explicitly
- **mapped** (bool optional, default=False) – return a explicit hydrogen mapped smiles, the atoms to be mapped can be controlled by supplying an atom map into the properties dictionary. If no mapping is passed all atoms will be mapped in order, else an atom map dictionary from the current atom index to the map id should be supplied with no duplicates. The map ids (values) should start from 0 or 1.

**Returns smiles** (*str*) – The SMILES of the input molecule.

**from\_smiles**(*smiles: str*, *hydrogens\_are\_explicit: bool = False*, *allow\_undefined\_stereo: bool = False*, *\_cls=None*)

Create a Molecule from a SMILES string using the RDKit toolkit.

**Warning:** This API is experimental and subject to change.

#### Parameters

- **smiles** (*str*) – The SMILES string to turn into a molecule
- **hydrogens\_are\_explicit** (*bool*, default=False) – If False, RDKit will perform hydrogen addition using Chem.AddHs
- **allow\_undefined\_stereo** (*bool*, default=False) – Whether to accept SMILES with undefined stereochemistry. If False, an exception will be raised if a SMILES with undefined stereochemistry is passed into this function.
- **\_cls** (*class*) – Molecule constructor

**Returns molecule** (*openff.toolkit.topology.Molecule*) – An OpenFF style molecule.

:raises RadicalsNotSupportedError : If any atoms in the RDKit molecule contain radical electrons.:

**from\_inchi**(*inchi: str*, *allow\_undefined\_stereo: bool = False*, *\_cls=None*)

Construct a Molecule from a InChI representation

#### Parameters

- **inchi** (*str*) – The InChI representation of the molecule.
- **allow\_undefined\_stereo** (*bool*, default=False) – Whether to accept InChI with undefined stereochemistry. If False, an exception will be raised if a InChI with undefined stereochemistry is passed into this function.
- **\_cls** (*class*) – Molecule constructor

**Returns molecule** (*openff.toolkit.topology.Molecule*)

**generate\_conformers**(*molecule: Molecule*, *n\_conformers: int = 1*, *rms\_cutoff: Optional[Quantity] = None*, *clear\_existing: bool = True*, *\_cls=None*, *make\_carboxylic\_acids\_cis: bool = False*)

Generate molecule conformers using RDKit.

**Warning:** This API is experimental and subject to change.

#### Parameters

- **molecule** (a `Molecule`) – The molecule to generate conformers for.
- **n\_conformers** (`int`, default=1) – Maximum number of conformers to generate.
- **rms\_cutoff** (unit-wrapped float, in units of distance, optional, default=None) – The minimum RMS value at which two conformers are considered redundant and one is deleted. If None, the cutoff is set to 1 Angstrom
- **clear\_existing** (`bool`, default=True) – Whether to overwrite existing conformers for the molecule.
- **\_cls** (class) – Molecule constructor
- **make\_carboxylic\_acids\_cis** (`bool`, default=False) – Guarantee all conformers have exclusively cis carboxylic acid groups (COOH) by rotating the proton in any trans carboxylic acids 180 degrees around the C-O bond.

`assign_partial_charges(molecule: Molecule, partial_charge_method: Optional[str] = None, use_conformers: Optional[List[Quantity]] = None, strict_n_conformers: bool = False, normalize_partial_charges: bool = True, _cls=None)`

Compute partial charges with RDKit, and assign the new values to the `partial_charges` attribute.

**Warning:** This API is experimental and subject to change.

#### Parameters

- **molecule** (`Molecule`) – Molecule for which partial charges are to be computed
- **partial\_charge\_method** (`str`, optional, default=None) – The charge model to use. One of ['mmff94', 'gasteiger']. If None, 'mmff94' will be used.
  - **'mmff94': Applies partial charges using the Merck Molecular Force Field (MMFF).** This method does not make use of conformers, and hence `use_conformers` and `strict_n_conformers` will not impact the partial charges produced.
- **use\_conformers** (iterable of unit-wrapped numpy arrays, each with) – shape (n\_atoms, 3) and dimension of distance. Optional, default = None Coordinates to use for partial charge calculation. If None, an appropriate number of conformers will be generated.
- **strict\_n\_conformers** (`bool`, default=False) – Whether to raise an exception if an invalid number of conformers is provided for the given charge method. If this is False and an invalid number of conformers is found, a warning will be raised.
- **normalize\_partial\_charges** (`bool`, default=True) – Whether to offset partial charges so that they sum to the total formal charge of the molecule. This is used to prevent accumulation of rounding errors when the partial charge generation method has low precision.
- **\_cls** (class) – Molecule constructor

#### Raises



- `ChargeMethodUnavailableError` if the requested charge method can not be handled by this toolkit –
- `ChargeCalculationError` if the charge method is supported by this toolkit, but fails –

`apply_elf_conformer_selection(molecule: Molecule, percentage: float = 2.0, limit: int = 10, rms_tolerance: Quantity = 0.05 * unit.angstrom)`

Applies the [ELF method](#) to select a set of diverse conformers which have minimal electrostatically strongly interacting functional groups from a molecules conformers.

The diverse conformer selection is performed by the `_elf_select_diverse_conformers` function, which attempts to greedily select conformers which are most distinct according to their RMS.

**Warning:**

- Although this function is inspired by the OpenEye ELF10 method, this implementation may yield slightly different conformers due to potential differences in this and the OE closed source implementation.

## Notes

- The input molecule should have a large set of conformers already generated to select the ELF10 conformers from.
- The selected conformers will be retained in the `molecule.conformers` list while unselected conformers will be discarded.
- Only heavy atoms are included when using the RMS to select diverse conformers.

**See also:**

`RDKitToolkitWrapper._elf_select_diverse_conformers`

## Parameters

- **molecule** – The molecule which contains the set of conformers to select from.
- **percentage** – The percentage of conformers with the lowest electrostatic interaction energies to greedily select from.
- **limit** – The maximum number of conformers to select.
- **rms\_tolerance** – Conformers whose RMS is within this amount will be treated as identical and the duplicate discarded.

`from_rdkit(rdmol, allow_undefined_stereo: bool = False, hydrogens_are_explicit: bool = False, _cls=None)`

Create a Molecule from an RDKit molecule.

Requires the RDKit to be installed.

**Warning:** This API is experimental and subject to change.

## Parameters

- **rdmol** (`rdkit.RDMol`) – An RDKit molecule
- **allow\_undefined\_stereo** (`bool`, `default=False`) – If false, raises an exception if rdmol contains undefined stereochemistry.
- **hydrogens\_are\_explicit** (`bool`, `default=False`) – If False, RDKit will perform hydrogen addition using `Chem.AddHs`
- **\_cls** (`class`) – Molecule constructor

**Returns** **molecule** (`openff.toolkit.topology.Molecule`) – An OpenFF molecule

### Examples

Create a molecule from an RDKit molecule

```
>>> from rdkit import Chem
>>> from openff.toolkit.tests.utils import get_data_file_path
>>> rdmol = Chem.MolFromMolFile(get_data_file_path('systems/monomers/ethanol.sdf'))
```

```
>>> toolkit_wrapper = RDKitToolkitWrapper()
>>> molecule = toolkit_wrapper.from_rdkit(rdmol)
```

**to\_rdkit**(*molecule*: `Molecule`, *aromaticity\_model*: `str` = `DEFAULT_AROMATICITY_MODEL`)

Create an RDKit molecule Requires the RDKit to be installed.

**Warning:** This API is experimental and subject to change.

**Parameters** **aromaticity\_model** (`str`, optional, `default="OEAroModel_MDL"`) – The aromaticity model to use. Only `OEAroModel_MDL` is supported.

**Returns** **rdmol** (`rdkit.RDMol`) – An RDKit molecule

### Examples

Convert a molecule to RDKit >>> from openff.toolkit import Molecule >>> ethanol = Molecule.from\_smiles('CCO') >>> rdmol = ethanol.to\_rdkit()

**to\_inchi**(*molecule*: `Molecule`, *fixed\_hydrogens*: `bool` = `False`)

Create an InChI string for the molecule using the RDKit Toolkit. InChI is a standardised representation that does not capture tautomers unless specified using the fixed hydrogen layer.

For information on InChi see here <https://iupac.org/who-we-are/divisions/division-details/inchi/>

#### Parameters

- **molecule** (An `openff.toolkit.topology.Molecule`) – The molecule to convert into a SMILES.
- **fixed\_hydrogens** (`bool`, `default=False`) – If a fixed hydrogen layer should be added to the InChI, if `True` this will produce a non standard specific InChI string of the molecule.

**Returns** **inchi** (`str`) – The InChI string of the molecule.

**to\_inchikey**(*molecule*: [Molecule](#), *fixed\_hydrogens*: *bool* = *False*) → *str*

Create an InChIKey for the molecule using the RDKit Toolkit. InChIKey is a standardised representation that does not capture tautomers unless specified using the fixed hydrogen layer.

For information on InChi see here <https://iupac.org/who-we-are/divisions/division-details/inchi/>

#### Parameters

- **molecule** ([Molecule](#)) – The molecule to convert into a SMILES.
- **fixed\_hydrogens** (*bool*, default=*False*) – If a fixed hydrogen layer should be added to the InChI, if *True* this will produce a non standard specific InChI string of the molecule.

**Returns** **inchi\_key** (*str*) – The InChIKey representation of the molecule.

**get\_tagged\_smarts\_connectivity**(*smarts*: *str*)

Returns a tuple of tuples indicating connectivity between tagged atoms in a SMARTS string. Does not return bond order.

**Parameters** **smarts** (*str*) – The tagged SMARTS to analyze

#### Returns

- **unique\_tags** (*tuple of int*) – A sorted tuple of all unique tagged atom map indices.
- **tagged\_atom\_connectivity** (*tuple of tuples of int, shape n\_tagged\_bonds x 2*) –  
A tuple of tuples, where each inner tuple is a pair of tagged atoms (**tag\_idx\_1**, **tag\_idx\_2**) which are bonded. The inner tuples are ordered smallest-to-largest, and the tuple of tuples is ordered lexically. So the return value for an improper torsion would be ((1, 2), (2, 3), (2, 4)).

**Raises** **SMIRKSParsingError** – If RDKit was unable to parse the provided smirks/tagged smarts

**find\_smarts\_matches**(*molecule*: [Molecule](#), *smarts*: *str*, *aromaticity\_model*: *str* = 'OEAroModel\_MD1', *unique*: *bool* = *False*) → *List[Tuple[int, ...]]*

Find all SMARTS matches for the specified molecule, using the specified aromaticity model.

**Warning:** This API is experimental and subject to change.

#### Parameters

- **molecule** ([Molecule](#)) – The molecule for which all specified SMARTS matches are to be located
- **smarts** (*str*) – SMARTS string with optional SMIRKS-style atom tagging
- **aromaticity\_model** (*str*, optional, default='OEAroModel\_MD1') – Molecule is prepared with this aromaticity model prior to querying.
- **unique** (*bool*, default=*False*) – If *True*, only return unique matches. If *False*, return all matches.
- **:** (*.. note*) – Currently:
- **OEAroModel\_MD1** (the only supported aromaticity\_model is) –

**atom\_is\_in\_ring**(*atom*: Atom) → bool

Return whether or not an atom is in a ring.

It is assumed that this atom is in molecule.

**Parameters** *atom* (Atom) – The molecule containing the atom of interest

**Returns** *is\_in\_ring* (bool) – Whether or not the atom is in a ring.

**Raises** `NotAttachedToMoleculeError` –

**bond\_is\_in\_ring**(*bond*: Bond) → bool

Return whether or not a bond is in a ring.

It is assumed that this atom is in molecule.

**Parameters** *bond* (Bond) – The molecule containing the atom of interest

**Returns** *is\_in\_ring* (bool) – Whether or not the bond of index *bond\_index* is in a ring

**Raises** `NotAttachedToMoleculeError` –

**property** `toolkit_file_read_formats`

List of file formats that this toolkit can read.

**property** `toolkit_installation_instructions`

Instructions on how to install the wrapped toolkit.

**property** `toolkit_name`

Return the name of the toolkit wrapped by this class as a str

**Warning:** This API is experimental and subject to change.

**Returns** `toolkit_name` (str) – The name of the wrapped toolkit

**property** `toolkit_version`

Return the version of the wrapped toolkit as a str

**Warning:** This API is experimental and subject to change.

**Returns** `toolkit_version` (str) – The version of the wrapped toolkit

### 13.1.5 AmberToolsToolkitWrapper

**class** `openff.toolkit.utils.toolkits.AmberToolsToolkitWrapper`

AmberTools toolkit wrapper

**Warning:** This API is experimental and subject to change.

`__init__()`

## Methods

<code>__init__()</code>	
<code>assign_fractional_bond_orders(molecule[, ...])</code>	Update and store list of bond orders this molecule.
<code>assign_partial_charges(molecule[, ...])</code>	Compute partial charges with AmberTools using antechamber/sqm, and assign the new values to the <code>partial_charges</code> attribute.
<code>from_file(file_path, file_format[, ...])</code>	Return an <code>openff.toolkit.topology.Molecule</code> from a file using this toolkit.
<code>from_file_obj(file_obj, file_format[, ...])</code>	Return an <code>openff.toolkit.topology.Molecule</code> from a file-like object (an object with a <code>".read()"</code> method using this toolkit.
<code>is_available()</code>	Check whether the AmberTools toolkit is installed
<code>requires_toolkit()</code>	

## Attributes

<code>toolkit_file_read_formats</code>	List of file formats that this toolkit can read.
<code>toolkit_file_write_formats</code>	List of file formats that this toolkit can write.
<code>toolkit_installation_instructions</code>	Instructions on how to install the wrapped toolkit.
<code>toolkit_name</code>	Return the name of the toolkit wrapped by this class as a str
<code>toolkit_version</code>	Return the version of the wrapped toolkit as a str

**static** `is_available()` → bool

Check whether the AmberTools toolkit is installed

**Returns** `is_installed` (bool) – True if AmberTools is installed, False otherwise.

**assign\_partial\_charges**(*molecule*: `Molecule`, *partial\_charge\_method*: *Optional*[str] = None, *use\_conformers*: *Optional*[List[Quantity]] = None, *strict\_n\_conformers*: bool = False, *normalize\_partial\_charges*: bool = True, *\_cls*=None)

Compute partial charges with AmberTools using antechamber/sqm, and assign the new values to the `partial_charges` attribute.

**Warning:** This API experimental and subject to change.

## Parameters

- **molecule** (`Molecule`) – Molecule for which partial charges are to be computed
- **partial\_charge\_method** (str, optional, default=None) – The charge model to use. One of ['gasteiger', 'am1bcc', 'am1-mulliken']. If None, 'am1-mulliken' will be used.

- **use\_conformers** (iterable of unit-wrapped numpy arrays, each) – with shape (n\_atoms, 3) and dimension of distance. Optional, default = None List of unit-wrapped numpy arrays to use for partial charge calculation. If None, an appropriate number of conformers will be generated.
- **strict\_n\_conformers** (bool, default=False) – Whether to raise an exception if an invalid number of conformers is provided for the given charge method. If this is False and an invalid number of conformers is found, a warning will be raised.
- **normalize\_partial\_charges** (bool, default=True) – Whether to offset partial charges so that they sum to the total formal charge of the molecule. This is used to prevent accumulation of rounding errors when the partial charge generation method has low precision.
- **\_cls** (class) – Molecule constructor

#### Raises

- **ChargeMethodUnavailableError** if the requested charge method can not be handled by this toolkit –
- **ChargeCalculationError** if the charge method is supported by this toolkit, but fails –

**assign\_fractional\_bond\_orders**(molecule: [Molecule](#), bond\_order\_model: *Optional*[str] = None, use\_conformers: *Optional*[List[str]] = None, \_cls=None)

Update and store list of bond orders this molecule. Bond orders are stored on each bond, in the *bond.fractional\_bond\_order* attribute.

**Warning:** This API is experimental and subject to change.

#### Parameters

- **molecule** (openff.toolkit.topology.molecule [Molecule](#)) – The molecule to assign wiberg bond orders to
- **bond\_order\_model** (str, optional, default=None) – The charge model to use. Only allowed value is ‘am1-wiberg’. If None, ‘am1-wiberg’ will be used.
- **use\_conformers** (iterable of unit-wrapped np.array with shape (n\_atoms, 3)) – and dimension of distance, optional, default=None The conformers to use for fractional bond order calculation. If None, an appropriate number of conformers will be generated by an available ToolkitWrapper.
- **\_cls** (class) – Molecule constructor

**from\_file**(file\_path, file\_format, allow\_undefined\_stereo=False)

Return an openff.toolkit.topology.Molecule from a file using this toolkit.

#### Parameters

- **file\_path** (str) – The file to read the molecule from
- **file\_format** (str) – Format specifier, usually file suffix (eg. ‘MOL2’, ‘SMI’) Note that not all toolkits support all formats. Check ToolkitWrapper.toolkit\_file\_read\_formats for details.

- **allow\_undefined\_stereo** (*bool*, default=False) – If false, raises an exception if any molecules contain undefined stereochemistry.
- **\_cls** (*class*) – Molecule constructor

**Returns** **molecules** (*Molecule or list of Molecules*) – a list of Molecule objects is returned.

**from\_file\_obj**(*file\_obj*, *file\_format*, *allow\_undefined\_stereo*=False, *\_cls*=None)

Return an `openff.toolkit.topology.Molecule` from a file-like object (an object with a “`read()`” method using this toolkit.

#### Parameters

- **file\_obj** (file-like object) – The file-like object to read the molecule from
- **file\_format** (*str*) – Format specifier, usually file suffix (eg. ‘MOL2’, ‘SMI’) Note that not all toolkits support all formats. Check `ToolkitWrapper.toolkit_file_read_formats` for details.
- **allow\_undefined\_stereo** (*bool*, default=False) – If false, raises an exception if any molecules contain undefined stereochemistry. If false, the function skips loading the molecule.
- **\_cls** (*class*) – Molecule constructor

**Returns** **molecules** (*Molecule or list of Molecules*) – a list of Molecule objects is returned.

**property** **toolkit\_file\_read\_formats**

List of file formats that this toolkit can read.

**property** **toolkit\_file\_write\_formats**

List of file formats that this toolkit can write.

**property** **toolkit\_installation\_instructions**

Instructions on how to install the wrapped toolkit.

**property** **toolkit\_name**

Return the name of the toolkit wrapped by this class as a str

**Warning:** This API is experimental and subject to change.

**Returns** **toolkit\_name** (*str*) – The name of the wrapped toolkit

**property** **toolkit\_version**

Return the version of the wrapped toolkit as a str

**Warning:** This API is experimental and subject to change.

**Returns** **toolkit\_version** (*str*) – The version of the wrapped toolkit

### 13.1.6 BuiltInToolkitWrapper

**class** openff.toolkit.utils.toolkits.**BuiltInToolkitWrapper**

Built-in ToolkitWrapper for very basic functionality. Intended for testing and not much more.

**Warning:** This API is experimental and subject to change.

`__init__()`

#### Methods

<code>__init__()</code>	
<code>assign_partial_charges(molecule[, ...])</code>	Compute partial charges with the built-in toolkit using simple arithmetic operations, and assign the new values to the <code>partial_charges</code> attribute.
<code>from_file(file_path, file_format[, ...])</code>	Return an <code>openff.toolkit.topology.Molecule</code> from a file using this toolkit.
<code>from_file_obj(file_obj, file_format[, ...])</code>	Return an <code>openff.toolkit.topology.Molecule</code> from a file-like object (an object with a <code>".read()"</code> method using this toolkit.
<code>is_available()</code>	Check whether the corresponding toolkit can be imported
<code>requires_toolkit()</code>	

#### Attributes

<code>toolkit_file_read_formats</code>	List of file formats that this toolkit can read.
<code>toolkit_file_write_formats</code>	List of file formats that this toolkit can write.
<code>toolkit_installation_instructions</code>	Instructions on how to install the wrapped toolkit.
<code>toolkit_name</code>	Return the name of the toolkit wrapped by this class as a str
<code>toolkit_version</code>	Return the version of the wrapped toolkit as a str

**assign\_partial\_charges**(*molecule*, *partial\_charge\_method*=None, *use\_conformers*=None, *strict\_n\_conformers*=False, *normalize\_partial\_charges*=True, *\_cls*=None)

Compute partial charges with the built-in toolkit using simple arithmetic operations, and assign the new values to the `partial_charges` attribute.

**Warning:** This API is experimental and subject to change.

#### Parameters

- **molecule** (`Molecule`) – Molecule for which partial charges are to be computed



- **partial\_charge\_method** (*str*, optional, default=None) – The charge model to use. One of ['zeros', 'formal\_charge']. If None, 'formal\_charge' will be used.
- **use\_conformers** (iterable of unit-wrapped numpy arrays, each with shape) – (n\_atoms, 3) and dimension of distance. Optional, default = None Coordinates to use for partial charge calculation. If None, an appropriate number of conformers will be generated.
- **strict\_n\_conformers** (*bool*, default=False) – Whether to raise an exception if an invalid number of conformers is provided for the given charge method. If this is False and an invalid number of conformers is found, a warning will be raised instead of an Exception.
- **normalize\_partial\_charges** (*bool*, default=True) – Whether to offset partial charges so that they sum to the total formal charge of the molecule. This is used to prevent accumulation of rounding errors when the partial charge generation method has low precision.
- **\_cls** (class) – Molecule constructor

#### Raises

- **ChargeMethodUnavailableError** if this toolkit cannot handle the requested charge method –
- **IncorrectNumConformersError** if **strict\_n\_conformers** is True and **use\_conformers** is provided –
- and specifies an invalid number of conformers for the requested method –
- **ChargeCalculationError** if the charge calculation is supported by this toolkit, but fails –

**from\_file**(*file\_path*, *file\_format*, *allow\_undefined\_stereo*=False)

Return an openff.toolkit.topology.Molecule from a file using this toolkit.

#### Parameters

- **file\_path** (*str*) – The file to read the molecule from
- **file\_format** (*str*) – Format specifier, usually file suffix (eg. 'MOL2', 'SMI') Note that not all toolkits support all formats. Check ToolkitWrapper.toolkit\_file\_read\_formats for details.
- **allow\_undefined\_stereo** (*bool*, default=False) – If false, raises an exception if any molecules contain undefined stereochemistry.
- **\_cls** (class) – Molecule constructor

**Returns molecules** (*Molecule or list of Molecules*) – a list of Molecule objects is returned.

**from\_file\_obj**(*file\_obj*, *file\_format*, *allow\_undefined\_stereo*=False, *\_cls*=None)

Return an openff.toolkit.topology.Molecule from a file-like object (an object with a “.read()” method using this toolkit.

#### Parameters

- **file\_obj** (file-like object) – The file-like object to read the molecule from

- **file\_format** (*str*) – Format specifier, usually file suffix (eg. ‘MOL2’, ‘SMI’) Note that not all toolkits support all formats. Check `ToolkitWrapper.toolkit_file_read_formats` for details.
- **allow\_undefined\_stereo** (*bool*, default=False) – If false, raises an exception if any molecules contain undefined stereochemistry. If false, the function skips loading the molecule.
- **\_cls** (*class*) – Molecule constructor

**Returns molecules** (*Molecule or list of Molecules*) – a list of Molecule objects is returned.

**classmethod is\_available()**

Check whether the corresponding toolkit can be imported

**Returns is\_installed** (*bool*) – True if corresponding toolkit is installed, False otherwise.

**property toolkit\_file\_read\_formats**

List of file formats that this toolkit can read.

**property toolkit\_file\_write\_formats**

List of file formats that this toolkit can write.

**property toolkit\_installation\_instructions**

Instructions on how to install the wrapped toolkit.

**property toolkit\_name**

Return the name of the toolkit wrapped by this class as a str

**Warning:** This API is experimental and subject to change.

**Returns toolkit\_name** (*str*) – The name of the wrapped toolkit

**property toolkit\_version**

Return the version of the wrapped toolkit as a str

**Warning:** This API is experimental and subject to change.

**Returns toolkit\_version** (*str*) – The version of the wrapped toolkit

## 13.2 Serialization support

---

`Serializable`

Mix-in to add serialization and deserialization support via JSON, YAML, BSON, TOML, MessagePack, and XML.

---

### 13.2.1 Serializable

**class** `openff.toolkit.utils.serialization.Serializable`

Mix-in to add serialization and deserialization support via JSON, YAML, BSON, TOML, MessagePack, and XML.

For more information on these formats, see: [JSON](#), [BSON](#), [YAML](#), [TOML](#), [MessagePack](#), and [XML](#).

To use this mix-in, the class inheriting from this class must have implemented `to_dict()` and `from_dict()` methods that utilize dictionaries containing only serializable Python objects.

**Warning:** The serialization/deserialization schemes used here place some strict constraints on what kinds of dict objects can be serialized. No effort is made to add further protection to ensure serialization is possible. Use with caution.

#### Examples

Example class using `Serializable` mix-in:

```
>>> from openff.toolkit.utils.serialization import Serializable
>>> class Thing(Serializable):
...     def __init__(self, description):
...         self.description = description
...
...     def to_dict(self):
...         return { 'description' : self.description }
...
...     @classmethod
...     def from_dict(cls, d):
...         return cls(d['description'])
...
>>> # Create an example object
>>> thing = Thing('blorb')
```

Get [JSON](#) representation:

```
>>> json_thing = thing.to_json()
```

Reconstruct an object from its [JSON](#) representation:

```
>>> thing_from_json = Thing.from_json(json_thing)
```

Get [BSON](#) representation:

```
>>> bson_thing = thing.to_bson()
```

Reconstruct an object from its [BSON](#) representation:

```
>>> thing_from_bson = Thing.from_bson(bson_thing)
```

Get [YAML](#) representation:

```
>>> yaml_thing = thing.to_yaml()
```

Reconstruct an object from its [YAML](#) representation:

```
>>> thing_from_yaml = Thing.from_yaml(yaml_thing)
```

Get [MessagePack](#) representation:

```
>>> messagepack_thing = thing.to_messagepack()
```

Reconstruct an object from its [MessagePack](#) representation:

```
>>> thing_from_messagepack = Thing.from_messagepack(messagepack_thing)
```

Get [XML](#) representation:

```
>>> xml_thing = thing.to_xml()
```

`__init__()`

## Methods

<code>__init__()</code>	
<code>from_bson(serialized)</code>	Instantiate an object from a BSON serialized representation.
<code>from_dict(d)</code>	
<code>from_json(serialized)</code>	Instantiate an object from a JSON serialized representation.
<code>from_messagepack(serialized)</code>	Instantiate an object from a MessagePack serialized representation.
<code>from_pickle(serialized)</code>	Instantiate an object from a pickle serialized representation.
<code>from_toml(serialized)</code>	Instantiate an object from a TOML serialized representation.
<code>from_xml(serialized)</code>	Instantiate an object from an XML serialized representation.
<code>from_yaml(serialized)</code>	Instantiate from a YAML serialized representation.
<code>to_bson()</code>	Return a BSON serialized representation.
<code>to_dict()</code>	
<code>to_json([indent])</code>	Return a JSON serialized representation.
<code>to_messagepack()</code>	Return a MessagePack representation.
<code>to_pickle()</code>	Return a pickle serialized representation.
<code>to_toml()</code>	Return a TOML serialized representation.
<code>to_xml([indent])</code>	Return an XML representation.
<code>to_yaml()</code>	Return a YAML serialized representation.

**to\_json**(*indent=None*) → *str*

Return a JSON serialized representation.

Specification: <https://www.json.org/>

**Parameters** *indent* (*int*, optional, default=None) – If not None, will pretty-print with specified number of spaces for indentation

**Returns** *serialized* (*str*) – A JSON serialized representation of the object

**classmethod** **from\_json**(*serialized: str*)

Instantiate an object from a JSON serialized representation.

Specification: <https://www.json.org/>

**Parameters** *serialized* (*str*) – A JSON serialized representation of the object

**Returns** *instance* (*cls*) – An instantiated object

**to\_bson**()

Return a BSON serialized representation.

Specification: <http://bsonspec.org/>

**Returns** *serialized* (*bytes*) – A BSON serialized representation of the object

**classmethod** **from\_bson**(*serialized*)

Instantiate an object from a BSON serialized representation.

Specification: <http://bsonspec.org/>

**Parameters** *serialized* (*bytes*) – A BSON serialized representation of the object

**Returns** *instance* (*cls*) – An instantiated object

**to\_toml**()

Return a TOML serialized representation.

Specification: <https://github.com/toml-lang/toml>

**Returns** *serialized* (*str*) – A TOML serialized representation of the object

**classmethod** **from\_toml**(*serialized*)

Instantiate an object from a TOML serialized representation.

Specification: <https://github.com/toml-lang/toml>

**Parameters** *serialized* (*str*) – A TOML serialized representation of the object

**Returns** *instance* (*cls*) – An instantiated object

**to\_yaml**()

Return a YAML serialized representation.

Specification: <http://yaml.org/>

**Returns** *serialized* (*str*) – A YAML serialized representation of the object

**classmethod** **from\_yaml**(*serialized*)

Instantiate from a YAML serialized representation.

Specification: <http://yaml.org/>

**Parameters** *serialized* (*str*) – A YAML serialized representation of the object

**Returns** *instance* (*cls*) – Instantiated object

**to\_messagepack()**

Return a MessagePack representation.

Specification: <https://msgpack.org/index.html>

**Returns** **serialized** (*bytes*) – A MessagePack-encoded bytes serialized representation of the object

**classmethod from\_messagepack(serialized)**

Instantiate an object from a MessagePack serialized representation.

Specification: <https://msgpack.org/index.html>

**Parameters** **serialized** (*bytes*) – A MessagePack-encoded bytes serialized representation

**Returns** **instance** (*cls*) – Instantiated object.

**to\_xml(indent=2)**

Return an XML representation.

Specification: <https://www.w3.org/XML/>

**Parameters** **indent** (*int*, optional, default=2) – If not None, will pretty-print with specified number of spaces for indentation

**Returns** **serialized** (*bytes*) – A MessagePack-encoded bytes serialized representation.

**classmethod from\_xml(serialized)**

Instantiate an object from an XML serialized representation.

Specification: <https://www.w3.org/XML/>

**Parameters** **serialized** (*bytes*) – An XML serialized representation

**Returns** **instance** (*cls*) – Instantiated object.

**to\_pickle()**

Return a pickle serialized representation.

**Warning:** This is not recommended for safe, stable storage since the pickle specification may change between Python versions.

**Returns** **serialized** (*str*) – A pickled representation of the object

**classmethod from\_pickle(serialized)**

Instantiate an object from a pickle serialized representation.

**Warning:** This is not recommended for safe, stable storage since the pickle specification may change between Python versions.

**Parameters** **serialized** (*str*) – A pickled representation of the object

**Returns** **instance** (*cls*) – An instantiated object

## 13.3 Collections

Custom collections for the toolkit

<code>ValidatedList</code>	A list that runs custom converter and validators when new elements are added.
<code>ValidatedDict</code>	A dict that runs custom converter and validators when new elements are added.

### 13.3.1 ValidatedList

**class** `openff.toolkit.utils.collections.ValidatedList(seq=(), converter=None, validator=None)`

A list that runs custom converter and validators when new elements are added.

Multiple converters and validators can be assigned to the list. These are executed in the given order with converters run before validators.

Validators must take the new element as the first argument and raise an exception if validation fails.

`validator(new_element) -> None`

Converters must also take the new element as the first argument, but they have to return the converted value.

`converter(new_element) -> converted_value`

#### Examples

We can define validator and converter functions that are run on each element of the list.

```
>>> def is_positive_validator(value):
...     if value <= 0:
...         raise TypeError('value must be positive')
...
>>> v1 = ValidatedList([1, -1], validator=is_positive_validator)
Traceback (most recent call last):
...
TypeError: value must be positive
```

Multiple converters that are run before the validators can be specified.

```
>>> v1 = ValidatedList([-1, '2', 3.0], converter=[float, abs],
...                 validator=is_positive_validator)
>>> v1
[1.0, 2.0, 3.0]
```

**\_\_init\_\_**(`seq=(), converter=None, validator=None`)

Initialize the list.

#### Parameters

- **seq** (Iterable) – A sequence of elements.
- **converter** (callable or List[callable]) – Functions that will be used to convert each new element of the list.

- **validator** (callable or List[callable]) – Functions that will be used to convert each new element of the list.

## Methods

<code>__init__([seq, converter, validator])</code>	Initialize the list.
<code>append(p_object)</code>	Append object to the end of the list.
<code>clear()</code>	Remove all items from list.
<code>copy()</code>	Return a shallow copy of the list.
<code>count(value, /)</code>	Return number of occurrences of value.
<code>extend(iterable)</code>	Extend list by appending elements from the iterable.
<code>index(value[, start, stop])</code>	Return first index of value.
<code>insert(index, p_object)</code>	Insert object before index.
<code>pop([index])</code>	Remove and return item at index (default last).
<code>remove(value, /)</code>	Remove first occurrence of value.
<code>reverse()</code>	Reverse <i>IN PLACE</i> .
<code>sort(*[, key, reverse])</code>	Sort the list in ascending order and return None.

### **extend(iterable)**

Extend list by appending elements from the iterable.

### **append(p\_object)**

Append object to the end of the list.

### **insert(index, p\_object)**

Insert object before index.

### **copy()**

Return a shallow copy of the list.

### **clear()**

Remove all items from list.

### **count(value, /)**

Return number of occurrences of value.

### **index(value, start=0, stop=9223372036854775807, /)**

Return first index of value.

Raises ValueError if the value is not present.

### **pop(index=- 1, /)**

Remove and return item at index (default last).

Raises IndexError if list is empty or index is out of range.

### **remove(value, /)**

Remove first occurrence of value.

Raises ValueError if the value is not present.

### **reverse()**

Reverse *IN PLACE*.



**sort**(\*, key=None, reverse=False)

Sort the list in ascending order and return None.

The sort is in-place (i.e. the list itself is modified) and stable (i.e. the order of two equal elements is maintained).

If a key function is given, apply it once to each list item and sort them, ascending or descending, according to their function values.

The reverse flag can be set to sort in descending order.

### 13.3.2 ValidatedDict

**class** openff.toolkit.utils.collections.**ValidatedDict**(mapping, converter=None, validator=None)

A dict that runs custom converter and validators when new elements are added.

Multiple converters and validators can be assigned to the dict. These are executed in the given order with converters run before validators.

Validators must take the new element as the first argument and raise an exception if validation fails.

validator(new\_element) -> None

Converters must also take the new element as the first argument, but they have to return the converted value.

converter(new\_element) -> converted\_value

#### Examples

We can define validator and converter functions that are run on each value of the dict.

```
>>> def is_positive_validator(value):
...     if value <= 0:
...         raise TypeError('value must be positive')
...
>>> v1 = ValidatedDict({'a': 1, 'b': -1}, validator=is_positive_validator)
Traceback (most recent call last):
...
TypeError: value must be positive
```

Multiple converters that are run before the validators can be specified.

```
>>> v1 = ValidatedDict({'c': -1, 'd': '2', 'e': 3.0}, converter=[float, abs],
...                    validator=is_positive_validator)
>>> v1
{'c': 1.0, 'd': 2.0, 'e': 3.0}
```

**\_\_init\_\_**(mapping, converter=None, validator=None)

Initialize the dict.

#### Parameters

- **mapping** (Mapping) – A mapping of elements, probably a dict.
- **converter** (callable or List[callable]) – Functions that will be used to convert each new element of the dict.

- **validator** (callable or List[callable]) – Functions that will be used to convert each new element of the dict.

## Methods

<code>__init__(mapping[, converter, validator])</code>	Initialize the dict.
<code>clear()</code>	
<code>copy()</code>	
<code>fromkeys([value])</code>	Create a new dictionary with keys from iterable and values set to value.
<code>get(key[, default])</code>	Return the value for key if key is in the dictionary, else default.
<code>items()</code>	
<code>keys()</code>	
<code>pop(k[,d])</code>	If key is not found, d is returned if given, otherwise <code>KeyError</code> is raised
<code>popitem()</code>	Remove and return a (key, value) pair as a 2-tuple.
<code>setdefault(key[, default])</code>	Insert key with a value of default if key is not in the dictionary.
<code>update([E, ]**F)</code>	If E is present and has a <code>.keys()</code> method, then does: for k in E: <code>D[k] = E[k]</code> If E is present and lacks a <code>.keys()</code> method, then does: for k, v in E: <code>D[k] = v</code> In either case, this is followed by: for k in F: <code>D[k] = F[k]</code>
<code>values()</code>	

**update**(`[E]`, `**F`) → None. Update D from dict/iterable E and F.

If E is present and has a `.keys()` method, then does: for k in E: `D[k] = E[k]` If E is present and lacks a `.keys()` method, then does: for k, v in E: `D[k] = v` In either case, this is followed by: for k in F: `D[k] = F[k]`

**copy**() → a shallow copy of D

**clear**() → None. Remove all items from D.

**fromkeys**(`value=None, /`)

Create a new dictionary with keys from iterable and values set to value.

**get**(`key, default=None, /`)

Return the value for key if key is in the dictionary, else default.

**items**() → a set-like object providing a view on D's items

**keys**() → a set-like object providing a view on D's keys

**pop**(`k[, d]`) → v, remove specified key and return the corresponding value.

If key is not found, d is returned if given, otherwise `KeyError` is raised

**popitem()**

Remove and return a (key, value) pair as a 2-tuple.

Pairs are returned in LIFO (last-in, first-out) order. Raises KeyError if the dict is empty.

**setdefault(key, default=None, /)**

Insert key with a value of default if key is not in the dictionary.

Return the value for key if key is in the dictionary, else default.

**values()** → an object providing a view on D's values

## 13.4 Miscellaneous utilities

Miscellaneous utility functions.

<code>inherit_docstrings</code>	Inherit docstrings from parent class
<code>all_subclasses</code>	Recursively retrieve all subclasses of the specified class
<code>temporary_cd</code>	Context to temporary change the working directory.
<code>get_data_file_path</code>	Get the full path to one of the reference files in test-systems.
<code>convert_0_1_smirnoff_to_0_2</code>	Convert an 0.1-compliant SMIRNOFF dict to an 0.2-compliant one.
<code>convert_0_2_smirnoff_to_0_3</code>	Convert an 0.2-compliant SMIRNOFF dict to an 0.3-compliant one.
<code>get_molecule_parameterIDs</code>	Process a list of molecules with a specified SMIRNOFF ffxml file and determine which parameters are used by which molecules, returning colated results.
<code>unit_to_string</code>	

### 13.4.1 inherit\_docstrings

`openff.toolkit.utils.utils.inherit_docstrings(cls)`

Inherit docstrings from parent class

### 13.4.2 all\_subclasses

`openff.toolkit.utils.utils.all_subclasses(cls)`

Recursively retrieve all subclasses of the specified class

### 13.4.3 temporary\_cd

`openff.toolkit.utils.utils.temporary_cd(dir_path)`

Context to temporary change the working directory.

**Parameters** `dir_path` (`str`) – The directory path to enter within the context

#### Examples

```
>>> dir_path = '/tmp'
>>> with temporary_cd(dir_path):
...     pass # do something in dir_path
```

### 13.4.4 get\_data\_file\_path

`openff.toolkit.utils.utils.get_data_file_path(relative_path)`

Get the full path to one of the reference files in testsystems. In the source distribution, these files are in `openff/toolkit/data/`, but on installation, they're moved to somewhere in the user's python site-packages directory.

**Parameters** `name` (`str`) – Name of the file to load (with respect to the repex folder).

### 13.4.5 convert\_0\_1\_smirnoff\_to\_0\_2

`openff.toolkit.utils.utils.convert_0_1_smirnoff_to_0_2(smirnoff_data_0_1)`

Convert an 0.1-compliant SMIRNOFF dict to an 0.2-compliant one. This involves renaming several tags, adding Electrostatics and ToolkitAM1BCC tags, and separating improper torsions into their own section.

**Parameters** `smirnoff_data_0_1` (`dict`) – Hierarchical dict representing a SMIRNOFF data structure according the the 0.1 spec

**Returns** `smirnoff_data_0_2` – Hierarchical dict representing a SMIRNOFF data structure according the the 0.2 spec

### 13.4.6 convert\_0\_2\_smirnoff\_to\_0\_3

`openff.toolkit.utils.utils.convert_0_2_smirnoff_to_0_3(smirnoff_data_0_2)`

Convert an 0.2-compliant SMIRNOFF dict to an 0.3-compliant one. This involves removing units from header tags and adding them to attributes of child elements. It also requires converting ProperTorsions and ImproperTorsions potentials from “charmm” to “fourier”.

**Parameters** `smirnoff_data_0_2` (`dict`) – Hierarchical dict representing a SMIRNOFF data structure according the the 0.2 spec

**Returns** `smirnoff_data_0_3` – Hierarchical dict representing a SMIRNOFF data structure according the the 0.3 spec

### 13.4.7 `get_molecule_parameterIDs`

`openff.toolkit.utils.utils.get_molecule_parameterIDs(molecules, forcefield)`

Process a list of molecules with a specified SMIRNOFF ffxml file and determine which parameters are used by which molecules, returning collated results.

#### Parameters

- **molecules** (list of `openff.toolkit.topology.Molecule`) – List of molecules (with explicit hydrogens) to parse
- **forcefield** (`ForceField`) – The ForceField to apply

#### Returns

- **parameters\_by\_molecule** (*dict*) – Parameter IDs used in each molecule, keyed by isomeric SMILES generated from provided OEMols. Each entry in the dict is a list which does not necessarily have unique entries; i.e. parameter IDs which are used more than once will occur multiple times.
- **parameters\_by\_ID** (*dict*) – Molecules in which each parameter ID occur, keyed by parameter ID. Each entry in the dict is a set of isomeric SMILES for molecules in which that parameter occurs. No frequency information is stored.

### 13.4.8 `unit_to_string`

`openff.toolkit.utils.utils.unit_to_string(input_unit: Unit) → str`

## 13.5 Exceptions

Exceptions raised by the Toolkit.

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exceptions

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### 13.5.1 `openff.toolkit.utils.exceptions`

#### Exceptions

<code>AntechamberNotFoundError(msg)</code>	The antechamber executable was not found
<code>AtomNotInTopologyError(msg)</code>	An atom was not found in a topology.
<code>BondExistsError(msg)</code>	The program attempted to add a bond that already exists
<code>BondNotInTopologyError(msg)</code>	An bond was not found in a topology.
<code>CallbackRegistrationError(msg)</code>	Error raised when callback registration fails.
<code>ChargeCalculationError(msg)</code>	An unhandled error occurred in an external toolkit during charge calculation
<code>ChargeMethodUnavailableError(msg)</code>	A toolkit does not support the requested <code>partial_charge_method</code> combination
<code>ConformerGenerationError(msg)</code>	Conformer generation via a wrapped toolkit failed.

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Table 1 – continued from previous page

<code>DuplicateParameterError(msg)</code>	Exception raised when trying to add a ParameterType that already exists
<code>DuplicateUniqueMoleculeError(msg)</code>	Exception for when the user provides indistinguishable unique molecules when trying to identify atoms from a PDB
<code>DuplicateVirtualSiteTypeException(msg)</code>	Exception raised when trying to register two different virtual site classes with the same 'type'
<code>FractionalBondOrderInterpolationMethodUnsupported(msg)</code>	Exception when an unsupported fractional bond order interpolation assignment method is called.
<code>GAFFAtomTypeWarning</code>	A warning raised if a loaded mol2 file possibly uses GAFF atom types.
<code>HierarchySchemeNotFoundException(msg)</code>	Exception raised when trying to access a HierarchyScheme from a molecule that doesn't have one with the given iterator name
<code>HierarchySchemeWithIteratorNameAlreadyRegistered(msg)</code>	Exception when trying to add a HierarchyScheme to a molecule that already has one with the same iterator name
<code>IncompatibleParameterError(msg)</code>	Exception for when a set of parameters is scientifically/technically incompatible with another
<code>IncompatibleUnitError(msg)</code>	Exception for when a parameter is in the wrong units for a ParameterHandler's unit system
<code>InconsistentStereochemistryError(msg)</code>	Error raised when stereochemistry is inconsistent before and after conversions between molecule representations.
<code>IncorrectNumConformersError(msg)</code>	The requested <code>partial_charge_method</code> expects a different number of conformers than was provided
<code>IncorrectNumConformersWarning</code>	The requested <code>partial_charge_method</code> expects a different number of conformers than was provided
<code>InvalidAromaticityModelError(msg)</code>	General exception for errors while setting the aromaticity model of a Topology.
<code>InvalidAtomMetadataError(msg)</code>	The program attempted to set atom metadata to an invalid type
<code>InvalidBondOrderError(msg)</code>	Exception for passing a non-int to <code>Molecule.bond_order</code>
<code>InvalidBoxVectorsError(msg)</code>	Exception for setting invalid box vectors
<code>InvalidConformerError(msg)</code>	This error is raised when the conformer added to the molecule has a different connectivity to that already defined.
<code>InvalidIUPACNameError(msg)</code>	Failed to parse IUPAC name
<code>InvalidPeriodicityError(msg)</code>	Exception for setting invalid periodicity
<code>InvalidToolkitError(msg)</code>	A non-toolkit object was received when a toolkit object was expected
<code>InvalidToolkitRegistryError(msg)</code>	An object other than a ToolkitRegistry or toolkit wrapper was received
<code>LicenseError(msg)</code>	This function requires a license that cannot be found.
<code>MissingIndexedAttributeError(msg)</code>	Error raised when an indexed attribute does not exist
<code>MissingPackageError(msg)</code>	This function requires a package that is not installed.

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<code>MissingPartialChargesError(msg)</code>	Error raised when a molecule is missing partial charges in a context in which it is expected to have them.
<code>MissingUniqueMoleculesError(msg)</code>	Exception for when <code>unique_molecules</code> is required but not found
<code>MoleculeNotInTopologyError(msg)</code>	A molecule was not found in a topology.
<code>MultipleMoleculesInPDLError(msg)</code>	Error raised when a multiple molecules are found when one was expected
<code>NotAttachedToMoleculeError(msg)</code>	Exception for when a component does not belong to a <code>Molecule</code> object, but is queried
<code>NotBondedError(msg)</code>	Exception for when a function requires a bond between two atoms, but none is present
<code>NotEnoughPointsForInterpolationError(msg)</code>	Exception for when less than two points are provided for interpolation
<code>NotInTopologyError(msg)</code>	An object was not found in a topology.
<code>OpenFFToolkitException(msg)</code>	Base exception for custom exceptions raised by the OpenFF Toolkit
<code>ParameterHandlerRegistrationError(msg)</code>	Exception for errors in <code>ParameterHandler</code> registration
<code>ParameterLookupError(msg)</code>	Exception raised when something goes wrong in a parameter lookup in <code>ParameterHandler</code> . <code>__getitem__</code>
<code>PartialChargeVirtualSitesError(msg)</code>	Exception thrown when partial charges cannot be computed for a <code>Molecule</code> because the <code>ForceField</code> applies virtual sites.
<code>RadicalsNotSupportedError(msg)</code>	The OpenFF Toolkit does not currently support parsing molecules with radicals.
<code>RemapIndexError(msg)</code>	An error with indices used to remap a molecule
<code>SMILESParseError(msg)</code>	The record could not be parsed into the given format
<code>SMIRKSMismatchError(msg)</code>	Exception for cases where smirks are inappropriate for the environment type they are being parsed into
<code>SMIRKSParsingError(msg)</code>	Exception for when SMIRKS are not parseable for any environment
<code>SMIRNOFFAromaticityError(msg)</code>	Exception thrown when an incompatible SMIRNOFF aromaticity model is checked for compatibility.
<code>SMIRNOFFParseError(msg)</code>	Error for when a SMIRNOFF data structure is not parseable by a <code>ForceField</code>
<code>SMIRNOFFSpecError(msg)</code>	Exception for when data is noncompliant with the SMIRNOFF data specification.
<code>SMIRNOFFSpecUnimplementedError(msg)</code>	Exception for when a portion of the SMIRNOFF specification is not yet implemented.
<code>SMIRNOFFVersionError(msg)</code>	Exception thrown when an incompatible SMIRNOFF version data structure is attempted to be read.
<code>SmilesParsingError(msg)</code>	This error is raised when parsing a SMILES string results in an error.
<code>ToolkitUnavailableException(msg)</code>	The requested toolkit is unavailable.
<code>UnassignedAngleParameterException(msg)</code>	Exception raised when there are angle terms for which a <code>ParameterHandler</code> can't find parameters.

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<code>UnassignedBondParameterException(msg)</code>	Exception raised when there are bond terms for which a <code>ParameterHandler</code> can't find parameters.
<code>UnassignedChemistryInPDBError([msg, ...])</code>	Error raised when a bond or atom in a polymer could not be assigned chemical information.
<code>UnassignedMoleculeChargeException(msg)</code>	Exception raised when no charge method is able to assign charges to a molecule.
<code>UnassignedProperTorsionParameterException(msg)</code>	Exception raised when there are proper torsion terms for which a <code>ParameterHandler</code> can't find parameters.
<code>UnassignedValenceParameterException(msg)</code>	Exception raised when there are valence terms for which a <code>ParameterHandler</code> can't find parameters.
<code>UndefinedStereochemistryError(msg)</code>	A molecule was attempted to be loaded with undefined stereochemistry
<code>UnsupportedFileTypeError(msg)</code>	Error raised when attempting to parse an unsupported file type.
<code>UnsupportedMoleculeConversionError(msg)</code>	Error raised when attempting to instantiate a <code>Molecule</code> with insufficient inputs.
<code>WrongShapeError(msg)</code>	Error raised when an array of the wrong shape is found

**exception** `openff.toolkit.utils.exceptions.OpenFFToolkitException(msg)`

Base exception for custom exceptions raised by the OpenFF Toolkit

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.IncompatibleUnitError(msg)`

Exception for when a parameter is in the wrong units for a `ParameterHandler`'s unit system

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.MissingPackageError(msg)`

This function requires a package that is not installed.

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.ToolkitUnavailableException(msg)`

The requested toolkit is unavailable.

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.LicenseError(msg)`

This function requires a license that cannot be found.

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.InvalidToolkitError(msg)`

A non-toolkit object was received when a toolkit object was expected

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.



**exception** `openff.toolkit.utils.exceptions.InvalidToolkitRegistryError(msg)`  
An object other than a ToolkitRegistry or toolkit wrapper was received

**with\_traceback()**  
Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.UndefinedStereochemistryError(msg)`  
A molecule was attempted to be loaded with undefined stereochemistry

**with\_traceback()**  
Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.GAFFAtomTypeWarning`  
A warning raised if a loaded mol2 file possibly uses GAFF atom types.

**with\_traceback()**  
Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.ChargeMethodUnavailableError(msg)`  
A toolkit does not support the requested partial\_charge\_method combination

**with\_traceback()**  
Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.IncorrectNumConformersError(msg)`  
The requested partial\_charge\_method expects a different number of conformers than was provided

**with\_traceback()**  
Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.IncorrectNumConformersWarning`  
The requested partial\_charge\_method expects a different number of conformers than was provided

**with\_traceback()**  
Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.ChargeCalculationError(msg)`  
An unhandled error occurred in an external toolkit during charge calculation

**with\_traceback()**  
Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.ConformerGenerationError(msg)`  
Conformer generation via a wrapped toolkit failed.

**with\_traceback()**  
Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.InvalidIUPACNameError(msg)`  
Failed to parse IUPAC name

**with\_traceback()**  
Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.AntechamberNotFoundError(msg)`  
The antechamber executable was not found

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**SMILESParseError**(msg)

The record could not be parsed into the given format

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**RadicalsNotSupportedError**(msg)

The OpenFF Toolkit does not currently support parsing molecules with radicals.

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**InvalidConformerError**(msg)

This error is raised when the conformer added to the molecule has a different connectivity to that already defined. or any other conformer related issues.

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**SmilesParsingError**(msg)

This error is raised when parsing a SMILES string results in an error.

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**NotAttachedToMoleculeError**(msg)

Exception for when a component does not belong to a Molecule object, but is queried

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**NotInTopologyError**(msg)

An object was not found in a topology.

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**RemapIndexError**(msg)

An error with indices used to remap a molecule

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**AtomNotInTopologyError**(msg)

An atom was not found in a topology.

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**BondNotInTopologyError**(msg)

An bond was not found in a topology.

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.MoleculeNotInTopologyError(msg)`

A molecule was not found in a topology.

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.InvalidAtomMetadataError(msg)`

The program attempted to set atom metadata to an invalid type

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.BondExistsError(msg)`

The program attempted to add a bond that already exists

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.DuplicateUniqueMoleculeError(msg)`

Exception for when the user provides indistinguishable unique molecules when trying to identify atoms from a PDB

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.NotBondedError(msg)`

Exception for when a function requires a bond between two atoms, but none is present

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.InvalidBondOrderError(msg)`

Exception for passing a non-int to *Molecule.bond\_order*

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.InvalidBoxVectorsError(msg)`

Exception for setting invalid box vectors

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.InvalidPeriodicityError(msg)`

Exception for setting invalid periodicity

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.MissingUniqueMoleculesError(msg)`

Exception for when unique\_molecules is required but not found

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.SMIRKSMismatchError(msg)`

Exception for cases where smirks are inappropriate for the environment type they are being parsed into

**with\_traceback()**  
Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**SMIRKSParsingError**(msg)  
Exception for when SMIRKS are not parseable for any environment

**with\_traceback()**  
Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**ParameterHandlerRegistrationError**(msg)  
Exception for errors in ParameterHandler registration

**with\_traceback()**  
Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**SMIRNOFFVersionError**(msg)  
Exception thrown when an incompatible SMIRNOFF version data structure is attempted to be read.

**with\_traceback()**  
Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**SMIRNOFFAromaticityError**(msg)  
Exception thrown when an incompatible SMIRNOFF aromaticity model is checked for compatibility.

**with\_traceback()**  
Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**InvalidAromaticityModelError**(msg)  
General exception for errors while setting the aromaticity model of a Topology.

**with\_traceback()**  
Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**SMIRNOFFParseError**(msg)  
Error for when a SMIRNOFF data structure is not parseable by a ForceField

**with\_traceback()**  
Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**PartialChargeVirtualSitesError**(msg)  
Exception thrown when partial charges cannot be computed for a Molecule because the ForceField applies virtual sites.

**with\_traceback()**  
Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**SMIRNOFFSpecError**(msg)  
Exception for when data is noncompliant with the SMIRNOFF data specification.

**with\_traceback()**  
Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**SMIRNOFFSpecUnimplementedError**(msg)  
Exception for when a portion of the SMIRNOFF specification is not yet implemented.

**with\_traceback()**  
Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.FractionalBondOrderInterpolationMethodUnsupportedError(msg)`  
Exception for when an unsupported fractional bond order interpolation assignment method is called.

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.NotEnoughPointsForInterpolationError(msg)`

Exception for when less than two points are provided for interpolation

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.IncompatibleParameterError(msg)`

Exception for when a set of parameters is scientifically/technically incompatible with another

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.UnassignedValenceParameterException(msg)`

Exception raised when there are valence terms for which a ParameterHandler can't find parameters.

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.UnassignedBondParameterException(msg)`

Exception raised when there are bond terms for which a ParameterHandler can't find parameters.

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.UnassignedAngleParameterException(msg)`

Exception raised when there are angle terms for which a ParameterHandler can't find parameters.

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.UnassignedProperTorsionParameterException(msg)`

Exception raised when there are proper torsion terms for which a ParameterHandler can't find parameters.

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.UnassignedMoleculeChargeException(msg)`

Exception raised when no charge method is able to assign charges to a molecule.

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.DuplicateParameterError(msg)`

Exception raised when trying to add a ParameterType that already exists

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.ParameterLookupError(msg)`

Exception raised when something goes wrong in a parameter lookup in ParameterHandler.\_\_getitem\_\_

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**DuplicateVirtualSiteTypeException**(msg)

Exception raised when trying to register two different virtual site classes with the same ‘type’

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**CallbackRegistrationError**(msg)

Error raised when callback registration fails.

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**HierarchySchemeWithIteratorNameAlreadyRegisteredException**(msg)

Exception raised when trying to add a HierarchyScheme to a molecule that already has one with the same iterator name

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**HierarchySchemeNotFoundException**(msg)

Exception raised when trying to access a HierarchyScheme from a molecule that doesn’t have one with the given iterator name

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**MissingIndexedAttributeError**(msg)

Error raised when an indexed attribute does not exist

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**MissingPartialChargesError**(msg)

Error raised when a molecule is missing partial charges in a context in which it is expected to have them.

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**UnsupportedMoleculeConversionError**(msg)

Error raised when attempting to instantiate a Molecule with insufficient inputs.

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**InconsistentStereochemistryError**(msg)

Error raised when stereochemistry is inconsistent before and after conversions between molecule representations.

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**UnsupportedFileTypeError**(msg)

Error raised when attempting to parse an unsupported file type.

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**MultipleMoleculesInPDBError**(msg)

Error raised when a multiple molecules are found when one was expected

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**WrongShapeError**(msg)

Error raised when an array of the wrong shape is found

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**UnassignedChemistryInPDBError**(msg: *Optional*[*str*] = *None*, substructure\_library: *Optional*[*Dict*[*str*, *Tuple*[*str*, *List*[*str*]]]] = *None*, omm\_top: *Optional*[*OpenMMTopology*] = *None*, unassigned\_bonds: *Optional*[*List*[*Tuple*[*int*, *int*]]] = *None*, unassigned\_atoms: *Optional*[*List*[*int*]] = *None*, matches: *Optional*[*DefaultDict*[*int*, *List*[*str*]]] = *None*)

Error raised when a bond or atom in a polymer could not be assigned chemical information.

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.





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