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# OpenFF Toolkit Documentation

*Release 0.15.0+0.gb824475.dirty*

Open Force Field Consortium

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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 mamba

The simplest way to install the Open Force Field Toolkit is via [Mamba](#), a drop-in replacement for the [Conda](#) package manager. We publish [packages](#) via [conda-forge](#). With Mamba installed, use it to install the OpenFF Toolkit into a new environment:

```
$ mamba create -n openff-toolkit -c conda-forge openff-toolkit
```

To use the new environment in a shell session, you must first activate it:

```
$ mamba activate openff-toolkit
```

If you do not have Mamba or Conda installed, see the *ecosystem installation documentation*.

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**Note:** Installation via the Mamba package manager is the recommended 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.

### 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 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 “built-in” 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](#).

### 1.3.1 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.

### 1.3.2 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.

### 1.3.3 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:

```
$ mamba install -c openeye 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.



### 1.3.4 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 attribute:

```
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

For users: These examples are best viewed at our [centralized documentation page](#), where you will find a variety of ways to view and run the notebooks.

For developers: The following examples live in [the OpenFF toolkit repository](#).

### 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 0.15.0

This release adds compatibility with QCFractal  $\geq 0.50.0$ , but removes compatibility with QCFractal  $< 0.50.0$ .

#### 3.1.1 API-breaking changes

- [PR #1760](#): Removes the private, unused `ParameterHandler._OPENMMTYPE` attribute.
- [PR #1763](#): Updates the OpenFF Toolkit to be compatible with QCFractal  $\geq 0.50$ . Removes the client named argument from `Molecule.from_qcschema`.

#### 3.1.2 Behavior changes

#### 3.1.3 Bugfixes

- [PR #1778](#): Ensures SD data tags are preserved in `Molecule.from_openeye` if the input is of type `oechem.OEGraphMol`.
- [PR #1811](#): Preserves hierarchy data in `_SimpleMolecule.from_molecule`

#### 3.1.4 New features

- [PR #1775](#): Re-exports `openff.units.unit` and `Quantity` at `openff.toolkit.unit` and `Quantity`.
- [PR #1805](#): Adds `_SimpleMolecule.__deepcopy__` and `_SimpleMolecule.to_topology`.

### 3.1.5 Improved documentation and warnings

- [PR #1732](#): Add documentation describing the use of PDB files with the toolkit.
- [PR #1804](#): Makes `ForceField.parse_sources` docstring consistent with implementation.

## 3.2 0.14.5

### 3.2.1 Bugfixes

- [PR #1740](#): Updates for Mypy 1.6.
- [PR #1749](#): Updates versioneer for Python 3.12 compatibility.
- [PR #1756](#): Fixes issue [#1739](#), where virtual sites would be double-created under some circumstances.

### 3.2.2 New features

- [PR #1731](#): Support SMIRNOFF vdW version 0.5.

### 3.2.3 Improved documentation and warnings

- [PR #1747](#): Warns if a SMILES with full atom mappings is passed to `Molecule.from_smiles`, which does not use the atom map for atom ordering (`Molecule.from_mapped_smiles` does).
- [PR #1743](#): Uses a longer stride in OpenMM DCD reporter in the toolkit showcase and should better utilize GPU resources, if available.
- [PR #1744](#): Updates the virtual site notebook to use new Interchange behavior.

## 3.3 0.14.4

### 3.3.1 Behavior changes

- [PR #1705](#): Do not raise warning when `allow_undefined_stereo=True`.
- [PR #1695](#): `ChemicalEnvironmentParsingError` is now raised when an underlying toolkit fails to parse a SMARTS/SMIRKS pattern it is given during substructure matching.
- [PR #1716](#): Adds deprecation warnings to `Molecule.from_polymer_pdb`, `Molecule.from_pdb_and_smiles`, and `RDKitToolkitWrapper.from_pdb_and_smiles` instead pointing users toward `Topology.from_pdb`.

### 3.3.2 Bugfixes

- [PR #1726](#): Fix error message in setting `scale12`, `scale13`, and `scale15` attributes.
- [PR #1728](#): Adds support for loading deprotonated cysteine (sometimes labeled as “CYM”) residues in `Topology.from_pdb`

### 3.3.3 New features

- [PR #1733](#): Makes `NAGLToolkitWrapper` and its associated module public.
- [PR #1698](#): Makes `openff.toolkit.utils.toolkit_registry.toolkit_registry_manager` public.
- [PR #1662](#): Adds hierarchy scheme iterators to `Topology`, i.e. `Topology.residues`, when schemes of the same iterator name are defines on all constituent `Molecules`.
- [PR #1700](#): Use `openff-nagl v0.3.0`.
- [PR #1623](#): Adds `Topology.visualize`.

### 3.3.4 Improved documentation and warnings

- [PR #1709](#): Update molecule cookbook to use the maximally capable `Topology.from_pdb` in lieu of the more limited `Molecule.from_pdb_and_smiles` and `Molecule.from_polymer_pdb`.
- [PR #1719](#): Remove out-of-date and unused `examples/environment.yaml` and various examples updates.

## 3.4 0.14.3

### 3.4.1 Bugfixes

- [PR #1689](#): Fixes [#1688](#) in which automatic up-conversion of version 0.3 of `vdwHandler` created via the Python API errored out if method was not specified.
- [PR #1690](#): Fixes a circular-import bug that occurs when attempting to print a “no cheminformatics toolkits available” warning.

## 3.5 0.14.2

### 3.5.1 Behavior changes

- [PR #1679](#): Version 0.3 `<vdw>` sections of OFFXML files will automatically be up-converted (in memory) to version 0.4 according to the recommendations provided in [OFF-EP 0008](#).

### 3.5.2 New features

- [PR #1631](#): Adds support for Python 3.11.

## 3.6 0.14.1

### 3.6.1 API-breaking changes

- [PR #1664](#): Removes `ChemicalEnvironment` and the entire `openff.toolkit.typing.chemistry` sub-module, which was deprecated in 0.12.0.

### 3.6.2 Behavior changes

- [PR #1675](#): Makes InChI parsing failures more informative and gives them their own exception type, `InChIParseError`.

### 3.6.3 New features

- [PR #1627](#): (beta release of major new feature by @connordavel) Adds experimental support for custom substructure loading in `Topology.from_pdb`, via the `_custom_substructures` keyword argument. This will be added to the public API (by removing the leading underscore) in a future feature release, but is available for testing now. This feature should allow for easier loading of modified amino acids, nucleic acids, and other polymers.

### 3.6.4 Bugfixes

- [PR #1662](#): Fixes issue [#1660](#) by forbidding the registration of `HierarchySchemes` with iterator names that conflict with existing `Molecule` attributes.
- [PR #1667](#): A more helpful exception is now raised when `Topology.from_openmm` is given an OpenMM `Topology` with virtual sites.

### 3.6.5 Examples updated

- [PR #1671](#): Re-rendered all examples using RDKit+AmberTools backend, and using most recent version of OFF Toolkit.

### 3.6.6 Improved documentation and warnings

## 3.7 0.14.0

### 3.7.1 API-breaking changes

- [PR #1649](#): Removes tests and associated modules from the public API.



- [PR #1508](#): Removes the `return_topology kwarg` from `ForceField.create_openmm_system` which was [deprecated in version 0.11.0](#). To access the Topology that results from parametrization, call `ForceField.create_interchange` and access the `.topology` attribute of the returned Interchange object.
- [PR #1506](#): Removes several classes and properties in the topology submodule that were [deprecated in version 0.11.0](#).

### 3.7.2 Behavior changes

- [PR #1652](#): Fixes issue [#1642](#) by making `AmberToolsToolkitWrapper` thread-safe (previously `AmberToolsToolkitWrapper.assign_partial_charges` and `assign_fractional_bond_orders` were not)

### 3.7.3 Bugfixes

- [PR #1654](#): Fixes issue [#1653](#), where a test that expected RDKit to fail began returning an error when RDKit became able to generate conformers for octahedral molecules.

### 3.7.4 Improved documentation and warnings

- [PR #1572](#): Improved installation guide in line with ecosystem docs.

### 3.7.5 Examples updated

- [PR #1644](#): Streamlines several examples by using `Interchange.to_openmm_simulation`.
- [PR #1651](#): Fix broken links in several examples.
- [PR #1648](#): Update examples to use `Topology.from_pdb` and other small cleanups.

## 3.8 0.13.2

### 3.8.1 Bugfixes

- [PR #1640](#): Fixes issue [#1633](#) in which some force field attributes were erroneously parsed as `Quantity` objects and issue [#1635](#) in which OpenFF 2.1.0 (“Sage”) could not be loaded with Pint 0.22.

### 3.8.2 Improved documentation and warnings

- [PR #1636](#) and [PR #1643](#): Make the Molecule Cookbook and `Molecule.from_qcschema` docstring only pull down QCF records with fully defined stereo.

## 3.9 0.13.1

### 3.9.1 Behavior changes

- [PR #1619](#): Fixes **silent error #1618**, by making `partial_charges.setter` more comprehensive in type and shape checking.

### 3.9.2 Bugfixes

- [PR #1617](#): Fixes [#1616](#), by converting NAGL charges to float and converting `partial_charges` to float before converting to `_openeye()`
- [PR #1622](#): Fixes [#1621](#) and [#1346](#) in which some file-loading methods would fail on `pathlib.Path`.

## 3.10 0.13.0

### 3.10.1 New features

- [PR #1567](#): Allows setting `Molecule.name` in `Molecule.from_smiles`, `from_inchi`, `from_polymer_pdb`, and `from_pdb_and_smiles`.
- [PR #1565](#): Adds `Topology.from_pdb`.

### 3.10.2 Behavior changes

- [PR #1569](#): Several instances of `Exception` being raised are now replaced with other exceptions being raised.
- [PR #1577](#): Drops support for Python 3.8, following [NEP-29](#).

### 3.10.3 Bugfixes

- [PR #1589](#): Fixes [Issue #1579](#), where `Molecule.from_polymer_pdb` could not handle `NH2` caps at C termini.
- [PR #1591](#): Fixes [#1563](#), where `from_rdkit` would sometimes raise an error about radicals if a molecule using a non-MDL aromaticity model was provided.

### 3.10.4 Improved documentation and warnings

- [PR #1564](#): Improve documentation of conformer selection in `Molecule.assign_partial_charges()`
- [PR #1574](#): Fix class method signature rendering throughout API docs
- [PR #1584](#): Update some outdated docstrings and add some annotations.

### 3.10.5 Examples updates

- [PR #1575](#): The Toolkit Showcase example has been simplified via use of `Topology.from_pdb`

## 3.11 0.12.1

### 3.11.1 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.

### 3.11.2 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.

### 3.11.3 Bugfixes

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

### 3.11.4 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").

## 3.12 0.12.0

### 3.12.1 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.

### 3.12.2 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.

### 3.12.3 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.

### 3.12.4 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`.

## 3.13 0.11.4 Bugfix release

### 3.13.1 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.

### 3.13.2 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`.

## 3.14 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.

### 3.14.1 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.

### 3.14.2 Examples updates

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

### 3.14.3 Improved documentation and warnings

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

### 3.14.4 Miscellaneous

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

## 3.15 0.11.2 Bugfix release

### 3.15.1 Behavior changes

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

### 3.15.2 Bug fixes

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

### 3.15.3 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.

## 3.16 0.11.1 Minor release forbidding loading radicals

### 3.16.1 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.

### 3.16.2 Examples changed

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

### 3.16.3 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()`

## 3.17 0.11.0 Major release adding support for proteins and refactoring the Topology class.

## 3.18 Migration guide

### 3.18.1 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.

### 3.18.2 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()
```

### 3.18.3 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)
```

### 3.18.4 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)
```

### 3.18.5 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`.

### 3.18.6 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)

### 3.18.7 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.

### 3.18.8 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`.

### 3.18.9 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
```

### 3.18.10 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.

### 3.18.11 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.

### 3.18.12 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
```

### 3.18.13 Breaking change: `MissingDependencyError` renamed `MissingPackageError`

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

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

### 3.18.14 `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')
```

### 3.18.15 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` 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.

### 3.18.16 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

### 3.18.17 Tests updated

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

## 3.19 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.

## 3.20 0.10.4 Bugfix release

### 3.20.1 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.

## 3.21 0.10.3 Bugfix release

### 3.21.1 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.

### 3.21.2 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.



### 3.21.3 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.

### 3.21.4 Behaviors changed and bugfixes

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

### 3.21.5 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.

### 3.21.6 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.

## 3.22 0.10.2 Bugfix release

### 3.22.1 API-breaking changes

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

### 3.22.2 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 file 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.

### 3.22.3 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.

### 3.22.4 Examples added

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

## 3.23 0.10.1 Minor feature and bugfix release

### 3.23.1 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`.

### 3.23.2 Tests updated

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

### 3.23.3 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.

## 3.24 0.10.0 Improvements for force field fitting

### 3.24.1 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.

### 3.24.2 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.

### 3.24.3 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.

### 3.24.4 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!

### 3.24.5 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.

## 3.25 0.9.2 Minor feature and bugfix release

### 3.25.1 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`.

### 3.25.2 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.

### 3.25.3 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.

## 3.26 Earlier releases

## 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 mamba/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 environment, explicitly passing the channels to be used, in-order:

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

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

## 4.10 My mamba/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 an `Interchange` for painless conversion to other 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.

```
from openff.toolkit import Molecule, Topology
```

### 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-ordinate 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)

# First index is the Nitrogen
assert mapped_smiles.atoms[0].atomic_number == 7

# Final indices are all H
assert all([a.atomic_number == 1 for a in mapped_smiles.atoms[6:]])

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:

```
from openff.toolkit.utils.exceptions import UndefinedStereochemistryError

try:
    smiles_non_isomeric = Molecule.from_smiles("CC([NH3+])C(=O)[O-]")
except UndefinedStereochemistryError as error:
    print(error)
```

```
Unable to make OFFMol from OEMol: OEMol has unspecified stereochemistry. oemol.GetTitle()='
    ↪'Problematic atoms are:
```

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```
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
```

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()
```

```
<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
    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")
```

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```

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,

```

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```

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

from_dictionary = Molecule.from_dict(molecule_dict)

from_dictionary.visualize()

<IPython.core.display.SVG object>

```

## 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()
```

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

### 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()
```

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

### 6.3.3 From PDB file

The `Topology.from_pdb()` method is now the recommended method for loading all PDB files. It can interpret proteins, waters, ions, and small molecules from a PDB file as a `Topology`. 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 input PDB file. The following block loads a PDB file containing a single protein.

```
from openff.toolkit.utils import get_data_file_path

path = get_data_file_path("proteins/T4-protein.pdb")
topology = Topology.from_pdb(path)
protein = topology.molecule(0)
protein.visualize("nglview")
```

```
NGLWidget()
```

The following block loads a PDB containing two small molecules from PDB and SMILES.

```
top_from_pdb_from_smiles = Topology.from_pdb(
    get_data_file_path("molecules/po4_phenylphosphate.pdb"),
    unique_molecules=[
        Molecule.from_smiles("P(=O)([O-])([O-])([O-])"),
        Molecule.from_smiles("C1=CC=CC=C1OP(=O)([O-])([O-])"),
    ],
)

top_from_pdb_from_smiles.molecule(0).visualize("nglview")
```

```
NGLWidget()
```

```
top_from_pdb_from_smiles.molecule(1).visualize("nglview")
```

```
NGLWidget()
```

And for a maximalist example, the following block loads a single PDB file containing a protein, waters, ions, and a small molecule (the chemical identity of any small molecules must be provided with the `unique_molecules` keyword argument, and any small molecules' connectivity must have corresponding CONECT records in the PDB file).

```
from openff.toolkit.utils import get_data_file_path

ligand_path = get_data_file_path("molecules/PT2385.sdf")
ligand = Molecule.from_file(ligand_path)

complex_path = get_data_file_path("proteins/5tbm_complex_solv_box.pdb")
topology = Topology.from_pdb(complex_path, unique_molecules=[ligand])

molecule_smilesees = [mol.to_smiles() for mol in topology.molecules]
counts = molecule_smilesees
for smiles in sorted(set(molecule_smilesees)):
    count = molecule_smilesees.count(smiles)
    if len(smiles) > 1000:
        smiles = "protein"
    print(smiles, ":", count, "molecule(s)")
```

```
[Cl-] : 12 molecule(s)
[H]O[H] : 4413 molecule(s)
protein : 1 molecule(s)
[H]c1c(c(c2c(c10c3c(c(c(c3[H])F)[H])C
→#N)[H])C(C([C@@]2([H])O[H])(F)F)([H])[H])S(=O)(=O)C([H])([H])[H])[H] : 1 molecule(s)
[Na+] : 17 molecule(s)
```

## 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-/m0/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, # Note these two mappings,
        4: 3, # which are flipped!
        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_mdtraj(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 PortalClient

client = PortalClient("https://api.qcarchive.molssi.org:443/")

record = [*client.query_molecules(molecular_formula="C16H20N3O5")][-1]

from_qcarchive = Molecule.from_qcschema(record)

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_dataset(
    dataset_type="optimization",
    dataset_name="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>
```

## COOKBOOK: USING PDB FILES WITH THE OPENFF TOOLKIT

PDB files are a common way to represent biopolymer structures, but they don't natively contain all of the chemical information required to construct Molecule objects. However, PDB files are used widely in the molecular simulation community, so OpenFF has implemented functionality to load them.

The recommended pathway for loading PDB files is `Topology.from_pdb`. Additionally, the PDB file must have the following characteristics:

For protein atoms (ATOM records):

- Atom names and residue names must be consistent with the [Chemical Components Dictionary](#)
- Only the 20 canonical amino acids are supported by default (including protonated/deprotonated variants)
- All hydrogens must be explicit

For small molecules, waters, and ions (HETATM records):

- The elemental symbol of each atom must be identified [according to the PDB spec](#) in text columns 77 and 78
- Bonds must be identified in the CONECT records at the bottom of the file
- All unique small molecules must be identified in the `unique_molecules` keyword argument

---

### Information

OpenFF Topology and Molecule objects store much more information than is in the PDB files they might be generated from. Don't be surprised if this Python code takes a few more seconds to load a PDB file than other tools.

---

## 7.1 PDB file with only a (single) protein

`6hvi_prepared.pdb` is protein from the [Merck free energy perturbation study](#). It was prepared for simulation using commercial tools by Schrodinger, and doesn't have any bulk water, ions, small molecules, or a box.

```
protein = Topology.from_pdb("6hvi_prepared.pdb")  
  
protein.visualize()
```

```
NGLWidget()
```

From here, you might use Packmol or PDBFixer to add water or other solvents without leaving Python (or there are tools available for water/solvent packing in AMBER, GROMACS, and many commercial packages). An example of using PDBFixer can be found in our “[Toolkit Showcase](#)” [example](#).

## 7.2 PDB file with a protein, waters, and ions

This PDB file comes from the [AMBER tutorial on making solvated simulations](#). We have slightly modified the procedure to create a file suitable for loading into the OpenFF Toolkit:

- TIP3P water is used instead of OPC (a four-site model)
- a cubic solvent box is used instead of an octohedron
- the N terminus of the protein is made neutral

```
ramp1 = Topology.from_pdb("RAMP1_solv_box_ions.pdb")
ramp1.visualize()
```

```
NGLWidget()
```

## 7.3 PDB file with one or more ligands

The following PDB is taken from the [GROMACS protein-ligand tutorial](#) (with manually-added CONECT records) and contains a protein, water, and a small molecule (ligand).

While the chemistry of water, ions, and proteins can be deduced from known templates (this is what happened under the hood in the previous two examples), small molecules are trickier. The number of amino acids and ions is relatively small, but the number of possible small molecules is tremendous so storing them in a database is not feasible. We instead ask the user to fill in the missing information that would be looked up from the CCD or hard-coded heuristics, specifically the bond order and stereochemistry. This information is stored in a `Molecule` object(s), which we ask the user to provide via the `unique_molecules` argument.

If you try to load a PDB file containing a small molecule, without providing the chemistry of the small molecule, you’ll get an error message identifying the atoms that couldn’t be loaded:

```
Topology.from_pdb("gromacs_solv_complex.pdb")
```

```
UnassignedChemistryInPDBError: Some bonds or atoms in the input could not be identified.
```

```
Hint: The following residue names with unassigned atoms were not found in the substructure_
↳ library. While the OpenFF Toolkit identifies residues by matching chemical substructures_
↳ rather than by residue name, it currently only supports the 20 'canonical' amino acids.
    JZ4
```

```
Hint: The following residues were assigned names that do not match the residue name in the_
↳ input, or could not be assigned residue names at all. This may indicate that atoms are_
↳ missing from the input or some other error. The OpenFF Toolkit requires all atoms,_
```

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```

↳including hydrogens, to be explicit in the input to avoid ambiguities in protonation state.
↳or bond order:
    Input residue X:JZ4#0001 contains atoms matching substructures {'No match'}

Error: The following 22 atoms exist in the input but could not be assigned chemical
information from the substructure library:
    Atom 2614 (C4) in residue X:JZ4#0001
    Atom 2615 (C7) in residue X:JZ4#0001
    Atom 2616 (C8) in residue X:JZ4#0001
    Atom 2617 (C9) in residue X:JZ4#0001
    Atom 2618 (C10) in residue X:JZ4#0001
    Atom 2619 (C11) in residue X:JZ4#0001
    Atom 2620 (C12) in residue X:JZ4#0001
    Atom 2621 (C13) in residue X:JZ4#0001
    Atom 2622 (C14) in residue X:JZ4#0001
    Atom 2623 (OAB) in residue X:JZ4#0001
    Atom 2624 (H1) in residue X:JZ4#0001
    Atom 2625 (H2) in residue X:JZ4#0001
    Atom 2626 (H3) in residue X:JZ4#0001
    Atom 2627 (H4) in residue X:JZ4#0001
    Atom 2628 (H5) in residue X:JZ4#0001
    Atom 2629 (H6) in residue X:JZ4#0001
    Atom 2630 (H7) in residue X:JZ4#0001
    Atom 2631 (H8) in residue X:JZ4#0001
    Atom 2632 (H9) in residue X:JZ4#0001
    Atom 2633 (H10) in residue X:JZ4#0001
    Atom 2634 (H11) in residue X:JZ4#0001
    Atom 2635 (H12) in residue X:JZ4#0001

```

Any OpenFF Molecule object with the appropriate atoms and connectivity can be used to identify the small molecule when loading the PDB file. See the Molecule Cookbook for some of the numerous ways to create them! Since the coordinates are specified in the PDB file, it's not necessary that this Molecule has conformers.

In this case we know the identity of the ligand and can look up a SMILES string, which is all that's needed to load this PDB file! Since there are many molecules in this file, it may take a few tens of seconds to load and visualize - this is expected and is a result of carefully checking and applying chemical information.

```

jz4 = Molecule.from_smiles("CCCC1=CC=CC=C1O")
complex = Topology.from_pdb("gromacs_solv_complex.pdb", unique_molecules=[jz4])

complex.visualize()

```

```

NGLWidget()

```



## SMIRNOFF (SMIRKS NATIVE OPEN FORCE FIELD)

### 8.1 The SMIRNOFF specification

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

### 8.2 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’.

### 9.1 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.

## 9.2 Ordering of atoms and virtual sites

The OpenFF Toolkit and Interchange currently add all new virtual particles to the "end" of a Topology, such that the particle indices of all newly-created virtual particles are higher than index of the last atom.

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 parents 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

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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.

## 10.1 Overview

### 10.1.1 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.

### 10.1.2 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.

## 10.1.3 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.

## 10.2 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.

### 10.2.1 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.

## 10.2.2 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.

### 10.2.3 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`.

### 10.2.4 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.

## 10.3 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.

### 10.3.1 Setting up a development environment

1. Install the mamba package manager as part of the [Miniforge or Mambaforge distributions](#) (an alternative to the [Anaconda Distribution](#))
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
mamba env create -n openff-dev -f devtools/conda-envs/test_env.yaml
mamba activate openff-dev
```

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```
# 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
mamba env update --name openff-dev --file docs/environment.yml
mamba install --name openff-dev -c conda-forge sphinx-autobuild
```

To build the documentation from scratch:

```
# Build the documentation
# From the openff-toolkit root directory
mamba 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
mamba activate openff-dev
sphinx-autobuild docs docs/_build/html --watch openff
# Then navigate your web browser to http://localhost:8000
```

## 10.3.2 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:

```
mamba install black isort flake8 -c conda-forge
black openff
isort openff
flake8 openff
```

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

### 10.3.3 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:

```
mamba 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.

You can also manually run all hooks outside of commit time with

```
pre-commit run
```

or an individual hook by name, i.e.

```
pre-commit run flake8
```

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.

## 10.4 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.

## 10.5 Supported Python versions

The OpenFF Toolkit roughly follows [NEP 29](#). As of April 2023 this means Python 3.9-3.10 are officially supported (3.11 is missing some upstream dependencies). 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:

## MOLECULE CONVERSION TO OTHER PACKAGES

Molecule conversion spec

### 11.1 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.









## 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](#)).

### 12.1 Primary objects

### 12.2 Secondary objects



## FORCE FIELD TYPING TOOLS

### 13.1 Force field typing engines

Engines for applying parameters to chemical systems

#### 13.1.1 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: str =  
    DEFAULT_AROMATICITY_MODEL,  
    parameter_handler_classes=None,  
    parameter_io_handler_classes=None,  
    disable_version_check: bool = False,  
    allow_cosmetic_attributes: bool = False,  
    load_plugins: bool = False)
```

A factory that assigns SMIRNOFF parameters to a molecular system

`ForceField` is a factory that constructs an OpenMM `System` object from a 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.toolkit 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: str = DEFAULT_AROMATICITY_MODEL,
        parameter_handler_classes=None, parameter_io_handler_classes=None,
        disable_version_check: bool = False, allow_cosmetic_attributes: bool = False, load_plugins:
        bool = 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)
```

### See also:

[parse\\_sources](#)



## 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** (iterable of string or file-like object or open file handle or URL) – An iterable 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, *, 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) → openmm.System`

Create an OpenMM System from this ForceField and a Topology.

Note that most force fields specify their own partial charges, and any partial charges defined on the `Molecule` objects in the topology are ignored. To use custom partial charges, see the `charge_from_molecules` argument.

#### 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.

```
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** (`openff.toolkit.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** (`openff.toolkit.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), ... ]`.

**get\_partial\_charges**(*molecule*: *Molecule*, *\*\*kwargs*) → 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** (`openff.units.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`.

<code>ParameterType</code>	Base class for SMIRNOFF parameter types.
<code>ConstraintType</code>	A SMIRNOFF constraint type
<code>BondType</code>	A SMIRNOFF bond type
<code>AngleType</code>	A SMIRNOFF angle type.
<code>ProperTorsionType</code>	A SMIRNOFF torsion type for proper torsions.
<code>ImproperTorsionType</code>	A SMIRNOFF torsion type for improper torsions.
<code>vdWType</code>	A SMIRNOFF vdWForce type.
<code>LibraryChargeType</code>	A SMIRNOFF Library Charge type.
<code>GBSAType</code>	A SMIRNOFF GBSA type.
<code>ChargeIncrementType</code>	A SMIRNOFF bond charge correction type.
<code>VirtualSiteType</code>	

## ParameterType

```
class openff.toolkit.typing.engines.smirnoff.parameters.ParameterType(smirks, al-
                                                                    low_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
... )
>>> 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")
... 
```

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```

...     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)
...     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.

### ConstraintType

```
class openff.toolkit.typing.engines.smirnoff.parameters.ConstraintType(smirks, allow_cosmetic_attributes=False, **kwargs)
```

A SMIRNOFF constraint type

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

**\_\_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>distance</code>
<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 serializaion

#### Returns

**smirnoff\_dict** (*dict*) – The SMIRNOFF-compliant dict representation of this object.

### BondType

**class** openff.toolkit.typing.engines.smirnoff.parameters.**BondType**(\*\**kwargs*)

A SMIRNOFF bond type

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

**\_\_init\_\_**(\*\**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__(**kwargs)</code>	Create a <code>ParameterType</code> .
<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>k</code>
<code>k_bondorder</code>
<code>length</code>
<code>length_bondorder</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 serializaion

**Returns**

**smirnoff\_dict** (*dict*) – The SMIRNOFF-compliant dict representation of this object.

**AngleType**

```
class openff.toolkit.typing.engines.smirnoff.parameters.AngleType(smirks, allow_cosmetic_attributes=False, **kwargs)
```

A SMIRNOFF angle type.

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

**\_\_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>angle</code>
<code>id</code>
<code>k</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.

### ProperTorsionType

**class** openff.toolkit.typing.engines.smirnoff.parameters.**ProperTorsionType**(*smirks, allow\_cosmetic\_attributes=False, \*\*kwargs*)

A SMIRNOFF torsion type for proper torsions.

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

**\_\_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>idivf</code>
<code>k</code>
<code>k_bondorder</code>
<code>parent_id</code>
<code>periodicity</code>
<code>phase</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.

**ImproperTorsionType**

```
class openff.toolkit.typing.engines.smirnoff.parameters.ImproperTorsionType(smirks, allow_cosmetic_attributes=False, **kwargs)
```

A SMIRNOFF torsion type for improper torsions.

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

**\_\_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>idivf</code>
<code>k</code>
<code>parent_id</code>
<code>periodicity</code>
<code>phase</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.

**vdWType**

**class** openff.toolkit.typing.engines.smirnoff.parameters.vdWType(*\*\*kwargs*)

A SMIRNOFF vdWForce type.

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

**\_\_init\_\_**(*\*\*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__(**kwargs)</code>	Create a <code>ParameterType</code> .
<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>epsilon</code>
<code>id</code>
<code>parent_id</code>
<code>rmin_half</code>
<code>sigma</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 serializaion

**Returns**

**smirnoff\_dict** (*dict*) – The SMIRNOFF-compliant dict representation of this object.

**LibraryChargeType**

**class** openff.toolkit.typing.engines.smirnoff.parameters.**LibraryChargeType**(*\*\*kwargs*)

A SMIRNOFF Library Charge type.

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

**\_\_init\_\_**(*\*\*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__(**kwargs)</code>	Create a <code>ParameterType</code> .
<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>from_molecule(molecule)</code>	Construct a <code>LibraryChargeType</code> from a molecule with existing partial charges.
<code>to_dict([discard_cosmetic_attributes, ...])</code>	Convert this object to dict format.

## Attributes

<code>charge</code>
<code>id</code>
<code>name</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.

**classmethod from\_molecule**(*molecule: Molecule*)

Construct a LibraryChargeType from a molecule with existing partial charges.

**Parameters**

**molecule** (`openff.toolkit.topology.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.:

**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.

**GBSAType**

```
class openff.toolkit.typing.engines.smirnoff.parameters.GBSAType(smirks,  
                                                             allow_cosmetic_attributes=False,  
                                                             **kwargs)
```

A SMIRNOFF GBSA type.

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

`__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>radius</code>
<code>scale</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.

### ChargeIncrementType

**class** openff.toolkit.typing.engines.smirnoff.parameters.ChargeIncrementType(*\*\*kwargs*)

A SMIRNOFF bond charge correction type.

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

**\_\_init\_\_**(*\*\*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__(**kwargs)</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>charge_increment</code>
<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 serializaiton

**Returns**

**smirnoff\_dict** (*dict*) – The SMIRNOFF-compliant dict representation of this object.

**VirtualSiteType**

**class** openff.toolkit.typing.engines.smirnoff.parameters.**VirtualSiteType**(*\*\*kwargs*)

**\_\_init\_\_**(*\*\*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__(**kwargs)</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.
<code>type_to_parent_index(type_)</code>	Returns the index of the atom matched by the SMIRKS pattern that should be considered the 'parent' to a given type of virtual site.

## Attributes

<code>charge_increment</code>	
<code>distance</code>	
<code>epsilon</code>	
<code>id</code>	
<code>inPlaneAngle</code>	
<code>match</code>	
<code>name</code>	
<code>outOfPlaneAngle</code>	
<code>parent_id</code>	
<code>parent_index</code>	Returns the index of the atom matched by the SMIRKS pattern that should be considered the 'parent' to the virtual site.
<code>rmin_half</code>	
<code>sigma</code>	
<code>smirks</code>	
<code>type</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.

**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.

**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.

```
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.

## 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.

ParameterList	Parameter list that also supports accessing items by SMARTS string.
ParameterHandler	Base class for parameter handlers.
ConstraintHandler	Handle SMIRNOFF <Constraints> tags
BondHandler	Handle SMIRNOFF <Bonds> tags
AngleHandler	Handle SMIRNOFF <AngleForce> tags
ProperTorsionHandler	Handle SMIRNOFF <ProperTorsionForce> tags
ImproperTorsionHandler	Handle SMIRNOFF <ImproperTorsionForce> tags
vdWHandler	Handle SMIRNOFF <vdW> tags
ElectrostaticsHandler	Handles SMIRNOFF <Electrostatics> tags.
LibraryChargeHandler	Handle SMIRNOFF <LibraryCharges> tags
ToolkitAM1BCCHandler	Handle SMIRNOFF <ToolkitAM1BCC> tags
GBSAHandler	Handle SMIRNOFF <GBSA> tags
ChargeIncrementModelHandler	Handle SMIRNOFF <ChargeIncrementModel> tags
VirtualSiteHandler	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 ParameterList, optionally providing a list of ParameterType objects to initially populate it.
<code>append(parameter)</code>	Add a ParameterType object to the end of the ParameterList
<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 ParameterList object to the end of the ParameterList
<code>index(item)</code>	Get the numerical index of a ParameterType object or SMIRKS in this ParameterList.
<code>insert(index, parameter)</code>	Add a ParameterType 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 ParameterList to a normal list, serializing each ParameterType 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.

<b>Warning:</b> 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.toolkit 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']
```

### `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]=,[:16:3]~[: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.toolkit 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** (openff.toolkit.topology.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 <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** `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 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.toolkit 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** (`openff.toolkit.topology.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.toolkit 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.

## 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__</code> (**kwargs)	Initialize a ParameterHandler, optionally with a list of parameters and other kwargs.
<code>add_cosmetic_attribute</code> (attr_name, attr_value)	Add a cosmetic attribute to this object.
<code>add_parameter</code> ([parameter_kwargs, parameter, ...])	Add a parameter to the force field, ensuring all parameters are valid.
<code>attribute_is_cosmetic</code> (attr_name)	Determine whether an attribute of this object is cosmetic.
<code>check_handler_compatibility</code> (other_handler)	Checks whether this ParameterHandler encodes compatible physics as another ParameterHandler.
<code>create_force</code> (*args, **kwargs)	Deprecated since version 0.11.0.
<code>delete_cosmetic_attribute</code> (attr_name)	Delete a cosmetic attribute from this object.
<code>find_matches</code> (entity[, unique])	Find the elements of the topology/molecule matched by a parameter type.
<code>get_parameter</code> (parameter_attrs)	Return the parameters in this ParameterHandler that match the parameter_attrs argument.
<code>to_dict</code> ([discard_cosmetic_attributes])	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 serializaition

#### 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.toolkit 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** (`openff.toolkit.topology.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.toolkit 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 <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>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>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 serializaion

**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.toolkit 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** (`openff.toolkit.topology.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.toolkit 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`.

**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.toolkit 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** (openff.toolkit.topology.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.toolkit 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__([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 improper torsions in 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>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** (`openff.toolkit.topology.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.toolkit 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.toolkit 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(\*\*kwargs)

Handle SMIRNOFF <vdW> 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> (**kwargs)	Initialize a ParameterHandler, optionally with a list of parameters and other kwargs.
<code>add_cosmetic_attribute</code> (attr_name, attr_value)	Add a cosmetic attribute to this object.
<code>add_parameter</code> ([parameter_kwargs, parameter, ...])	Add a parameter to the force field, ensuring all parameters are valid.
<code>attribute_is_cosmetic</code> (attr_name)	Determine whether an attribute of this object is cosmetic.
<code>check_handler_compatibility</code> (other_handler)	Checks whether this ParameterHandler encodes compatible physics as another ParameterHandler.
<code>create_force</code> (*args, **kwargs)	Deprecated since version 0.11.0.
<code>delete_cosmetic_attribute</code> (attr_name)	Delete a cosmetic attribute from this object.
<code>find_matches</code> (entity[, unique])	Find the elements of the topology/molecule matched by a parameter type.
<code>get_parameter</code> (parameter_attrs)	Return the parameters in this ParameterHandler that match the parameter_attrs argument.
<code>to_dict</code> ([discard_cosmetic_attributes])	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>nonperiodic_method</code>	
<code>parameters</code>	The ParameterList that holds this ParameterHandler's parameter objects
<code>periodic_method</code>	
<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.toolkit 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** (`openff.toolkit.topology.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.toolkit 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> (**kwargs)	Initialize a ParameterHandler, optionally with a list of parameters and other kwargs.
<code>add_cosmetic_attribute</code> (attr_name, attr_value)	Add a cosmetic attribute to this object.
<code>add_parameter</code> ([parameter_kwargs, parameter, ...])	Add a parameter to the force field, ensuring all parameters are valid.
<code>attribute_is_cosmetic</code> (attr_name)	Determine whether an attribute of this object is cosmetic.
<code>check_handler_compatibility</code> (other_handler)	Checks whether this ParameterHandler encodes compatible physics as another ParameterHandler.
<code>create_force</code> (*args, **kwargs)	Deprecated since version 0.11.0.
<code>delete_cosmetic_attribute</code> (attr_name)	Delete a cosmetic attribute from this object.
<code>find_matches</code> (entity[, unique])	Find the elements of the topology/molecule matched by a parameter type.
<code>get_parameter</code> (parameter_attrs)	Return the parameters in this ParameterHandler that match the parameter_attrs argument.
<code>to_dict</code> ([discard_cosmetic_attributes])	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.toolkit 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** (`openff.toolkit.topology.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.toolkit 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 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** `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** (`openff.toolkit.topology.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** (`openff.toolkit.topology.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.toolkit 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.toolkit 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.

## ToolkitAM1BCCHandler

```
class openff.toolkit.typing.engines.smirnoff.parameters.ToolkitAM1BCCHandler(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.toolkit 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** (`openff.toolkit.topology.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.toolkit 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 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>gb_model</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>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 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.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.toolkit 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** (`openff.toolkit.topology.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.toolkit 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** (`openff.toolkit.topology.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.toolkit 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.toolkit 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 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 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 <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']`)  $\rightarrow$  `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 serializaion

#### 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.toolkit 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** (`openff.toolkit.topology.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.toolkit import unit
>>> handler = BondHandler(skip_version_check=True)
>>> handler.add_parameter(
...     {
...         'smirks': '[*:1]-[:2]',
...         'length': 1*unit.angstrom,
```

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```

...     '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.

ParameterIOHandler	Base class for handling serialization/deserialization of SMIRNOFF ForceField objects
XMLParameterIOHandler	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

<b>__init__()</b>	Create a new ParameterIOHandler.
<b>parse_file(file_path)</b>	<b>param file_path</b>
<b>parse_string(data)</b>	Parse a SMIRNOFF force field definition in a serialized format
<b>to_file(file_path, smirnoff_data)</b>	Write the current force field parameter set to a file.
<b>to_string(smirnoff_data)</b>	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.

ParameterAttribute	A descriptor for ParameterType attributes.
IndexedParameterAttribute	The attribute of a parameter with an unspecified number of terms.
MappedParameterAttribute	The attribute of a parameter in which each term is a mapping.
IndexedMappedParameterAttribute	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.toolkit 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 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).

### IndexedParameterAttribute

```
class openff.toolkit.typing.engines.smirnoff.parameters.IndexedParameterAttribute(default: Any
                                         =
                                         UNDEFINED,
                                         unit: Op-
                                         tional[Unit]
                                         = None,
                                         converter:
                                         Op-
                                         tional[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.toolkit 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])
```

---

```
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).

## 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.toolkit 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])
```

```
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).

## 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.toolkit 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)
...
>>> 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

### 14.1 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.

To temporarily change the state of GLOBAL\_TOOLKIT\_REGISTRY, we provide the toolkit\_registry\_manager context manager.

```
>>> from openff.toolkit.utils.toolkits import RDKitToolkitWrapper, AmberToolsToolkitWrapper, GLOBAL_TOOLKIT_REGISTRY
>>> from openff.toolkit.utils import toolkit_registry_manager
>>> print(len(GLOBAL_TOOLKIT_REGISTRY.registered_toolkits))
4
>>> with toolkit_registry_manager(ToolkitRegistry([RDKitToolkitWrapper(), AmberToolsToolkitWrapper()])):
...     print(len(GLOBAL_TOOLKIT_REGISTRY.registered_toolkits))
2
```

To remove ToolkitWrappers permanently from a ToolkitRegistry, the deregister\_toolkit method can be used:

```
>>> from openff.toolkit.utils.toolkits import OpenEyeToolkitWrapper, BuiltInToolkitWrapper
>>> from openff.toolkit.utils.toolkits import GLOBAL_TOOLKIT_REGISTRY as toolkit_registry
>>> print(len(toolkit_registry.registered_toolkits))
4
>>> toolkit_registry.deregister_toolkit(RDKitToolkitWrapper)
>>> print(len(toolkit_registry.registered_toolkits))
3
>>> toolkit_registry.register_toolkit(RDKitToolkitWrapper)
>>> print(len(toolkit_registry.registered_toolkits))
4
```

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(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]
```

ToolkitRegistry	Registry for ToolkitWrapper objects
ToolkitWrapper	Toolkit wrapper base class.
OpenEyeToolkitWrapper	OpenEye toolkit wrapper
RDKitToolkitWrapper	RDKit toolkit wrapper
AmberToolsToolkitWrapper	AmberTools toolkit wrapper
BuiltInToolkitWrapper	Built-in ToolkitWrapper for very basic functionality.



### 14.1.1 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)
```

### 14.1.2 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 openff.toolkit.topology.Molecule from a file using this toolkit.
<code>from_file_obj(file_obj, file_format[, ...])</code>	Return an openff.toolkit.topology.Molecule from a file-like object (an object with a ".read()" 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

<b>Warning:</b> 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.

### 14.1.3 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, ...])</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 OpenEye OEChem Toolkit.
<code>to_inchikey(molecule[, fixed_hydrogens])</code>	Create an InChIKey for the molecule using the OpenEye OEChem 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 protomers.

#### Parameters

- **molecule** (`openff.toolkit.topology.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** (`openff.toolkit.topology.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** (`openff.toolkit.topology.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.

*OEAtom*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 *OEAtom*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 *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

- **oemol** (`openeye.oechem.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

OEAto`m`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 OEAto`m`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 OEAto`m` 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** (openff.toolkit.topology.molecule.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** (openff.toolkit.topology.molecule.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 OpenEye OEChem 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 OpenEye OEChem 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** (openff.toolkit.topology.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, name: str = ""*) → 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
- **name** (*str*, default="") – An optional name for the output molecule

### 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, name: str = ""*) → 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
- **name** (str, default="") – An optional name for the output molecule

**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[pint.util.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** (`openff.toolkit.topology.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*[*pint.util.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** (`openff.toolkit.topology.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

#### 14.1.4 RDKitToolkitWrapper

**class** openff.toolkit.utils.toolkits.RDKitToolkitWrapper  
RDKit toolkit wrapper

<b>Warning:</b> 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, ...])</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`, *name*: `str` = `"`)

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
- **name** (*str*, default="") – An optional name for the output molecule

**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 RDMol 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 RDMol 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** (openff.toolkit.topology.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** (openff.toolkit.topology.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** (openff.toolkit.topology.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*, *name*: *str* = "")

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
- **name** (*str*, default="") – An optional name to pass to the `_cls` 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*, *name*: *str* = "")

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[pint.util.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** (*openff.toolkit.topology.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** (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.

**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\_MDL', *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** (*openff.toolkit.topology.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') – 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\_MDL** (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** (*openff.toolkit.topology.molecule.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** (*openff.toolkit.topology.molecule.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

### 14.1.5 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*[*pint.util.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** (`openff.toolkit.topology.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

### 14.1.6 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** (`openff.toolkit.topology.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

---

`toolkit_registry_manager`

A context manager that temporarily changes the ToolkitWrappers in the GLOBAL\_TOOLKIT\_REGISTRY.

---

### 14.1.7 toolkit\_registry\_manager

`openff.toolkit.utils.toolkit_registry.toolkit_registry_manager(toolkit_registry: Union[ToolkitRegistry, ToolkitWrapper])`

A context manager that temporarily changes the ToolkitWrappers in the GLOBAL\_TOOLKIT\_REGISTRY. This can be useful in cases where one would otherwise need to otherwise manually specify the use of a specific ToolkitWrapper or ToolkitRegistry repeatedly in a block of code, or in cases where there isn't another way to switch the ToolkitWrappers used for a particular operation.

## Examples

```
>>> from openff.toolkit import Molecule, RDKitToolkitWrapper, AmberToolsToolkitWrapper
>>> from openff.toolkit.utils import toolkit_registry_manager, ToolkitRegistry
>>> mol = Molecule.from_smiles("CCO")
>>> print(mol.to_smiles()) # This will use the OpenEye backend (if installed and_
↳ licensed)
[H]C([H])([H])C([H])([H])O[H]
>>> with toolkit_registry_manager(ToolkitRegistry([RDKitToolkitWrapper()])):
...     print(mol.to_smiles())
[H][O][C]([H])([H])[C]([H])([H])[H]
```

## 14.2 Serialization support

Serializable

Mix-in to add serialization and deserialization support via JSON, YAML, BSON, TOML, MessagePack, and XML.

### 14.2.1 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):
```

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```
...         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)`**  $\rightarrow$  *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

## 14.3 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.

### 14.3.1 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.

### 14.3.2 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, default 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, default 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

## 14.4 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 col-lated results.
<code>unit_to_string</code>	

### 14.4.1 inherit\_docstrings

`openff.toolkit.utils.utils.inherit_docstrings(cls)`

Inherit docstrings from parent class

### 14.4.2 all\_subclasses

`openff.toolkit.utils.utils.all_subclasses(cls)`

Recursively retrieve all subclasses of the specified class

### 14.4.3 temporary\_cd

`openff.toolkit.utils.utils.temporary_cd(dir_path)`

Context to temporarily 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
```

### 14.4.4 get\_data\_file\_path

`openff.toolkit.utils.utils.get_data_file_path(relative_path: str) → str`

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 `openff/toolkit/data/`)

### 14.4.5 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 to the 0.1 spec

#### Returns

*smirnoff\_data\_0\_2* – Hierarchical dict representing a SMIRNOFF data structure according to the 0.2 spec

### 14.4.6 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 to the 0.2 spec



**Returns**

*smirnoff\_data\_0\_3* – Hierarchical dict representing a SMIRNOFF data structure according to the 0.3 spec

**14.4.7 get\_molecule\_parameterIDs**

`openff.toolkit.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.

**14.4.8 unit\_to\_string**

`openff.toolkit.utils.unit_to_string(input_unit: Unit) → str`

**14.5 Exceptions**

Exceptions raised by the Toolkit.

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`exceptions`

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**14.5.1 openff.toolkit.utils.exceptions****Exceptions**

<code>AmbiguousAtomChemicalAssignment(res_name, ...)</code>	Exception raised when substructure does not contain enough information
<code>AmbiguousBondChemicalAssignment(res_name, ...)</code>	Exception raised when substructure does not contain enough information
<code>AntechamberNotFoundError(msg)</code>	The antechamber executable was not found

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<code>AtomMappingWarning</code>	A warning when dealing with atom mapping or indices.
<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>ChemicalEnvironmentParsingError(msg)</code>	Exception for when SMARTS/SMIRKS are not parseable by a wrapped toolkit
<code>ConformerGenerationError(msg)</code>	Conformer generation via a wrapped toolkit failed.
<code>ConstraintExistsError(msg)</code>	Attempting to override a constraint that already exists with a specified distance.
<code>DuplicateParameterError(msg)</code>	Exception raised when trying to add a <code>ParameterType</code> 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>FractionalBondOrderInterpolationMethodUnsupportedError(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>HierarchyIteratorNameConflictError(msg)</code>	Exception raised when trying to access a hierarchy scheme with a name that already exists as a <i>Topology</i> or <i>Molecule</i> attribute.
<code>HierarchySchemeNotFoundException(msg)</code>	Exception raised when trying to access a <code>HierarchyScheme</code> from a molecule that doesn't have one with the given iterator name
<code>HierarchySchemeWithIteratorNameAlreadyRegisteredError(msg)</code>	Exception when trying to add a <code>HierarchyScheme</code> to a molecule that already has one with the same iterator name
<code>InChIParseError(msg)</code>	The InChI record could not be parsed.
<code>IncompatibleParameterError(msg)</code>	Exception for when a set of parameters is scientifically/technically incompatible with another
<code>IncompatibleShapeError(msg)</code>	Exception for when a value is in the wrong shape
<code>IncompatibleTypeError(msg)</code>	Exception for when a value is in an incompatible type
<code>IncompatibleUnitError(msg)</code>	Exception for when a parameter is in the wrong units for a <code>ParameterHandler</code> '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

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<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 <i>Molecule.bond_order</i>
<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>InvalidQCInputError(msg)</code>	This error is raised when an input to <i>Molecule.from_qcschema</i> is invalid.
<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 <i>ToolkitRegistry</i> or toolkit wrapper was received
<code>LicenseError(msg)</code>	This function requires a license that cannot be found.
<code>MissingCMILESError(msg)</code>	Error raised when attempting to convert an QC input to an OFF Molecule, but the CMILES can't be found or isn't present.
<code>MissingConformersError(msg)</code>	Error raised when a molecule is missing conformer(s) in a context in which it is expected to have them.
<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.
<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 <i>unique_molecules</i> is required but not found
<code>MoleculeNotInTopologyError(msg)</code>	A molecule was not found in a topology.
<code>MoleculeParseError(msg)</code>	The molecule could not be created from the given format
<code>MultipleMoleculesInPDBError(msg)</code>	Error raised when a multiple molecules are found when one was expected
<code>NonUniqueSubstructureName(duplicate_keys)</code>	Exception raised when nonunique names are given
<code>NotAttachedToMoleculeError(msg)</code>	Exception for when a component does not belong to a <i>Molecule</i> 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>OpenEyeError(msg)</code>	Error raised when an OpenEye Toolkits operation fails.

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<code>OpenEyeImportError(msg)</code>	Error raised when importing an OpenEye module fails.
<code>OpenFFToolkitException(msg)</code>	Base exception for custom exceptions raised by the OpenFF Toolkit
<code>ParameterHandlerRegistrationError(msg)</code>	Exception for errors in ParameterHandler registration
<code>ParameterLookupError(msg)</code>	Exception raised when something goes wrong in a parameter lookup in ParameterHandler. <code>__getitem__</code>
<code>PartialChargeVirtualSitesError(msg)</code>	Exception thrown when partial charges cannot be computed for a Molecule because the ForceField 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 ForceField
<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>SubstructureAtomSmartsInvalid(name, ...)</code>	Exception raised when atom or bond smarts are found to be improperly formatted
<code>SubstructureBondSmartsInvalid(name, bond, ...)</code>	
<code>SubstructureImproperlySpecified(name, reason)</code>	Exception raised when substructure does not contain enough information
<code>ToolkitUnavailableException(msg)</code>	The requested toolkit is unavailable.
<code>UnassignedAngleParameterException(msg)</code>	Exception raised when there are angle terms for which a ParameterHandler can't find parameters.
<code>UnassignedBondParameterException(msg)</code>	Exception raised when there are bond terms for which a ParameterHandler 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.

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Table 1 – continued from previous page

<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>VirtualSitesUnsupportedError(msg)</code>	Exception raised when trying to store virtual sites in a <i>Molecule</i> or <i>Topology</i> object.
<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.IncompatibleShapeError(msg)`

Exception for when a value is in the wrong shape

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.IncompatibleTypeError(msg)`

Exception for when a value is in an incompatible type

**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.MoleculeParseError(msg)`  
The molecule could not be created from the given format  
**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.AtomMappingWarning`  
A warning when dealing with atom mapping or indices.  
**with\_traceback()**  
Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.InChIParseError(msg)`  
The InChI record could not be parsed.  
**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.InvalidQCInputError(msg)`  
This error is raised when an input to `Molecule.from_qcschema` is invalid.  
**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.**ConstraintExistsError**(msg)  
Attempting to override a constraint that already exists with a specified distance.

**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.ChemicalEnvironmentParsingError(msg)`  
Exception for when SMARTS/SMIRKS are not parseable by a wrapped toolkit

**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.HierarchyIteratorNameConflictError(msg)

Exception raised when trying to access a hierarchy scheme with a name that already exists as a *Topology* or *Molecule* attribute.

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.VirtualSitesUnsupportedError(msg)

Exception raised when trying to store virtual sites in a *Molecule* or *Topology* object.

**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.MissingConformersError(msg)

Error raised when a molecule is missing conformer(s) 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.MissingCMILESError(msg)

Error raised when attempting to convert an QC input to an OFF Molecule, but the CMILES can't be found or isn't present.

**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.OpenEyeError(msg)`  
 Error raised when an OpenEye Toolkits operation fails.

**with\_traceback()**  
 Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** `openff.toolkit.utils.exceptions.OpenEyeImportError(msg)`  
 Error raised when importing an OpenEye module fails.

**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.

**exception** openff.toolkit.utils.exceptions.**NonUniqueSubstructureName**(*duplicate\_keys*)

Exception raised when nonunique names are given

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**SubstructureAtomSmartsInvalid**(*name*, *atom\_smarts*,  
*smarts*, *reason*)

Exception raised when atom or bond smarts are found to be improperly formatted

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**SubstructureBondSmartsInvalid**(*name*, *bond*,  
*valid\_bond\_types*)

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**SubstructureImproperlySpecified**(*name*, *reason*)

Exception raised when substructure does not contain enough information

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**AmbiguousAtomChemicalAssignment**(*res\_name*, *mol\_atom*,  
*query\_atom*, *reason*)

Exception raised when substructure does not contain enough information

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** openff.toolkit.utils.exceptions.**AmbiguousBondChemicalAssignment**(*res\_name*, *mol\_bond*,  
*query\_bond*, *reason*)

Exception raised when substructure does not contain enough information

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

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