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**WC***ontodocumentation*

***Release 0.0.2***

**Karr Lab**

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Ontology for whole-cell modeling.

The following example illustrates how to use the ontology in Python:

```
from wc_onto import onto
species_term = onto['WC:species']
```



## 1.1 Installation

### 1.1.1 Prerequisites

- Python
- Pip

### 1.1.2 Installing the ontology for use in Python

1. Install this Python package with pip:

```
pip install git+https://github.com/KarrLab/wc_onto.git#egg=wc_onto[all]
```

This command will install this Python package, including the ontology (in OBO format) and the Python code for using the ontology. Once installed, the ontology will be located at `pkg_resources.resource_filename('wc_onto', 'onto.obo')`.

2. Obtain a [BioPortal API key](#)
3. Save your BioPortal API key to a configuration file (`~/.wc/wc_onto.cfg`):

```
[wc_onto]
[[biportal]]
    key = <BioPortal API key>
```

4. Import the package. The other ontologies which `wc_onto` references will automatically be downloaded the first time that the package is imported.:

```
from wc_onto import onto
```

### 1.1.3 Downloading the ontology

Alternatively, the ontology can be downloaded (in OBO format) from GitHub or BioPortal

- Download [latest revision](#) from GitHub
- Download [latest snapshot](#) from BioPortal

## 1.2 About

### 1.2.1 License

The software is released under the MIT license

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### 1.2.2 Development team

This package was developed by the [Karr Lab](#) at the Icahn School of Medicine at Mount Sinai in New York, USA.

### 1.2.3 Acknowledgements

### 1.2.4 Questions and comments

Please contact the [Karr Lab](#) with any questions or comments.