

## Namespace PyCamcoil

### Sub-modules

- [PyCamcoil.camcoil](#)
- [PyCamcoil.src](#)

## Module PyCamcoil.camcoil

### Functions

#### Function main

```
def main(  
    sequence=None,  
    pH=None,  
    f_out=None  
)
```

This is the main function that is called to initiate the camcoil\_engine prediction.

:param sequence: (string) of amino-acids.

:param pH: (float) determines the specific random coil (reference) values that will be used to generate the predictions.

:param f\_out: (path) if given, the output will be saved there instead of the screen.

:return: None.

## Module PyCamcoil.src

### Sub-modules

- [PyCamcoil.src.camcoil\\_engine](#)
- [PyCamcoil.src.camcoil\\_properties](#)

## Module PyCamcoil.src.camcoil\_engine

This module provides a “Python implementation” of the camcoil program (originally written in C) to estimate the random coil chemical shift values from a sequence (string) of amino-acids.

The work is described in detail at:

1. Alfonso De Simone, Andrea Cavalli, Shang-Te Danny Hsu, Wim Vranken and Michele Vendruscolo (2009) (<https://doi.org/10.1021/ja904937a>). “Accurate Random Coil Chemical Shifts from an Analysis of Loop Regions in Native States of Proteins”. Journal of the American Chemical Society (JACS), 131 (45), 16332 - 16333.

Note —= The txt files: ‘corr\_1L’, ‘corr\_2L’, ‘corr\_1R’, ‘corr\_2R’, are required for the estimation of the random coil values. They should be placed in the same directory with the module file. If they do not exist the code will exit with an error.

## Classes

### Class CamCoil

```
class CamCoil(  
    pH=7.0  
)
```

This class implements the CamCoil code in Python.

Initializes the camcoil object. The pH is given as option during the initialization of the object even though only two actual implementations exist at the moment (i.e., pH=2 and pH=7).

If the user selects another pH value, this will be set automatically to one of these two in the code.

:param pH: (float) the default pH value is set to 7.0.

### Instance variables

**Variable df** Return an attribute of instance, which is of type owner.

**Variable pH** Accessor (getter) of the pH parameter.

:return: the pH value.

### Methods

#### Method predict

```
def predict(  
    self,  
    seq=None,  
    verbose=False  
)
```

Accepts a string amino-acid sequence, and returns a prediction with the random coil chemical shifts.

:param seq: (string) The input amino-acid sequence.

:param verbose: (bool) If the flag is set to True it will print more information on the screen.

:return: a pandas DataFrame, with the results.

## Module PyCamcoil.src.camcoil\_properties

Properties for the CamCoil implementation. These include:

1. ACCEPTED\_RES\_ONE
2. pH2\_prop
3. pH7\_prop
4. weights
5. weights\_LFP

## Classes

### Class ChemShifts

```
class ChemShifts(  
    N,  
    C,  
    CA,  
    CB,  
    H,  
    HA  
)
```

ChemShifts(N, C, CA, CB, H, HA)

### Ancestors (in MRO)

- [builtins.tuple](#)

### Instance variables

**Variable C** Random coil chemical shift value for ‘C’.

**Variable CA** Random coil chemical shift value for ‘CA’.

**Variable CB** Random coil chemical shift value for ‘CB’.

**Variable H** Random coil chemical shift value for ‘H’.

**Variable HA** Random coil chemical shift value for ‘HA’.

**Variable N** Random coil chemical shift value for ‘N’.

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