

The Biopython Structural Bioinformatics FAQ

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1 Introduction

The Biopython Project is an international association of developers of freely available Python (<http://www.python.org/>) for computational biology. For more information, see the Biopython FAQ at <http://www.biopython.org/wiki/FAQ>.

Judging from requests for features and information, Bio.PDB is also used by several LPCs (Large Pharmaceutical Companies :-).

4 Is there a Bio.PDB reference?

How do I extract a specific Atom/Residue/Chain/Model from a Structure?

Easy. Here are some examples:

```
model = structure[0]
chain = model [ ' A' ]
residue = chain [ 100 ]
atom = residue [ ' CA' ]
```

Note that you can use a shortcut:

```
atom = structure[0][ ' A' ][ 100 ][ ' CA' ]
```

What is a model id?

The model id is an integer which denotes the rank of the model in the PDB/mmCIF file. The model id starts at 0. Crystal structures generally have only one model (with id 0), while NMR files usually have several models.

What is a chain id?

The chain id is specified in the PDB/mmCIF file, and is a single character (typically a letter).

What is a residue id?


```
# Calculate classical coordination number exp_fs=hse.calc_fs_exposure(model)
# Print HSEalpha for a residue
print exp_ca[some_residue]
```

How do I map the residues of two related structures onto each other?

First, create an alignment file in FASTA format, then use the `StructureAlignment` class. This class can also be used for alignments with more than two structures.

How do I test if a Residue object is an amino acid?

Use `is_aa(residue)`.

Can I do vector operations on atomic coordinates?

Atom objects return a `Vector`

