

# A simple example

A simple example of pKa titration of lysozyme.

- [A simple MCCE example of pH titration](#)

# A simple MCCE example of pH titration

## Run MCCE

Prepare a working directory:

```
$ mkdir test_lysozyme  
$ cd test_lysozyme
```

Get a pdb file

```
$ getpdb 1dpx
```

You now have a PDB file 1DPX.pdb in the working directory.

The simplest way to run MCCE is with these four steps:

## Step 1: Make PDB file into MCCE PDB

This step proofreads the structure file and cuts terminal residues and complex cofactors into smaller ones if necessary.

```
$ step1.py 1DPX.pdb
```

## Step 2: Create side chain conformers

This step makes alternative side chain locations and ionization states.

```
$ step2.py
```

## Step 3: Calculate energy table

This step calculates conformer self energy and pairwise interaction table.

```
$ step3.py
```

## Step 4: Simulate a titration with Monte Carlo sampling

This step simulates a titration and writes out the conformation and ionization states of each side chain at various conditions.

```
$ step4.py
```

## Notes

### Command help "-h"

- For more detailed command usages, use "-h" switch in each command above.

### Run in background

- Some steps take hours to finish, so it is recommended to run at the background. For example:

```
step3.py > run.log &
```

- For more exhaustive work, we recommend using tools like `p_batch` to process many runs at once in the background.

## Jupyter notebook

Here is a Jupyter note book template: [mcce.ipynb](https://mcce.ipynb)