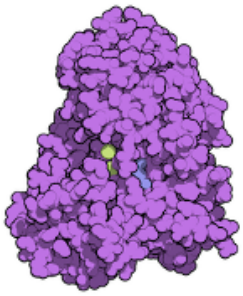
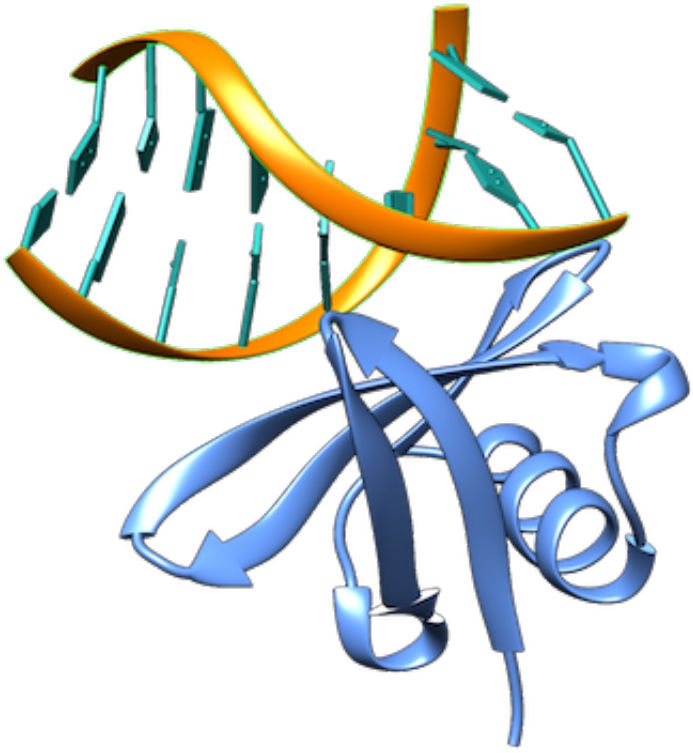


LightDock

LightDock 1AZP Protein-DNA example

This is a complete example of the LightDock protocol when residue restraints are specified using the 1AZP protein-DNA complex as an example.



All the files used in this example can be found in the path examples/1AZP.

IMPORTANT: We recommend you to create a new folder and to copy the starting files `1AZP_A.pdb`, `1AZP_B.pdb` and `restraints.list` to that folder in case you would like to run this example.

1. Setup

1.1. Removing and adding hydrogen atoms

First of all, we need the protein partner to have the correct hydrogen atoms in order for the `dna` scoring function to work properly (`dna` scoring function is based in AMBER force-field). To do it so, we will use the software `reduce` which can be downloaded from GitHub.

We remove the previous hydrogens and them rebuild them according to reduce:

```
reduce -Trim 1AZP_A.pdb > 1AZP_A_noh.pdb
reduce -BUILD 1AZP_A_noh.pdb > 1AZP_A_h.pdb
```

1.2. LightDock setup

First, run the setup:

```
lightdock_setup 1AZP_A_h.pdb 1AZP_B.pdb 400 200 -anm -rst restraints.list
```

The output should be something like this:

```
@> ProDy is configured: verbosity='info'
[lightdock_setup] INFO: Reading structure from 1AZP_A_h.pdb PDB file...
[lightdock_setup] INFO: 1094 atoms, 66 residues read.
[lightdock_setup] INFO: Reading structure from 1AZP_B.pdb PDB file...
[pdb] WARNING: Possible problem: [ResidueNonStandardError] Can not check non-stand
ard residue DG.1
[pdb] WARNING: Possible problem: [ResidueNonStandardError] Can not check non-stand
ard residue DC.2
[pdb] WARNING: Possible problem: [ResidueNonStandardError] Can not check non-stand
ard residue DG.3
[pdb] WARNING: Possible problem: [ResidueNonStandardError] Can not check non-stand
ard residue DA.4
[pdb] WARNING: Possible problem: [ResidueNonStandardError] Can not check non-stand
ard residue DT.5
[pdb] WARNING: Possible problem: [ResidueNonStandardError] Can not check non-stand
ard residue DC.6
[pdb] WARNING: Possible problem: [ResidueNonStandardError] Can not check non-stand
ard residue DG.7
[pdb] WARNING: Possible problem: [ResidueNonStandardError] Can not check non-stand
ard residue DC.8
[pdb] WARNING: Possible problem: [ResidueNonStandardError] Can not check non-stand
ard residue DG.9
[pdb] WARNING: Possible problem: [ResidueNonStandardError] Can not check non-stand
ard residue DC.10
[pdb] WARNING: Possible problem: [ResidueNonStandardError] Can not check non-stand
ard residue DG.11
[pdb] WARNING: Possible problem: [ResidueNonStandardError] Can not check non-stand
```

```
ard residue DA.12
[pdb] WARNING: Possible problem: [ResidueNonStandardError] Can not check non-stand
ard residue DT.13
[pdb] WARNING: Possible problem: [ResidueNonStandardError] Can not check non-stand
ard residue DC.14
[pdb] WARNING: Possible problem: [ResidueNonStandardError] Can not check non-stand
ard residue DG.15
[pdb] WARNING: Possible problem: [ResidueNonStandardError] Can not check non-stand
ard residue DC.16
[lightdock_setup] INFO: 328 atoms, 16 residues read.
[lightdock_setup] INFO: Calculating reference points for receptor 1AZP_A_h.pdb...
[lightdock_setup] INFO: Done.
[lightdock_setup] INFO: Calculating reference points for ligand 1AZP_B.pdb...
[lightdock_setup] INFO: Done.
[lightdock_setup] INFO: Saving processed structure to PDB file...
[lightdock_setup] INFO: Done.
[lightdock_setup] INFO: Saving processed structure to PDB file...
[lightdock_setup] INFO: Done.
[lightdock_setup] INFO: Calculating ANM for receptor molecule...
[lightdock_setup] INFO: 10 normal modes calculated
[lightdock_setup] INFO: Calculating ANM for ligand molecule...
[lightdock_setup] INFO: 10 normal modes calculated
[lightdock_setup] INFO: Reading restraints from restraints.list
[lightdock_setup] INFO: Number of receptor restraints is: 3 (active), 0 (passive)
[lightdock_setup] INFO: Number of ligand restraints is: 0 (active), 0 (passive)
[lightdock_setup] INFO: Calculating starting positions...
[lightdock_setup] INFO: Generated 27 positions files
[lightdock_setup] INFO: Done.
[lightdock_setup] INFO: Number of swarms is 27 after applying restraints
[lightdock_setup] INFO: Preparing environment
[lightdock_setup] INFO: Done.
[lightdock_setup] INFO: LightDock setup OK
```

At the moment, LightDock is not checking the structure of the nucleotides, so that is the reason of the several warning appearing. It is safe to ignore them.

2. Simulation

We can run our simulation in a local machine or in a HPC cluster. For the first option, simply run the following command:

```
lightdock setup.json 100 -s dna -c 8
```

Where the flag `-c 8` indicates LightDock to use 8 available cores. For this example we will run `100` steps of the protocol and the DNA scoring function `-s dna`.

To run a LightDock job on a HPC cluster, a Portable Batch System (PBS) file can be generated. This PBS file defines the commands and cluster resources used for the job. A PBS file is a plain-text file that can be easily edited with any UNIX editor. For example, create a `submit_job.sh` file containing:

```
#PBS -N LightDock-1AZP
#PBS -q medium
#PBS -l nodes=1:ppn=16
#PBS -S /bin/bash
#PBS -d ./
#PBS -e ./lightdock.err
#PBS -o ./lightdock.out

lightdock setup.json 100 -s dna -c 16
```

This script tells the PBS queue manager to use 16 cores of a single node in a queue with name `medium`, with job name `LigthDock-1AZP` and with standard output to `lightdock.out` and error output redirected to `lightdock.err`.

To run this script you can do it so:

```
qsub < submit_job.sh
```