Intro to Rosetta Part 2

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De Novo Structure Prediction

- Needs 4 files:
 - Fasta sequence
 - 9mer and 3mer fragment files
 - o Options file
- Can generate fragment files from Robetta
- Do Novo program found in main/source/bin/
 - Called
 AbinitioRelax.default.linuxgccrelease

```
ιn¬
        -file-
                -fasta input nanobody/nanobody.fasta-
                -frag3 input nanobody/aat000 03 05.200 v1 3-
                -frag9 input nanobody/aat000 09 05.200 v1 3-
-abinitio-
        -relax-
        -increase cycles 10-
        -rg reweight 0.5-
        -rsd wt helix 0.5-
        -rsd wt loop 0.5-
-relax-
        -fast-
-out-
        -pdb-
        -nstruct 300-
        -file-
                -scorefile score.sc-
-overwrite-
```

Run with

./AbinitioRelax.default.linuxgccrelease @options

Generates S_0001.pdb and score.sc

Open with pymol S_0001.pdb