

MobyleNet tutorial

Homology modeling pipeline

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Synopsis

We illustrate here how to take advantage of the MobyleNet to model the 3D structure of the sunflower protein corresponding to the HuCL01857C002 genomic information.

- tools at the three nodes (LIPM, Pasteur and RPBS) can be chained to complete the modeling
- *nota bene* : all calls are performed within the RPBS (remote imported services) portal

The screenshot shows a web-based search interface. At the top, there's a search bar with the text "results". Below it, a section titled "Fasta formatted sequences (Sequence)" contains a file named "sequences.FASTA" with its contents displayed:

```
>lc1|HuCL01857C002_1 AA acc=HuCL01857C002_1_AA len=171 sp= type= begin=1 end=517 strand+= chr=HuCL0
DSSYHSPKTQTLFLSQINQMDQLTDDQISEFKEAFSLFDKDGCGI
TTKELGTVMRSLGQNQPTAEALQDMINEVDADGNGTIDFPEFLNLMARKHK
DTDSEELKLEAFRVRFDKDQNGFISAAEELRHVMTNLGEKLTDEEVDEMIRE
ADVGDGDQINYEEOFVKVMMAK
```

At the bottom of the interface, there are several buttons: "full screen view", "bookmark", "as:", "sequences.FA", and "PDBBlast2 (query)". The "PDBBlast2 (query)" button is highlighted with a red rectangular border.

The full tutorial is available at :

<http://mobylenet.rpbs.univ-paris-diderot.fr/doc/tutorials/network.html>



MobyleNet : Homology Modeling Pipeline

