Welcome to iPBA webserver. A powerful method for structural alignment based on a structural alphabet.

Alignment of protein alphafold2 (chain A) and protein omegafold (chain A)

Summary

Color code for Quality of alignment

\- +

Normalized score	364.99
RMSD	1.81
Alignment length	126
Aligned residues	74
Fraction aligned	58.73 %
GDT TS	44.87

Alignment

```
Position        1                    11        21         31        41        51         61
PB              zzahaa cd            ddddehjbfbdcddddddfk bccddfbfklmmmmmmmmmnopacdddddd fklm m
alphafold2 A  ---MDKGDV-TA----------LPMKKWFTTNYHYLVPEVEP-SAEIKLNSTKPFDEFNEAKSLGVETKPVFI-GPYT-F
Identity        |                    ||||||||||||||||||||||||||||||||||||||  |    |
omegafold A   MDKGDVTALP-MKKWFTTNYHYLV----------------PEVEPSAEIKLNSTKPFDEFNEAKSLGVETKPVFIG-P-YTF
PB              zzghiacghh ehhklnomklmcc                cddfklccddfbfklmmmmmmmmmnopacddddehj l mmm
Position        1          11        21                       31        41        51          61
```

Anchor(s) used by iPBA apears in **Bold**

Download output files

Download pdb files:

- Download first pdb file (alphafold2) aligned to second pdb file (omegafold)
- Download second pdb file (omegafold)
- Download the two aligned pdb files (alphafold2 is chain A and omegafold is chain B)

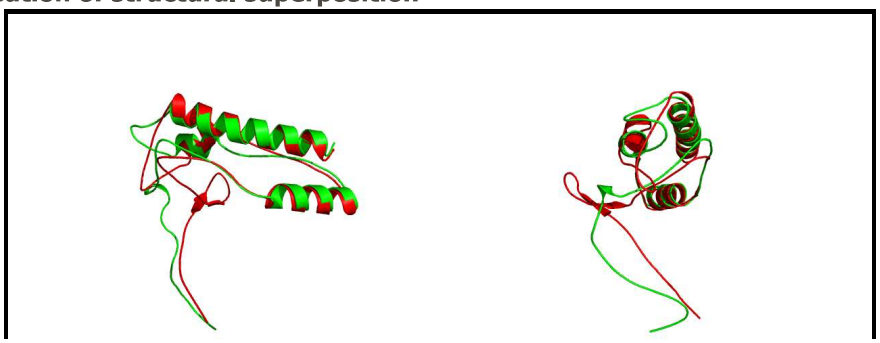
Use pml file for visualisation in pymol:

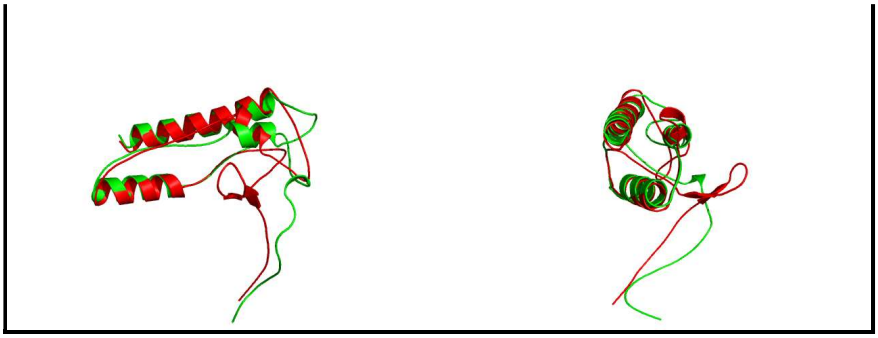
- Download first the two pdb files:[alphafold2] [omegafold]
- Then download pml to use with pymol

Download summary of results

- Summary

Visualisation of structural superposition





Molecule needs Java 1.4

Show Trace only
Show Backbone only
Show Cartoon only

Show only alphafold2
Show only omegafold
Show All