

Web Service

Alignment

Secondary Structure Prediction

Protein Disorder

Analysis

Conservation

Fetch DB References

```
? SANTQ-- S L F G L K S - GTAR
-----
? FANTQ-- S L F G L K S - STAR
? FANTQ-- S L F G L K S - STAR
L PAAKV-- G I M G R S A - S S R R
? L R L R V -- A V A K P L A - A P M R
```

<http://www.compbio.dundee.ac.uk/jabaws>

Tcoffee with Defaults

Edit settings and run ...

Run Tcoffee with preset

Probcons with Defaults

Edit settings and run ...

Muscle with Defaults

Edit settings and run ...

Run Muscle with preset

Mafft with Defaults

Edit settings and run ...

Run Mafft with preset

Clustal

Realign with Clustal

ClustalO

Realign with ClustalO