


Clustal Omega

Multiple Sequence Alignment (MSA)

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We need your help! Has Job Dispatcher saved you time or effort? Please take 15 minutes to fill in a survey and help EMBL-EBI make the case for why open data resources are critical to life science research.

Survey link: [https://www.surveymonkey.com/r/QGFMBH8?channel=\[webpage\]](https://www.surveymonkey.com/r/QGFMBH8?channel=[webpage])

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Results for Job ID

clustalo-l20250718-072312-0155-59470595-p1m

Copy

Resubmission

Tool Output

Alignments

Guide Tree

Phylogenetic Tree

Results Viewers

Result Files

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Phylogenetic Tree

```
(
(
3I40_1|Chain:0.00000,
(
4E7U_1|Chains:0.04762,
(
5JYQ_1|Chain:0.23158,
(
(
(
(
3I40_2|Chain:0.00000,
4E7U_2|Chains:0.00000)
:0.00000,
1ZNI_2|Chains:0.00000)
:0.00000,
4INS_2|Chains:0.00000)
:0.37569,
5JYQ_2|Chain:0.38622)
:0.15063)
:0.27080)
:0.04762)
:0.00000,
1ZNI_1|Chains:0.00000,
4INS_1|Chains:0.00000);
```

Phylogram

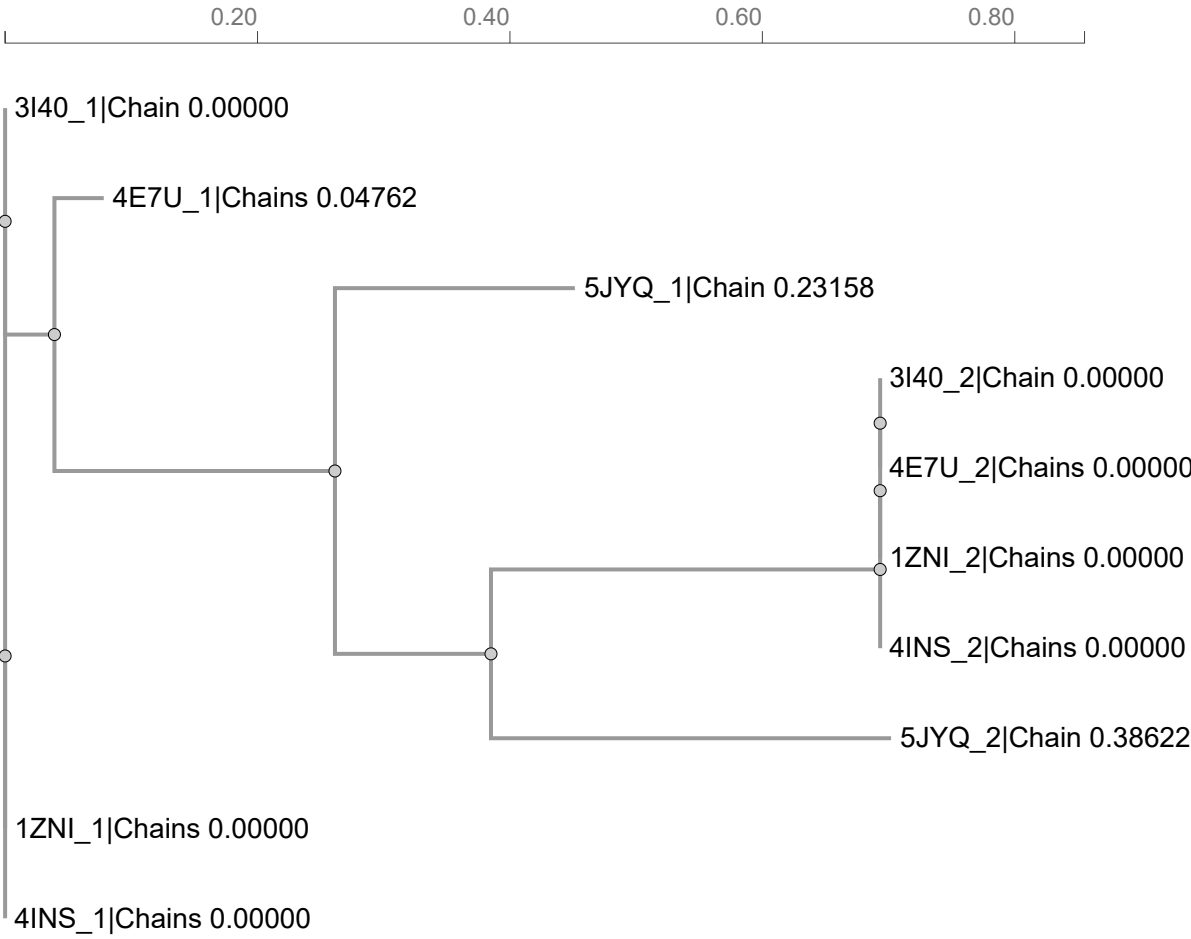


☐ Radial

Selected

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 branches with c



If you use this service, please consider citing the following publication: [The EMBL-EBI Job Dispatcher sequence analysis tools framework in 2024](#). More information about this bioinformatics application can be found in its [bio.tools](#) record.

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