

Clustal Omega

Multiple Sequence Alignment (MSA)

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

Results for Job ID

clustalo-l20250718-063254-0826-7058527-p1m

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Resubmission



Tool Output

Alignments

Guide Tree

Phylogenetic Tree

Results Viewers

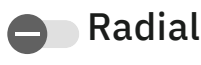
Result Files

S

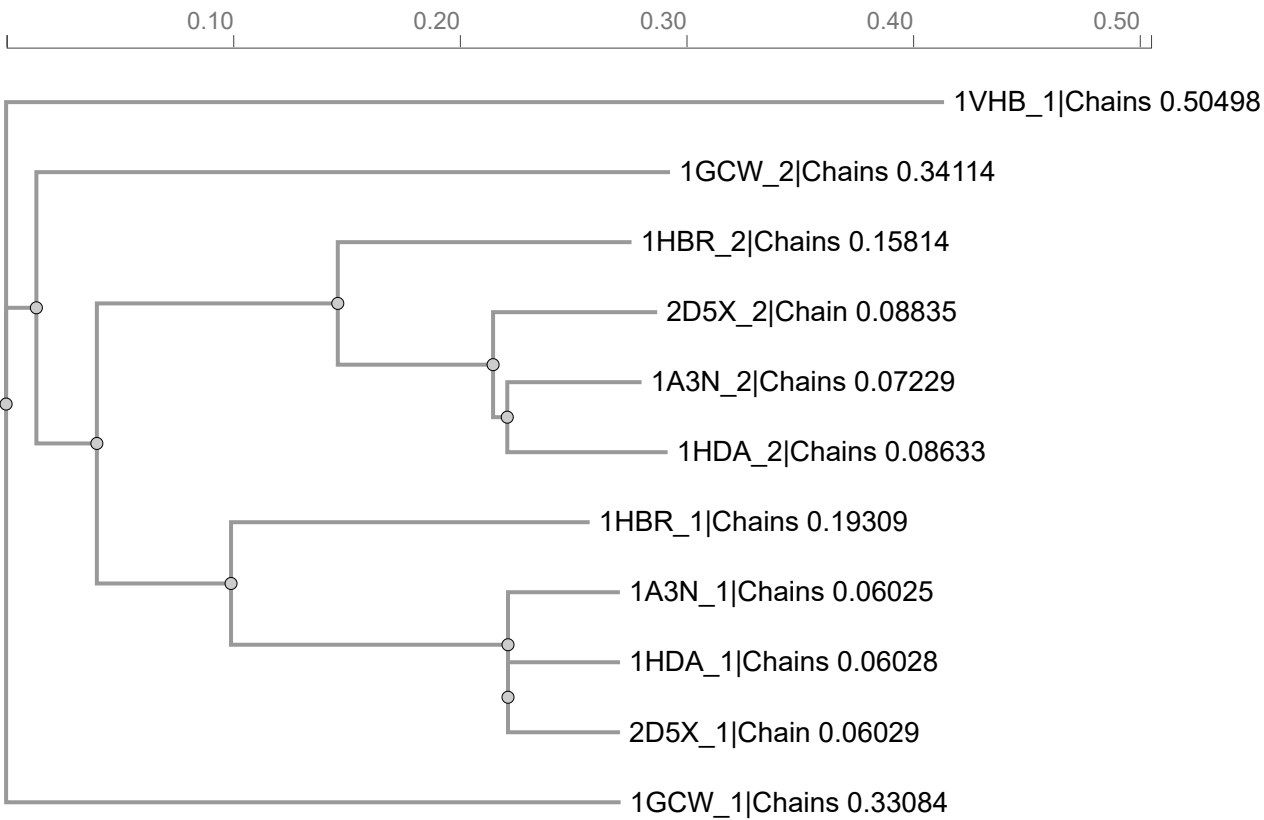
Phylogenetic Tree

(
1VHB_1|Chains:0.50498,
(
1GCW_2|Chains:0.34114,
(
(
1HBR_2|Chains:0.15814,
(
2D5X_2|Chain:0.08835,
(
1A3N_2|Chains:0.07229,
1HDA_2|Chains:0.08633)
:0.00764)
:0.08361)
:0.12971,
(
1HBR_1|Chains:0.19309,
(
1A3N_1|Chains:0.06025,
(
1HDA_1|Chains:0.06028,
2D5X_1|Chain:0.06029)
:0.00000)
:0.14911)
:0.07224)
:0.03256)
:0.01630,
1GCW_1|Chains:0.33084);

Phylogram



Selected **0** 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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