

Clustal Omega

Multiple Sequence Alignment (MSA)

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Results for Job ID

clustalo-l20250718-063254-0826-7058527-p1m

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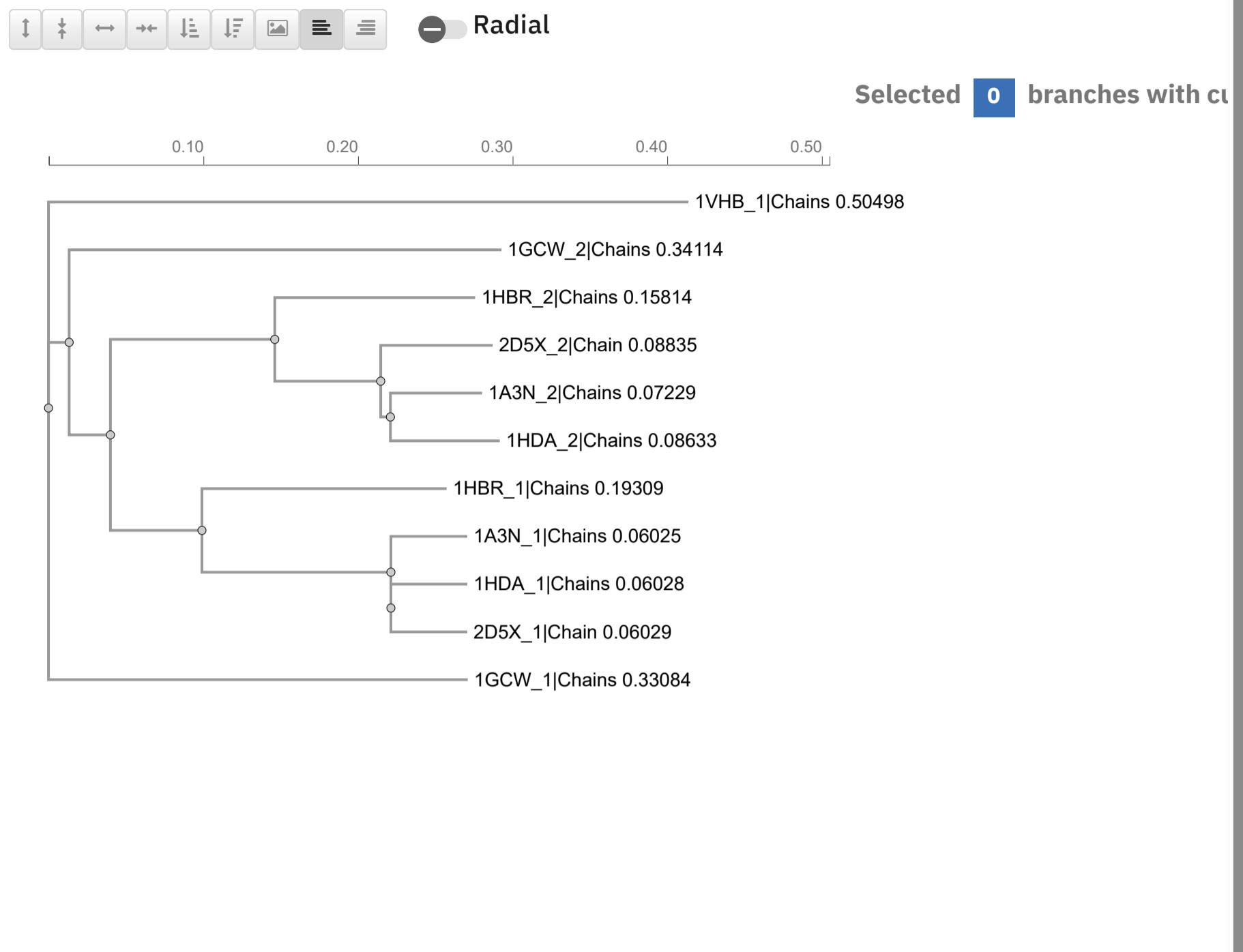


Tool Output Alignments Guide Tree Phylogenetic Tree Results Viewers Result Files S

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



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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