Clustal Omega

Tools (/Tools/) > Multiple Sequence Alignment (/Tools/msa) > Clustal Omega

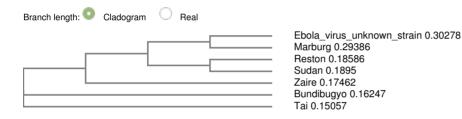
Service Retirement

We remind you that it is not long until the EBI's Wise2DBA (https://www.ebi.ac.uk/Tools/psa/wise2dba/) and Promoterwise (https://www.ebi.ac.uk/Tools/psa/promoterwise/) services are retired on 15th April 2018. Alternatives can be found at Exonerate (https://www.ebi.ac.uk/about/vertebrate-genomics/software/exonerate), BWA (http://bio-bwa.sourceforge.net) or BLAT (http://genome.ucsc.edu/FAQ/FAQblat). If you have any concerns, please contact us via support (https://www.ebi.ac.uk/support/sequence-alignment).

Results for job clustalo-I20180205-084704-0016-90365492-pg

Phylogenetic Tree

This is a Neighbour-joining tree without distance corrections.



Tree Data

```
(
(
(
(
(
Ebola_virus_unknown_strain:0.30278,
Marburg:0.29386)
:0.03491,
(
Reston:0.18586,
Sudan:0.18950)
:0.01346)
:0.01179,
Zaire:0.17462)
:0.01093,
Bundibugyo:0.16247,
Tai:0.15057);
```

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