

Alphafold

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Tags: *1_Drylab*

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(_ Written by Filip König_)

The target sequence was provided in form of fasta file and uploaded to the server.

A fasta file with the {3| number of chains in the target complex} target sequences were prepared and uploaded to the server.

To specify the template search space, the maximum template release date was set to {2021-01-01|maximum template release date}.

The multiple sequence alignments were generated with the default AlphaFold2 workflow.

The 5 resulting models have predicted LDDT scores of {92.53525399548542, 91.87078500440556, 91.7663773031415, 91.4853350371071, 91.34376681863755|pLDDT scores}.

AlphaFold Multimer provides confidence scores in form of a weighted linear combination of the predicted TM-score (pTM) and the interface predicted TM-score (ipTM). The 5 resulting models have scores of {0.2978001561893409, 0.27671591900244097, 0.25441992194655294, 0.24924325150457788, 0.2137227415772075|ipTM+pTM scores}. The predicted alignment errors are provided as plots as well as csv files.