<Section | Protein Domain Prediction>

The target sequence was submitted to the TopDomain server. The top five templates identified by TopDomain were {3N25\_A, 4YJ5\_A, 3GR4\_A, 1A49\_A, 6DU6\_B| template\_pdbs} with sequence identities of {99%, 93%, 93%, 100%, 63% | template\_identities}, coverages of {95%, 97%, 97%, 97%, 96%| template\_coverages}, and predicted TM-Score of {0.96, 0.96, 0.96, 0.96, 0.93 | template\_confidences}, respectively. TopDomain predicted {5|topdomain\_boundary\_number} boundary locations at positions {38, 115, 217, 324, 389|(comment, also only integers) topdomain\_positions} with peak boundary confidence scores of {0.83, 0.94, 0.91, 0.71, 0.95|topdomain\_confidences} respectively. TopDomainSeq predicted {4|topdomain\_seq\_boundary\_number} boundary locations at positions {39, 115, 215, 388|(comment, also only integers) topdomain\_seq\_positions} with peak boundary confidence scores of {0.65, 0.76, 0.73, 0.73|topdomain\_seq\_confidences} respectively.

<Section | Protein Property Prediction >

The target sequence was submitted to the TopProperty server. TopProperty predicted {10|(comment: this can only be integer) tm\_segments} trans-membrane segments and indicated that the fold is a {transmembrane helix bundle| (comment: This can only be 4 values: “transmembrane helix bundle, transmembrane beta barrel, transmembrane anchored protein and globular protein) tm\_protein\_class}.

<Section | Protein Structure Prediction >

Structure prediction was performed with { TopModel | (comment: only 3 options: TopModel, AlphaFold2, AlphaFoldMultimer) modelling\_method }. The model quality of the predicted structure was estimated by {AlphaFold2, TopScore| mqap\_method } with a final {pTM,TopScore|mqap\_score} score of {0.7|mqap\_value}. Residue-wise model quality showed that the majority of the protein was nicely predicted, but that residue regions {1-35,150-161|disorder\_regions} are likely disordered and has a low model confidence.

< ‘if’|method|=|TopModel>

The top five templates identified by TopModel were {3N25\_A, 4YJ5\_A, 3GR4\_A, 1A49\_A, 6DU6\_B| template\_pdbs} with identities of {99%, 93%, 93%, 100%, 63% | template\_identities}, coverages of { 95%, 97%, 97%, 97%, 96%| template\_coverages}, and predicted TM-Score of {0.96, 0.96, 0.96, 0.96, 0.93 | template\_confidences} , respectively.

<Section | Protein Structure Prediction >

Protein complex prediction was performed with {HADDOCK|(comment: only 3 options: HADDOCK, TopInterface and AlphaFoldMultimer) complex\_method}.

< ‘if’|method|=|HADDOCK>

For HADDOCK, {TopInterface | (comment: 4 different options: TopInterface, Experimental, Manual, Random) docking\_restraints } docking restraints were used to guide HADDOCK to the right docking solution. The lowest energy decoy from the largest cluster was selected as the final docking solution.

< ‘if’|method|=|AlphaFoldMultimer>

The final complex prediction showed a predicted TM-Score of {0.9|complex\_score}.