

Case Study

MODELING GPCR STRUCTURES IN NOVAFOLD

Using proprietary structure data or libraries of specific subdomains to enhance and refine structure prediction results.

Overview

Here we present a study using custom libraries for modeling a GPCR structure without a known experimental structure. We used a library with all public 350 GPCR structures to construct a base GPCR model by homology modeling. A separate structure was predicted for the extracellular region using the general-purpose NovaFold library. Then the two models were grafted together to create the final structure

Workflow

1

Model structure in NovaFold

Use the custom library of GPCR proteins to model the entire structure of the GPCR sheep viral sequence.

2

Model extracellular region

Using the default NovaFold library from the Protein Data Bank, model just the extracellular region of the GPCR protein.

3

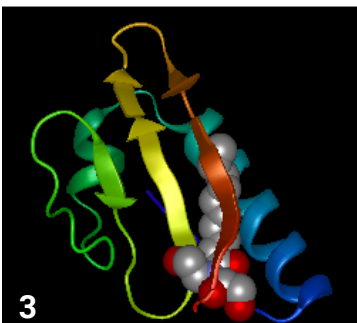
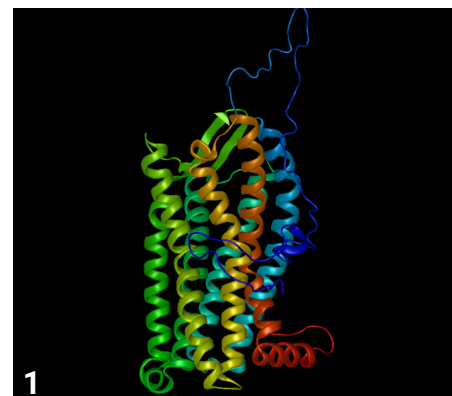
Identify extracellular region

View GO term functionality, similar structures and ligand binding sites using predicted protein function workflow to help identify the function of the extracellular part of the GPCR.

4

Align structures

Export subdomain of transmembrane portion of GPCR structure to a new PDB file, then import both the GPCR domain and the extracellular domain and align structures in Protean 3D.



<input type="checkbox"/>	Rank	Ligand	Method	Confidence	Template	Site Residues
<input checked="" type="checkbox"/>	1	2CV	TM-SITE	0.14	2y04A	13,17,20,21,24
<input type="checkbox"/>	2	CLA	TM-SITE	0.12	6iqzK	21,24,25
<input type="checkbox"/>	3	CA	S-SITE	0.05	2z8sA	61,62,63,64,65,67
<input type="checkbox"/>	4	UNL	TM-SITE	0.05	2h88C	19,22,26
<input type="checkbox"/>	5	BCL	TM-SITE	0.04	5y5sY	12,13,16,19,20,24
<input type="checkbox"/>	6	ZN	TM-SITE	0.03	5grqA	9,12,75
<input type="checkbox"/>	7	MUN	TM-SITE	0.03	6eyuA	21,25,66,67
<input type="checkbox"/>	8	CLA	TM-SITE	0.01	2d2cA	20,73
<input type="checkbox"/>	9	CA	TM-SITE	0.01	5bv9A	12,14
<input type="checkbox"/>	10	2CV	TM-SITE	0.01	2y00A	14,18



Results

The templates selected from homology modeling can help identify the class of GPCR being modeled. The independent modeling of the extracellular subdomain helps give insight into the function and structure of that region.

Custom libraries are available for a wide variety of projects, and can be created for proprietary or public data. Contact support@dnastar.com for more information.