

# 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

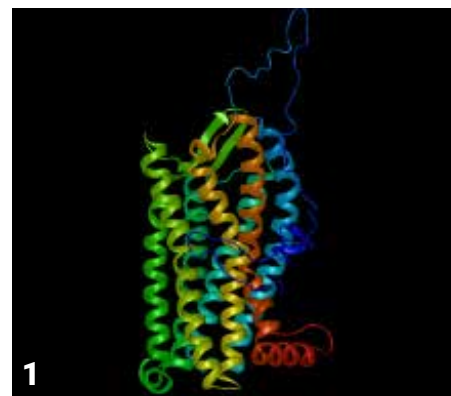
#### Identify extracellular region

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.



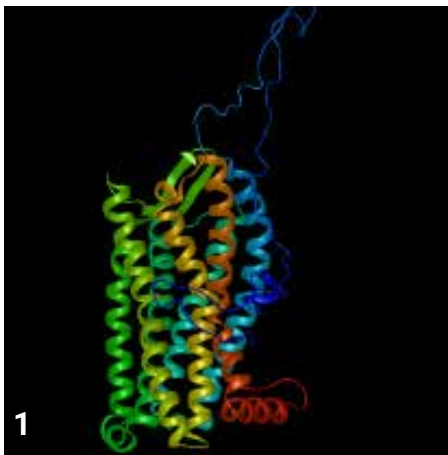
	Rank	Ligand	Method	Confidence	Template	Site Residues
<input checked="" type="checkbox"/>	1	2CV	TIM-S-TE	0.14	2y04A	13,17,20,21,24
<input type="checkbox"/>	2	CLA	TIM-S-TE	0.12	6iq4K	21,24,25
<input type="checkbox"/>	3	CA	S-SITE	0.05	2d8vA	61,62,63,64,65,67
<input type="checkbox"/>	4	UNIL	TIM-S-TE	0.05	2i88C	19,22,26
<input type="checkbox"/>	5	BCL	TIM-S-TE	0.04	5y5yY	12,13,16,19,20,24
<input type="checkbox"/>	6	ZN	TIM-S-TE	0.03	5uq4A	9,12,75
<input type="checkbox"/>	7	VLN	TIM-S-TE	0.03	6gyuA	21,25,66,67
<input type="checkbox"/>	8	CLA	TIM-S-TE	0.01	2u2cA	20,73
<input type="checkbox"/>	9	CA	TIM-S-TE	0.01	5lv9A	12,14
<input type="checkbox"/>	10	2CV	TIM-S-TE	0.01	2y02A	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.**





## Workflow

The following steps can be completed using NovaFold and any custom structure library.

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 Databank, model just the extracellular region of the GPCR protein.

3

### Identify extracellular region

View GO term functionality, similar structures and ligand binding sites from Coach and CoFactor methods 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 and then import both the GPCR domain and the extracellular domain and align structures using TM-Align in Protean 3D.



<input type="checkbox"/>	Rank	Ligand	Method	Confidence	Template	Site Residues
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<input type="checkbox"/>	9	CA	TM-SITE	0.01	5b09A	12,14
<input type="checkbox"/>	10	2CV	TM-SITE	0.01	2y02A	14,18

## Results

Modeling the GPCR using the homology modeling threader templates helps identify the type of GPCR structure by reviewing the templates used in the creation of the model. The independent modeling of the extracellular subdomain helps give insight into the function and structure of that region.

## Create your own library

Custom libraries are available for a wide variety of projects, and can be created for proprietary and public data. Contact support@dnastar.com to get started!