
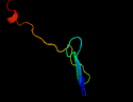

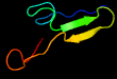



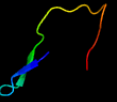

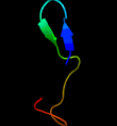
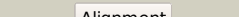

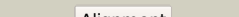
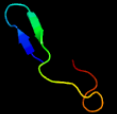

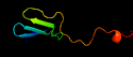

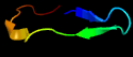

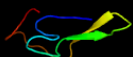


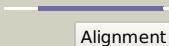
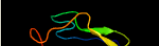
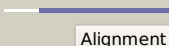
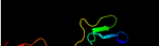
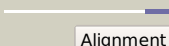

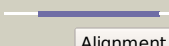
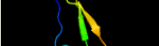
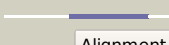


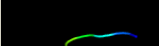

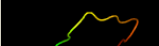
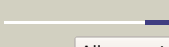



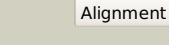
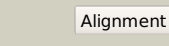
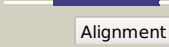
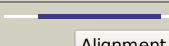
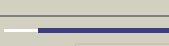

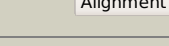
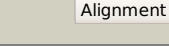
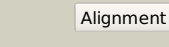


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2386A_(RVBD2386A)_2680468_2680677
Date	Mon Aug 5 13:25:54 BST 2019
Unique Job ID	69765ede0a82aed6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1jz8a4</a>	 Alignment		52.0	15	<b>Fold:</b> Supersandwich <b>Superfamily:</b> Galactose mutarotase-like <b>Family:</b> beta-Galactosidase, domain 5
2	<a href="#">d2omwb1</a>	 Alignment		20.4	14	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Cadherin-like <b>Family:</b> Cadherin
3	<a href="#">c3ff8B_</a>	 Alignment		17.7	27	<b>PDB header:</b> cell adhesion/immune system <b>Chain:</b> B: <b>PDB Molecule:</b> epithelial cadherin; <b>PDBTitle:</b> structure of nk cell receptor klrp1 bound to e-cadherin
4	<a href="#">d1l3wa1</a>	 Alignment		15.8	28	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Cadherin-like <b>Family:</b> Cadherin
5	<a href="#">c1nciB_</a>	 Alignment		15.3	29	<b>PDB header:</b> cell adhesion protein <b>Chain:</b> B: <b>PDB Molecule:</b> n-cadherin; <b>PDBTitle:</b> structural basis of cell-cell adhesion by cadherins
6	<a href="#">d2omzb1</a>	 Alignment		14.0	28	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Cadherin-like <b>Family:</b> Cadherin
7	<a href="#">c4zmtF_</a>	 Alignment		14.0	20	<b>PDB header:</b> cell adhesion <b>Chain:</b> F: <b>PDB Molecule:</b> cadherin-3; <b>PDBTitle:</b> crystal structure of human p-cadherin (ss-x-dimer-long)
8	<a href="#">c3mv14_</a>	 Alignment		13.4	12	<b>PDB header:</b> hydrolase <b>Chain:</b> 4: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> e.coli (lacz) beta-galactosidase (r599a) in complex with guanidinium
9	<a href="#">c3ff7B_</a>	 Alignment		13.3	29	<b>PDB header:</b> cell adhesion/immune system <b>Chain:</b> B: <b>PDB Molecule:</b> epithelial cadherin; <b>PDBTitle:</b> structure of nk cell receptor klrp1 bound to e-cadherin
10	<a href="#">c1nciA_</a>	 Alignment		13.2	18	<b>PDB header:</b> cell adhesion protein <b>Chain:</b> A: <b>PDB Molecule:</b> n-cadherin; <b>PDBTitle:</b> structural basis of cell-cell adhesion by cadherins
11	<a href="#">d1ncia_</a>	 Alignment		13.2	18	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Cadherin-like <b>Family:</b> Cadherin

12	<a href="#">c1nchB</a>	 Alignment		12.4	16	<b>PDB header:</b> cell adhesion protein <b>Chain:</b> B: <b>PDB Molecule:</b> n-cadherin; <b>PDBTitle:</b> structural basis of cell-cell adhesion by cadherins
13	<a href="#">c1jz6C</a>	 Alignment		11.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> e. coli (lacz) beta-galactosidase in complex with galacto-2 tetrazole
14	<a href="#">c2rqxA</a>	 Alignment		11.4	50	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> polymyxin b resistance protein; <b>PDBTitle:</b> solution nmr structure of pmrd from klebsiella pneumoniae
15	<a href="#">c1ncgA</a>	 Alignment		11.3	17	<b>PDB header:</b> cell adhesion protein <b>Chain:</b> A: <b>PDB Molecule:</b> n-cadherin; <b>PDBTitle:</b> structural basis of cell-cell adhesion by cadherins
16	<a href="#">c1zxcB</a>	 Alignment		11.1	25	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> cadherin-8; <b>PDBTitle:</b> crystal structure of cadherin8 ec1 domain
17	<a href="#">c2p6yA</a>	 Alignment		7.5	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein vca0587; <b>PDBTitle:</b> x-ray structure of the protein q9km02_vibch from vibrio cholerae at2 the resolution 1.63 a. northeast structural genomics consortium3 target vcr80.
18	<a href="#">c1nchA</a>	 Alignment		7.3	29	<b>PDB header:</b> cell adhesion protein <b>Chain:</b> A: <b>PDB Molecule:</b> n-cadherin; <b>PDBTitle:</b> structural basis of cell-cell adhesion by cadherins
19	<a href="#">c2jsoA</a>	 Alignment		7.1	40	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> polymyxin resistance protein pmrd; <b>PDBTitle:</b> antimicrobial resistance protein
20	<a href="#">d1igqa</a>	 Alignment		7.0	21	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> C-terminal domain of transcriptional repressors <b>Family:</b> Transcriptional repressor protein KorB
21	<a href="#">c1zvnA</a>	 Alignment	not modelled	6.9	24	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> cadherin 1; <b>PDBTitle:</b> crystal structure of chick mn-cadherin ec1
22	<a href="#">d2f9zc1</a>	 Alignment	not modelled	6.6	29	<b>Fold:</b> CNF1/YfiH-like putative cysteine hydrolases <b>Superfamily:</b> CNF1/YfiH-like putative cysteine hydrolases <b>Family:</b> CheD-like
23	<a href="#">c1dgiA</a>	 Alignment	not modelled	6.5	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aldehyde oxidoreductase; <b>PDBTitle:</b> crystal structure of the aldehyde oxidoreductase from2 desulfovibrio desulfuricans atcc 27774
24	<a href="#">c4lq8B</a>	 Alignment	not modelled	6.3	24	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> sca-family protein; <b>PDBTitle:</b> rickettsia rickettsii cell surface antigen 4 (sca4) head domain2 (residues 21-360)
25	<a href="#">c3hwuA</a>	 Alignment	not modelled	6.2	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative dna-binding protein; <b>PDBTitle:</b> crystal structure of putative dna-binding protein (yp_299413.1) from2 ralstonia eutropha jmp134 at 1.30 a resolution
26	<a href="#">c1zxcA</a>	 Alignment	not modelled	6.2	24	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> cadherin-8; <b>PDBTitle:</b> crystal structure of cadherin8 ec1 domain
27	<a href="#">d1igub</a>	 Alignment	not modelled	6.1	21	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> C-terminal domain of transcriptional repressors <b>Family:</b> Transcriptional repressor protein KorB
28	<a href="#">d1a0ia1</a>	 Alignment	not modelled	6.1	29	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> DNA ligase/mRNA capping enzyme postcatalytic domain
29	<a href="#">c5xkaE</a>	 Alignment	not modelled	5.8	45	<b>PDB header:</b> transferase/signaling protein <b>Chain:</b> E: <b>PDB Molecule:</b> epidermal patterning factor-like protein 4;

29	<a href="#">c3xslE_</a>	Alignment	not modelled	5.8	43	<b>PDBTitle:</b> crystal structure of plant receptor erl2 in complexe with epfl4
30	<a href="#">c5xknF_</a>	Alignment	not modelled	5.8	45	<b>PDB header:</b> transferase/signaling protein <b>Chain:</b> F; <b>PDB Molecule:</b> epidermal patterning factor-like protein 4; <b>PDBTitle:</b> crystal structure of plant receptor erl2 in complexe with epfl4
31	<a href="#">c5kwbA_</a>	Alignment	not modelled	5.6	29	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> spike glycoprotein; <b>PDBTitle:</b> crystal structure of the receptor binding domain of the spike2 glycoprotein of human betacoronavirus hku1 (hku1 1a-ctd, 1.93 angstrom, molecular replacement)
32	<a href="#">d2qlva1</a>	Alignment	not modelled	5.5	20	<b>Fold:</b> TBP-like <b>Superfamily:</b> KA1-like <b>Family:</b> Ssp2 C-terminal domain-like
33	<a href="#">c5ghaF_</a>	Alignment	not modelled	5.4	41	<b>PDB header:</b> transferase/transport protein <b>Chain:</b> F; <b>PDB Molecule:</b> sulfur carrier ttub; <b>PDBTitle:</b> sulfur transferase ttua in complex with sulfur carrier ttub
34	<a href="#">c3htrB_</a>	Alignment	not modelled	5.4	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized prc-barrel domain protein; <b>PDBTitle:</b> crystal structure of prc-barrel domain protein from2 rhodopseudomonas palustris
35	<a href="#">c3hlzA_</a>	Alignment	not modelled	5.3	50	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein bt_1490; <b>PDBTitle:</b> crystal structure of bt_1490 (np_810393.1) from bacteroides2 thetaiotaomicron vpi-5482 at 1.50 a resolution
36	<a href="#">c4eogA_</a>	Alignment	not modelled	5.3	33	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of csx1 of pyrococcus furiosus