
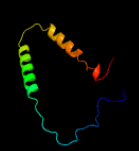
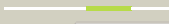
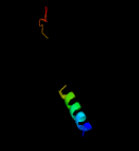

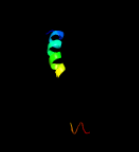

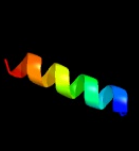

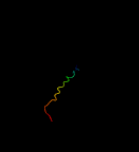

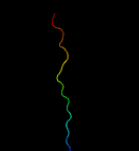

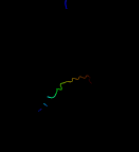

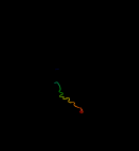





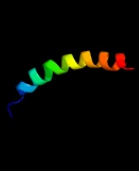
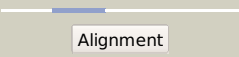

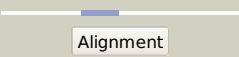
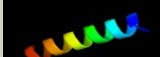
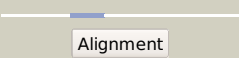

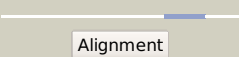
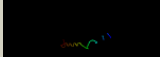
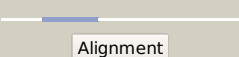

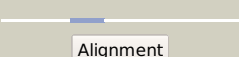

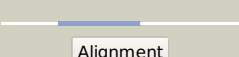
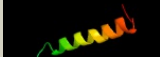
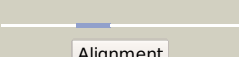

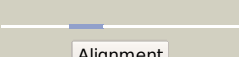

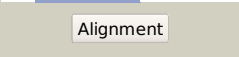
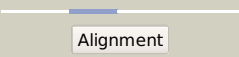
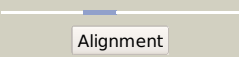
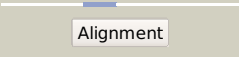
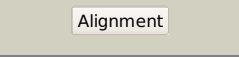
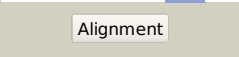
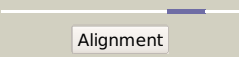
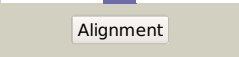


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3705A (-) _4149269_4149658
Date	Fri Aug 9 18:20:40 BST 2019
Unique Job ID	753b29425f36d1d1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4ymkA_</a>	 Alignment		82.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> acyl-coa desaturase 1; <b>PDBTitle:</b> crystal structure of stearyl-coenzyme a desaturase 1
2	<a href="#">c2m0qA_</a>	 Alignment		69.5	23	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> potassium voltage-gated channel subfamily e member 2; <b>PDBTitle:</b> solution nmr analysis of intact kcne2 in detergent micelles2 demonstrate a straight transmembrane helix
3	<a href="#">c2k21A_</a>	 Alignment		54.5	27	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> potassium voltage-gated channel subfamily e <b>PDBTitle:</b> nmr structure of human kcne1 in Impg micelles at ph 6.0 and2 40 degree c
4	<a href="#">c6a69B_</a>	 Alignment		48.4	29	<b>PDB header:</b> structural protein <b>Chain:</b> B; <b>PDB Molecule:</b> neuroplastin; <b>PDBTitle:</b> cryo-em structure of a p-type atpase
5	<a href="#">c6a0aA_</a>	 Alignment		38.7	48	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> collagen type iii peptide; <b>PDBTitle:</b> structure of a triple-helix region of human collagen type iii
6	<a href="#">c1x1kF_</a>	 Alignment		36.8	68	<b>PDB header:</b> structural protein <b>Chain:</b> F; <b>PDB Molecule:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp- <b>PDBTitle:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
7	<a href="#">c6a0aC_</a>	 Alignment		34.0	52	<b>PDB header:</b> structural protein <b>Chain:</b> C; <b>PDB Molecule:</b> collagen type iii peptide; <b>PDBTitle:</b> structure of a triple-helix region of human collagen type iii
8	<a href="#">c6a0aB_</a>	 Alignment		34.0	52	<b>PDB header:</b> structural protein <b>Chain:</b> B; <b>PDB Molecule:</b> collagen type iii peptide; <b>PDBTitle:</b> structure of a triple-helix region of human collagen type iii
9	<a href="#">c2jo1A_</a>	 Alignment		29.2	23	<b>PDB header:</b> hydrolase regulator <b>Chain:</b> A; <b>PDB Molecule:</b> phospholemman; <b>PDBTitle:</b> structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
10	<a href="#">c6nhyA_</a>	 Alignment		29.0	38	<b>PDB header:</b> immune system <b>Chain:</b> A; <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 10b; <b>PDBTitle:</b> structure of the transmembrane domain of the death receptor 5 mutant2 (g217y) - trimer only
11	<a href="#">c6nhyB_</a>	 Alignment		29.0	38	<b>PDB header:</b> immune system <b>Chain:</b> B; <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 10b; <b>PDBTitle:</b> structure of the transmembrane domain of the death receptor 5 mutant2 (g217y) - trimer only

12	<a href="#">c6nhyC_</a>			29.0	38	<b>PDB header:</b> immune system <b>Chain:</b> C; <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 10b; <b>PDBTitle:</b> structure of the transmembrane domain of the death receptor 5 mutant2 (g217y) - trimer only
13	<a href="#">c2mkvA_</a>			28.7	23	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> sodium/potassium-transporting atpase subunit gamma; <b>PDBTitle:</b> structure of the na,k-atpase regulatory protein fxyd2b in micelles
14	<a href="#">c3jcuJ_</a>			28.5	47	<b>PDB header:</b> membrane protein <b>Chain:</b> J; <b>PDB Molecule:</b> photosystem ii reaction center protein j; <b>PDBTitle:</b> cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
15	<a href="#">c6a0cB_</a>			28.1	48	<b>PDB header:</b> structural protein <b>Chain:</b> B; <b>PDB Molecule:</b> collagen type iii peptide; <b>PDBTitle:</b> structure of a triple-helix region of human collagen type iii
16	<a href="#">c6hwhB_</a>			26.2	13	<b>PDB header:</b> electron transport <b>Chain:</b> B; <b>PDB Molecule:</b> ubiquinol-cytochrome c reductase iron-sulfur subunit; <b>PDBTitle:</b> structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
17	<a href="#">c5xnmj_</a>			25.9	44	<b>PDB header:</b> membrane protein <b>Chain:</b> J; <b>PDB Molecule:</b> photosystem ii reaction center protein j; <b>PDBTitle:</b> structure of unstacked c2s2m2-type psii-lhcii supercomplex from pisum2 sativum
18	<a href="#">c4zyoA_</a>			25.1	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> acyl-coa desaturase; <b>PDBTitle:</b> crystal structure of human integral membrane stearyl-coa desaturase2 with substrate
19	<a href="#">c2k1vB_</a>			25.0	54	<b>PDB header:</b> hormone <b>Chain:</b> B; <b>PDB Molecule:</b> relaxin-3; <b>PDBTitle:</b> r3/i5 relaxin chimera
20	<a href="#">c2k1aA_</a>			24.6	13	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> integrin alpha-iib; <b>PDBTitle:</b> bicelle-embedded integrin alpha(iib) transmembrane segment
21	<a href="#">c2ndjA_</a>		not modelled	24.5	25	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> potassium voltage-gated channel subfamily e member 3; <b>PDBTitle:</b> structural basis for kcne3 and estrogen modulation of the kcnq12 channel
22	<a href="#">c2jp3A_</a>		not modelled	24.4	21	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> fxyd domain-containing ion transport regulator 4; <b>PDBTitle:</b> solution structure of the human fxyd4 (chif) protein in sds2 micelles
23	<a href="#">c5oqtC_</a>		not modelled	23.6	45	<b>PDB header:</b> transport protein <b>Chain:</b> C; <b>PDB Molecule:</b> uncharacterized protein ynem; <b>PDBTitle:</b> crystal structure of a bacterial cationic amino acid transporter (cat)2 homologue
24	<a href="#">c6f34C_</a>		not modelled	23.6	45	<b>PDB header:</b> membrane protein <b>Chain:</b> C; <b>PDB Molecule:</b> mgts; <b>PDBTitle:</b> crystal structure of a bacterial cationic amino acid transporter (cat)2 homologue bound to arginine.
25	<a href="#">c6a0cC_</a>		not modelled	23.5	52	<b>PDB header:</b> structural protein <b>Chain:</b> C; <b>PDB Molecule:</b> collagen type iii peptide; <b>PDBTitle:</b> structure of a triple-helix region of human collagen type iii
26	<a href="#">c6a0cA_</a>		not modelled	23.5	52	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> collagen type iii peptide; <b>PDBTitle:</b> structure of a triple-helix region of human collagen type iii
27	<a href="#">c3a0mD_</a>		not modelled	19.9	64	<b>PDB header:</b> structural protein <b>Chain:</b> D; <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
28	<a href="#">c2k9hA_</a>		not modelled	19.9	67	<b>PDB header:</b> metal binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> glycoprotein; <b>PDBTitle:</b> the hantavirus glycoprotein g1 tail contains a dual cchc-2 type classical zinc fingers

29	<a href="#">c6c14B_</a>	Alignment	not modelled	19.0	15	<b>PDB header:</b> membrane protein, metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> lhfp1 tetraspan subfamily member 5 protein; <b>PDBTitle:</b> cryoem structure of mouse pcdh15-1ec-lhfp15 complex
30	<a href="#">c3a0mB_</a>	Alignment	not modelled	18.8	65	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
31	<a href="#">c4yzfA_</a>	Alignment	not modelled	18.5	19	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> band 3 anion transport protein; <b>PDBTitle:</b> crystal structure of the anion exchanger domain of human erythrocyte2 band 3
32	<a href="#">c3a0mE_</a>	Alignment	not modelled	17.9	58	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
33	<a href="#">c3a0mC_</a>	Alignment	not modelled	17.9	64	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
34	<a href="#">c2v53C_</a>	Alignment	not modelled	17.6	54	<b>PDB header:</b> cell adhesion <b>Chain:</b> C: <b>PDB Molecule:</b> collagen alpha-1(iii) chain; <b>PDBTitle:</b> crystal structure of a sparc-collagen complex
35	<a href="#">c2v53D_</a>	Alignment	not modelled	17.6	54	<b>PDB header:</b> cell adhesion <b>Chain:</b> D: <b>PDB Molecule:</b> collagen alpha-1(iii) chain; <b>PDBTitle:</b> crystal structure of a sparc-collagen complex
36	<a href="#">c2v53B_</a>	Alignment	not modelled	17.6	54	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> collagen alpha-1(iii) chain; <b>PDBTitle:</b> crystal structure of a sparc-collagen complex
37	<a href="#">c2k1kA_</a>	Alignment	not modelled	17.4	83	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ephrin type-a receptor 1; <b>PDBTitle:</b> nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
38	<a href="#">c2k1kB_</a>	Alignment	not modelled	17.4	83	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> ephrin type-a receptor 1; <b>PDBTitle:</b> nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
39	<a href="#">c2k1kA_</a>	Alignment	not modelled	17.4	83	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ephrin type-a receptor 1; <b>PDBTitle:</b> nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
40	<a href="#">c2k1kB_</a>	Alignment	not modelled	17.4	83	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> ephrin type-a receptor 1; <b>PDBTitle:</b> nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
41	<a href="#">c3ctwB_</a>	Alignment	not modelled	17.0	40	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> rcda; <b>PDBTitle:</b> crystal structure of rcda from caulobacter crescentus cb15
42	<a href="#">d1ug0a_</a>	Alignment	not modelled	17.0	18	<b>Fold:</b> Surp module (SWAP domain) <b>Superfamily:</b> Surp module (SWAP domain) <b>Family:</b> Surp module (SWAP domain)
43	<a href="#">c3a1hA_</a>	Alignment	not modelled	16.2	58	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure analysis of the collagen-like peptide, (ppg)4-otg-2 (ppg)4
44	<a href="#">c2kncA_</a>	Alignment	not modelled	15.3	13	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiB; <b>PDBTitle:</b> platelet integrin alfaIIB-beta3 transmembrane-cytoplasmic2 heterocomplex
45	<a href="#">c3a0mA_</a>	Alignment	not modelled	15.2	64	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
46	<a href="#">c6caaA_</a>	Alignment	not modelled	14.8	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> electrogenic sodium bicarbonate cotransporter 1; <b>PDBTitle:</b> cryoem structure of human slc4a4 sodium-coupled acid-base transporter2 nbce1
47	<a href="#">c3a1hF_</a>	Alignment	not modelled	14.7	65	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure analysis of the collagen-like peptide, (ppg)4-otg-2 (ppg)4
48	<a href="#">c3hclB_</a>	Alignment	not modelled	14.5	40	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> peptide methionine sulfoxide reductase; <b>PDBTitle:</b> structure of msrb from xanthomonas campestris (oxidized2 form)
49	<a href="#">c6nhwC_</a>	Alignment	not modelled	13.6	54	<b>PDB header:</b> immune system <b>Chain:</b> C: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 10b; <b>PDBTitle:</b> structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
50	<a href="#">c6nhwE_</a>	Alignment	not modelled	13.6	54	<b>PDB header:</b> immune system <b>Chain:</b> E: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 10b; <b>PDBTitle:</b> structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
51	<a href="#">c6nhwF_</a>	Alignment	not modelled	13.6	54	<b>PDB header:</b> immune system <b>Chain:</b> F: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 10b; <b>PDBTitle:</b> structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
52	<a href="#">c6nhwB_</a>	Alignment	not modelled	13.6	54	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 10b; <b>PDBTitle:</b> structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
53	<a href="#">c3a1hE_</a>	Alignment	not modelled	13.5	64	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure analysis of the collagen-like peptide,

						(ppg)4-otg-2 (ppg)4
54	<a href="#">c3a1hC_</a>	Alignment	not modelled	13.5	64	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure analysis of the collagen-like peptide, (ppg)4-otg-2 (ppg)4
55	<a href="#">c3a1hD_</a>	Alignment	not modelled	13.5	64	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure analysis of the collagen-like peptide, (ppg)4-otg-2 (ppg)4
56	<a href="#">c3n23E_</a>	Alignment	not modelled	13.3	42	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> na+/k+ atpase gamma subunit transcript variant a; <b>PDBTitle:</b> crystal structure of the high affinity complex between ouabain and the e2p form of the sodium-potassium pump
57	<a href="#">d1x4oa1</a>	Alignment	not modelled	13.1	29	<b>Fold:</b> Surp module (SWAP domain) <b>Superfamily:</b> Surp module (SWAP domain) <b>Family:</b> Surp module (SWAP domain)
58	<a href="#">c4xydB_</a>	Alignment	not modelled	13.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> norc-like protein; <b>PDBTitle:</b> nitric oxide reductase from roseobacter denitrificans (rdnor)
59	<a href="#">d1qhda1</a>	Alignment	not modelled	12.8	83	<b>Fold:</b> A virus capsid protein alpha-helical domain <b>Superfamily:</b> A virus capsid protein alpha-helical domain <b>Family:</b> vp6, the major capsid protein of group A rotavirus
60	<a href="#">c6irtA_</a>	Alignment	not modelled	12.7	25	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> 4f2 cell-surface antigen heavy chain; <b>PDBTitle:</b> human lat1-4f2hc complex bound with bch
61	<a href="#">d1xcra1</a>	Alignment	not modelled	12.3	32	<b>Fold:</b> AF0104/ALDC/Ptd012-like <b>Superfamily:</b> AF0104/ALDC/Ptd012-like <b>Family:</b> PTD012-like
62	<a href="#">c3gcfC_</a>	Alignment	not modelled	12.2	62	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> terminal oxygenase component of carbazole 1,9a- <b>PDBTitle:</b> terminal oxygenase of carbazole 1,9a-dioxygenase from <i>Nocardioides aromaticivorans</i> ic177
63	<a href="#">c3a1hB_</a>	Alignment	not modelled	12.2	58	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure analysis of the collagen-like peptide, (ppg)4-otg-2 (ppg)4
64	<a href="#">d2hlya1</a>	Alignment	not modelled	11.4	33	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Atu2299-like
65	<a href="#">c5sv9B_</a>	Alignment	not modelled	11.4	9	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> bor1p boron transporter; <b>PDBTitle:</b> structure of the slc4 transporter bor1p in an inward-facing conformation
66	<a href="#">d2axtj1</a>	Alignment	not modelled	11.4	50	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Photosystem II reaction center protein J, Psbj <b>Family:</b> Psbj-like
67	<a href="#">c3a0hj_</a>	Alignment	not modelled	11.4	50	<b>PDB header:</b> electron transport <b>Chain:</b> J: <b>PDB Molecule:</b> photosystem ii reaction center protein j; <b>PDBTitle:</b> crystal structure of i-substituted photosystem ii complex
68	<a href="#">c6ae1B_</a>	Alignment	not modelled	11.1	50	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> crispr-associated protein, tm1810 family; <b>PDBTitle:</b> crystal structure of csm2 of the type iii-a crispr-cas effector2 complex
69	<a href="#">c4bklG_</a>	Alignment	not modelled	11.1	100	<b>PDB header:</b> immune system <b>Chain:</b> G: <b>PDB Molecule:</b> j1 epitope; <b>PDBTitle:</b> crystal structure of the arthritogenic antibody m2139 (fab2 fragment) in complex with the triple-helical j1 peptide
70	<a href="#">c2e5zA_</a>	Alignment	not modelled	11.0	23	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> splicing factor, arginine/serine-rich 8; <b>PDBTitle:</b> solution structure of the surp2 domain in splicing factor, 2 arginine/serine-rich 8
71	<a href="#">c2hmnA_</a>	Alignment	not modelled	10.9	83	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> naphthalene 1,2-dioxygenase alpha subunit; <b>PDBTitle:</b> crystal structure of the naphthalene 1,2-dioxygenase f352v2 mutant bound to anthracene.
72	<a href="#">c1z01D_</a>	Alignment	not modelled	10.8	62	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-oxo-1,2-dihydroquinoline 8-monoxygenase, oxygenase <b>PDBTitle:</b> 2-oxoquinoline 8-monoxygenase component: active site modulation by 2 rieske-[2fe-2s] center oxidation/reduction
73	<a href="#">c3jcul_</a>	Alignment	not modelled	10.6	29	<b>PDB header:</b> membrane protein <b>Chain:</b> I: <b>PDB Molecule:</b> protein photosystem ii reaction center protein i; <b>PDBTitle:</b> cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom resolution
74	<a href="#">c3kdpH_</a>	Alignment	not modelled	10.2	36	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> na+/k+ atpase gamma subunit transcript variant a; <b>PDBTitle:</b> crystal structure of the sodium-potassium pump
75	<a href="#">c3kdpG_</a>	Alignment	not modelled	10.2	36	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> na+/k+ atpase gamma subunit transcript variant a; <b>PDBTitle:</b> crystal structure of the sodium-potassium pump
76	<a href="#">c2hacB_</a>	Alignment	not modelled	10.2	33	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> t-cell surface glycoprotein cd3 zeta chain; <b>PDBTitle:</b> structure of zeta-zeta transmembrane dimer
77	<a href="#">c2hacA_</a>	Alignment	not modelled	10.2	33	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> t-cell surface glycoprotein cd3 zeta chain; <b>PDBTitle:</b> structure of zeta-zeta transmembrane dimer
78	<a href="#">c3nvnA_</a>	Alignment	not modelled	10.1	57	<b>PDB header:</b> viral protein/signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> evm139; <b>PDBTitle:</b> molecular mechanism of guidance cue recognition

79	<a href="#">c3gzkA_</a>	Alignment	not modelled	9.9	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulase; <b>PDBTitle:</b> structure of a. acidocaldarius cellulase cela
80	<a href="#">d2axti1</a>	Alignment	not modelled	9.8	35	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Photosystem II reaction center protein I, Psbl <b>Family:</b> Psbl-like
81	<a href="#">c3a0hi_</a>	Alignment	not modelled	9.8	35	<b>PDB header:</b> electron transport <b>Chain:</b> I: <b>PDB Molecule:</b> photosystem ii reaction center protein i; <b>PDBTitle:</b> crystal structure of i-substituted photosystem ii complex
82	<a href="#">c6c3rB_</a>	Alignment	not modelled	9.8	63	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> cricket paralysis virus 1a protein; <b>PDBTitle:</b> cricket paralysis virus rna1 suppressor protein crpv-1a
83	<a href="#">c4hqjG_</a>	Alignment	not modelled	9.8	36	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> G: <b>PDB Molecule:</b> na+/k+ atpase gamma subunit transcript variant a; <b>PDBTitle:</b> crystal structure of na+,k+-atpase in the na+-bound state
84	<a href="#">c5vnyA_</a>	Alignment	not modelled	9.7	71	<b>PDB header:</b> endocytosis, protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> lethal (2) giant discs 1, isoform b; <b>PDBTitle:</b> crystal structure of dm14-3 domain of lgd
85	<a href="#">c1wqlA_</a>	Alignment	not modelled	9.1	62	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> iron-sulfur protein large subunit of cumene dioxygenase; <b>PDBTitle:</b> cumene dioxygenase (cuma1a2) from pseudomonas fluorescens ip01
86	<a href="#">c4hqjE_</a>	Alignment	not modelled	8.9	36	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> E: <b>PDB Molecule:</b> na+/k+ atpase gamma subunit transcript variant a; <b>PDBTitle:</b> crystal structure of na+,k+-atpase in the na+-bound state
87	<a href="#">c3abnC_</a>	Alignment	not modelled	8.9	65	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-asp-gly-(pro-pro-gly)4 at 1.022 a
88	<a href="#">c3admC_</a>	Alignment	not modelled	8.8	64	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
89	<a href="#">c2de7B_</a>	Alignment	not modelled	8.7	54	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> terminal oxygenase component of carbazole; <b>PDBTitle:</b> the substrate-bound complex between oxygenase and 2 ferredoxin in carbazole 1,9a-dioxygenase
90	<a href="#">c3admD_</a>	Alignment	not modelled	8.6	64	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
91	<a href="#">c3a0aF_</a>	Alignment	not modelled	8.6	65	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
92	<a href="#">c4bmtB_</a>	Alignment	not modelled	8.5	37	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ribonucleoside-diphosphate reductase subunit beta; <b>PDBTitle:</b> crystal structure of ribonucleotide reductase di-iron nrd2 from bacillus cereus
93	<a href="#">c3a0aA_</a>	Alignment	not modelled	8.5	58	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
94	<a href="#">c2elpA_</a>	Alignment	not modelled	8.4	63	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger protein 406; <b>PDBTitle:</b> solution structure of the 13th c2h2 zinc finger of human2 zinc finger protein 406
95	<a href="#">c3a08F_</a>	Alignment	not modelled	8.2	65	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-oog-(ppg)4, monoclinic, twinned crystal
96	<a href="#">c3abnB_</a>	Alignment	not modelled	8.2	64	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-asp-gly-(pro-pro-gly)4 at 1.022 a
97	<a href="#">c3eamB_</a>	Alignment	not modelled	7.8	23	<b>PDB header:</b> membrane protein, transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> glr4197 protein; <b>PDBTitle:</b> an open-pore structure of a bacterial pentameric ligand-2 gated ion channel
98	<a href="#">c3a08E_</a>	Alignment	not modelled	7.8	58	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-oog-(ppg)4, monoclinic, twinned crystal
99	<a href="#">c2kogA_</a>	Alignment	not modelled	7.6	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> vesicle-associated membrane protein 2; <b>PDBTitle:</b> lipid-bound synaptobrevin solution nmr structure