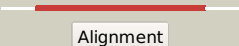
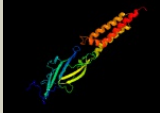


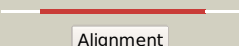
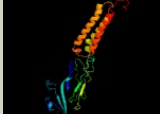

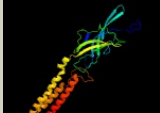


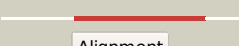


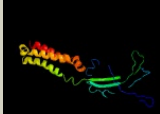





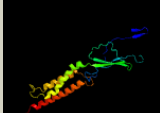

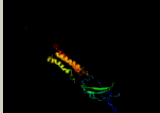
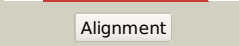
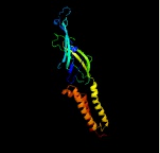



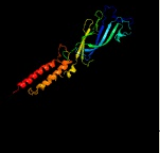

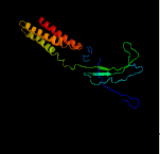
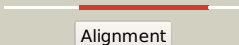

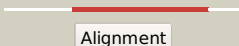

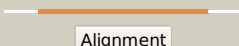
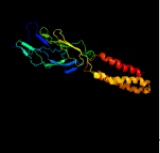
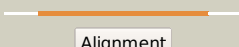

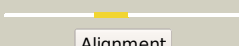

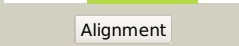
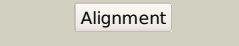
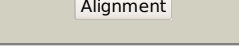
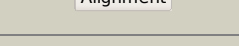


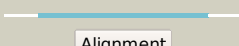



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3435c (- )_3854119_3854973
Date	Fri Aug 9 18:20:10 BST 2019
Unique Job ID	826de3ab3d337452

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3riaC_</a>	 Alignment		97.1	15	<b>PDB header:</b> transport protein/immune system <b>Chain:</b> C: <b>PDB Molecule:</b> avermectin-sensitive glutamate-gated chloride channel glucl <b>PDBTitle:</b> c. elegans glutamate-gated chloride channel (glucl) in complex with2 fab, ivermectin and iodide.
2	<a href="#">c4pirD_</a>	 Alignment		96.9	21	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> 5-hydroxytryptamine receptor 3a; <b>PDBTitle:</b> x-ray structure of the mouse serotonin 5-ht3 receptor
3	<a href="#">c3jadC_</a>	 Alignment		96.8	13	<b>PDB header:</b> signaling protein/antagonist <b>Chain:</b> C: <b>PDB Molecule:</b> glycine receptor subunit alphaz1; <b>PDBTitle:</b> structure of alpha-1 glycine receptor by single particle electron2 cryo-microscopy, strychnine-bound state
4	<a href="#">c3eamB_</a>	 Alignment		96.6	15	<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
5	<a href="#">c6d6uB_</a>	 Alignment		96.4	13	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> gamma-aminobutyric acid receptor subunit alpha-1,gamma- <b>PDBTitle:</b> human gaba-a receptor alpha1-beta2-gamma2 subtype in complex with gaba2 and flumazenil, conformation a
6	<a href="#">c4cofC_</a>	 Alignment		96.3	17	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> gamma-aminobutyric acid receptor subunit beta-3; <b>PDBTitle:</b> crystal structure of a human gamma-aminobutyric acid receptor, the2 gaba(a)r-beta3 homopentamer
7	<a href="#">c4aq5C_</a>	 Alignment		96.2	14	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> acetylcholine receptor delta subunit; <b>PDBTitle:</b> gating movement in acetylcholine receptor analysed by time-resolved2 electron cryo-microscopy (closed class)
8	<a href="#">c2vl0A_</a>	 Alignment		95.7	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> elic pentameric ligand gated ion channel from <b>PDBTitle:</b> x-ray structure of a pentameric ligand gated ion channel2 from erwinia chrysanthemi (elic)
9	<a href="#">c2bg9C_</a>	 Alignment		95.6	13	<b>PDB header:</b> ion channel/receptor <b>Chain:</b> C: <b>PDB Molecule:</b> acetylcholine receptor protein, delta chain; <b>PDBTitle:</b> refined structure of the nicotinic acetylcholine receptor2 at 4a resolution.
10	<a href="#">c5kxiA_</a>	 Alignment		95.6	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> neuronal acetylcholine receptor subunit alpha-4; <b>PDBTitle:</b> x-ray structure of the human alpha4beta2 nicotinic receptor
11	<a href="#">c4aq5B_</a>	 Alignment		95.4	12	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> acetylcholine receptor beta subunit; <b>PDBTitle:</b> gating movement in acetylcholine receptor analysed by time-resolved2 electron cryo-microscopy (closed class)

12	<a href="#">c6fvqE_</a>	 Alignment		94.9	11	<b>PDB header:</b> membrane protein <b>Chain:</b> E: <b>PDB Molecule:</b> cys-loop ligand-gated ion channel; <b>PDBTitle:</b> the active form of a pentameric ion channel (stelic) gated by alkaline2 ph - r86a
13	<a href="#">c5kxiC_</a>	 Alignment		94.5	14	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> neuronal acetylcholine receptor subunit beta-2; <b>PDBTitle:</b> x-ray structure of the human alpha4beta2 nicotinic receptor
14	<a href="#">c6hinA_</a>	 Alignment		94.4	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> 5-hydroxytryptamine receptor 3a; <b>PDBTitle:</b> mouse serotonin 5-ht3 receptor, serotonin-bound, f conformation
15	<a href="#">c4aq9E_</a>	 Alignment		94.3	16	<b>PDB header:</b> membrane protein <b>Chain:</b> E: <b>PDB Molecule:</b> acetylcholine receptor gamma subunit; <b>PDBTitle:</b> gating movement in acetylcholine receptor analysed by time- resolved2 electron cryo-microscopy (open class)
16	<a href="#">c2bg9E_</a>	 Alignment		94.3	16	<b>PDB header:</b> ion channel/receptor <b>Chain:</b> E: <b>PDB Molecule:</b> acetylcholine receptor protein, gamma chain; <b>PDBTitle:</b> refined structure of the nicotinic acetylcholine receptor2 at 4a resolution.
17	<a href="#">c2bg9B_</a>	 Alignment		92.8	11	<b>PDB header:</b> ion channel/receptor <b>Chain:</b> B: <b>PDB Molecule:</b> acetylcholine receptor protein, beta chain; <b>PDBTitle:</b> refined structure of the nicotinic acetylcholine receptor2 at 4a resolution.
18	<a href="#">c2bg9A_</a>	 Alignment		86.9	13	<b>PDB header:</b> ion channel/receptor <b>Chain:</b> A: <b>PDB Molecule:</b> acetylcholine receptor protein, alpha chain; <b>PDBTitle:</b> refined structure of the nicotinic acetylcholine receptor2 at 4a resolution.
19	<a href="#">c4aq5A_</a>	 Alignment		83.7	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> acetylcholine receptor subunit alpha; <b>PDBTitle:</b> gating movement in acetylcholine receptor analysed by time-resolved2 electron cryo-microscopy (closed class)
20	<a href="#">c5jxpA_</a>	 Alignment		74.8	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> asp/glu-specific dipeptidyl-peptidase; <b>PDBTitle:</b> crystal structure of porphyromonas endodontalis dpp11 in alternate2 conformation
21	<a href="#">c6d6tE_</a>	 Alignment	not modelled	66.8	16	<b>PDB header:</b> transport protein <b>Chain:</b> E: <b>PDB Molecule:</b> human gaba-a receptor subunit gamma-2; <b>PDBTitle:</b> human gaba-a receptor alpha1-beta2-gamma2 subtype in complex with gaba2 and flumazenil, conformation b
22	<a href="#">c3wolB_</a>	 Alignment	not modelled	64.5	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dipeptidyl aminopeptidase bii; <b>PDBTitle:</b> crystal structure of the dap bii dipeptide complex i
23	<a href="#">c5jxfA_</a>	 Alignment	not modelled	63.3	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> asp/glu-specific dipeptidyl-peptidase; <b>PDBTitle:</b> crystal structure of flavobacterium psychrophilum dpp11 in complex2 with dipeptide arg-asp
24	<a href="#">c4y01B_</a>	 Alignment	not modelled	54.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> peptidase s46; <b>PDBTitle:</b> crystal structure of dipeptidyl peptidase 11 (dpp11) from2 porphyromonas gingivalis
25	<a href="#">c2m59A_</a>	 Alignment	not modelled	38.7	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> vascular endothelial growth factor receptor 2; <b>PDBTitle:</b> spatial structure of dimeric vegfr2 membrane domain in dpc micelles
26	<a href="#">c2m59B_</a>	 Alignment	not modelled	38.7	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> vascular endothelial growth factor receptor 2; <b>PDBTitle:</b> spatial structure of dimeric vegfr2 membrane domain in dpc micelles
27	<a href="#">c6d6uE_</a>	 Alignment	not modelled	30.0	14	<b>PDB header:</b> transport protein <b>Chain:</b> E: <b>PDB Molecule:</b> gamma-aminobutyric acid receptor subunit gamma-2,gamma- <b>PDBTitle:</b> human gaba-a receptor alpha1-beta2-gamma2 subtype in complex with gaba2 and flumazenil, conformation a
		 Alignment				<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> sarcoplasmic/endoplasmic reticulum

28	<a href="#">c2voyB_</a>	Alignment	not modelled	29.4	24	calcium atpase 1; <b>PDBTitle:</b> cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus <b>PDB header:</b> membrane protein <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein y57a10a.10; <b>PDBTitle:</b> structure of a trimeric intracellular cation channel from c. elegans2 with bound ca2+
29	<a href="#">c5egiB_</a>	Alignment	not modelled	26.6	21	<b>PDB header:</b> membrane protein <b>Chain:</b> G; <b>PDB Molecule:</b> trimeric intracellular cation channel type b-b; <b>PDBTitle:</b> crystal structure analysis of tric counter-ion channels in calcium2 release
30	<a href="#">c6iz4G_</a>	Alignment	not modelled	23.7	33	<b>PDB header:</b> virus <b>Chain:</b> A; <b>PDB Molecule:</b> porcine circovirus 2 (pcv2) capsid protein; <b>PDBTitle:</b> the 2.3 a structure of porcine circovirus 2
31	<a href="#">c3r0rA_</a>	Alignment	not modelled	22.9	28	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> trimeric intracellular cation channel type a; <b>PDBTitle:</b> crystal structure analysis of a eukaryotic membrane protein
32	<a href="#">c6iz0A_</a>	Alignment	not modelled	19.0	28	<b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> S; <b>PDB Molecule:</b> cytochrome b-c1 complex subunit 8; <b>PDBTitle:</b> iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
33	<a href="#">c6hu9s_</a>	Alignment	not modelled	18.4	50	<b>PDB header:</b> apoptosis <b>Chain:</b> C; <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 6; <b>PDBTitle:</b> transmembrane domain of mouse fas/cd95 death receptor
34	<a href="#">c2na6C_</a>	Alignment	not modelled	17.5	17	<b>PDB header:</b> apoptosis <b>Chain:</b> A; <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 6; <b>PDBTitle:</b> transmembrane domain of mouse fas/cd95 death receptor
35	<a href="#">c2na6A_</a>	Alignment	not modelled	17.5	17	<b>PDB header:</b> apoptosis <b>Chain:</b> B; <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 6; <b>PDBTitle:</b> transmembrane domain of mouse fas/cd95 death receptor
36	<a href="#">c2na6B_</a>	Alignment	not modelled	17.5	17	<b>PDB header:</b> apoptosis <b>Chain:</b> B; <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 6; <b>PDBTitle:</b> transmembrane domain of mouse fas/cd95 death receptor
37	<a href="#">c5jqkB_</a>	Alignment	not modelled	17.4	57	<b>PDB header:</b> solute binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> pfvft1; <b>PDBTitle:</b> crystal structure of plasmodium falciparum pf3d7_0606800 (pfvft1)
38	<a href="#">c5mhjA_</a>	Alignment	not modelled	17.0	25	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> major viral transcription factor icp4; <b>PDBTitle:</b> icp4 dna-binding domain, lacking intrinsically disordered region, in2 complex with 12mer dna duplex from its own promoter
39	<a href="#">c6hu9e_</a>	Alignment	not modelled	17.0	18	<b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> E; <b>PDB Molecule:</b> cytochrome b-c1 complex subunit rieske, mitochondrial; <b>PDBTitle:</b> iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
40	<a href="#">c5j09F_</a>	Alignment	not modelled	16.8	20	<b>PDB header:</b> virus <b>Chain:</b> F; <b>PDB Molecule:</b> beak and feather disease virus capsid protein; <b>PDBTitle:</b> crystal structure of decameric bfdv capsid protein
41	<a href="#">c6hu9g_</a>	Alignment	not modelled	16.8	50	<b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> G; <b>PDB Molecule:</b> cytochrome b-c1 complex subunit 7; <b>PDBTitle:</b> iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
42	<a href="#">c5eikA_</a>	Alignment	not modelled	13.0	17	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein y57a10a.28; <b>PDBTitle:</b> structure of a trimeric intracellular cation channel from c. elegans2 in the absence of ca2+
43	<a href="#">c4gucA_</a>	Alignment	not modelled	10.2	22	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> protein ba_2500; <b>PDBTitle:</b> 1.4 angstrom resolution crystal structure of uncharacterized protein2 ba_2500 from bacillus anthracis str. ames
44	<a href="#">d2hyma1</a>	Alignment	not modelled	9.0	13	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III
45	<a href="#">c1q90L_</a>	Alignment	not modelled	8.8	23	<b>PDB header:</b> photosynthesis <b>Chain:</b> L; <b>PDB Molecule:</b> cytochrome b6f complex subunit pet1; <b>PDBTitle:</b> structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
46	<a href="#">d1q90L_</a>	Alignment	not modelled	8.8	23	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> PetL subunit of the cytochrome b6f complex <b>Family:</b> PetL subunit of the cytochrome b6f complex
47	<a href="#">d1x4ka2</a>	Alignment	not modelled	8.8	13	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
48	<a href="#">c1wcuA_</a>	Alignment	not modelled	8.1	12	<b>PDB header:</b> carbohydrate binding <b>Chain:</b> A; <b>PDB Molecule:</b> non-catalytic protein 1; <b>PDBTitle:</b> cbm29_1, a family 29 carbohydrate binding module from2 piromyces equi
49	<a href="#">d1qwma_</a>	Alignment	not modelled	7.6	13	<b>Fold:</b> Galactose-binding domain-like <b>Superfamily:</b> Galactose-binding domain-like <b>Family:</b> Family 29 carbohydrate binding module, CBM29
50	<a href="#">c3g43F_</a>	Alignment	not modelled	7.4	43	<b>PDB header:</b> metal binding protein <b>Chain:</b> F; <b>PDB Molecule:</b> voltage-dependent l-type calcium channel subunit alpha-1c; <b>PDBTitle:</b> crystal structure of the calmodulin-bound cav1.2 c-terminal regulatory2 domain dimer
51	<a href="#">c3j1rR_</a>	Alignment	not modelled	7.2	29	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> R; <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
52	<a href="#">c3j1rG_</a>	Alignment	not modelled	7.2	29	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> G; <b>PDB Molecule:</b> archaeal adhesion filament core;

52	<a href="#">c3j1r9_</a>	Alignment	not modelled	7.2	29	<b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices <b>PDB header:</b> cell adhesion, structural protein
53	<a href="#">c3j1rI_</a>	Alignment	not modelled	7.2	29	<b>Chain:</b> I: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices <b>PDB header:</b> cell adhesion, structural protein
54	<a href="#">c3j1rT_</a>	Alignment	not modelled	7.2	29	<b>Chain:</b> T: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices <b>PDB header:</b> cell adhesion, structural protein
55	<a href="#">c3j1rJ_</a>	Alignment	not modelled	7.2	29	<b>Chain:</b> J: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices <b>PDB header:</b> cell adhesion, structural protein
56	<a href="#">c3j1rQ_</a>	Alignment	not modelled	7.2	29	<b>Chain:</b> Q: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices <b>PDB header:</b> cell adhesion, structural protein
57	<a href="#">c3j1rO_</a>	Alignment	not modelled	7.2	29	<b>Chain:</b> O: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices <b>PDB header:</b> cell adhesion, structural protein
58	<a href="#">c3j1rS_</a>	Alignment	not modelled	7.2	29	<b>Chain:</b> S: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices <b>PDB header:</b> cell adhesion, structural protein
59	<a href="#">c3j1rN_</a>	Alignment	not modelled	7.2	29	<b>Chain:</b> N: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices <b>PDB header:</b> cell adhesion, structural protein
60	<a href="#">c3j1rK_</a>	Alignment	not modelled	7.2	29	<b>Chain:</b> K: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices <b>PDB header:</b> cell adhesion, structural protein
61	<a href="#">c3j1rH_</a>	Alignment	not modelled	7.2	29	<b>Chain:</b> H: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices <b>PDB header:</b> cell adhesion, structural protein
62	<a href="#">c3j1rM_</a>	Alignment	not modelled	7.2	29	<b>Chain:</b> M: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices <b>PDB header:</b> cell adhesion, structural protein
63	<a href="#">c3j1rE_</a>	Alignment	not modelled	7.2	29	<b>Chain:</b> E: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices <b>PDB header:</b> cell adhesion, structural protein
64	<a href="#">c3j1rC_</a>	Alignment	not modelled	7.2	29	<b>Chain:</b> C: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices <b>PDB header:</b> cell adhesion, structural protein
65	<a href="#">c3j1rF_</a>	Alignment	not modelled	7.2	29	<b>Chain:</b> F: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices <b>PDB header:</b> cell adhesion, structural protein
66	<a href="#">c3j1rD_</a>	Alignment	not modelled	7.2	29	<b>Chain:</b> D: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices <b>PDB header:</b> cell adhesion, structural protein
67	<a href="#">c3j1rP_</a>	Alignment	not modelled	7.2	29	<b>Chain:</b> P: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices <b>PDB header:</b> cell adhesion, structural protein
68	<a href="#">c3j1rL_</a>	Alignment	not modelled	7.2	29	<b>Chain:</b> L: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices <b>PDB header:</b> cell adhesion, structural protein
69	<a href="#">c3j1rB_</a>	Alignment	not modelled	7.2	29	<b>Chain:</b> B: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices <b>PDB header:</b> cell adhesion, structural protein
70	<a href="#">c3j1rU_</a>	Alignment	not modelled	7.2	29	<b>Chain:</b> U: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices <b>PDB header:</b> cell adhesion, structural protein
71	<a href="#">c3j1rA_</a>	Alignment	not modelled	7.2	29	<b>Chain:</b> A: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices <b>PDB header:</b> protein binding
72	<a href="#">c2qc1B_</a>	Alignment	not modelled	7.2	13	<b>Chain:</b> B: <b>PDB Molecule:</b> acetylcholine receptor subunit alpha; <b>PDBTitle:</b> crystal structure of the extracellular domain of the nicotinic2 acetylcholine receptor 1 subunit bound to alpha-bungarotoxin at 1.9 a3 resolution <b>PDB header:</b> hydrolase
73	<a href="#">c5xyhA_</a>	Alignment	not modelled	7.1	58	<b>Chain:</b> A: <b>PDB Molecule:</b> cbsa; <b>PDBTitle:</b> crystal structure of catalytic domain of 1,4-beta-cellobiosidase2 (cbsa) from xanthomonas oryzae pv. oryzae <b>PDB header:</b> metal binding protein
74	<a href="#">c4m1IB_</a>	Alignment	not modelled	6.8	33	<b>Chain:</b> B: <b>PDB Molecule:</b> iq domain-containing protein g; <b>PDBTitle:</b> complex of iqcg and ca2+-bound cam <b>PDB header:</b> membrane protein
75	<a href="#">d1vq3a_</a>	Alignment	not modelled	6.6	11	<b>Fold:</b> PurS-like <b>Superfamily:</b> PurS-like <b>Family:</b> PurS subunit of FGAM synthetase <b>PDB header:</b> cell adhesion
76	<a href="#">c5kyhS_</a>	Alignment	not modelled	6.5	19	<b>Chain:</b> S: <b>PDB Molecule:</b> ih0670; <b>PDBTitle:</b> structure of ih0670 flagellar-like filament <b>PDB header:</b> membrane protein
77	<a href="#">c4m5bA_</a>	Alignment	not modelled	6.3	18	<b>Chain:</b> A: <b>PDB Molecule:</b> cobalamin biosynthesis protein cbim; <b>PDBTitle:</b> crystal structure of an truncated transition metal transporter <b>PDB header:</b> membrane protein

78	<a href="#">c4m5cA_</a>	Alignment	not modelled	6.3	18	<b>Chain:</b> A; <b>PDB Molecule:</b> cobalamin biosynthesis protein cbim; <b>PDBTitle:</b> crystal structure of an truncated transition metal transporter
79	<a href="#">d1ttza_</a>	Alignment	not modelled	6.3	39	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
80	<a href="#">d1hc1a3</a>	Alignment	not modelled	5.7	17	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Arthropod hemocyanin, C-terminal domain
81	<a href="#">c2voyG_</a>	Alignment	not modelled	5.6	11	<b>PDB header:</b> hydrolase <b>Chain:</b> G; <b>PDB Molecule:</b> sarcoplasmic/endoplasmic reticulum calcium atpase 1; <b>PDBTitle:</b> cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
82	<a href="#">c4jx0A_</a>	Alignment	not modelled	5.5	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a two domain protein with unknown function2 (bf3416) from bacteroides fragilis nctc 9343 at 2.90 a resolution
83	<a href="#">c3n91A_</a>	Alignment	not modelled	5.4	16	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a structural genomics, unknown function2 (bacova_03430) from bacteroides ovatus at 2.40 a resolution
84	<a href="#">c5nbbA_</a>	Alignment	not modelled	5.4	31	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> rna chaperone proq; <b>PDBTitle:</b> structure of the c-terminal domain of the escherichia coli proq rna2 binding protein
85	<a href="#">c6c14A_</a>	Alignment	not modelled	5.1	11	<b>PDB header:</b> membrane protein, metal transport <b>Chain:</b> A; <b>PDB Molecule:</b> protocadherin-15; <b>PDBTitle:</b> cryoem structure of mouse pcdh15-1ec-lhfp15 complex