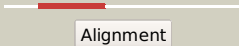




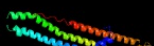

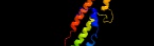
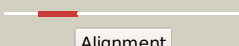

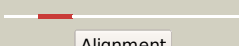

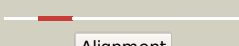

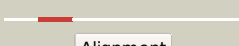
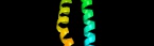



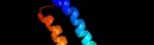




# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD0280\_(PPE3)\_339364\_340974  
 Date Tue Jul 23 14:50:34 BST 2019  
 Unique Job ID cb4f4fce49a4d3ed

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5xfsB_</a>	 Alignment		100.0	39	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> ppe family protein ppe15; <b>PDBTitle:</b> crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
2	<a href="#">c2g38B_</a>	 Alignment		100.0	30	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> ppe family protein; <b>PDBTitle:</b> a pe/ppe protein complex from mycobacterium tuberculosis
3	<a href="#">d2g38b1</a>	 Alignment		100.0	30	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> PE/PPE dimer-like <b>Family:</b> PPE
4	<a href="#">c4xy3A_</a>	 Alignment		100.0	19	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> esx-1 secretion-associated protein espb; <b>PDBTitle:</b> structure of esx-1 secreted protein espb
5	<a href="#">c4wj2A_</a>	 Alignment		97.9	20	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> antigen mtb48; <b>PDBTitle:</b> mycobacterial protein
6	<a href="#">c2vs0B_</a>	 Alignment		97.6	11	<b>PDB header:</b> cell invasion <b>Chain:</b> B: <b>PDB Molecule:</b> virulence factor esxa; <b>PDBTitle:</b> structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	<a href="#">c4iogD_</a>	 Alignment		97.4	14	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> secreted protein esxb; <b>PDBTitle:</b> the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. Sterne
8	<a href="#">c3gvmA_</a>	 Alignment		97.3	14	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein sag1039; <b>PDBTitle:</b> structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
9	<a href="#">c3zbhC_</a>	 Alignment		97.1	15	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> esxa; <b>PDBTitle:</b> geobacillus thermodenitrificans esxa crystal form i
10	<a href="#">d1wa8a1</a>	 Alignment		96.4	18	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
11	<a href="#">c4lwsB_</a>	 Alignment		93.5	18	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	<a href="#">c4lwsA_</a>	Alignment		93.3	12	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> esxa : esxb (semet) hetero-dimer from thermomonospora curvata
13	<a href="#">d1wa8b1</a>	Alignment		92.9	17	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
14	<a href="#">c4i0xA_</a>	Alignment		91.4	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> esat-6-like protein mab_3112; <b>PDBTitle:</b> crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
15	<a href="#">c2kg7B_</a>	Alignment		86.0	19	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> esat-6-like protein eshx; <b>PDBTitle:</b> structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
16	<a href="#">c4i0xJ_</a>	Alignment		56.1	30	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> J: <b>PDB Molecule:</b> esat-6-like protein mab_3113; <b>PDBTitle:</b> crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
17	<a href="#">d1ui5a2</a>	Alignment		45.0	22	<b>Fold:</b> Tetracyclin repressor-like, C-terminal domain <b>Superfamily:</b> Tetracyclin repressor-like, C-terminal domain <b>Family:</b> Tetracyclin repressor-like, C-terminal domain
18	<a href="#">d1zeea1</a>	Alignment		25.1	42	<b>Fold:</b> Indolic compounds 2,3-dioxygenase-like <b>Superfamily:</b> Indolic compounds 2,3-dioxygenase-like <b>Family:</b> Indoleamine 2,3-dioxygenase-like
19	<a href="#">c3zfsA_</a>	Alignment		24.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> f420-reducing hydrogenase, subunit alpha; <b>PDBTitle:</b> cryo-em structure of the f420-reducing nife-hydrogenase from a2 methanogenic archaeon with bound substrate
20	<a href="#">c4xb6D_</a>	Alignment		17.2	22	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> alpha-d-ribose 1-methylphosphonate 5-phosphate c-p lyase; <b>PDBTitle:</b> structure of the e. coli c-p lyase core complex
21	<a href="#">c5I85B_</a>	Alignment	not modelled	16.5	36	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> nuclear fragile x mental retardation-interacting protein 1; <b>PDBTitle:</b> solution structure of the complex between human znhit3 and nufip12 proteins
22	<a href="#">c3sjrB_</a>	Alignment	not modelled	16.4	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of conserved unkown function protein cv_1783 from2 chromobacterium violaceum atcc 12472
23	<a href="#">c2nvjA_</a>	Alignment	not modelled	15.8	40	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 25mer peptide from vacuolar atp synthase subunit <b>PDBTitle:</b> nmr structures of transmembrane segment from subunit a from2 the yeast proton v-atpase
24	<a href="#">c2ahmG_</a>	Alignment	not modelled	15.7	29	<b>PDB header:</b> viral protein, replication <b>Chain:</b> G: <b>PDB Molecule:</b> replicase polyprotein 1ab, heavy chain; <b>PDBTitle:</b> crystal structure of sars-cov super complex of non-structural2 proteins: the hexadecamer
25	<a href="#">c3j00Z_</a>	Alignment	not modelled	14.6	4	<b>PDB header:</b> ribosome/ribosomal protein <b>Chain:</b> Z: <b>PDB Molecule:</b> cell division protein ftsq; <b>PDBTitle:</b> structure of the ribosome-secye complex in the membrane environment
26	<a href="#">d1dipa1</a>	Alignment	not modelled	13.2	12	<b>Fold:</b> beta-Prism II <b>Superfamily:</b> alpha-D-mannose-specific plant lectins <b>Family:</b> alpha-D-mannose-specific plant lectins
27	<a href="#">c6aokA_</a>	Alignment	not modelled	12.7	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ceg4; <b>PDBTitle:</b> crystal structure of legionella pneumophila effector ceg4 with n-2 terminal tev protease cleavage sequence
28	<a href="#">d1vifn1</a>	Alianment	not modelled	12.3	100	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Cna protein B-type domain

						<b>Family:</b> Cna protein B-type domain
29	<a href="#">c1bkvA</a>	Alignment	not modelled	11.6	44	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
30	<a href="#">c6cgjA</a>	Alignment	not modelled	11.4	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> effector protein lem4 (lpg1101); <b>PDBTitle:</b> structure of the had domain of effector protein lem4 (lpg1101) from2 legionella pneumophila
31	<a href="#">c1bkvC</a>	Alignment	not modelled	11.2	44	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
32	<a href="#">c1bkvB</a>	Alignment	not modelled	11.2	44	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
33	<a href="#">c3ub0D</a>	Alignment	not modelled	10.8	17	<b>PDB header:</b> replication <b>Chain:</b> D: <b>PDB Molecule:</b> non-structural protein 6, nsp6,; <b>PDBTitle:</b> crystal structure of the nonstructural protein 7 and 8 complex of2 feline coronavirus
34	<a href="#">c2wseE</a>	Alignment	not modelled	9.2	30	<b>PDB header:</b> photosynthesis <b>Chain:</b> E: <b>PDB Molecule:</b> photosystem i reaction center subunit iv a, chloroplastic; <b>PDBTitle:</b> improved model of plant photosystem i
35	<a href="#">d1dmua</a>	Alignment	not modelled	8.8	44	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> Restriction endonuclease BglI
36	<a href="#">c1bzgA</a>	Alignment	not modelled	8.8	14	<b>PDB header:</b> hormone <b>Chain:</b> A: <b>PDB Molecule:</b> parathyroid hormone-related protein; <b>PDBTitle:</b> the solution structure of human parathyroid hormone-related2 protein (1-34) in near-physiological solution, nmr, 303 structures
37	<a href="#">c2kg7A</a>	Alignment	not modelled	8.8	59	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein esxg (pe family protein); <b>PDBTitle:</b> structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
38	<a href="#">c4u39Q</a>	Alignment	not modelled	8.6	36	<b>PDB header:</b> cell cycle <b>Chain:</b> Q: <b>PDB Molecule:</b> cell division factor; <b>PDBTitle:</b> crystal structure of ftsz:mciz complex from bacillus subtilis
39	<a href="#">c4f3fC</a>	Alignment	not modelled	8.5	38	<b>PDB header:</b> immune system <b>Chain:</b> C: <b>PDB Molecule:</b> mesothelin; <b>PDBTitle:</b> crystal structure of msln7-64 morab-009 fab complex
40	<a href="#">c5hl8B</a>	Alignment	not modelled	8.2	40	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> type ii secretion system protein I; <b>PDBTitle:</b> 1.93 angstrom resolution crystal structure of a pullulanase-specific2 type ii secretion system integral cytoplasmic membrane protein gspI3 (c-terminal fragment; residues 309-397) from klebsiella pneumoniae4 subsp. pneumoniae ntuH-k2044
41	<a href="#">d1nkt4</a>	Alignment	not modelled	8.1	58	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
42	<a href="#">c6nbiP</a>	Alignment	not modelled	7.9	60	<b>PDB header:</b> signaling protein <b>Chain:</b> P: <b>PDB Molecule:</b> long-acting parathyroid hormone analog; <b>PDBTitle:</b> cryo-em structure of parathyroid hormone receptor type 1 in complex2 with a long-acting parathyroid hormone analog and g protein
43	<a href="#">c2m5IA</a>	Alignment	not modelled	7.6	50	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> ns5a protein; <b>PDBTitle:</b> ns5a308
44	<a href="#">c1vytF</a>	Alignment	not modelled	7.5	50	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> voltage-dependent l-type calcium channel <b>PDBTitle:</b> beta3 subunit complexed with aid
45	<a href="#">c5dn4A</a>	Alignment	not modelled	7.0	43	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidoglycan hydrolase flgJ; <b>PDBTitle:</b> structure of the glycoside hydrolase domain from salmonella2 typhimurium flgJ
46	<a href="#">c4gyxC</a>	Alignment	not modelled	6.9	38	<b>PDB header:</b> structural protein, blood clotting <b>Chain:</b> C: <b>PDB Molecule:</b> type iii collagen fragment in a host peptide stabilized by <b>PDBTitle:</b> the von willebrand factor a3 domain binding region of type iii2 collagen stabilized by the cysteine knot
47	<a href="#">c2jtwA</a>	Alignment	not modelled	6.9	50	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> transmembrane helix 7 of yeast vatpase; <b>PDBTitle:</b> solution structure of tm7 bound to dpc micelles
48	<a href="#">c3ogrA</a>	Alignment	not modelled	6.8	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> complex structure of beta-galactosidase from trichoderma reesei with2 galactose
49	<a href="#">d1fcda3</a>	Alignment	not modelled	6.8	40	<b>Fold:</b> CO dehydrogenase flavoprotein C-domain-like <b>Superfamily:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain <b>Family:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain
50	<a href="#">c6fxoA</a>	Alignment	not modelled	6.8	67	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional autolysin; <b>PDBTitle:</b> crystal structure of major bifunctional autolysin
51	<a href="#">d2apla1</a>	Alignment	not modelled	6.4	32	<b>Fold:</b> PG0816-like <b>Superfamily:</b> PG0816-like <b>Family:</b> PG0816-like
52	<a href="#">c6gp2A</a>	Alignment	not modelled	6.4	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonucleoside-diphosphate reductase beta chain; <b>PDBTitle:</b> ribonucleotide reductase class ie r2 from mesoplasma florum, dopa-2 active form
						<b>PDB header:</b> immune system

53	<a href="#">c2lkqA_</a>	Alignment	not modelled	6.4	56	<b>Chain:</b> A: <b>PDB Molecule:</b> immunoglobulin lambda-like polypeptide 1; <b>PDBTitle:</b> nmr structure of the lambda 5 22-45 peptide
54	<a href="#">c3e6qL_</a>	Alignment	not modelled	6.3	20	<b>PDB header:</b> isomerase <b>Chain:</b> L: <b>PDB Molecule:</b> putative 5-carboxymethyl-2-hydroxymuconate isomerase; <b>PDBTitle:</b> putative 5-carboxymethyl-2-hydroxymuconate isomerase from pseudomonas2 aeruginosa.
55	<a href="#">c4dmtB_</a>	Alignment	not modelled	6.3	38	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen iii derived peptide; <b>PDBTitle:</b> crystal structure of a vwf binding collagen iii derived triple helical2 peptide
56	<a href="#">c4dmtC_</a>	Alignment	not modelled	6.3	38	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen iii derived peptide; <b>PDBTitle:</b> crystal structure of a vwf binding collagen iii derived triple helical2 peptide
57	<a href="#">c4dmtA_</a>	Alignment	not modelled	6.3	38	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen iii derived peptide; <b>PDBTitle:</b> crystal structure of a vwf binding collagen iii derived triple helical2 peptide
58	<a href="#">c2iunD_</a>	Alignment	not modelled	6.2	50	<b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> avian adenovirus celo long fibre; <b>PDBTitle:</b> structure of the c-terminal head domain of the avian adenovirus celo2 long fibre (p21 crystal form)
59	<a href="#">c4cuaB_</a>	Alignment	not modelled	6.2	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> unravelling the multiple functions of the architecturally2 intricate streptococcus pneumoniae beta-galactosidase, bgaa
60	<a href="#">c2zycA_</a>	Alignment	not modelled	6.0	60	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidoglycan hydrolase flgj; <b>PDBTitle:</b> crystal structure of peptidoglycan hydrolase from2 sphingomonas sp. a1
61	<a href="#">c1t0jC_</a>	Alignment	not modelled	6.0	43	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> voltage-dependent l-type calcium channel alpha-1c subunit; <b>PDBTitle:</b> crystal structure of a complex between voltage-gated calcium channel2 beta2a subunit and a peptide of the alpha1c subunit
62	<a href="#">c5uc0B_</a>	Alignment	not modelled	6.0	100	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein cog5400; <b>PDBTitle:</b> crystal structure of beta-barrel-like, uncharacterized protein of2 cog5400 from brucella abortus
63	<a href="#">c6qpiA_</a>	Alignment	not modelled	5.9	19	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> anoctamin-6; <b>PDBTitle:</b> cryo-em structure of calcium-free mtmem16f lipid scramblase in2 nanodisc
64	<a href="#">c4mveB_</a>	Alignment	not modelled	5.8	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of tcur_1030 protein from thermomonospora curvata
65	<a href="#">c1vytE_</a>	Alignment	not modelled	5.8	50	<b>PDB header:</b> transport protein <b>Chain:</b> E: <b>PDB Molecule:</b> voltage-dependent l-type calcium channel <b>PDBTitle:</b> beta3 subunit complexed with aid
66	<a href="#">c2d9zA_</a>	Alignment	not modelled	5.7	35	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein kinase c, nu type; <b>PDBTitle:</b> solution structure of the ph domain of protein kinase c, nu2 type from human
67	<a href="#">c4gyxA_</a>	Alignment	not modelled	5.7	45	<b>PDB header:</b> structural protein, blood clotting <b>Chain:</b> A: <b>PDB Molecule:</b> type iii collagen fragment in a host peptide stabilized by <b>PDBTitle:</b> the von willebrand factor a3 domain binding region of type iii2 collagen stabilized by the cysteine knot
68	<a href="#">c4gyxB_</a>	Alignment	not modelled	5.7	45	<b>PDB header:</b> structural protein, blood clotting <b>Chain:</b> B: <b>PDB Molecule:</b> type iii collagen fragment in a host peptide stabilized by <b>PDBTitle:</b> the von willebrand factor a3 domain binding region of type iii2 collagen stabilized by the cysteine knot
69	<a href="#">c6et5U_</a>	Alignment	not modelled	5.7	58	<b>PDB header:</b> photosynthesis <b>Chain:</b> U: <b>PDB Molecule:</b> light-harvesting protein b-1015 gamma chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
70	<a href="#">c6et5g_</a>	Alignment	not modelled	5.7	58	<b>PDB header:</b> photosynthesis <b>Chain:</b> G: <b>PDB Molecule:</b> light-harvesting protein b-1015 beta chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
71	<a href="#">c6et5d_</a>	Alignment	not modelled	5.7	58	<b>PDB header:</b> photosynthesis <b>Chain:</b> D: <b>PDB Molecule:</b> <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
72	<a href="#">c6et5l_</a>	Alignment	not modelled	5.7	58	<b>PDB header:</b> photosynthesis <b>Chain:</b> L: <b>PDB Molecule:</b> light-harvesting protein b-1015 gamma chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
73	<a href="#">c6et5R_</a>	Alignment	not modelled	5.7	58	<b>PDB header:</b> photosynthesis <b>Chain:</b> R: <b>PDB Molecule:</b> light-harvesting protein b-1015 gamma chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
74	<a href="#">c6et5s_</a>	Alignment	not modelled	5.7	58	<b>PDB header:</b> photosynthesis <b>Chain:</b> S: <b>PDB Molecule:</b> light-harvesting protein b-1015 alpha chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
75	<a href="#">c6et5a_</a>	Alignment	not modelled	5.7	58	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
76	<a href="#">c6et5v_</a>	Alignment	not modelled	5.7	58	<b>PDB header:</b> photosynthesis <b>Chain:</b> V: <b>PDB Molecule:</b> light-harvesting protein b-1015 alpha chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
77	<a href="#">c6et5m_</a>	Alignment	not modelled	5.7	58	<b>PDB header:</b> photosynthesis <b>Chain:</b> M: <b>PDB Molecule:</b> reaction center protein m chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis

78	<a href="#">c6et5p_</a>	Alignment	not modelled	5.7	58	<b>PDB header:</b> photosynthesis <b>Chain:</b> P: <b>PDB Molecule:</b> light-harvesting protein b-1015 alpha chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
79	<a href="#">c6et52_</a>	Alignment	not modelled	5.7	58	<b>PDB header:</b> photosynthesis <b>Chain:</b> 2: <b>PDB Molecule:</b> light-harvesting protein b-1015 gamma chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
80	<a href="#">c6et50_</a>	Alignment	not modelled	5.7	58	<b>PDB header:</b> photosynthesis <b>Chain:</b> O: <b>PDB Molecule:</b> light-harvesting protein b-1015 gamma chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
81	<a href="#">c6et5j_</a>	Alignment	not modelled	5.7	58	<b>PDB header:</b> photosynthesis <b>Chain:</b> J: <b>PDB Molecule:</b> <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
82	<a href="#">c6et5y_</a>	Alignment	not modelled	5.7	58	<b>PDB header:</b> photosynthesis <b>Chain:</b> Y: <b>PDB Molecule:</b> light-harvesting protein b-1015 alpha chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
83	<a href="#">c6et5X_</a>	Alignment	not modelled	5.7	58	<b>PDB header:</b> photosynthesis <b>Chain:</b> X: <b>PDB Molecule:</b> light-harvesting protein b-1015 gamma chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
84	<a href="#">c6et55_</a>	Alignment	not modelled	5.7	58	<b>PDB header:</b> photosynthesis <b>Chain:</b> 5: <b>PDB Molecule:</b> light-harvesting protein b-1015 gamma chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
85	<a href="#">c4qdnA_</a>	Alignment	not modelled	5.7	80	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> flagellar protein flgJ [peptidoglycan hydrolase]; <b>PDBTitle:</b> crystal structure of the endo-beta-n-acetylglucosaminidase from2 thermotoga maritima
86	<a href="#">c2vwaE_</a>	Alignment	not modelled	5.6	25	<b>PDB header:</b> unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> putative uncharacterized protein pf13_0012; <b>PDBTitle:</b> crystal structure of a sporozoite protein essential for2 liver stage development of malaria parasite
87	<a href="#">c6dzsD_</a>	Alignment	not modelled	5.5	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> mycobacterial homoserine dehydrogenase thra in complex with nadp
88	<a href="#">c3qi7A_</a>	Alignment	not modelled	5.5	57	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of a putative transcriptional regulator2 (yp_001089212.1) from clostridium difficile 630 at 1.86 a resolution
89	<a href="#">c4dexB_</a>	Alignment	not modelled	5.5	50	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> voltage-dependent n-type calcium channel subunit alpha-1b; <b>PDBTitle:</b> crystal structure of the voltage dependent calcium channel beta-22 subunit in complex with the cav2.2 i-ii linker.
90	<a href="#">d1otga_</a>	Alignment	not modelled	5.5	23	<b>Fold:</b> Tautomerase/MIF <b>Superfamily:</b> Tautomerase/MIF <b>Family:</b> 5-carboxymethyl-2-hydroxymuconate isomerase (CHMI)
91	<a href="#">c1e1hD_</a>	Alignment	not modelled	5.4	60	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> botulinum neurotoxin type a light chain; <b>PDBTitle:</b> crystal structure of recombinant botulinum neurotoxin type a light2 chain, self-inhibiting zn endopeptidase.
92	<a href="#">c6iqzE_</a>	Alignment	not modelled	5.4	31	<b>PDB header:</b> plant protein <b>Chain:</b> E: <b>PDB Molecule:</b> psae; <b>PDBTitle:</b> structure of psi-lhci
93	<a href="#">c4lzxB_</a>	Alignment	not modelled	5.3	31	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> iq domain-containing protein g; <b>PDBTitle:</b> complex of iqcg and ca2+-free cam
94	<a href="#">c5vmoB_</a>	Alignment	not modelled	5.3	50	<b>PDB header:</b> viral protein/apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> bcl-2 interacting mediator of cell death; <b>PDBTitle:</b> crystal structure of grouper iridovirus giv66:bim complex
95	<a href="#">c3fi7A_</a>	Alignment	not modelled	5.3	80	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lmo1076 protein; <b>PDBTitle:</b> crystal structure of the autolysin auto (lmo1076) from listeria2 monocytogenes, catalytic domain
96	<a href="#">c4m1lB_</a>	Alignment	not modelled	5.2	36	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> iq domain-containing protein g; <b>PDBTitle:</b> complex of iqcg and ca2+-bound cam
97	<a href="#">d1jyaa_</a>	Alignment	not modelled	5.2	19	<b>Fold:</b> Secretion chaperone-like <b>Superfamily:</b> Type III secretory system chaperone-like <b>Family:</b> Type III secretory system chaperone
98	<a href="#">c2o01E_</a>	Alignment	not modelled	5.1	38	<b>PDB header:</b> photosynthesis <b>Chain:</b> E: <b>PDB Molecule:</b> photosystem i reaction center subunit iv a, chloroplast; <b>PDBTitle:</b> the structure of a plant photosystem i supercomplex at 3.4 angstrom2 resolution