

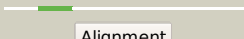

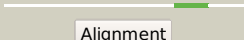
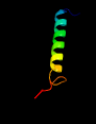
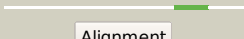
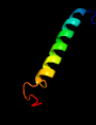
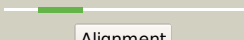

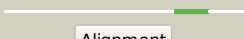

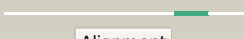
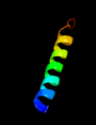

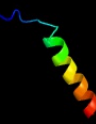
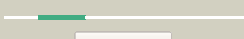




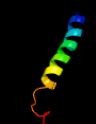


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3694c_(-)_4136300_4137292
Date	Fri Aug 9 18:20:38 BST 2019
Unique Job ID	3de674ae3e0f10cb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6hwhX_</a>	 Alignment		92.2	14	<b>PDB header:</b> electron transport <b>Chain:</b> X: <b>PDB Molecule:</b> cytochrome c oxidase polypeptide 4; <b>PDBTitle:</b> structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
2	<a href="#">c2lo0B_</a>	 Alignment		58.6	19	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of the get5 carboxyl domain from a. fumigatus
3	<a href="#">c2momB_</a>	 Alignment		58.2	26	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> lysosome-associated membrane glycoprotein 2; <b>PDBTitle:</b> structural insights of tm domain of lamp-2a in dpc micelles
4	<a href="#">c2momC_</a>	 Alignment		58.2	26	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> lysosome-associated membrane glycoprotein 2; <b>PDBTitle:</b> structural insights of tm domain of lamp-2a in dpc micelles
5	<a href="#">d1g7oa1</a>	 Alignment		56.8	17	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
6	<a href="#">c5lc5c_</a>	 Alignment		55.5	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nadh dehydrogenase [ubiquinone] iron-sulfur protein 3, <b>PDBTitle:</b> structure of mammalian respiratory complex i, class2
7	<a href="#">c3jcul_</a>	 Alignment		49.6	24	<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 angstrom2 resolution
8	<a href="#">c5ldwc_</a>	 Alignment		47.6	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nadh dehydrogenase [ubiquinone] iron-sulfur protein 3, <b>PDBTitle:</b> structure of mammalian respiratory complex i, class1
9	<a href="#">c5yo8B_</a>	 Alignment		45.4	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> tetraprenyl-beta-curcumene synthase; <b>PDBTitle:</b> crystal structure of beta-c25/c30/c35-prene synthase
10	<a href="#">d1alla_</a>	 Alignment		41.6	10	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Phycocyanin-like phycobilisome proteins
11	<a href="#">c3a0hi_</a>	 Alignment		39.5	21	<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

12	<a href="#">c4po5E_</a>	Alignment		38.0	8	<b>PDB header:</b> photosynthesis <b>Chain:</b> E: <b>PDB Molecule:</b> allophycocyanin subunit alpha-b; <b>PDBTitle:</b> crystal structure of allophycocyanin b from synechocystis pcc 6803
13	<a href="#">c2vmlA_</a>	Alignment		37.8	18	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> phycocyanin alpha chain; <b>PDBTitle:</b> the monoclinic structure of phycocyanin from gloeobacter violaceus
14	<a href="#">d2axti1</a>	Alignment		35.8	21	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Photosystem II reaction center protein I, Psbl <b>Family:</b> Psbl-like
15	<a href="#">d1ha7b_</a>	Alignment		34.4	16	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Phycocyanin-like phycobilisome proteins
16	<a href="#">c2c7jB_</a>	Alignment		33.1	20	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> phycocerythrocyanin beta chain; <b>PDBTitle:</b> phycocerythrocyanin from mastigocladus laminosus, 295 k, 3.0 a
17	<a href="#">d1cpcb_</a>	Alignment		32.9	20	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Phycocyanin-like phycobilisome proteins
18	<a href="#">d1cpca_</a>	Alignment		29.7	21	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Phycocyanin-like phycobilisome proteins
19	<a href="#">c6ajjA_</a>	Alignment		29.5	16	<b>PDB header:</b> membrane protein, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> drug exporters of the rnd superfamily-like protein, <b>PDBTitle:</b> crystal structure of mycolic acid transporter mmp13 from mycobacterium2 smegmatis complexed with ica38
20	<a href="#">c2jo8B_</a>	Alignment		28.6	32	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase 4; <b>PDBTitle:</b> solution structure of c-terminal domain of human mammalian2 sterile 20-like kinase 1 (mst1)
21	<a href="#">c4l0nG_</a>	Alignment	not modelled	27.5	32	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> serine/threonine-protein kinase 3; <b>PDBTitle:</b> crystal structure of stk3 (mst2) sarah domain
22	<a href="#">d1f99b_</a>	Alignment	not modelled	27.5	16	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Phycocyanin-like phycobilisome proteins
23	<a href="#">c5azdA_</a>	Alignment	not modelled	27.2	18	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> bacteriorhodopsin; <b>PDBTitle:</b> crystal structure of thermophilic rhodopsin.
24	<a href="#">d1xg0c_</a>	Alignment	not modelled	26.4	16	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Phycocyanin-like phycobilisome proteins
25	<a href="#">c2dcoA_</a>	Alignment	not modelled	25.2	21	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> s1p4 first extracellular loop peptidomimetic; <b>PDBTitle:</b> s1p4 first extracellular loop peptidomimetic
26	<a href="#">d1jboa_</a>	Alignment	not modelled	23.9	18	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Phycocyanin-like phycobilisome proteins
27	<a href="#">c6nyyC_</a>	Alignment	not modelled	22.8	19	<b>PDB header:</b> translocase <b>Chain:</b> C: <b>PDB Molecule:</b> afg3-like protein 2; <b>PDBTitle:</b> human m-aaa protease afg3l2, substrate-bound
28	<a href="#">d2ofya1</a>	Alignment	not modelled	21.2	12	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
29	<a href="#">d1eyxb_</a>	Alignment	not modelled	21.0	15	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like

						<b>Family:</b> Phycocyanin-like phycobilisome proteins
30	<a href="#">c3i3aC</a>	Alignment	not modelled	19.8	15	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> acyl-[acyl-carrier-protein]-udp-n- <b>PDBTitle:</b> structural basis for the sugar nucleotide and acyl chain2 selectivity of leptospira interrogans lpxa
31	<a href="#">c4aj5M</a>	Alignment	not modelled	19.1	26	<b>PDB header:</b> cell cycle <b>Chain:</b> M: <b>PDB Molecule:</b> spindle and kinetochore-associated protein 2; <b>PDBTitle:</b> crystal structure of the ska core complex
32	<a href="#">c5ip1A</a>	Alignment	not modelled	18.5	17	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoprotein; <b>PDBTitle:</b> tomato spotted wilt tospovirus nucleocapsid protein
33	<a href="#">c4jo8B</a>	Alignment	not modelled	18.5	13	<b>PDB header:</b> immune system/viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> killer cell lectin-like receptor 8; <b>PDBTitle:</b> crystal structure of the activating ly49h receptor in complex with2 m157 (g1f strain)
34	<a href="#">c2mc0A</a>	Alignment	not modelled	18.3	16	<b>PDB header:</b> transcription activator/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional activator tipa; <b>PDBTitle:</b> structural basis of a thiopeptide antibiotic multidrug resistance2 system from streptomyces lividans:nosiheptide in complex with tipas
35	<a href="#">d1liaa</a>	Alignment	not modelled	17.9	11	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Phycocyanin-like phycobilisome proteins
36	<a href="#">c3sboA</a>	Alignment	not modelled	17.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadp-specific glutamate dehydrogenase; <b>PDBTitle:</b> structure of e.coli gdh from native source
37	<a href="#">d1eyxa</a>	Alignment	not modelled	17.2	14	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Phycocyanin-like phycobilisome proteins
38	<a href="#">c3r3eA</a>	Alignment	not modelled	16.8	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yqjg; <b>PDBTitle:</b> the glutathione bound structure of yqjg, a glutathione transferase2 homolog from escherichia coli k-12
39	<a href="#">d1kn1a</a>	Alignment	not modelled	16.6	10	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Phycocyanin-like phycobilisome proteins
40	<a href="#">c3pxpA</a>	Alignment	not modelled	16.1	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> helix-turn-helix domain protein; <b>PDBTitle:</b> crystal structure of a pas and dna binding domain containing protein2 (caur_2278) from chloroflexus aurantiacus j-10-fl at 2.30 a3 resolution
41	<a href="#">c5d3aA</a>	Alignment	not modelled	16.0	14	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> kinesin-like protein kif21a; <b>PDBTitle:</b> kif21a regulatory coiled coil
42	<a href="#">c3a7kD</a>	Alignment	not modelled	15.6	21	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> halorhodopsin; <b>PDBTitle:</b> crystal structure of halorhodopsin from natronomonas2 pharaonis
43	<a href="#">c4xxkA</a>	Alignment	not modelled	15.5	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phycobiliprotein apce; <b>PDBTitle:</b> crystal structure of the semet-derivative of the bilin-binding domain2 of phycobilisome core-membrane linker apce
44	<a href="#">d1liab</a>	Alignment	not modelled	15.3	13	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Phycocyanin-like phycobilisome proteins
45	<a href="#">c4kppA</a>	Alignment	not modelled	15.1	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of h+/ca2+ exchanger cax
46	<a href="#">c4ptsB</a>	Alignment	not modelled	15.0	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione s-transferase; <b>PDBTitle:</b> crystal structure of a glutathione transferase from gordonia2 bronchialis dsm 43247, target efi-507405
47	<a href="#">c6hhaA</a>	Alignment	not modelled	13.9	21	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> l-rhamnose mutarotase; <b>PDBTitle:</b> crystal structure of l-rhamnose mutarotase fa22100 from formosa2 agariphila
48	<a href="#">c3okqA</a>	Alignment	not modelled	13.8	25	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> bud site selection protein 6; <b>PDBTitle:</b> crystal structure of a core domain of yeast actin nucleation cofactor2 bud6
49	<a href="#">c3zplE</a>	Alignment	not modelled	13.7	18	<b>PDB header:</b> transcription/dna <b>Chain:</b> E: <b>PDB Molecule:</b> putative marr-family transcriptional repressor; <b>PDBTitle:</b> crystal structure of sco3205, a marr family transcriptional regulator2 from streptomyces coelicolor, in complex with dna
50	<a href="#">c3jz0B</a>	Alignment	not modelled	13.7	11	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> B: <b>PDB Molecule:</b> lincosamide nucleotidyltransferase; <b>PDBTitle:</b> linb complexed with clindamycin and ampcpp
51	<a href="#">d1b33a</a>	Alignment	not modelled	13.6	11	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Phycocyanin-like phycobilisome proteins
52	<a href="#">c2lvsA</a>	Alignment	not modelled	13.2	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> nmr solution structure of a crispr repeat binding protein
53	<a href="#">c2qlxA</a>	Alignment	not modelled	12.7	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> l-rhamnose mutarotase; <b>PDBTitle:</b> crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum in complex with l-rhamnose
54	<a href="#">c2qlwA</a>	Alignment	not modelled	12.7	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> rhau; <b>PDBTitle:</b> crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum
55	<a href="#">c4hwcA</a>	Alignment	not modelled	12.4	44	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phospholipase b-like 1;

55	<a href="#">c4bwA</a>	Alignment	not modelled	12.4	44	<b>PDBTitle:</b> x-ray structure of a phospholipase b like protein 1 from2 bovine kidneys <b>PDB header:</b> hydrolase
56	<a href="#">c3fgrA</a>	Alignment	not modelled	12.3	56	<b>Chain:</b> A; <b>PDB Molecule:</b> putative phospholipase b-like 2 28 kda form; <b>PDBTitle:</b> two chain form of the 66.3 kda protein at 1.8 angstrom
57	<a href="#">c5tw9D</a>	Alignment	not modelled	12.2	20	<b>PDB header:</b> lipid-binding protein <b>Chain:</b> D; <b>PDB Molecule:</b> iron uptake system component efeo; <b>PDBTitle:</b> 1.50 angstrom crystal structure of c-terminal fragment (residues 322-2 384) of iron uptake system component efeo from yersinia pestis.
58	<a href="#">c2vmID</a>	Alignment	not modelled	12.0	16	<b>PDB header:</b> photosynthesis <b>Chain:</b> D; <b>PDB Molecule:</b> phycocyanin beta chain; <b>PDBTitle:</b> the monoclinic structure of phycocyanin from gloeobacter violaceus
59	<a href="#">d1x8da1</a>	Alignment	not modelled	11.7	13	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> YiIL-like
60	<a href="#">c5lj3H</a>	Alignment	not modelled	11.5	13	<b>PDB header:</b> splicing <b>Chain:</b> H; <b>PDB Molecule:</b> cwc22; <b>PDBTitle:</b> structure of the core of the yeast spliceosome immediately after2 branching
61	<a href="#">c3bpjD</a>	Alignment	not modelled	11.3	19	<b>PDB header:</b> translation <b>Chain:</b> D; <b>PDB Molecule:</b> eukaryotic translation initiation factor 3 subunit j; <b>PDBTitle:</b> crystal structure of human translation initiation factor 3, subunit 12 alpha
62	<a href="#">c5tmxA</a>	Alignment	not modelled	11.1	27	<b>PDB header:</b> transcription regulator <b>Chain:</b> A; <b>PDB Molecule:</b> protein sini; <b>PDBTitle:</b> solution structure of sini, antagonist to the master biofilm-regulator2 sinr in bacillus subtilis
63	<a href="#">c6bn1A</a>	Alignment	not modelled	11.1	24	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> serine/threonine-protein kinase hippo; <b>PDBTitle:</b> salvador hippo sarah domain complex
64	<a href="#">c3hxrA</a>	Alignment	not modelled	10.9	5	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> nucleoporin nup120; <b>PDBTitle:</b> nucleoporin nup120 from s.cerevisiae (aa 1-757)
65	<a href="#">c2kxA</a>	Alignment	not modelled	10.7	50	<b>PDB header:</b> viral protein, immune system <b>Chain:</b> A; <b>PDB Molecule:</b> haemagglutinin ha2 chain peptide; <b>PDBTitle:</b> the hemagglutinin fusion peptide (h1 subtype) at ph 7.4
66	<a href="#">d1aw9a1</a>	Alignment	not modelled	10.7	17	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
67	<a href="#">c5mqfT</a>	Alignment	not modelled	10.6	18	<b>PDB header:</b> splicing <b>Chain:</b> T; <b>PDB Molecule:</b> pre-mrna-splicing factor cwc22 homolog; <b>PDBTitle:</b> cryo-em structure of a human spliceosome activated for step 2 of2 splicing (c* complex)
68	<a href="#">c1vw4R</a>	Alignment	not modelled	10.3	17	<b>PDB header:</b> ribosome <b>Chain:</b> R; <b>PDB Molecule:</b> 54s ribosomal protein l2, mitochondrial; <b>PDBTitle:</b> structure of the yeast mitochondrial large ribosomal subunit
69	<a href="#">c3io1B</a>	Alignment	not modelled	10.3	7	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> aminobenzoyl-glutamate utilization protein; <b>PDBTitle:</b> crystal structure of aminobenzoyl-glutamate utilization2 protein from klebsiella pneumoniae
70	<a href="#">d1ug2a</a>	Alignment	not modelled	10.1	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Myb/SANT domain
71	<a href="#">c1nogA</a>	Alignment	not modelled	10.0	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> conserved hypothetical protein ta0546; <b>PDBTitle:</b> crystal structure of conserved protein 0546 from thermoplasma2 acidophilum
72	<a href="#">d1noga</a>	Alignment	not modelled	10.0	28	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Cobalamin adenosyltransferase-like <b>Family:</b> Cobalamin adenosyltransferase
73	<a href="#">c2jagA</a>	Alignment	not modelled	9.9	21	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> halorhodopsin; <b>PDBTitle:</b> l1-intermediate of halorhodopsin t203v
74	<a href="#">c3jlzP</a>	Alignment	not modelled	9.7	14	<b>PDB header:</b> metal transport <b>Chain:</b> P; <b>PDB Molecule:</b> cation efflux family protein; <b>PDBTitle:</b> inward-facing conformation of the zinc transporter yiiip revealed by2 cryo-electron microscopy
75	<a href="#">d1e12a</a>	Alignment	not modelled	9.7	20	<b>Fold:</b> Family A G protein-coupled receptor-like <b>Superfamily:</b> Family A G protein-coupled receptor-like <b>Family:</b> Bacteriorhodopsin-like
76	<a href="#">c2jxfA</a>	Alignment	not modelled	9.6	23	<b>PDB header:</b> viral protein, membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> genome polyprotein; <b>PDBTitle:</b> the solution structure of hcv ns4b(40-69)
77	<a href="#">c4wqoD</a>	Alignment	not modelled	9.6	10	<b>PDB header:</b> transcription <b>Chain:</b> D; <b>PDB Molecule:</b> cullin-2; <b>PDBTitle:</b> structure of vhl-elob-eloc-cul2
78	<a href="#">d1ha7a</a>	Alignment	not modelled	9.4	17	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Phycocyanin-like phycobilisome proteins
79	<a href="#">c4fquF</a>	Alignment	not modelled	9.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F; <b>PDB Molecule:</b> putative glutathione transferase; <b>PDBTitle:</b> glutathionyl-hydroquinone reductase pcpf of sphingobium2 chlorophenicum
80	<a href="#">c6et5O</a>	Alignment	not modelled	9.1	29	<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 <b>PDB header:</b> photosynthesis

81	<a href="#">c6et5s_</a>	Alignment	not modelled	9.1	29	<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
82	<a href="#">c6et5v_</a>	Alignment	not modelled	9.1	29	<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
83	<a href="#">c6et5a_</a>	Alignment	not modelled	9.1	29	<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
84	<a href="#">c6et5l_</a>	Alignment	not modelled	9.1	29	<b>PDB header:</b> photosynthesis <b>Chain:</b> I; <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="#">c6et55_</a>	Alignment	not modelled	9.1	29	<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
86	<a href="#">c6et5m_</a>	Alignment	not modelled	9.1	29	<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
87	<a href="#">c6et5X_</a>	Alignment	not modelled	9.1	29	<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
88	<a href="#">c6et5j_</a>	Alignment	not modelled	9.1	29	<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
89	<a href="#">c6et5y_</a>	Alignment	not modelled	9.1	29	<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
90	<a href="#">c6et5g_</a>	Alignment	not modelled	9.1	29	<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
91	<a href="#">c6et5R_</a>	Alignment	not modelled	9.1	29	<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
92	<a href="#">c6et5d_</a>	Alignment	not modelled	9.1	29	<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
93	<a href="#">c6et5U_</a>	Alignment	not modelled	9.1	29	<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
94	<a href="#">c6et52_</a>	Alignment	not modelled	9.1	29	<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
95	<a href="#">c6et5p_</a>	Alignment	not modelled	9.1	29	<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
96	<a href="#">c5f42B_</a>	Alignment	not modelled	8.8	22	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine o- <b>PDBTitle:</b> activity and crystal structure of francisella novicida udp-n-2 acetylglucosamine acyltransferase
97	<a href="#">c4m5bA_</a>	Alignment	not modelled	8.7	20	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> cobalamin biosynthesis protein cbim; <b>PDBTitle:</b> crystal structure of an truncated transition metal transporter
98	<a href="#">c4m5cA_</a>	Alignment	not modelled	8.7	20	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> cobalamin biosynthesis protein cbim; <b>PDBTitle:</b> crystal structure of an truncated transition metal transporter
99	<a href="#">d1b8db_</a>	Alignment	not modelled	8.5	14	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Phycocyanin-like phycobilisome proteins