






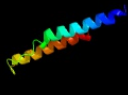





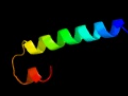



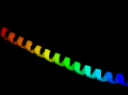






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1779c (-) _2012693_2014486
Date	Fri Aug 2 13:30:38 BST 2019
Unique Job ID	1916e0980f571890

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5voxb_</a>	 Alignment		74.4	8	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> v-type proton atpase subunit b; <b>PDBTitle:</b> yeast v-atpase in complex with legionella pneumophila effector sidk2 (rotational state 1)
2	<a href="#">c6o7ua_</a>	 Alignment		73.8	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> <b>PDBTitle:</b> saccharomyces cerevisiae v-atpase stv1-vo
3	<a href="#">c4cdiC_</a>	 Alignment		64.3	28	<b>PDB header:</b> membrane protein <b>Chain:</b> C; <b>PDB Molecule:</b> predicted protein; <b>PDBTitle:</b> crystal structure of acrb-acrz complex
4	<a href="#">c6o7xa_</a>	 Alignment		63.8	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> vacuolar atp synthase catalytic subunit a; <b>PDBTitle:</b> saccharomyces cerevisiae v-atpase stv1-v1vo state 3
5	<a href="#">c5gasN_</a>	 Alignment		56.8	25	<b>PDB header:</b> hydrolase <b>Chain:</b> N; <b>PDB Molecule:</b> archaeal/vacuolar-type h+-atpase subunit i; <b>PDBTitle:</b> thermus thermophilus v/a-atpase, conformation 2
6	<a href="#">c2kncA_</a>	 Alignment		48.3	17	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> integrin alpha-iiib; <b>PDBTitle:</b> platelet integrin alfaiaib-beta3 transmembrane-cytoplasmic2 heterocomplex
7	<a href="#">c6cfwB_</a>	 Alignment		46.7	23	<b>PDB header:</b> membrane protein <b>Chain:</b> B; <b>PDB Molecule:</b> monovalent cation/h+ antiporter subunit f; <b>PDBTitle:</b> cryoem structure of a respiratory membrane-bound hydrogenase
8	<a href="#">c5ew5C_</a>	 Alignment		36.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> colicin-e9; <b>PDBTitle:</b> crystal structure of colicin e9 in complex with its immunity protein2 im9
9	<a href="#">c5kc1H_</a>	 Alignment		35.8	12	<b>PDB header:</b> endocytosis <b>Chain:</b> H; <b>PDB Molecule:</b> autophagy-related protein 38; <b>PDBTitle:</b> structure of the c-terminal dimerization domain of atg38
10	<a href="#">c2mx4A_</a>	 Alignment		30.1	21	<b>PDB header:</b> translation,protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> eukaryotic translation initiation factor 4e-binding protein <b>PDBTitle:</b> nmr structure of phosphorylated 4e-bp2
11	<a href="#">c5nbtC_</a>	 Alignment		28.1	19	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> katanin p80 wd40 repeat-containing subunit b1; <b>PDBTitle:</b> apo structure of p60n/p80c katanin

12	<a href="#">c4rfsS_</a>	Alignment		27.0	14	<b>PDB header:</b> hydrolase, transport protein <b>Chain:</b> S; <b>PDB Molecule:</b> substrate binding prtein s; <b>PDBTitle:</b> structure of a pantothenate energy coupling factor transporter
13	<a href="#">c2l8sA_</a>	Alignment		24.7	21	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> integrin alpha-1; <b>PDBTitle:</b> solution nmr structure of transmembrane and cytosolic regions of f2 integrin alpha1 in detergent micelles
14	<a href="#">c6hu9e_</a>	Alignment		24.4	21	<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
15	<a href="#">c2lqtA_</a>	Alignment		21.8	33	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> coiled-coil-helix-coiled-coil-helix domain-containing <b>PDBTitle:</b> solution structure of chchd7
16	<a href="#">c1ciiA_</a>	Alignment		21.2	8	<b>PDB header:</b> transmembrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> colicin ia; <b>PDBTitle:</b> colicin ia
17	<a href="#">d2fmla1</a>	Alignment		20.7	41	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Nudix-associated domain
18	<a href="#">c4rnbA_</a>	Alignment		19.9	11	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> orexin receptor type 2, glga glycogen synthase; <b>PDBTitle:</b> crystal structure of the human ox2 orexin receptor bound to the2 insomnia drug suvorexant
19	<a href="#">c6f2dj_</a>	Alignment		19.6	18	<b>PDB header:</b> protein transport <b>Chain:</b> J; <b>PDB Molecule:</b> flagellar biosynthetic protein fliq; <b>PDBTitle:</b> a flipqr complex forms the core of the salmonella type iii secretion2 system export apparatus.
20	<a href="#">c6f2dl_</a>	Alignment		19.6	18	<b>PDB header:</b> protein transport <b>Chain:</b> I; <b>PDB Molecule:</b> flagellar biosynthetic protein fliq; <b>PDBTitle:</b> a flipqr complex forms the core of the salmonella type iii secretion2 system export apparatus.
21	<a href="#">c6r6bl_</a>	Alignment	not modelled	19.4	18	<b>PDB header:</b> protein transport <b>Chain:</b> I; <b>PDB Molecule:</b> surface presentation of antigens protein spaq; <b>PDBTitle:</b> structure of the core shigella flexneri type iii secretion system2 export gate complex sctrst (spa24/spa9/spa29).
22	<a href="#">c2y69Q_</a>	Alignment	not modelled	17.8	20	<b>PDB header:</b> electron transport <b>Chain:</b> Q; <b>PDB Molecule:</b> cytochrome c oxidase subunit 4 isoform 1; <b>PDBTitle:</b> bovine heart cytochrome c oxidase re-refined with molecular oxygen
23	<a href="#">c2momC_</a>	Alignment	not modelled	17.6	24	<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
24	<a href="#">c2momB_</a>	Alignment	not modelled	17.6	24	<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
25	<a href="#">c5mg3D_</a>	Alignment	not modelled	17.6	18	<b>PDB header:</b> chaperone <b>Chain:</b> D; <b>PDB Molecule:</b> protein translocase subunit secD; <b>PDBTitle:</b> em fitted model of bacterial holo-translocon
26	<a href="#">c2yvxD_</a>	Alignment	not modelled	17.1	16	<b>PDB header:</b> transport protein <b>Chain:</b> D; <b>PDB Molecule:</b> mg2+ transporter mgte; <b>PDBTitle:</b> crystal structure of magnesium transporter mgte
27	<a href="#">c4dgwA_</a>	Alignment	not modelled	16.2	15	<b>PDB header:</b> splicing <b>Chain:</b> A; <b>PDB Molecule:</b> pre-mrna-splicing factor prp9; <b>PDBTitle:</b> crystal structure of the sf3a splicing factor complex of u2 snrnp
						<b>PDB header:</b> transport protein

28	<a href="#">c3k07A_</a>	Alignment	not modelled	16.2	13	<b>Chain:</b> A: <b>PDB Molecule:</b> cation efflux system protein cusa; <b>PDBTitle:</b> crystal structure of cusa
29	<a href="#">c5tj5A_</a>	Alignment	not modelled	15.5	8	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> v-type proton atpase subunit a; <b>PDBTitle:</b> atomic model for the membrane-embedded motor of a eukaryotic v-atpase
30	<a href="#">d1v54d_</a>	Alignment	not modelled	15.5	20	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Mitochondrial cytochrome c oxidase subunit IV <b>Family:</b> Mitochondrial cytochrome c oxidase subunit IV
31	<a href="#">d1kpla_</a>	Alignment	not modelled	15.5	13	<b>Fold:</b> Clc chloride channel <b>Superfamily:</b> Clc chloride channel <b>Family:</b> Clc chloride channel
32	<a href="#">c6iiuA_</a>	Alignment	not modelled	13.9	10	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> soluble cytochrome b562,thromboxane a2 receptor,rubredoxin, <b>PDBTitle:</b> crystal structure of the human thromboxane a2 receptor bound to2 ramatroban
33	<a href="#">c4i7zE_</a>	Alignment	not modelled	13.7	24	<b>PDB header:</b> photosynthesis <b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 6; <b>PDBTitle:</b> crystal structure of cytochrome b6f in dogg, with disordered rieske2 iron-sulfur protein soluble domain
34	<a href="#">c4pv1E_</a>	Alignment	not modelled	13.7	24	<b>PDB header:</b> electron transport/inhibitor <b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 6; <b>PDBTitle:</b> cytochrome b6f structure from m. laminosus with the quinone analog2 inhibitor stigmatellin
35	<a href="#">c2kr6A_</a>	Alignment	not modelled	13.7	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> presenilin-1; <b>PDBTitle:</b> solution structure of presenilin-1 ctf subunit
36	<a href="#">d1xo1a1</a>	Alignment	not modelled	12.9	19	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> 5' to 3' exonuclease, C-terminal subdomain <b>Family:</b> 5' to 3' exonuclease, C-terminal subdomain
37	<a href="#">c6mctF_</a>	Alignment	not modelled	12.7	30	<b>PDB header:</b> de novo protein <b>Chain:</b> F: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
38	<a href="#">c6mctJ_</a>	Alignment	not modelled	12.7	30	<b>PDB header:</b> de novo protein <b>Chain:</b> J: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
39	<a href="#">c6mctM_</a>	Alignment	not modelled	12.7	30	<b>PDB header:</b> de novo protein <b>Chain:</b> M: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
40	<a href="#">c6mctO_</a>	Alignment	not modelled	12.7	30	<b>PDB header:</b> de novo protein <b>Chain:</b> O: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
41	<a href="#">c6mctA_</a>	Alignment	not modelled	12.7	30	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
42	<a href="#">c6mctI_</a>	Alignment	not modelled	12.7	30	<b>PDB header:</b> de novo protein <b>Chain:</b> I: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
43	<a href="#">c6mctC_</a>	Alignment	not modelled	12.7	30	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
44	<a href="#">c6mq2D_</a>	Alignment	not modelled	12.7	30	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c22212 form-2
45	<a href="#">c6mpwA_</a>	Alignment	not modelled	12.7	30	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> de novo design of membrane protein--mini-evgl membrane protein, c22212 form-1
46	<a href="#">c6mctL_</a>	Alignment	not modelled	12.7	30	<b>PDB header:</b> de novo protein <b>Chain:</b> L: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
47	<a href="#">c6mctB_</a>	Alignment	not modelled	12.7	30	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
48	<a href="#">c6mctK_</a>	Alignment	not modelled	12.7	30	<b>PDB header:</b> de novo protein <b>Chain:</b> K: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
49	<a href="#">c6mctE_</a>	Alignment	not modelled	12.7	30	<b>PDB header:</b> de novo protein <b>Chain:</b> E: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
50	<a href="#">c6mctN_</a>	Alignment	not modelled	12.7	30	<b>PDB header:</b> de novo protein <b>Chain:</b> N: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
51	<a href="#">c6mctG_</a>	Alignment	not modelled	12.7	30	<b>PDB header:</b> de novo protein <b>Chain:</b> G: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
52	<a href="#">c6mctD_</a>	Alignment	not modelled	12.7	30	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
53	<a href="#">c6mctH_</a>	Alignment	not modelled	12.7	30	<b>PDB header:</b> de novo protein <b>Chain:</b> H: <b>PDB Molecule:</b> mini-evgl membrane protein; <b>PDBTitle:</b> a designed pentameric membrane protein stabilized by van der waals2 interaction
						<b>PDB header:</b> structural genomics, unknown function

54	<a href="#">c3fgxA</a>	Alignment	not modelled	12.7	17	<b>Chain:</b> A; <b>PDB Molecule:</b> rbstp2171; <b>PDBTitle:</b> structure of uncharacterised protein rbstp2171 from bacillus2 stearothermophilus
55	<a href="#">c4nawK</a>	Alignment	not modelled	12.1	60	<b>PDB header:</b> protein transport/ligase <b>Chain:</b> K; <b>PDB Molecule:</b> autophagy-related protein 16-1; <b>PDBTitle:</b> crystal structure of human atg12~atg5-atg16n in complex with a2 fragment of atg3
56	<a href="#">c4gdkC</a>	Alignment	not modelled	12.1	60	<b>PDB header:</b> protein binding <b>Chain:</b> C; <b>PDB Molecule:</b> autophagy-related protein 16-1; <b>PDBTitle:</b> crystal structure of human atg12~atg5 conjugate in complex with an n-2 terminal fragment of atg16l1
57	<a href="#">c4nawC</a>	Alignment	not modelled	12.1	60	<b>PDB header:</b> protein transport/ligase <b>Chain:</b> C; <b>PDB Molecule:</b> autophagy-related protein 16-1; <b>PDBTitle:</b> crystal structure of human atg12~atg5-atg16n in complex with a2 fragment of atg3
58	<a href="#">c4gdlC</a>	Alignment	not modelled	12.1	60	<b>PDB header:</b> protein binding <b>Chain:</b> C; <b>PDB Molecule:</b> autophagy-related protein 16-1; <b>PDBTitle:</b> crystal structure of human atg12~atg5 conjugate in complex with an n-2 terminal fragment of atg16l1
59	<a href="#">c4gdkF</a>	Alignment	not modelled	11.9	60	<b>PDB header:</b> protein binding <b>Chain:</b> F; <b>PDB Molecule:</b> autophagy-related protein 16-1; <b>PDBTitle:</b> crystal structure of human atg12~atg5 conjugate in complex with an n-2 terminal fragment of atg16l1
60	<a href="#">c2e74E</a>	Alignment	not modelled	11.8	24	<b>PDB header:</b> photosynthesis <b>Chain:</b> E; <b>PDB Molecule:</b> cytochrome b6-f complex subunit 6; <b>PDBTitle:</b> crystal structure of the cytochrome b6f complex from m.laminosus
61	<a href="#">d2e74e1</a>	Alignment	not modelled	11.8	24	<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
62	<a href="#">c1vf5E</a>	Alignment	not modelled	11.8	24	<b>PDB header:</b> photosynthesis <b>Chain:</b> E; <b>PDB Molecule:</b> protein pet I; <b>PDBTitle:</b> crystal structure of cytochrome b6f complex from m.laminosus
63	<a href="#">c2e75E</a>	Alignment	not modelled	11.8	24	<b>PDB header:</b> photosynthesis <b>Chain:</b> E; <b>PDB Molecule:</b> cytochrome b6-f complex subunit 6; <b>PDBTitle:</b> crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
64	<a href="#">c1vf5R</a>	Alignment	not modelled	11.8	24	<b>PDB header:</b> photosynthesis <b>Chain:</b> R; <b>PDB Molecule:</b> protein pet I; <b>PDBTitle:</b> crystal structure of cytochrome b6f complex from m.laminosus
65	<a href="#">c4h0IE</a>	Alignment	not modelled	11.8	24	<b>PDB header:</b> photosynthesis <b>Chain:</b> E; <b>PDB Molecule:</b> cytochrome b6-f complex subunit 6; <b>PDBTitle:</b> cytochrome b6f complex crystal structure from mastigocladus laminosus2 with n-side inhibitor nqno
66	<a href="#">c4h13E</a>	Alignment	not modelled	11.8	24	<b>PDB header:</b> photosynthesis <b>Chain:</b> E; <b>PDB Molecule:</b> cytochrome b6-f complex subunit 6; <b>PDBTitle:</b> crystal structure of the cytochrome b6f complex from mastigocladus2 laminosus with tds
67	<a href="#">c2e76E</a>	Alignment	not modelled	11.8	24	<b>PDB header:</b> photosynthesis <b>Chain:</b> E; <b>PDB Molecule:</b> cytochrome b6-f complex subunit 6; <b>PDBTitle:</b> crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
68	<a href="#">c1i8tB</a>	Alignment	not modelled	11.7	20	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> udp-galactopyranose mutase; <b>PDBTitle:</b> strcuture of udp-galactopyranose mutase from e.coli
69	<a href="#">c6gv9K</a>	Alignment	not modelled	11.7	40	<b>PDB header:</b> protein fibril <b>Chain:</b> K; <b>PDB Molecule:</b> prepilin peptidase-dependent protein d; <b>PDBTitle:</b> structure of the type iv pilus from enterohemorrhagic escherichia coli2 (ehec)
70	<a href="#">c2lonA</a>	Alignment	not modelled	11.6	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> hig1 domain family member 1b; <b>PDBTitle:</b> backbone structure of human membrane protein higd1b
71	<a href="#">c2ht2B</a>	Alignment	not modelled	11.5	10	<b>PDB header:</b> membrane protein <b>Chain:</b> B; <b>PDB Molecule:</b> h(+)/cl(-) exchange transporter clca; <b>PDBTitle:</b> structure of the escherichia coli clc chloride channel2 y445h mutant and fab complex
72	<a href="#">c1z8yN</a>	Alignment	not modelled	11.2	29	<b>PDB header:</b> virus <b>Chain:</b> N; <b>PDB Molecule:</b> spike glycoprotein e2; <b>PDBTitle:</b> mapping the e2 glycoprotein of alphaviruses
73	<a href="#">c1z8yP</a>	Alignment	not modelled	11.2	29	<b>PDB header:</b> virus <b>Chain:</b> P; <b>PDB Molecule:</b> spike glycoprotein e2; <b>PDBTitle:</b> mapping the e2 glycoprotein of alphaviruses
74	<a href="#">c1z8yJ</a>	Alignment	not modelled	11.2	29	<b>PDB header:</b> virus <b>Chain:</b> J; <b>PDB Molecule:</b> spike glycoprotein e2; <b>PDBTitle:</b> mapping the e2 glycoprotein of alphaviruses
75	<a href="#">c1z8yL</a>	Alignment	not modelled	11.2	29	<b>PDB header:</b> virus <b>Chain:</b> L; <b>PDB Molecule:</b> spike glycoprotein e2; <b>PDBTitle:</b> mapping the e2 glycoprotein of alphaviruses
76	<a href="#">c2lomA</a>	Alignment	not modelled	11.2	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> hig1 domain family member 1a; <b>PDBTitle:</b> backbone structure of human membrane protein higd1a
77	<a href="#">c2mbhB</a>	Alignment	not modelled	11.0	33	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> krueppel-like factor 1; <b>PDBTitle:</b> nmr structure of ekf(22-40)/ubiquitin complex
78	<a href="#">c2k1aA</a>	Alignment	not modelled	10.8	18	<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
79	<a href="#">c5mdxX</a>	Alignment	not modelled	10.7	32	<b>PDB header:</b> photosynthesis <b>Chain:</b> X; <b>PDB Molecule:</b> photosystem ii reaction center protein x; <b>PDBTitle:</b> cryo-em structure of the psii supercomplex from arabidopsis thaliana
80	<a href="#">c5mdxx</a>	Alignment	not modelled	10.7	32	<b>PDB header:</b> photosynthesis <b>Chain:</b> X; <b>PDB Molecule:</b> photosystem ii reaction center protein x; <b>PDBTitle:</b> cryo-em structure of the psii supercomplex from

						arabidopsis thaliana
81	<a href="#">c4mo2A_</a>	Alignment	not modelled	10.7	25	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-galactopyranose mutase; <b>PDBTitle:</b> crystal structure of udp-n-acetylgalactopyranose mutase from2 campylobacter jejuni
82	<a href="#">d1scfa_</a>	Alignment	not modelled	10.5	18	<b>Fold:</b> 4-helical cytokines <b>Superfamily:</b> 4-helical cytokines <b>Family:</b> Short-chain cytokines
83	<a href="#">c1scfA_</a>	Alignment	not modelled	10.5	18	<b>PDB header:</b> hormone/growth factor <b>Chain:</b> A: <b>PDB Molecule:</b> stem cell factor; <b>PDBTitle:</b> human recombinant stem cell factor
84	<a href="#">c4nawO_</a>	Alignment	not modelled	10.0	60	<b>PDB header:</b> protein transport/ligase <b>Chain:</b> O: <b>PDB Molecule:</b> autophagy-related protein 16-1; <b>PDBTitle:</b> crystal structure of human atg12~atg5-atg16n in complex with a2 fragment of atg3
85	<a href="#">c4nawG_</a>	Alignment	not modelled	10.0	60	<b>PDB header:</b> protein transport/ligase <b>Chain:</b> G: <b>PDB Molecule:</b> autophagy-related protein 16-1; <b>PDBTitle:</b> crystal structure of human atg12~atg5-atg16n in complex with a2 fragment of atg3
86	<a href="#">d2imja1</a>	Alignment	not modelled	10.0	42	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> PFL3262-like
87	<a href="#">c4b03A_</a>	Alignment	not modelled	9.4	7	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> dengue virus 1 e protein; <b>PDBTitle:</b> 6a electron cryomicroscopy structure of immature dengue virus serotype2 1
88	<a href="#">c5m1gB_</a>	Alignment	not modelled	9.2	21	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> gag protein; <b>PDBTitle:</b> structure of a spumaretrovirus gag central domain reveals an ancient2 retroviral capsid
89	<a href="#">c5azcA_</a>	Alignment	not modelled	9.2	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> prolipoprotein diacylglycerol transferase; <b>PDBTitle:</b> crystal structure of escherichia coli lgt in complex with2 phosphatidylglycerol
90	<a href="#">c5a63C_</a>	Alignment	not modelled	9.1	12	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> gamma-secretase subunit aph-1a; <b>PDBTitle:</b> cryo-em structure of the human gamma-secretase complex at 3.4 angstrom2 resolution.
91	<a href="#">c4yu5A_</a>	Alignment	not modelled	9.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> immune inhibitor a, metalloprotease; <b>PDBTitle:</b> crystal structure of selenomethionine variant of bacillus anthracis2 immune inhibitor a2 peptidase zymogen
92	<a href="#">d1zvca1</a>	Alignment	not modelled	8.9	34	<b>Fold:</b> AOC barrel-like <b>Superfamily:</b> Allene oxide cyclase-like <b>Family:</b> Allene oxide cyclase-like
93	<a href="#">c4l6rA_</a>	Alignment	not modelled	8.7	11	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> soluble cytochrome b562 and glucagon receptor chimera; <b>PDBTitle:</b> structure of the class b human glucagon g protein coupled receptor
94	<a href="#">c2qzvB_</a>	Alignment	not modelled	8.6	23	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> major vault protein; <b>PDBTitle:</b> draft crystal structure of the vault shell at 9 angstroms2 resolution
95	<a href="#">c1ltxR_</a>	Alignment	not modelled	8.6	20	<b>PDB header:</b> transferase/protein binding <b>Chain:</b> R: <b>PDB Molecule:</b> rab escort protein 1; <b>PDBTitle:</b> structure of rab escort protein-1 in complex with rab geranylgeranyl2 transferase and isoprenoid
96	<a href="#">c2e1mA_</a>	Alignment	not modelled	8.6	44	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-glutamate oxidase; <b>PDBTitle:</b> crystal structure of l-glutamate oxidase from streptomyces sp. x-119-6
97	<a href="#">c5ws4A_</a>	Alignment	not modelled	8.5	20	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> macrolide export atp-binding/permease protein macb; <b>PDBTitle:</b> crystal structure of tripartite-type abc transporter macb from2 acinetobacter baumannii
98	<a href="#">c1emzA_</a>	Alignment	not modelled	8.1	57	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelope glycoprotein e1; <b>PDBTitle:</b> solution structure of fragment (350-370) of the2 transmembrane domain of hepatitis c envelope glycoprotein3 e1
99	<a href="#">d2dw4a2</a>	Alignment	not modelled	8.0	20	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain