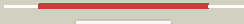




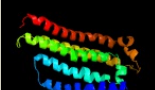















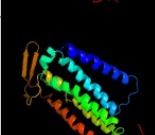


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1623c_cydA_1824437_1825894
Date	Fri Aug 2 13:30:21 BST 2019
Unique Job ID	8ec71fc089a1e834

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5ir6A_</a>	 Alignment		100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> bd-type quinol oxidase subunit i; <b>PDBTitle:</b> the structure of bd oxidase from geobacillus thermodenitrificans
2	<a href="#">c3mk7K_</a>	 Alignment		96.5	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> K: <b>PDB Molecule:</b> cytochrome c oxidase, cbb3-type, subunit n; <b>PDBTitle:</b> the structure of cbb3 cytochrome oxidase
3	<a href="#">c6elhA_</a>	 Alignment		94.3	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nitric-oxide reductase; <b>PDBTitle:</b> low resolution structure of neisseria meningitidis qnor
4	<a href="#">c5ir6B_</a>	 Alignment		93.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> bd-type quinol oxidase subunit ii; <b>PDBTitle:</b> the structure of bd oxidase from geobacillus thermodenitrificans
5	<a href="#">c2yevA_</a>	 Alignment		91.0	15	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c oxidase polypeptide i+iii; <b>PDBTitle:</b> structure of caa3-type cytochrome oxidase
6	<a href="#">c4xydA_</a>	 Alignment		89.2	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nitric-oxide reductase subunit b; <b>PDBTitle:</b> nitric oxide reductase from roseobacter denitrificans (rdnor)
7	<a href="#">c1fftF_</a>	 Alignment		88.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> ubiquinol oxidase; <b>PDBTitle:</b> the structure of ubiquinol oxidase from escherichia coli
8	<a href="#">d1ffta_</a>	 Alignment		88.4	15	<b>Fold:</b> Cytochrome c oxidase subunit I-like <b>Superfamily:</b> Cytochrome c oxidase subunit I-like <b>Family:</b> Cytochrome c oxidase subunit I-like
9	<a href="#">c3eh4A_</a>	 Alignment		87.1	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c oxidase subunit 1; <b>PDBTitle:</b> structure of the reduced form of cytochrome ba3 oxidase from thermus2 thermophilus
10	<a href="#">c3aygA_</a>	 Alignment		85.5	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nitric oxide reductase; <b>PDBTitle:</b> crystal structure of nitric oxide reductase complex with hqno
11	<a href="#">c6hwhQ_</a>	 Alignment		81.6	16	<b>PDB header:</b> electron transport <b>Chain:</b> Q: <b>PDB Molecule:</b> cytochrome c oxidase subunit 1; <b>PDBTitle:</b> structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis

12	<a href="#">c4wgwA_</a>	Alignment		81.4	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> divalent metal cation transporter mnth; <b>PDBTitle:</b> staphylococcus capitis divalent metal ion transporter (dmt) in complex2 with manganese
13	<a href="#">c4wgvC_</a>	Alignment		81.4	16	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> divalent metal cation transporter mnth; <b>PDBTitle:</b> crystal structure of staphylococcus capitis divalent metal ion2 transporter (dmt) in complex with nanobody
14	<a href="#">d1xmea1</a>	Alignment		80.8	16	<b>Fold:</b> Cytochrome c oxidase subunit I-like <b>Superfamily:</b> Cytochrome c oxidase subunit I-like <b>Family:</b> Cytochrome c oxidase subunit I-like
15	<a href="#">c6o7ua_</a>	Alignment		75.3	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> <b>PDBTitle:</b> saccharomyces cerevisiae v-atpase stv1-vo
16	<a href="#">c5voxb_</a>	Alignment		74.6	11	<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)
17	<a href="#">d1ar1a_</a>	Alignment		73.9	14	<b>Fold:</b> Cytochrome c oxidase subunit I-like <b>Superfamily:</b> Cytochrome c oxidase subunit I-like <b>Family:</b> Cytochrome c oxidase subunit I-like
18	<a href="#">d3dtua1</a>	Alignment		67.9	17	<b>Fold:</b> Cytochrome c oxidase subunit I-like <b>Superfamily:</b> Cytochrome c oxidase subunit I-like <b>Family:</b> Cytochrome c oxidase subunit I-like
19	<a href="#">c3o0rB_</a>	Alignment		65.7	8	<b>PDB header:</b> immune system/oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nitric oxide reductase subunit b; <b>PDBTitle:</b> crystal structure of nitric oxide reductase from pseudomonas2 aeruginosa in complex with antibody fragment
20	<a href="#">c6hu9m_</a>	Alignment		63.8	15	<b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> M: <b>PDB Molecule:</b> cytochrome b-c1 complex subunit 2, mitochondrial; <b>PDBTitle:</b> iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
21	<a href="#">d1v54a_</a>	Alignment	not modelled	61.1	14	<b>Fold:</b> Cytochrome c oxidase subunit I-like <b>Superfamily:</b> Cytochrome c oxidase subunit I-like <b>Family:</b> Cytochrome c oxidase subunit I-like
22	<a href="#">c1m56G_</a>	Alignment	not modelled	58.7	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> cytochrome c oxidase; <b>PDBTitle:</b> structure of cytochrome c oxidase from rhodobactor2 sphaeroides (wild type)
23	<a href="#">c4djiA_</a>	Alignment	not modelled	53.8	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable glutamate/gamma-aminobutyrate antiporter; <b>PDBTitle:</b> structure of glutamate-gaba antiporter gadc
24	<a href="#">c5i6xA_</a>	Alignment	not modelled	50.4	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium-dependent serotonin transporter; <b>PDBTitle:</b> x-ray structure of the ts3 human serotonin transporter complexed with2 paroxetine at the central site
25	<a href="#">c4tqvl_</a>	Alignment	not modelled	50.1	13	<b>PDB header:</b> transport protein <b>Chain:</b> I: <b>PDB Molecule:</b> algm1; <b>PDBTitle:</b> crystal structure of a bacterial abc transporter involved in the2 import of the acidic polysaccharide alginate
26	<a href="#">c4l6rA_</a>	Alignment	not modelled	49.7	17	<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
27	<a href="#">c6btmF_</a>	Alignment	not modelled	45.4	13	<b>PDB header:</b> membrane protein <b>Chain:</b> F: <b>PDB Molecule:</b> alternative complex iii subunit f; <b>PDBTitle:</b> structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
28	<a href="#">c6iiuA_</a>	Alignment	not modelled	44.0	14	<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
29	<a href="#">c5nf8A_</a>	Alignment	not modelled	35.9	18	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> respiratory supercomplex factor 1, mitochondrial; <b>PDBTitle:</b> solution structure of detergent-solubilized rcf1, a yeast2 mitochondrial inner membrane protein involved in respiratory complex3 iii/iv supercomplex formation
30	<a href="#">c4ainB_</a>	Alignment	not modelled	28.4	12	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> glycine betaine transporter betp; <b>PDBTitle:</b> crystal structure of betp with asymmetric protomers.
31	<a href="#">c6nbxG_</a>	Alignment	not modelled	27.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit j; <b>PDBTitle:</b> t.elongatus ndh (data-set 2)
32	<a href="#">c6btmC_</a>	Alignment	not modelled	25.9	13	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> alternative complex iii subunit c; <b>PDBTitle:</b> structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
33	<a href="#">c3kp9A_</a>	Alignment	not modelled	23.4	24	<b>PDB header:</b> blood coagulation,oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> vkorc1/thioredoxin domain protein; <b>PDBTitle:</b> structure of a bacterial homolog of vitamin k epoxide reductase
34	<a href="#">d2j8c1l</a>	Alignment	not modelled	20.4	14	<b>Fold:</b> Bacterial photosystem II reaction centre, L and M subunits <b>Superfamily:</b> Bacterial photosystem II reaction centre, L and M subunits <b>Family:</b> Bacterial photosystem II reaction centre, L and M subunits
35	<a href="#">c5i1mV_</a>	Alignment	not modelled	18.5	16	<b>PDB header:</b> membrane protein <b>Chain:</b> V: <b>PDB Molecule:</b> v-type proton atpase subunit a, vacuolar isoform; <b>PDBTitle:</b> yeast v-atpase average of densities, a subunit segment
36	<a href="#">c5tj5A_</a>	Alignment	not modelled	18.2	10	<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
37	<a href="#">c5lnkq_</a>	Alignment	not modelled	16.6	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> Q: <b>PDB Molecule:</b> <b>PDBTitle:</b> entire ovine respiratory complex i
38	<a href="#">c5gasN_</a>	Alignment	not modelled	16.4	14	<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
39	<a href="#">c4or2A_</a>	Alignment	not modelled	15.9	14	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> soluble cytochrome b562, metabotropic glutamate receptor 1; <b>PDBTitle:</b> human class c g protein-coupled metabotropic glutamate receptor 1 in2 complex with a negative allosteric modulator
40	<a href="#">d2p3ha1</a>	Alignment	not modelled	15.5	15	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
41	<a href="#">c6f0kC_</a>	Alignment	not modelled	15.2	13	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> polysulphide reductase nrfd; <b>PDBTitle:</b> alternative complex iii
42	<a href="#">c6iedA_</a>	Alignment	not modelled	14.8	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> heme a synthase; <b>PDBTitle:</b> crystal structure of heme a synthase from bacillus subtilis
43	<a href="#">c6gcsW_</a>	Alignment	not modelled	14.8	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> W: <b>PDB Molecule:</b> nb6m subunit; <b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica
44	<a href="#">c2l9uA_</a>	Alignment	not modelled	14.5	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbb-3; <b>PDBTitle:</b> spatial structure of dimeric erbb3 transmembrane domain
45	<a href="#">c2l9uB_</a>	Alignment	not modelled	14.5	13	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbb-3; <b>PDBTitle:</b> spatial structure of dimeric erbb3 transmembrane domain
46	<a href="#">c3lw52_</a>	Alignment	not modelled	14.4	13	<b>PDB header:</b> photosynthesis <b>Chain:</b> 2: <b>PDB Molecule:</b> type ii chlorophyll a/b binding protein from photosystem i; <b>PDB Fragment:</b> residues 81-246; <b>PDBTitle:</b> improved model of plant photosystem i
47	<a href="#">d2r2za1</a>	Alignment	not modelled	14.3	38	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
48	<a href="#">c3wkxA_</a>	Alignment	not modelled	14.3	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> non-reducing end beta-l-arabinofuranosidase; <b>PDBTitle:</b> crystal structure of gh127 beta-l-arabinofuranosidase hypba1 from2 bifidobacterium longum arabinose complex form
49	<a href="#">d2r6gf2</a>	Alignment	not modelled	14.0	11	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
50	<a href="#">c5z62N_</a>	Alignment	not modelled	13.8	20	<b>PDB header:</b> electron transport <b>Chain:</b> N: <b>PDB Molecule:</b> cytochrome c oxidase subunit ndufa4; <b>PDBTitle:</b> structure of human cytochrome c oxidase
51	<a href="#">c2bbjB_</a>	Alignment	not modelled	13.5	22	<b>PDB header:</b> metal transport/membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> divalent cation transport-related protein; <b>PDBTitle:</b> crystal structure of the cora mg2+ transporter
52	<a href="#">c5yq7L_</a>	Alignment	not modelled	12.7	12	<b>PDB header:</b> photosynthesis <b>Chain:</b> L: <b>PDB Molecule:</b> precursor for l subunits of photosynthetic reaction center; <b>PDBTitle:</b> cryo-em structure of the rc-lh core complex from roseiflexus2 castenholzii
53	<a href="#">c6ex6A_</a>	Alignment	not modelled	12.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> six-hairpin glycosidase; <b>PDBTitle:</b> the gh127, beta-arabinofuranosidase, bt3674

54	<a href="#">d3deda1</a>	Alignment	not modelled	12.5	38	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
55	<a href="#">d1eysm_</a>	Alignment	not modelled	12.0	19	<b>Fold:</b> Bacterial photosystem II reaction centre, L and M subunits <b>Superfamily:</b> Bacterial photosystem II reaction centre, L and M subunits <b>Family:</b> Bacterial photosystem II reaction centre, L and M subunits
56	<a href="#">d2o3ga1</a>	Alignment	not modelled	11.8	31	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
57	<a href="#">c3mepC_</a>	Alignment	not modelled	11.5	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein eca2234; <b>PDBTitle:</b> crystal structure of eca2234 protein from erwinia carotovora_2 northeast structural genomics consortium target ewr44
58	<a href="#">c5o31Z_</a>	Alignment	not modelled	11.4	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> Z: <b>PDB Molecule:</b> nadh dehydrogenase [ubiquinone] 1 alpha subcomplex subunit <b>PDBTitle:</b> mitochondrial complex i in the deactive state
59	<a href="#">c5kbuA_</a>	Alignment	not modelled	11.2	19	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate receptor 2,voltage-dependent calcium channel <b>PDBTitle:</b> cryo-em structure of glua2-2xstz complex at 7.8 angstrom resolution
60	<a href="#">c5yq7M_</a>	Alignment	not modelled	11.0	18	<b>PDB header:</b> photosynthesis <b>Chain:</b> M: <b>PDB Molecule:</b> precursor for m subunits of photosynthetic reaction center; <b>PDBTitle:</b> cryo-em structure of the rc-lh core complex from roseiflexus2 castenholzii
61	<a href="#">c3dedB_</a>	Alignment	not modelled	10.4	38	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable hemolysin; <b>PDBTitle:</b> c-terminal domain of probable hemolysin from chromobacterium violaceum
62	<a href="#">c6cxhC_</a>	Alignment	not modelled	10.0	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> particulate methane monooxygenase, c subunit; <b>PDBTitle:</b> crystal structure of particulate methane monooxygenase from2 methylomicrobium alcaliphilum 20z
63	<a href="#">c5mqoA_</a>	Alignment	not modelled	9.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> non-reducing end beta-l-arabinofuranosidase; <b>PDBTitle:</b> glycoside hydrolase bt_1003
64	<a href="#">c3lemA_</a>	Alignment	not modelled	9.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> fructosyltransferase; <b>PDBTitle:</b> crystal structure of fructosyltransferase (d191a) from a. japonicus in2 complex with nystose
65	<a href="#">c4eqvA_</a>	Alignment	not modelled	9.5	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> invertase 2; <b>PDBTitle:</b> structure of saccharomyces cerevisiae invertase
66	<a href="#">c2lomA_</a>	Alignment	not modelled	9.5	9	<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
67	<a href="#">c3fh6F_</a>	Alignment	not modelled	9.5	12	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> maltose transport system permease protein malf; <b>PDBTitle:</b> crystal structure of the resting state maltose transporter from e.2 coli
68	<a href="#">c4ev6E_</a>	Alignment	not modelled	9.5	23	<b>PDB header:</b> metal transport <b>Chain:</b> E: <b>PDB Molecule:</b> magnesium transport protein cora; <b>PDBTitle:</b> the complete structure of cora magnesium transporter from2 methanocaldococcus jannaschii
69	<a href="#">d2j8cm1</a>	Alignment	not modelled	9.4	20	<b>Fold:</b> Bacterial photosystem II reaction centre, L and M subunits <b>Superfamily:</b> Bacterial photosystem II reaction centre, L and M subunits <b>Family:</b> Bacterial photosystem II reaction centre, L and M subunits
70	<a href="#">c5opiA_</a>	Alignment	not modelled	9.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> rhamnogalacturonan lyase; <b>PDBTitle:</b> rhamnogalacturonan lyase
71	<a href="#">c2km1A_</a>	Alignment	not modelled	9.2	18	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> protein dre2; <b>PDBTitle:</b> solution structure of the n-terminal domain of the yeast protein dre2
72	<a href="#">d2oaa1</a>	Alignment	not modelled	9.0	38	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
73	<a href="#">c5fk8B_</a>	Alignment	not modelled	8.8	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-fructofuranosidase; <b>PDBTitle:</b> structure of d80a-fructofuranosidase from xanthophyllomyces2 dendrorhous complexed with neo-erlose
74	<a href="#">d2nqwa1</a>	Alignment	not modelled	8.7	15	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
75	<a href="#">d2gz4a1</a>	Alignment	not modelled	8.5	8	<b>Fold:</b> HD-domain/PDEase-like <b>Superfamily:</b> HD-domain/PDEase-like <b>Family:</b> HD domain
76	<a href="#">c2ls4A_</a>	Alignment	not modelled	8.4	29	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> high affinity copper uptake protein 1; <b>PDBTitle:</b> 1h chemical shift assignments for the third transmembrane domain from2 the human copper transport 1
77	<a href="#">d2rk5a1</a>	Alignment	not modelled	8.2	38	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
78	<a href="#">d2i5nm1</a>	Alignment	not modelled	8.2	19	<b>Fold:</b> Bacterial photosystem II reaction centre, L and M subunits <b>Superfamily:</b> Bacterial photosystem II reaction centre, L and M subunits <b>Family:</b> Bacterial photosystem II reaction centre, L and M subunits <b>PDB header:</b> hydrolase

79	<a href="#">c5xh9A_</a>	Alignment	not modelled	8.1	20	<b>Chain:</b> A: <b>PDB Molecule:</b> extracellular invertase; <b>PDBTitle:</b> aspergillus kawachii beta-fructofuranosidase
80	<a href="#">c5n9yB_</a>	Alignment	not modelled	8.0	12	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> zinc transport protein zntb; <b>PDBTitle:</b> the full-length structure of zntb
81	<a href="#">c4tkrB_</a>	Alignment	not modelled	7.9	17	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> thiamine transporter thia; <b>PDBTitle:</b> native-sad phasing for thit from listeria monocytogenes serovar.
82	<a href="#">d2plsA1</a>	Alignment	not modelled	7.9	31	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
83	<a href="#">c3j20J_</a>	Alignment	not modelled	7.9	67	<b>PDB header:</b> ribosome <b>Chain:</b> J: <b>PDB Molecule:</b> 30s ribosomal protein s8e; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
84	<a href="#">d2bh1x1</a>	Alignment	not modelled	7.9	20	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> EspE N-terminal domain-like <b>Family:</b> GSPiI protein E N-terminal domain-like
85	<a href="#">c2bh1Y_</a>	Alignment	not modelled	7.9	20	<b>PDB header:</b> transport protein <b>Chain:</b> Y: <b>PDB Molecule:</b> general secretion pathway protein e.; <b>PDBTitle:</b> x-ray structure of the general secretion pathway complex of2 the n-terminal domain of epse and the cytosolic domain of3 epsl of vibrio cholerae
86	<a href="#">c4pw2A_</a>	Alignment	not modelled	7.8	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> d-glucuronyl c5 epimerase b; <b>PDBTitle:</b> crystal structure of d-glucuronyl c5 epimerase
87	<a href="#">c2lonA_</a>	Alignment	not modelled	7.8	9	<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
88	<a href="#">c1zzaA_</a>	Alignment	not modelled	7.4	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> stannin; <b>PDBTitle:</b> solution nmr structure of the membrane protein stannin
89	<a href="#">c3llbA_</a>	Alignment	not modelled	7.3	31	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of the protein pa3983 with unknown2 function from pseudomonas aeruginosa pao1
90	<a href="#">d2a65a1</a>	Alignment	not modelled	7.2	18	<b>Fold:</b> SNF-like <b>Superfamily:</b> SNF-like <b>Family:</b> SNF-like
91	<a href="#">c1hgvA_</a>	Alignment	not modelled	7.2	26	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> ph75 inovirus major coat protein; <b>PDBTitle:</b> filamentous bacteriophage ph75
92	<a href="#">d1fftb2</a>	Alignment	not modelled	7.2	12	<b>Fold:</b> Transmembrane helix hairpin <b>Superfamily:</b> Cytochrome c oxidase subunit II-like, transmembrane region <b>Family:</b> Cytochrome c oxidase subunit II-like, transmembrane region
93	<a href="#">c4qk0C_</a>	Alignment	not modelled	7.1	23	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> gh127 beta-l-arabinofuranoside; <b>PDBTitle:</b> crystal structure of ara127n-se, a gh127 beta-l-arabinofuranosidase2 from geobacillus stearothermophilus t6
94	<a href="#">d1j7db_</a>	Alignment	not modelled	7.0	14	<b>Fold:</b> UBC-like <b>Superfamily:</b> UBC-like <b>Family:</b> UBC-related
95	<a href="#">c2o014_</a>	Alignment	not modelled	6.9	14	<b>PDB header:</b> photosynthesis <b>Chain:</b> 4: <b>PDB Molecule:</b> psi light-harvesting antenna chlorophyll a/b-binding <b>PDBTitle:</b> the structure of a plant photosystem i supercomplex at 3.4 angstrom2 resolution
96	<a href="#">c3k11A_</a>	Alignment	not modelled	6.9	3	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative glycosyl hydrolase; <b>PDBTitle:</b> crystal structure of putative glycosyl hydrolase (np_813087.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.80 a resolution
97	<a href="#">c1hgzA_</a>	Alignment	not modelled	6.8	29	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> ph75 inovirus major coat protein; <b>PDBTitle:</b> filamentous bacteriophage ph75
98	<a href="#">c2kcoA_</a>	Alignment	not modelled	6.8	50	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> 30s ribosomal protein s8e; <b>PDBTitle:</b> solution nmr structure of ribosomal protein sso0164 from2 sulfolobus solfataricus. northeast structural genomics3 consortium (nesg) target sst4.
99	<a href="#">c2oarA_</a>	Alignment	not modelled	6.6	11	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> large-conductance mechanosensitive channel; <b>PDBTitle:</b> mechanosensitive channel of large conductance (mscl)