

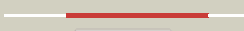






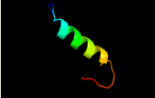

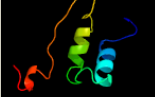

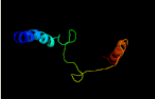








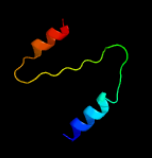

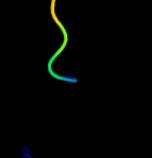
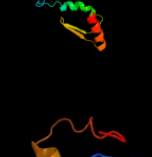
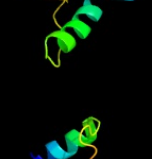
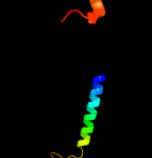
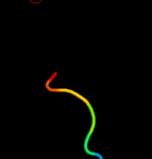
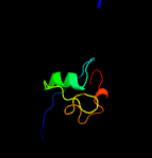
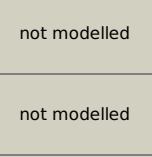


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2553c_(-)_2872022_2873275
Date	Wed Aug 7 12:50:19 BST 2019
Unique Job ID	945861177ab11699

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4iiwB_</a>	 Alignment		100.0	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> lmo1499 protein; <b>PDBTitle:</b> 2.6 angstrom crystal structure of putative yceg-like protein lmo14992 from listeria monocytogenes
2	<a href="#">c2r1fB_</a>	 Alignment		100.0	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> predicted aminodeoxychorismate lyase; <b>PDBTitle:</b> crystal structure of predicted aminodeoxychorismate lyase from escherichia coli
3	<a href="#">c4fetA_</a>	 Alignment		96.9	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> spore cortex-lytic enzyme prepeptide; <b>PDBTitle:</b> catalytic domain of germination-specific lytic tansglycosylase sleb2 from bacillus anthracis
4	<a href="#">c4f55A_</a>	 Alignment		96.6	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> spore cortex-lytic enzyme; <b>PDBTitle:</b> crystal structure of the catalytic domain of the bacillus cereus sleb2 protein
5	<a href="#">d3bz6a1</a>	 Alignment		51.4	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> PSPTO2686-like
6	<a href="#">c2v3sB_</a>	 Alignment		49.8	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase osr1; <b>PDBTitle:</b> structural insights into the recognition of substrates and 2 activators by the osr1 kinase
7	<a href="#">c5mg3F_</a>	 Alignment		49.8	16	<b>PDB header:</b> chaperone <b>Chain:</b> F: <b>PDB Molecule:</b> protein translocase subunit secf; <b>PDBTitle:</b> em fitted model of bacterial holo-translocon
8	<a href="#">d1dt9a3</a>	 Alignment		47.1	18	<b>Fold:</b> N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1 <b>Superfamily:</b> N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1 <b>Family:</b> N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1
9	<a href="#">d1gjja2</a>	 Alignment		40.5	29	<b>Fold:</b> LEM/SAP HeH motif <b>Superfamily:</b> LEM domain <b>Family:</b> LEM domain
10	<a href="#">d1h9fa_</a>	 Alignment		39.3	29	<b>Fold:</b> LEM/SAP HeH motif <b>Superfamily:</b> LEM domain <b>Family:</b> LEM domain
11	<a href="#">c3bz6A_</a>	 Alignment		36.6	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0502 protein pspto_2686; <b>PDBTitle:</b> crystal structure of a conserved protein of unknown function from pseudomonas syringae pv. tomato str. dc3000

12	<a href="#">c3e20C_</a>	Alignment		33.8	15	<b>PDB header:</b> translation <b>Chain:</b> C: <b>PDB Molecule:</b> eukaryotic peptide chain release factor subunit 1; <b>PDBTitle:</b> crystal structure of s.pombe erf1/erf3 complex
13	<a href="#">c5u8jA_</a>	Alignment		33.3	19	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0502 protein bfj73_07745; <b>PDBTitle:</b> crystal structure of a protein of unknown function ecI_02571 involved2 in membrane biogenesis from enterobacter cloacae
14	<a href="#">d1jeia_</a>	Alignment		32.0	14	<b>Fold:</b> LEM/SAP HeH motif <b>Superfamily:</b> LEM domain <b>Family:</b> LEM domain
15	<a href="#">d1ztwa1</a>	Alignment		28.7	12	<b>Fold:</b> DNA/RNA polymerases <b>Superfamily:</b> DNA/RNA polymerases <b>Family:</b> Reverse transcriptase
16	<a href="#">d1e0ga_</a>	Alignment		27.8	27	<b>Fold:</b> LysM domain <b>Superfamily:</b> LysM domain <b>Family:</b> LysM domain
17	<a href="#">d1eq7a_</a>	Alignment		27.7	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
18	<a href="#">c6btmA_</a>	Alignment		27.3	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> alternative complex iii subunit a; <b>PDBTitle:</b> structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
19	<a href="#">c1qjjA_</a>	Alignment		25.5	29	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> lap2; <b>PDBTitle:</b> n-terminal constant region of the nuclear envelope protein2 lap2
20	<a href="#">c5fimA_</a>	Alignment		25.2	17	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ygau; <b>PDBTitle:</b> the structure of kbp.k from e. coli
21	<a href="#">c6d5fF_</a>	Alignment	not modelled	24.9	56	<b>PDB header:</b> virus <b>Chain:</b> F: <b>PDB Molecule:</b> fimbrial protein; <b>PDBTitle:</b> cryo-em reconstruction of membrane-enveloped filamentous virus sfv12 (sulfolobus filamentous virus 1)
22	<a href="#">c3lwfD_</a>	Alignment	not modelled	24.3	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of putative transcriptional regulator (np_470886.1)2 from listeria innocua at 2.06 a resolution
23	<a href="#">d1wxqa2</a>	Alignment	not modelled	24.2	10	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> TGS-like <b>Family:</b> G domain-linked domain
24	<a href="#">c3ipdB_</a>	Alignment	not modelled	24.1	8	<b>PDB header:</b> exocytosis <b>Chain:</b> B: <b>PDB Molecule:</b> syntaxin-1a; <b>PDBTitle:</b> helical extension of the neuronal snare complex into the2 membrane, spacegroup i 21 21 21
25	<a href="#">d1l0wa2</a>	Alignment	not modelled	23.9	32	<b>Fold:</b> DCoH-like <b>Superfamily:</b> GAD domain-like <b>Family:</b> GAD domain
26	<a href="#">c5x8rx_</a>	Alignment	not modelled	23.9	33	<b>PDB header:</b> ribosome <b>Chain:</b> X: <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of the 30s small subunit of chloroplast ribosome from2 spinach
27	<a href="#">c2kogA_</a>	Alignment	not modelled	23.9	11	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> vesicle-associated membrane protein 2; <b>PDBTitle:</b> lipid-bound synaptobrevin solution nmr structure
28	<a href="#">c3r85F_</a>	Alignment	not modelled	23.2	21	<b>PDB header:</b> apoptosis <b>Chain:</b> F: <b>PDB Molecule:</b> heme-binding protein 2; <b>PDBTitle:</b> crystal structure of human soul bh3 domain in complex with bcl-xl <b>PDB header:</b> ligase

29	<a href="#">c3do6B_</a>	Alignment	not modelled	23.1	20	<b>Chain:</b> B: <b>PDB Molecule:</b> formate--tetrahydrofolate ligase; <b>PDBTitle:</b> crystal structure of putative formyltetrahydrofolate synthetase2 (tm1766) from thermotoga maritima at 1.85 a resolution
30	<a href="#">c3r85H_</a>	Alignment	not modelled	23.0	21	<b>PDB header:</b> apoptosis <b>Chain:</b> H: <b>PDB Molecule:</b> heme-binding protein 2; <b>PDBTitle:</b> crystal structure of human soul bh3 domain in complex with bcl-xl
31	<a href="#">c3r85E_</a>	Alignment	not modelled	22.9	17	<b>PDB header:</b> apoptosis <b>Chain:</b> E: <b>PDB Molecule:</b> heme-binding protein 2; <b>PDBTitle:</b> crystal structure of human soul bh3 domain in complex with bcl-xl
32	<a href="#">c2h8kA_</a>	Alignment	not modelled	22.1	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sult1c3 splice variant d; <b>PDBTitle:</b> human sulfotranferase sult1c3 in complex with pap
33	<a href="#">c6f0kA_</a>	Alignment	not modelled	22.1	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c family protein; <b>PDBTitle:</b> alternative complex iii
34	<a href="#">c3r85G_</a>	Alignment	not modelled	22.1	18	<b>PDB header:</b> apoptosis <b>Chain:</b> G: <b>PDB Molecule:</b> heme-binding protein 2; <b>PDBTitle:</b> crystal structure of human soul bh3 domain in complex with bcl-xl
35	<a href="#">c2zktB_</a>	Alignment	not modelled	21.3	24	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> 2,3-bisphosphoglycerate-independent phosphoglycerate <b>PDBTitle:</b> structure of ph0037 protein from pyrococcus horikoshii
36	<a href="#">d2fug13</a>	Alignment	not modelled	21.2	17	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Nqo1 middle domain-like <b>Family:</b> Nqo1 middle domain-like
37	<a href="#">c6raoG_</a>	Alignment	not modelled	19.4	19	<b>PDB header:</b> virus like particle <b>Chain:</b> G: <b>PDB Molecule:</b> afp7; <b>PDBTitle:</b> cryo-em structure of the anti-feeding prophage (afp) baseplate, 6-fold2 symmetrised
38	<a href="#">d2bgca1</a>	Alignment	not modelled	19.1	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CAP C-terminal domain-like
39	<a href="#">c6jzbD_</a>	Alignment	not modelled	18.2	15	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> moad/this family protein; <b>PDBTitle:</b> structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
40	<a href="#">c5a4jC_</a>	Alignment	not modelled	17.3	25	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> formate--tetrahydrofolate ligase; <b>PDBTitle:</b> crystal structure of fthfs1 from t.acetoxydans re1
41	<a href="#">c3po0A_</a>	Alignment	not modelled	16.6	12	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> small archaeal modifier protein 1; <b>PDBTitle:</b> crystal structure of samp1 from haloferax volcanii
42	<a href="#">c6jc0A_</a>	Alignment	not modelled	16.5	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative molybdenum cofactor biosynthesis protein d2 <b>PDBTitle:</b> structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
43	<a href="#">c5jceA_</a>	Alignment	not modelled	16.5	17	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> chitin elicitor-binding protein; <b>PDBTitle:</b> crystal structure of oscebip complex
44	<a href="#">c2vztA_</a>	Alignment	not modelled	16.5	5	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein ttha1756; <b>PDBTitle:</b> crystal structure of uncharacterized conserved protein from thermus2 thermophilus hb8
45	<a href="#">d1uw4a_</a>	Alignment	not modelled	16.3	31	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Smg-4/UPF3
46	<a href="#">c5fwIE_</a>	Alignment	not modelled	16.0	9	<b>PDB header:</b> chaperone <b>Chain:</b> E: <b>PDB Molecule:</b> hsp90 co-chaperone cdc37; <b>PDBTitle:</b> atomic cryoem structure of hsp90-cdc37-cdk4 complex
47	<a href="#">c5aweA_</a>	Alignment	not modelled	15.6	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative acetoin utilization protein, acetoin <b>PDBTitle:</b> crystal structure of a hypothetical protein, ttha0829 from thermus2 thermophilus hb8, composed of cystathionine-beta-synthase (cbs) and3 aspartate-kinase chorismate-mutase tyra (act) domains
48	<a href="#">c4uplC_</a>	Alignment	not modelled	15.5	9	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> sulfatase family protein; <b>PDBTitle:</b> dimeric sulfatase spas2 from silicibacter pomeroyi
49	<a href="#">c3hd7A_</a>	Alignment	not modelled	15.4	12	<b>PDB header:</b> exocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> vesicle-associated membrane protein 2; <b>PDBTitle:</b> helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
50	<a href="#">d1nr6a_</a>	Alignment	not modelled	13.9	33	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
51	<a href="#">c3vw7A_</a>	Alignment	not modelled	13.8	14	<b>PDB header:</b> signaling protein/antagonist <b>Chain:</b> A: <b>PDB Molecule:</b> proteinase-activated receptor 1, lysozyme; <b>PDBTitle:</b> crystal structure of human protease-activated receptor 1 (par1) bound2 with antagonist vorapaxar at 2.2 angstrom
52	<a href="#">c1ezjA_</a>	Alignment	not modelled	13.7	23	<b>PDB header:</b> viral protein, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleocapsid phosphoprotein; <b>PDBTitle:</b> crystal structure of the multimerization domain of the phosphoprotein2 from sendai virus
53	<a href="#">c5mpoA_</a>	Alignment	not modelled	13.7	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin synthase sulfur carrier subunit; <b>PDBTitle:</b> crystal structure of human molybdopterin synthase complex
						<b>PDB header:</b> protein binding

54	<a href="#">c3f1iH_</a>	Alignment	not modelled	13.7	35	<b>Chain:</b> H: <b>PDB Molecule:</b> hepatocyte growth factor-regulated tyrosine kinase <b>PDBTitle:</b> human escrt-0 core complex
55	<a href="#">c3gb8B_</a>	Alignment	not modelled	13.5	19	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> snurportin-1; <b>PDBTitle:</b> crystal structure of crm1/snurportin-1 complex
56	<a href="#">c2qieB_</a>	Alignment	not modelled	13.2	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> molybdopterin synthase small subunit; <b>PDBTitle:</b> staphylococcus aureus molybdopterin synthase in complex with precursor2 z
57	<a href="#">d2ysca1</a>	Alignment	not modelled	13.1	60	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
58	<a href="#">c2zomC_</a>	Alignment	not modelled	12.9	4	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> protein cuta, chloroplast, putative, expressed; <b>PDBTitle:</b> crystal structure of cuta1 from oryza sativa
59	<a href="#">c2nuhA_</a>	Alignment	not modelled	12.9	16	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic divalent cation tolerance protein; <b>PDBTitle:</b> crystal structure of cuta from the phytopathgen bacterium xylella2 fastidiosa
60	<a href="#">c4ug4H_</a>	Alignment	not modelled	12.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> choline sulfatase; <b>PDBTitle:</b> crystal structure of a choline sulfatase from sinorhizobium2 melliloti
61	<a href="#">c3e4eA_</a>	Alignment	not modelled	12.8	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 2e1; <b>PDBTitle:</b> human cytochrome p450 2e1 in complex with the inhibitor 4-2 methylpyrazole
62	<a href="#">c3wqbB_</a>	Alignment	not modelled	12.7	18	<b>PDB header:</b> hydrolase/chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> open reading frame 2; <b>PDBTitle:</b> crystal structure of aeromonas sobria serine protease (asp) and the2 chaperone (orf2) complex
63	<a href="#">d1vjka_</a>	Alignment	not modelled	12.7	21	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> MoaD/ThiS <b>Family:</b> MoaD
64	<a href="#">d2rc3a1</a>	Alignment	not modelled	11.8	8	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
65	<a href="#">c4p7dA_</a>	Alignment	not modelled	11.6	14	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> antitoxin hicb3; <b>PDBTitle:</b> antitoxin hicb3 crystal structure
66	<a href="#">c4imyH_</a>	Alignment	not modelled	11.6	0	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> af4/fmr2 family member 4; <b>PDBTitle:</b> the aff4 scaffold binds human p-tefb adjacent to hiv tat
67	<a href="#">c4xalA_</a>	Alignment	not modelled	11.3	13	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> tegument protein vp22; <b>PDBTitle:</b> crystal structure of the conserved core domain of vp22 from hsv-1
68	<a href="#">c3gbyA_</a>	Alignment	not modelled	11.3	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ct1051; <b>PDBTitle:</b> crystal structure of a protein with unknown function ct10512 from chlorobium tepidum
69	<a href="#">c3kopB_</a>	Alignment	not modelled	11.3	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of protein with a cyclophilin-like fold2 (yp_831253.1) from arthrobacter sp. fb24 at 1.90 a resolution
70	<a href="#">c4imyl_</a>	Alignment	not modelled	11.1	0	<b>PDB header:</b> transferase <b>Chain:</b> I: <b>PDB Molecule:</b> af4/fmr2 family member 4; <b>PDBTitle:</b> the aff4 scaffold binds human p-tefb adjacent to hiv tat
71	<a href="#">c4imyG_</a>	Alignment	not modelled	11.1	0	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> af4/fmr2 family member 4; <b>PDBTitle:</b> the aff4 scaffold binds human p-tefb adjacent to hiv tat
72	<a href="#">c5t1aA_</a>	Alignment	not modelled	10.8	11	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> chimera protein of cc chemokine receptor type 2 isoform b <b>PDBTitle:</b> structure of cc chemokine receptor 2 with orthosteric and allosteric2 antagonists
73	<a href="#">c4o2tB_</a>	Alignment	not modelled	10.7	30	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a duf4827 family protein (bdi_1692) from2 parabacteroides distasonis atcc 8503 at 2.40 a resolution
74	<a href="#">d1a9xa1</a>	Alignment	not modelled	10.4	33	<b>Fold:</b> Carbamoyl phosphate synthetase, large subunit connection domain <b>Superfamily:</b> Carbamoyl phosphate synthetase, large subunit connection domain <b>Family:</b> Carbamoyl phosphate synthetase, large subunit connection domain
75	<a href="#">c2zfhA_</a>	Alignment	not modelled	10.2	6	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> cuta; <b>PDBTitle:</b> crystal structure of putative cuta1 from homo sapiens at 2.05a2 resolution
76	<a href="#">c4u4iA_</a>	Alignment	not modelled	9.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cu/zn superoxide dismutase; <b>PDBTitle:</b> megavirus chilensis superoxide dismutase
77	<a href="#">c4p6vF_</a>	Alignment	not modelled	9.7	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> na(+)-translocating nadh-quinone reductase subunit f; <b>PDBTitle:</b> crystal structure of the na+-translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae
78	<a href="#">c5wwoB_</a>	Alignment	not modelled	9.7	11	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> essential nuclear protein 1; <b>PDBTitle:</b> crystal structure of enp1
79	<a href="#">c2m10A_</a>	Alignment	not modelled	9.5	16	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin converting factor subunit 1;

79	<a href="#">c2m19A_</a>	Alignment	not modelled	9.3	10	<b>PDBTitle:</b> solution structure of the haloferax volcanii hvo 2177 protein
80	<a href="#">d1p1la_</a>	Alignment	not modelled	9.4	20	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> Divalent ion tolerance proteins CutA (CutA1)
81	<a href="#">d1nzaa_</a>	Alignment	not modelled	9.4	12	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> Divalent ion tolerance proteins CutA (CutA1)
82	<a href="#">d1vhfa_</a>	Alignment	not modelled	9.4	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> Divalent ion tolerance proteins CutA (CutA1)
83	<a href="#">c6m9tA_</a>	Alignment	not modelled	9.2	11	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> prostaglandin e2 receptor ep3 subtype, endolysin chimera; <b>PDBTitle:</b> crystal structure of ep3 receptor bound to misoprostol-fa
84	<a href="#">c3mk7F_</a>	Alignment	not modelled	9.2	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> cytochrome c oxidase, cbb3-type, subunit p; <b>PDBTitle:</b> the structure of cbb3 cytochrome oxidase
85	<a href="#">c3ahpA_</a>	Alignment	not modelled	9.1	16	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> cuta1; <b>PDBTitle:</b> crystal structure of stable protein, cuta1, from a psychrotrophic2 bacterium shewanella sp. sib1
86	<a href="#">d1ukua_</a>	Alignment	not modelled	9.0	28	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> Divalent ion tolerance proteins CutA (CutA1)
87	<a href="#">c3a0mF_</a>	Alignment	not modelled	8.9	33	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
88	<a href="#">d1naqa_</a>	Alignment	not modelled	8.8	8	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> Divalent ion tolerance proteins CutA (CutA1)
89	<a href="#">c4upiA_</a>	Alignment	not modelled	8.8	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfatase family protein; <b>PDBTitle:</b> dimeric sulfatase spas1 from silicibacter pomeroyi
90	<a href="#">c5ylwA_</a>	Alignment	not modelled	8.7	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferruginol synthase; <b>PDBTitle:</b> cyp76ah1 from salvia miltiorrhiza
91	<a href="#">c5k9xA_</a>	Alignment	not modelled	8.6	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha chain from legionella2 pneumophila subsp. pneumophila
92	<a href="#">c5lnko_</a>	Alignment	not modelled	8.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> <b>PDBTitle:</b> entire ovine respiratory complex i
93	<a href="#">c3v2yA_</a>	Alignment	not modelled	8.6	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sphingosine 1-phosphate receptor 1, lysozyme chimera <b>PDBTitle:</b> crystal structure of a lipid g protein-coupled receptor at 2.80a
94	<a href="#">d1sr8a_</a>	Alignment	not modelled	8.4	9	<b>Fold:</b> CbiD-like <b>Superfamily:</b> CbiD-like <b>Family:</b> CbiD-like
95	<a href="#">d1fcqa_</a>	Alignment	not modelled	8.4	25	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Bee venom hyaluronidase
96	<a href="#">c1w9qB_</a>	Alignment	not modelled	8.4	8	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> syntenin 1; <b>PDBTitle:</b> crystal structure of the pdz tandem of human syntenin in complex with2 tnefaf peptide
97	<a href="#">c1xk5A_</a>	Alignment	not modelled	8.3	19	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> snurportin-1; <b>PDBTitle:</b> crystal structure of the m3g-cap-binding domain of2 snurportin1 in complex with a m3gpppg-cap dinucleotide
98	<a href="#">d2ef7a1</a>	Alignment	not modelled	8.3	17	<b>Fold:</b> CBS-domain pair <b>Superfamily:</b> CBS-domain pair <b>Family:</b> CBS-domain pair
99	<a href="#">c3ebsA_</a>	Alignment	not modelled	8.3	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 2a6; <b>PDBTitle:</b> human cytochrome p450 2a6 i208s/i300f/g301a/s369g in complex2 with phenacetin