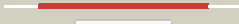










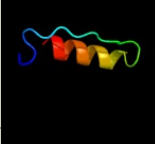

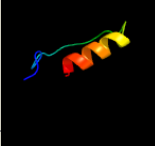







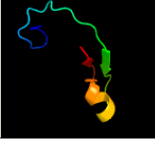


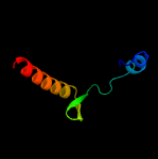
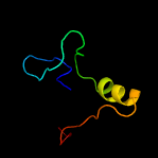



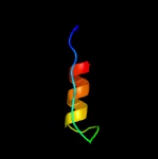
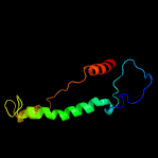


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2631 (-) _2957582_2958880
Date	Wed Aug 7 12:50:27 BST 2019
Unique Job ID	b8e2dd48bf1fe934

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1uc2a_</a>	 Alignment		100.0	54	<b>Fold:</b> Hypothetical protein PH1602 <b>Superfamily:</b> Hypothetical protein PH1602 <b>Family:</b> Hypothetical protein PH1602
2	<a href="#">c2epgB_</a>	 Alignment		100.0	54	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein ttha1785; <b>PDBTitle:</b> crystal structure of ttha1785
3	<a href="#">c5exkG_</a>	 Alignment		51.3	14	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> lipoyl synthase; <b>PDBTitle:</b> crystal structure of m. tuberculosis lipoyl synthase with 6-2 thiooctanoyl peptide intermediate
4	<a href="#">d2pd4a1</a>	 Alignment		47.1	11	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
5	<a href="#">d2h7ma1</a>	 Alignment		37.8	14	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
6	<a href="#">c4m87B_</a>	 Alignment		37.4	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-[acyl-carrier-protein] reductase [nadh]; <b>PDBTitle:</b> crystal structure of enoyl-acyl carrier protein reductase (fabI) from2 neisseria meningitidis in complex with nad+
7	<a href="#">c3ek2D_</a>	 Alignment		33.7	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> enoyl-(acyl-carrier-protein) reductase (nadh); <b>PDBTitle:</b> crystal structure of enoyl-(acyl carrier protein) reductase from2 burkholderia pseudomallei 1719b
8	<a href="#">c3grkE_</a>	 Alignment		33.7	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> enoyl-(acyl-carrier-protein) reductase (nadh); <b>PDBTitle:</b> crystal structure of short chain dehydrogenase reductase2 sdr glucose-ribitol dehydrogenase from brucella melitensis
9	<a href="#">c4nk4E_</a>	 Alignment		32.4	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> enoyl-[acyl-carrier-protein] reductase [nadh]; <b>PDBTitle:</b> crystal structure of fabI from candidatus liberibacter asiaticus
10	<a href="#">c2jyD_</a>	 Alignment		31.4	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> enoyl-[acyl-carrier-protein] reductase; <b>PDBTitle:</b> crystal structure of francisella tularensis enoyl reductase2 (ftfabI) with bound nad
11	<a href="#">c2btwA_</a>	 Alignment		28.6	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> alr0975 protein; <b>PDBTitle:</b> crystal structure of alr0975

12	<a href="#">d2bu3a1</a>	Alignment		25.7	18	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Phytochelatin synthase
13	<a href="#">c2c4rL_</a>	Alignment		24.2	25	<b>PDB header:</b> hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> ribonuclease e; <b>PDBTitle:</b> catalytic domain of e. coli rnase e
14	<a href="#">c2zdiC_</a>	Alignment		24.0	17	<b>PDB header:</b> chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> prefoldin subunit alpha; <b>PDBTitle:</b> crystal structure of prefoldin from pyrococcus horikoshii2 ot3
15	<a href="#">d1kvva_</a>	Alignment		23.5	14	<b>Fold:</b> SRP19 <b>Superfamily:</b> SRP19 <b>Family:</b> SRP19
16	<a href="#">c2bpbB_</a>	Alignment		22.5	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> sulfite\;cytochrome c oxidoreductase subunit b; <b>PDBTitle:</b> sulfite dehydrogenase from starkeya novella
17	<a href="#">d1jmxal</a>	Alignment		21.2	18	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
18	<a href="#">d1pbya1</a>	Alignment		21.1	15	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
19	<a href="#">c2o2sA_</a>	Alignment		21.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-acyl carrier reductase; <b>PDBTitle:</b> the structure of t. gondii enoyl acyl carrier protein reductase in2 complex with nad and triclosan
20	<a href="#">c3ja7L_</a>	Alignment		21.0	15	<b>PDB header:</b> viral protein <b>Chain:</b> L: <b>PDB Molecule:</b> portal protein gp20; <b>PDBTitle:</b> cryo-em structure of the bacteriophage t4 portal protein assembly at2 near-atomic resolution
21	<a href="#">c4u0pB_</a>	Alignment	not modelled	19.5	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> lipoyl synthase 2; <b>PDBTitle:</b> the crystal structure of lipoyl synthase in complex with s-adenosyl2 homocysteine
22	<a href="#">c2p91A_</a>	Alignment	not modelled	19.5	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-[acyl-carrier-protein] reductase [nadh]; <b>PDBTitle:</b> crystal structure of enoyl-[acyl-carrier-protein] reductase (nadh)2 from aquifex aeolicus vf5
23	<a href="#">c4alnE_</a>	Alignment	not modelled	19.5	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> enoyl-[acyl-carrier-protein] reductase [nadph]; <b>PDBTitle:</b> crystal structure of s. aureus fabi (p32)
24	<a href="#">d1wvec1</a>	Alignment	not modelled	19.4	9	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
25	<a href="#">c3sx2F_</a>	Alignment	not modelled	19.4	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> putative 3-ketoacyl-(acyl-carrier-protein) reductase; <b>PDBTitle:</b> crystal structure of a putative 3-ketoacyl-(acyl-carrier-protein)2 reductase from mycobacterium paratuberculosis in complex with nad
26	<a href="#">c3dp5A_</a>	Alignment	not modelled	19.4	18	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c family protein; <b>PDBTitle:</b> crystal structure of geobacter sulfurreducens omcf with n-2 terminal strep-tag ii
27	<a href="#">c1jmuE_</a>	Alignment	not modelled	19.3	67	<b>PDB header:</b> viral protein <b>Chain:</b> E: <b>PDB Molecule:</b> protein mu-1; <b>PDBTitle:</b> crystal structure of the reovirus mu1/sigma3 complex
						<b>Fold:</b> SRP19

28	<a href="#">d1lnga_</a>	Alignment	not modelled	19.1	18	<b>Superfamily:</b> SRP19 <b>Family:</b> SRP19
29	<a href="#">c6fn6A_</a>	Alignment	not modelled	18.9	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid synthase 1, isoform a; <b>PDBTitle:</b> modifying region (dh-er-kr) of an insect fatty acid synthase (fas)
30	<a href="#">d1kx7a_</a>	Alignment	not modelled	18.8	18	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
31	<a href="#">c2kknA_</a>	Alignment	not modelled	18.5	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of themotoga maritima protein tm1076:2 northeast structural genomics consortium target vt57
32	<a href="#">c6f0kE_</a>	Alignment	not modelled	18.5	20	<b>PDB header:</b> membrane protein <b>Chain:</b> E: <b>PDB Molecule:</b> quinol:cytochrome c oxidoreductase monoheme cytochrome <b>PDBTitle:</b> alternative complex iii
33	<a href="#">c2w1oA_</a>	Alignment	not modelled	18.4	23	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> 60s acidic ribosomal protein p2; <b>PDBTitle:</b> nmr structure of dimerization domain of human ribosomal2 protein p2
34	<a href="#">d1qsga_</a>	Alignment	not modelled	18.0	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
35	<a href="#">c4dyvA_</a>	Alignment	not modelled	18.0	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase sdr; <b>PDBTitle:</b> crystal structure of a short-chain dehydrogenase/reductase sdr from2 xanthobacter autotrophicus py2
36	<a href="#">c2ptgA_</a>	Alignment	not modelled	17.8	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-acyl carrier reductase; <b>PDBTitle:</b> crystal structure of eimeria tenella enoyl reductase
37	<a href="#">d1fxkc_</a>	Alignment	not modelled	17.7	13	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Prefoldin <b>Family:</b> Prefoldin
38	<a href="#">c3gdfA_</a>	Alignment	not modelled	17.4	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable nadp-dependent mannitol dehydrogenase; <b>PDBTitle:</b> crystal structure of the nadp-dependent mannitol dehydrogenase from2 cladosporium herbarum.
39	<a href="#">c4q9nD_</a>	Alignment	not modelled	17.1	15	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> enoyl-[acyl-carrier-protein] reductase [nadh]; <b>PDBTitle:</b> crystal structure of chlamydia trachomatis enoyl-acp reductase (fabI)2 in complex with nadh and afn-1252
40	<a href="#">d1el6a_</a>	Alignment	not modelled	16.7	38	<b>Fold:</b> Baseplate structural protein gp11 <b>Superfamily:</b> Baseplate structural protein gp11 <b>Family:</b> Baseplate structural protein gp11
41	<a href="#">c5koiH_</a>	Alignment	not modelled	16.6	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> enoyl-[acyl-carrier-protein] reductase [nadh]; <b>PDBTitle:</b> crystal structure of a possible enoyl-(acyl-carrier-protein) reductase2 from brucella melitensis
42	<a href="#">c3qivA_</a>	Alignment	not modelled	16.1	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> short-chain dehydrogenase or 3-oxoacyl-[acyl-carrier- <b>PDBTitle:</b> crystal structure of a putative short-chain dehydrogenase or 3-2 oxoacyl-[acyl-carrier-protein] reductase from mycobacterium3 paratuberculosis atcc baa-968 / k-10
43	<a href="#">d2rhca1</a>	Alignment	not modelled	16.0	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
44	<a href="#">c3cu4A_</a>	Alignment	not modelled	15.9	18	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c family protein; <b>PDBTitle:</b> omcf, outer membrane cytochrome f from geobacter2 sulfurreducers
45	<a href="#">c3tl3A_</a>	Alignment	not modelled	15.6	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> short-chain type dehydrogenase/reductase; <b>PDBTitle:</b> structure of a short-chain type dehydrogenase/reductase from2 mycobacterium ulcerans
46	<a href="#">c5jc8C_</a>	Alignment	not modelled	15.3	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative short-chain dehydrogenase/reductase; <b>PDBTitle:</b> crystal structure of a putative short-chain dehydrogenase/reductase2 from burkholderia xenovorans
47	<a href="#">d1r0ua_</a>	Alignment	not modelled	15.2	28	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Hypothetical protein YwiB
48	<a href="#">c2vqzB_</a>	Alignment	not modelled	14.9	20	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> polymerase basic protein 2; <b>PDBTitle:</b> structure of the cap-binding domain of influenza virus2 polymerase subunit pb2 with bound m7gtp
49	<a href="#">c3ktwA_</a>	Alignment	not modelled	14.6	23	<b>PDB header:</b> rna/rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle 19 kda protein; <b>PDBTitle:</b> crystal structure of the srp19/s-domain srp rna complex of sulfobolus2 solfataricus
50	<a href="#">c4zjuA_</a>	Alignment	not modelled	14.3	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-[acyl-carrier-protein] reductase [nadh]; <b>PDBTitle:</b> structure of a nadh-dependent enoyl-acp reductase from acinetobacter2 baumannii in complex with nad
51	<a href="#">c6btmE_</a>	Alignment	not modelled	14.2	27	<b>PDB header:</b> membrane protein <b>Chain:</b> E: <b>PDB Molecule:</b> alternative complex iii subunit e; <b>PDBTitle:</b> structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
52	<a href="#">d1wf7a_</a>	Alianment	not modelled	14.0	22	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like

						Family:PDZ domain
53	<a href="#">c2ehdB</a>	Alignment	not modelled	13.6	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase, short-chain dehydrogenase/reductase family; <b>PDBTitle:</b> crystal structure analysis of oxidoreductase
54	<a href="#">c2d0sA</a>	Alignment	not modelled	13.3	8	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c; <b>PDBTitle:</b> crystal structure of the cytochrome c552 from moderate2 thermophilic bacterium, hydrogenophilus thermoluteolus
55	<a href="#">c2foiB</a>	Alignment	not modelled	13.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-acyl carrier reductase; <b>PDBTitle:</b> synthesis, biological activity, and x-ray crystal structural analysis2 of diaryl ether inhibitors of malarial enoyl acp reductase.
56	<a href="#">c2nq8B</a>	Alignment	not modelled	13.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-acyl carrier reductase; <b>PDBTitle:</b> malarial enoyl acyl acp reductase bound with inh-nad adduct
57	<a href="#">c2v07A</a>	Alignment	not modelled	13.1	18	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c6; <b>PDBTitle:</b> structure of the arabidopsis thaliana cytochrome c6a v52q variant
58	<a href="#">c1zmoF</a>	Alignment	not modelled	13.1	9	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> halohydrin dehalogenase; <b>PDBTitle:</b> apo structure of haloalcohol dehalogenase hhea of2 arthrobacter sp. ad2
59	<a href="#">c3afnC</a>	Alignment	not modelled	13.1	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> carbonyl reductase; <b>PDBTitle:</b> crystal structure of aldose reductase a1-r complexed with nadp
60	<a href="#">c4kmsB</a>	Alignment	not modelled	12.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> acetoacetyl-coa reductase; <b>PDBTitle:</b> crystal structure of acetoacetyl-coa reductase from rickettsia felis
61	<a href="#">c3gr6A</a>	Alignment	not modelled	12.9	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-[acyl-carrier-protein] reductase [nadh]; <b>PDBTitle:</b> crystal structure of the staphylococcus aureus enoyl-acyl carrier2 protein reductase (fabI) in complex with nadp and triclosan
62	<a href="#">d1cc5a</a>	Alignment	not modelled	12.8	27	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
63	<a href="#">c3sjaG</a>	Alignment	not modelled	12.8	40	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> G: <b>PDB Molecule:</b> golgi to er traffic protein 1; <b>PDBTitle:</b> crystal structure of s. cerevisiae get3 in the open state in complex2 with get1 cytosolic domain
64	<a href="#">d1ulua</a>	Alignment	not modelled	12.8	20	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
65	<a href="#">c4j20B</a>	Alignment	not modelled	12.7	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome c-555; <b>PDBTitle:</b> x-ray structure of the cytochrome c-554 from chlorobaculum tepidum
66	<a href="#">c3u4kA</a>	Alignment	not modelled	12.6	22	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> fimbria adhesion protein; <b>PDBTitle:</b> crystal structure of the receptor binding domain of plasmid-born2 adhesin mrkd1p of klebsiella pneumoniae
67	<a href="#">c5mpyB</a>	Alignment	not modelled	12.6	29	<b>PDB header:</b> plant protein <b>Chain:</b> B: <b>PDB Molecule:</b> multiple organellar rna editing factor 9, chloroplastic; <b>PDBTitle:</b> crystal structure of arabidopsis thaliana rna editing factor morf9
68	<a href="#">c2l4fA</a>	Alignment	not modelled	12.3	27	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> defective in cullin neddylation protein 1; <b>PDBTitle:</b> nmr structure of the uba domain of s. cerevisiae dcn1 bound to2 ubiquitin
69	<a href="#">c4e3zA</a>	Alignment	not modelled	12.2	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oxidoreductase protein; <b>PDBTitle:</b> crystal structure of a oxidoreductase from rhizobium etli cfn 42
70	<a href="#">c4gydA</a>	Alignment	not modelled	12.1	27	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c6; <b>PDBTitle:</b> nostoc sp cytochrome c6
71	<a href="#">c3sjbC</a>	Alignment	not modelled	12.1	40	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> golgi to er traffic protein 1; <b>PDBTitle:</b> crystal structure of s. cerevisiae get3 in the open state in complex2 with get1 cytosolic domain
72	<a href="#">d1fcdc1</a>	Alignment	not modelled	12.0	22	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Two-domain cytochrome c
73	<a href="#">c3ku1E</a>	Alignment	not modelled	12.0	20	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of streptococcus pneumoniae sp1610, a putative trna2 (m1a22) methyltransferase, in complex with s-adenosyl-l-methionine
74	<a href="#">c4yn3B</a>	Alignment	not modelled	12.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cucumisin; <b>PDBTitle:</b> crystal structure of cucumisin complex with pro-peptide
75	<a href="#">d1wkqa</a>	Alignment	not modelled	11.9	36	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Deoxycytidylate deaminase-like
76	<a href="#">d1uh5a</a>	Alignment	not modelled	11.9	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
77	<a href="#">d1ulza2</a>	Alignment	not modelled	11.9	71	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like <b>PDB header:</b> oxidoreductase

78	<a href="#">c3tfoD_</a>	Alignment	not modelled	11.9	24	<b>Chain:</b> D: <b>PDB Molecule:</b> putative 3-oxoacyl-(acyl-carrier-protein) reductase; <b>PDBTitle:</b> crystal structure of a putative 3-oxoacyl-(acyl-carrier-protein)2 reductase from sinorhizobium meliloti
79	<a href="#">c4nqzF_</a>	Alignment	not modelled	11.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> enoyl-[acyl-carrier-protein] reductase [nadh] fabi; <b>PDBTitle:</b> crystal structure of the pseudomonas aeruginosa enoyl-acyl carrier2 protein reductase (fabi) in apo form
80	<a href="#">c3iz5w_</a>	Alignment	not modelled	11.9	18	<b>PDB header:</b> ribosome <b>Chain:</b> W: <b>PDB Molecule:</b> 60s ribosomal protein l22 (l22e); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
81	<a href="#">c3izcw_</a>	Alignment	not modelled	11.8	26	<b>PDB header:</b> ribosome <b>Chain:</b> W: <b>PDB Molecule:</b> 60s ribosomal protein rpl22 (l22e); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
82	<a href="#">c6q56C_</a>	Alignment	not modelled	11.8	40	<b>PDB header:</b> rna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> trna (adenine(22)-n(1))-methyltransferase; <b>PDBTitle:</b> crystal structure of the b. subtilis m1a22 trna methyltransferase trmk
83	<a href="#">c3ezlA_</a>	Alignment	not modelled	11.7	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acetoacetyl-coa reductase; <b>PDBTitle:</b> crystal structure of acetylacetyl-coa reductase from2 burkholderia pseudomallei 1710b
84	<a href="#">c5mxzA_</a>	Alignment	not modelled	11.6	22	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c-552 ks_3358; <b>PDBTitle:</b> kustc0563 y40f mutant
85	<a href="#">c2lklA_</a>	Alignment	not modelled	11.5	33	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> erythrocyte membrane protein 1 (pfemp1); <b>PDBTitle:</b> structure of the core intracellular domain of pfemp1
86	<a href="#">c5zvtM_</a>	Alignment	not modelled	11.5	67	<b>PDB header:</b> virus <b>Chain:</b> M: <b>PDB Molecule:</b> n-terminus of outer capsid protein vp5; <b>PDBTitle:</b> structure of rna polymerase complex and genome within a dsrna virus2 provides insights into the mechanisms of transcription and assembly
87	<a href="#">c4behB_</a>	Alignment	not modelled	11.4	23	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> 60s acidic ribosomal protein p2; <b>PDBTitle:</b> solution structure of human ribosomal protein p1.p2 heterodimer
88	<a href="#">c3d7lG_</a>	Alignment	not modelled	11.3	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> G: <b>PDB Molecule:</b> lin1944 protein; <b>PDBTitle:</b> the crystal structure of the protein lin1944 from listeria innocua .
89	<a href="#">c3dluA_</a>	Alignment	not modelled	11.3	20	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle 19 kda protein; <b>PDBTitle:</b> structures of srp54 and srp19, the two proteins assembling the2 ribonucleic core of the signal recognition particle from the archaeon3 pyrococcus furiosus.
90	<a href="#">c3edmD_</a>	Alignment	not modelled	11.2	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> short chain dehydrogenase; <b>PDBTitle:</b> crystal structure of a short chain dehydrogenase from agrobacterium2 tumefaciens
91	<a href="#">c5glijB_</a>	Alignment	not modelled	11.1	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrosine-protein phosphatase non-receptor type 13; <b>PDBTitle:</b> crystal structure of pdz1 domain of human protein tyrosine phosphatase2 ptp-bas
92	<a href="#">d2d1ya1</a>	Alignment	not modelled	11.1	37	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
93	<a href="#">c2fwmX_</a>	Alignment	not modelled	11.1	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> X: <b>PDB Molecule:</b> 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase; <b>PDBTitle:</b> crystal structure of e. coli enta, a 2,3-dihydrodihydroxy benzoate2 dehydrogenase
94	<a href="#">c5jy1C_</a>	Alignment	not modelled	11.1	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative short-chain dehydrogenase/reductase; <b>PDBTitle:</b> crystal structure of putative short-chain dehydrogenase/reductase from2 burkholderia xenovorans lb400 bound to nad
95	<a href="#">c6mn5A_</a>	Alignment	not modelled	11.0	21	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> aminoglycoside n(3)-acetyltransferase, aac(3)-iva; <b>PDBTitle:</b> crystal structure of aminoglycoside acetyltransferase aac(3)-iva,2 h154a mutant, in complex with gentamicin c1a
96	<a href="#">c2qioA_</a>	Alignment	not modelled	11.0	13	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-(acyl-carrier-protein) reductase; <b>PDBTitle:</b> x-ray structure of enoyl-acyl carrier protein reductase from bacillus2 anthracis with triclosan
97	<a href="#">d2o23a1</a>	Alignment	not modelled	10.9	29	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
98	<a href="#">c1j6qA_</a>	Alignment	not modelled	10.9	15	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c maturation protein e; <b>PDBTitle:</b> solution structure and characterization of the heme2 chaperone ccme
99	<a href="#">d1j6qa_</a>	Alignment	not modelled	10.9	15	<b>Fold:</b> OB-fold <b>Superfamily:</b> Heme chaperone CcmE <b>Family:</b> Heme chaperone CcmE