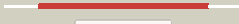



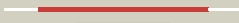


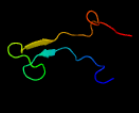

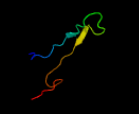

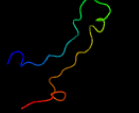

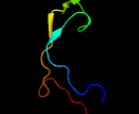

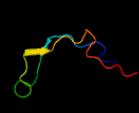

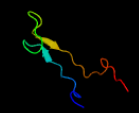




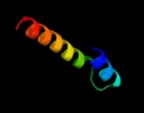
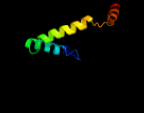
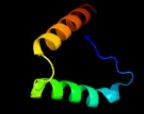



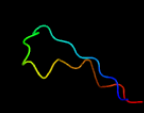




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1632c_(-)_1836394_1836837
Date	Fri Aug 2 13:30:22 BST 2019
Unique Job ID	24dcad558acafc4f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2p12a1</a>	 Alignment		100.0	59	<b>Fold:</b> FomD barrel-like <b>Superfamily:</b> FomD-like <b>Family:</b> FomD-like
2	<a href="#">c3exmA</a>	 Alignment		99.6	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> phosphatase sc4828; <b>PDBTitle:</b> crystal structure of the phosphatase sc4828 with the non-hydrolyzable2 nucleotide gpcp
3	<a href="#">c5zdnA</a>	 Alignment		99.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> fomd; <b>PDBTitle:</b> the complex structure of fomd with cdp
4	<a href="#">c1rrjA</a>	 Alignment		83.6	16	<b>PDB header:</b> isomerase/dna <b>Chain:</b> A; <b>PDB Molecule:</b> dna topoisomerase i; <b>PDBTitle:</b> structural mechanisms of camptothecin resistance by2 mutations in human topoisomerase i
5	<a href="#">c1a31A</a>	 Alignment		81.8	16	<b>PDB header:</b> isomerase/dna <b>Chain:</b> A; <b>PDB Molecule:</b> protein (topoisomerase i); <b>PDBTitle:</b> human reconstituted dna topoisomerase i in covalent complex2 with a 22 base pair dna duplex
6	<a href="#">c1nh3A</a>	 Alignment		81.3	16	<b>PDB header:</b> isomerase/dna <b>Chain:</b> A; <b>PDB Molecule:</b> dna topoisomerase i; <b>PDBTitle:</b> human topoisomerase i ara-c complex
7	<a href="#">d1k4ta3</a>	 Alignment		81.1	16	<b>Fold:</b> Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment <b>Superfamily:</b> Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment <b>Family:</b> Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment
8	<a href="#">c2b9sA</a>	 Alignment		74.3	22	<b>PDB header:</b> isomerase/dna <b>Chain:</b> A; <b>PDB Molecule:</b> topoisomerase i-like protein; <b>PDBTitle:</b> crystal structure of heterodimeric I. donovani topoisomerase i-2 vanadate-dna complex
9	<a href="#">d1oisa</a>	 Alignment		73.9	19	<b>Fold:</b> Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment <b>Superfamily:</b> Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment <b>Family:</b> Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment
10	<a href="#">c5htIA</a>	 Alignment		50.3	26	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> msha biogenesis protein mshe; <b>PDBTitle:</b> structure of mshe with cdg
11	<a href="#">d1nvpd1</a>	 Alignment		40.0	17	<b>Fold:</b> Transcription factor IIA (TFIIA), alpha-helical domain <b>Superfamily:</b> Transcription factor IIA (TFIIA), alpha-helical domain <b>Family:</b> Transcription factor IIA (TFIIA), alpha-helical domain

12	<a href="#">d1nh2d1</a>	Alignment		40.0	17	<b>Fold:</b> Transcription factor IIA (TFIIA), alpha-helical domain <b>Superfamily:</b> Transcription factor IIA (TFIIA), alpha-helical domain <b>Family:</b> Transcription factor IIA (TFIIA), alpha-helical domain
13	<a href="#">c3wo8B</a>	Alignment		39.1	9	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-n-acetylglucosaminidase; <b>PDBTitle:</b> crystal structure of the beta-n-acetylglucosaminidase from thermotoga2 maritima
14	<a href="#">c5bzaA</a>	Alignment		38.4	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-n-acetylhexosaminidase; <b>PDBTitle:</b> crystal structure of cbsa from thermotoga neapolitana
15	<a href="#">c5mj1A</a>	Alignment		33.7	35	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> cd83 antigen; <b>PDBTitle:</b> extracellular domain of human cd83 - rhombohedral crystal form
16	<a href="#">c3cr8C</a>	Alignment		33.3	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> sulfate adenylyltransferase, adenylylsulfate kinase; <b>PDBTitle:</b> hexameric aps kinase from thiobacillus denitrificans
17	<a href="#">c5mz2L</a>	Alignment		32.7	19	<b>PDB header:</b> photosynthesis <b>Chain:</b> I: <b>PDB Molecule:</b> rubisco small subunit; <b>PDBTitle:</b> rubisco from thalassiosira antarctica
18	<a href="#">d1bwvs</a>	Alignment		32.5	19	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
19	<a href="#">c5nv3P</a>	Alignment		32.3	28	<b>PDB header:</b> lyase <b>Chain:</b> P: <b>PDB Molecule:</b> ribulose bisphosphate carboxylase small chain 1; <b>PDBTitle:</b> structure of rubisco from rhodobacter sphaeroides in complex with cabp
20	<a href="#">d1bxni</a>	Alignment		32.0	28	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
21	<a href="#">c6ejfQ</a>	Alignment	not modelled	32.0	32	<b>PDB header:</b> motor protein <b>Chain:</b> Q: <b>PDB Molecule:</b> type iv pilus assembly protein pilf; <b>PDBTitle:</b> thermus thermophilus pilf atpase (apoprotein form)
22	<a href="#">d1svdm1</a>	Alignment	not modelled	31.7	22	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
23	<a href="#">d2nn4a1</a>	Alignment	not modelled	29.3	16	<b>Fold:</b> YqqQ-like <b>Superfamily:</b> YqqQ-like <b>Family:</b> YqqQ-like
24	<a href="#">d1g5ta</a>	Alignment	not modelled	29.0	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
25	<a href="#">c1nvpD</a>	Alignment	not modelled	28.9	19	<b>PDB header:</b> transcription/dna <b>Chain:</b> D: <b>PDB Molecule:</b> transcription initiation factor iia gamma chain; <b>PDBTitle:</b> human tfiia/tbp/dna complex
26	<a href="#">c2ybvN</a>	Alignment	not modelled	28.5	17	<b>PDB header:</b> lyase <b>Chain:</b> N: <b>PDB Molecule:</b> ribulose bisphosphate carboxylase small subunit; <b>PDBTitle:</b> structure of rubisco from thermosynechococcus elongatus
27	<a href="#">d1rbli</a>	Alignment	not modelled	28.4	14	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
28	<a href="#">d2oqoa1</a>	Alignment	not modelled	28.4	35	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> PBP transglycosylase domain-like
						<b>PDB header:</b> ribosome

29	<a href="#">c6nd4P_</a>	Alignment	not modelled	28.0	20	<b>Chain:</b> P; <b>PDB Molecule:</b> utp6; <b>PDBTitle:</b> conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
30	<a href="#">d1uzhc1</a>	Alignment	not modelled	25.6	28	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
31	<a href="#">c5ydcA_</a>	Alignment	not modelled	25.5	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator rv1828; <b>PDBTitle:</b> crystal structure of mercury soaked c-terminal domain of rv1828 from2 mycobacterium tuberculosis
32	<a href="#">c2n03A_</a>	Alignment	not modelled	25.5	29	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> plectin; <b>PDBTitle:</b> solution nmr structure plectin repeat domain 6 (4403-4606) of plectin2 from homo sapiens, northeast structural genomics consortium (nesg)3 target hr6354e
33	<a href="#">c1nh2D_</a>	Alignment	not modelled	25.4	19	<b>PDB header:</b> transcription/dna <b>Chain:</b> D; <b>PDB Molecule:</b> transcription initiation factor iia small chain; <b>PDBTitle:</b> crystal structure of a yeast tfiia/tbp/dna complex
34	<a href="#">d1g64b_</a>	Alignment	not modelled	25.2	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
35	<a href="#">c2jobA_</a>	Alignment	not modelled	24.9	26	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> antilipopolysaccharide factor; <b>PDBTitle:</b> solution structure of an antilipopolysaccharide factor from2 shrimp and its possible lipid a binding site
36	<a href="#">c5iobC_</a>	Alignment	not modelled	24.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> beta-glucosidase-related glycosidases; <b>PDBTitle:</b> crystal structure of beta-n-acetylglucosaminidase-like protein from2 corynebacterium glutamicum
37	<a href="#">c4jglA_</a>	Alignment	not modelled	23.2	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a streptavidin-like protein (bacegg_01519) from2 bacteroides eggerthii dsm 20697 at 1.25 a resolution
38	<a href="#">c4yvfC_</a>	Alignment	not modelled	23.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> beta-n-acetylhexosaminidase; <b>PDBTitle:</b> the crystal structure of a glycosyl hydrolase of gh3 family member2 from [mycobacterium smegmatis str. mc2 155
39	<a href="#">c5lqdB_</a>	Alignment	not modelled	22.8	21	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> alpha,alpha-trehalose-phosphate synthase; <b>PDBTitle:</b> trehalose-6-phosphate synthase, gdp-glucose-dependent otsa
40	<a href="#">c5cwnA_</a>	Alignment	not modelled	22.4	27	<b>PDB header:</b> de novo protein <b>Chain:</b> A; <b>PDB Molecule:</b> designed helical repeat protein; <b>PDBTitle:</b> crystal structure of de novo designed helical repeat protein dhr71
41	<a href="#">c6f8lj_</a>	Alignment	not modelled	22.0	26	<b>PDB header:</b> motor protein <b>Chain:</b> J; <b>PDB Molecule:</b> type iv pilus assembly protein pilf; <b>PDBTitle:</b> thermus thermophilus pilf atpase (amppnp-bound form)
42	<a href="#">d1wpua1</a>	Alignment	not modelled	21.8	18	<b>Fold:</b> Hut operon positive regulatory protein HutP <b>Superfamily:</b> Hut operon positive regulatory protein HutP <b>Family:</b> Hut operon positive regulatory protein HutP
43	<a href="#">d2csba1</a>	Alignment	not modelled	21.2	24	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> Topoisomerase V repeat domain
44	<a href="#">c4hdnA_</a>	Alignment	not modelled	21.2	30	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> arsa; <b>PDBTitle:</b> crystal structure of arsa in the substrate-free state.
45	<a href="#">c4g2nA_</a>	Alignment	not modelled	20.5	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> d-isomer specific 2-hydroxyacid dehydrogenase, nad-binding; <b>PDBTitle:</b> crystal structure of putative d-isomer specific 2-hydroxyacid2 dehydrogenase, nad-binding from polaromonas sp. js6 66
46	<a href="#">c6b5fB_</a>	Alignment	not modelled	20.2	19	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> nicotinate-nucleotide--dimethylbenzimidazole <b>PDBTitle:</b> crystal structure of nicotinate mononucleotide-5,6-2 dimethylbenzimidazole phosphoribosyltransferase cobt from yersinia3 enterocolitica
47	<a href="#">c1fuiB_</a>	Alignment	not modelled	20.1	19	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> l-fucose isomerase; <b>PDBTitle:</b> l-fucose isomerase from escherichia coli
48	<a href="#">c2irtA_</a>	Alignment	not modelled	19.8	39	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> nmr solution structure of the protein coded by gene2 rhos4_12090 of rhodobacter sphaeroides. northeast3 structural genomics target rhr5
49	<a href="#">d1ir1s_</a>	Alignment	not modelled	19.8	39	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
50	<a href="#">c1t7IA_</a>	Alignment	not modelled	19.6	19	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> 5-methyltetrahydropteroyltryglutamate--homocysteine <b>PDBTitle:</b> crystal structure of cobalamin-independent methionine synthase from t.2 maritima
51	<a href="#">d1l5oa_</a>	Alignment	not modelled	18.3	22	<b>Fold:</b> Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) <b>Superfamily:</b> Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) <b>Family:</b> Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT)
52	<a href="#">c3n0iD_</a>	Alignment	not modelled	17.9	24	<b>PDB header:</b> ligase <b>Chain:</b> D; <b>PDB Molecule:</b> tyrosyl-trna synthetase;

52	<a href="#">c3pvpB</a>	Alignment	not modelled	17.5	24	<b>PDBTitle:</b> leishmania major tyrosyl-trna synthetase in complex with tyrosinol,2 triclinic crystal form 1
53	<a href="#">c4hdnB</a>	Alignment	not modelled	17.6	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> arsrb; <b>PDBTitle:</b> crystal structure of arsab in the substrate-free state.
54	<a href="#">d1mlaa1</a>	Alignment	not modelled	17.3	16	<b>Fold:</b> FabD/lysophospholipase-like <b>Superfamily:</b> FabD/lysophospholipase-like <b>Family:</b> FabD-like
55	<a href="#">c3hzsA</a>	Alignment	not modelled	17.2	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> monofunctional glycosyltransferase; <b>PDBTitle:</b> s. aureus monofunctional glycosyltransferase (mtga)in complex with2 moenomycin
56	<a href="#">d1x2ga1</a>	Alignment	not modelled	17.1	13	<b>Fold:</b> SufE/NifU <b>Superfamily:</b> SufE/NifU <b>Family:</b> SP1160 C-terminal domain-like
57	<a href="#">c3vmtA</a>	Alignment	not modelled	16.5	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> monofunctional glycosyltransferase; <b>PDBTitle:</b> crystal structure of staphylococcus aureus membrane-bound2 transglycosylase in complex with a lipid ii analog
58	<a href="#">d2oa4a1</a>	Alignment	not modelled	15.5	33	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> SPO1678-like
59	<a href="#">c4prkB</a>	Alignment	not modelled	15.5	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-phosphoerythronate dehydrogenase; <b>PDBTitle:</b> crystal structure of d-lactate dehydrogenase (d-ldh) from2 lactobacillus jensenii
60	<a href="#">d1j33a</a>	Alignment	not modelled	15.3	30	<b>Fold:</b> Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) <b>Superfamily:</b> Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) <b>Family:</b> Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT)
61	<a href="#">c2pi1C</a>	Alignment	not modelled	15.2	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> d-lactate dehydrogenase; <b>PDBTitle:</b> crystal structure of d-lactate dehydrogenase from aquifex2 aeolicus complexed with nad and lactic acid
62	<a href="#">c3o10D</a>	Alignment	not modelled	13.7	19	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> sacsin; <b>PDBTitle:</b> crystal structure of the hepn domain from human saccin
63	<a href="#">c2omeA</a>	Alignment	not modelled	13.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> c-terminal-binding protein 2; <b>PDBTitle:</b> crystal structure of human ctbp2 dehydrogenase complexed with nad(h)
64	<a href="#">d1sc6a1</a>	Alignment	not modelled	13.5	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
65	<a href="#">c3bazA</a>	Alignment	not modelled	13.4	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxyphenylpyruvate reductase; <b>PDBTitle:</b> structure of hydroxyphenylpyruvate reductase from coleus blumei in2 complex with nadp+
66	<a href="#">c2w2kB</a>	Alignment	not modelled	13.3	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> d-mandelate dehydrogenase; <b>PDBTitle:</b> crystal structure of the apo forms of rhodotorula graminis2 d-mandelate dehydrogenase at 1.8a.
67	<a href="#">c2gqcB</a>	Alignment	not modelled	13.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxylate reductase/hydroxypyruvate reductase; <b>PDBTitle:</b> ternary crystal structure of human glyoxylate2 reductase/hydroxypyruvate reductase
68	<a href="#">d2hf5a1</a>	Alignment	not modelled	13.1	17	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
69	<a href="#">c5j23D</a>	Alignment	not modelled	13.1	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-hydroxyacid dehydrogenase; <b>PDBTitle:</b> crystal structure of nadph-dependent glyoxylate/hydroxypyruvate2 reductase smc04462 (smghrb) from sinorhizobium meliloti in complex3 with 2'-phospho- adp-ribose
70	<a href="#">d1ej7s</a>	Alignment	not modelled	12.9	39	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
71	<a href="#">c6p2iA</a>	Alignment	not modelled	12.6	12	<b>PDB header:</b> oxidoreductase, biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycerate dehydrogenase; <b>PDBTitle:</b> acyclic imino acid reductase (bsp5) in complex with nadph and d-arg
72	<a href="#">d2caza1</a>	Alignment	not modelled	12.1	13	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Endosomal sorting complex assembly domain <b>Family:</b> VPS23 C-terminal domain
73	<a href="#">c5ydnA</a>	Alignment	not modelled	12.0	28	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> gene product j; <b>PDBTitle:</b> mu pahge neck subunit
74	<a href="#">c5m4sA</a>	Alignment	not modelled	11.9	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription initiation factor iia subunit 2,transcription <b>PDBTitle:</b> transcription factor tfiia as a single chain protein
75	<a href="#">c2cazD</a>	Alignment	not modelled	11.8	13	<b>PDB header:</b> protein transport <b>Chain:</b> D: <b>PDB Molecule:</b> suppressor protein stp22 of temperature-sensitive alpha- <b>PDBTitle:</b> escrt-i core
76	<a href="#">c4xcvA</a>	Alignment	not modelled	11.7	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadp-dependent 2-hydroxyacid dehydrogenase; <b>PDBTitle:</b> probable 2-hydroxyacid dehydrogenase from rhizobium etli cfn 42 in2 complex with nadph
77	<a href="#">c3gvxA</a>	Alignment	not modelled	11.7	4	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerate dehydrogenase related protein; <b>PDBTitle:</b> crystal structure of glycerate dehydrogenase related2

						protein from thermoplasma acidophilum <b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> putative glucoamylase; <b>PDBTitle:</b> crystal structure of putative glucoamylase (yp_210071.1) from2 bacteroides fragilis nctc 9343 at 2.12 a resolution
78	<a href="#">c3eu8D_</a>	Alignment	not modelled	11.5	15	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> twitching motility protein pilt; <b>PDBTitle:</b> the crystal structure of the c-terminal domain of aquifex2 aeolicus pilt
79	<a href="#">c2eyuA_</a>	Alignment	not modelled	11.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> dehydrogenase; <b>PDBTitle:</b> crystal structure ph0520 protein from pyrococcus horikoshii ot3
80	<a href="#">c2d0iC_</a>	Alignment	not modelled	11.4	23	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
81	<a href="#">d1dxya1</a>	Alignment	not modelled	11.2	23	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Amine oxidase N-terminal region <b>Family:</b> Amine oxidase N-terminal region
82	<a href="#">d1w7ca3</a>	Alignment	not modelled	11.2	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of phosphoglycerate dehydrogenase from pyrococcus2 horikoshii ot3
83	<a href="#">c1wwkA_</a>	Alignment	not modelled	11.2	15	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> large exoprotein involved in heme utilization or adhesion; <b>PDBTitle:</b> crystal structure of cdia-ct/cdii complex from y. kristensenii 33638
84	<a href="#">c5e3eB_</a>	Alignment	not modelled	11.1	29	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional 3'-phosphoadenosine 5'-phosphosulfate <b>PDBTitle:</b> aps complex of human paps synthetase 1
85	<a href="#">c1xnjB_</a>	Alignment	not modelled	11.1	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-lactate dehydrogenase; <b>PDBTitle:</b> structure of salmonella d-lactate dehydrogenase in complex2 with nadh
86	<a href="#">c4cukA_</a>	Alignment	not modelled	10.9	11	<b>PDB header:</b> toxin <b>Chain:</b> H: <b>PDB Molecule:</b> tcda1; <b>PDBTitle:</b> crystal structure of tcda1
87	<a href="#">c1vw2H_</a>	Alignment	not modelled	10.9	27	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> paratox; <b>PDBTitle:</b> crystal structure of paratox
88	<a href="#">c6ckaB_</a>	Alignment	not modelled	10.8	27	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ggdef domain protein; <b>PDBTitle:</b> crystal structure of the azotobacter vinelandii globin-2 coupled oxygen sensor in the aquo-met form
89	<a href="#">c4uiiB_</a>	Alignment	not modelled	10.8	20	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Endosomal sorting complex assembly domain <b>Family:</b> VPS23 C-terminal domain
90	<a href="#">d2f6ma1</a>	Alignment	not modelled	10.8	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> I: <b>PDB Molecule:</b> homogentisate 1,2-dioxygenase; <b>PDBTitle:</b> resting state of homogentisate 1,2-dioxygenase
91	<a href="#">c4aq2L_</a>	Alignment	not modelled	10.7	31	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> 122aa long conserved hypothetical protein; <b>PDBTitle:</b> crystal structure of st0689, an archaeal hepn homologue
92	<a href="#">c1wolA_</a>	Alignment	not modelled	10.7	12	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
93	<a href="#">d2dl da1</a>	Alignment	not modelled	10.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-lactate dehydrogenase; <b>PDBTitle:</b> insights into domain closure, substrate specificity and2 catalysis of d-lactate dehydrogenase from lactobacillus3 bulgaricus
94	<a href="#">c1j4aA_</a>	Alignment	not modelled	10.7	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
95	<a href="#">d1mx3a1</a>	Alignment	not modelled	10.5	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Protease propeptides/inhibitors <b>Family:</b> Subtilase propeptides/inhibitors
96	<a href="#">d1tlea2</a>	Alignment	not modelled	10.5	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-lactate dehydrogenase; <b>PDBTitle:</b> a novel d-lactate dehydrogenase from sporolactobacillus sp
97	<a href="#">c4xkjA_</a>	Alignment	not modelled	10.5	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> d-isomer specific 2-hydroxyacid dehydrogenase; <b>PDBTitle:</b> crystal structure of d-isomer specific 2-hydroxyacid dehydrogenase2 from lactobacillus delbrueckii ssp. bulgaricus
98	<a href="#">c2yq4C_</a>	Alignment	not modelled	10.4	23	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
99	<a href="#">d1qp8a1</a>	Alignment	not modelled	10.3	23	