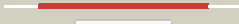



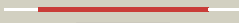

















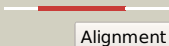

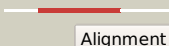

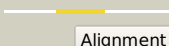



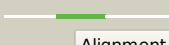
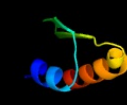
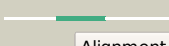


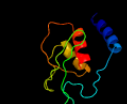




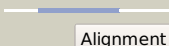
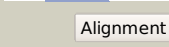
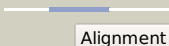
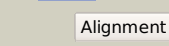
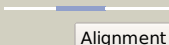
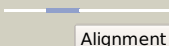
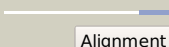



# Phyre2

Email: mdejesus@rockefeller.edu  
 Description: RVBD1601\_(hisB)\_1802042\_1802674  
 Date: Fri Aug 2 13:30:19 BST 2019  
 Unique Job ID: 3e458a9d819032d3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6fwhH_</a>	 Alignment		100.0	47	<b>PDB header:</b> lyase <b>Chain:</b> H; <b>PDB Molecule:</b> imidazoleglycerol-phosphate dehydratase; <b>PDBTitle:</b> acanthamoeba igpd in complex with r-c348 to 1.7a resolution
2	<a href="#">c6ezmL_</a>	 Alignment		100.0	44	<b>PDB header:</b> lyase <b>Chain:</b> L; <b>PDB Molecule:</b> imidazoleglycerol-phosphate dehydratase; <b>PDBTitle:</b> imidazoleglycerol-phosphate dehydratase from saccharomyces cerevisiae
3	<a href="#">c4lomA_</a>	 Alignment		100.0	100	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> imidazoleglycerol-phosphate dehydratase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis hisb in complex with2 its substrate
4	<a href="#">c2f1dP_</a>	 Alignment		100.0	51	<b>PDB header:</b> lyase <b>Chain:</b> P; <b>PDB Molecule:</b> imidazoleglycerol-phosphate dehydratase 1; <b>PDBTitle:</b> x-ray structure of imidazoleglycerol-phosphate dehydratase
5	<a href="#">c5dnIA_</a>	 Alignment		100.0	38	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> imidazoleglycerol-phosphate dehydratase; <b>PDBTitle:</b> crystal structure of igpd from pyrococcus furiosus in complex with2 (s)-c348
6	<a href="#">c1rhyB_</a>	 Alignment		100.0	39	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> imidazole glycerol phosphate dehydratase; <b>PDBTitle:</b> crystal structure of imidazole glycerol phosphate dehydratase
7	<a href="#">c2ae8C_</a>	 Alignment		100.0	33	<b>PDB header:</b> lyase <b>Chain:</b> C; <b>PDB Molecule:</b> imidazoleglycerol-phosphate dehydratase; <b>PDBTitle:</b> crystal structure of imidazoleglycerol-phosphate dehydratase from2 staphylococcus aureus subsp. aureus n315
8	<a href="#">d2f1da2</a>	 Alignment		100.0	51	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Imidazole glycerol phosphate dehydratase
9	<a href="#">d1rhya2</a>	 Alignment		100.0	35	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Imidazole glycerol phosphate dehydratase
10	<a href="#">d2ae8a2</a>	 Alignment		100.0	36	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Imidazole glycerol phosphate dehydratase
11	<a href="#">d2f1da1</a>	 Alignment		100.0	51	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Imidazole glycerol phosphate dehydratase

12	<a href="#">d1rhya1</a>	 Alignment		100.0	43	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Imidazole glycerol phosphate dehydratase
13	<a href="#">d2ae8a1</a>	 Alignment		100.0	30	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Imidazole glycerol phosphate dehydratase
14	<a href="#">d2ja9a2</a>	 Alignment		78.0	15	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
15	<a href="#">c2ja9A_</a>	 Alignment		65.4	14	<b>PDB header:</b> rna-binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> exosome complex exonuclease rrp40; <b>PDBTitle:</b> structure of the n-terminal deletion of yeast exosome2 component rrp40
16	<a href="#">c4ifdG_</a>	 Alignment		55.0	14	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> G; <b>PDB Molecule:</b> exosome complex component rrp40; <b>PDBTitle:</b> crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna
17	<a href="#">d2nn6g3</a>	 Alignment		42.0	15	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
18	<a href="#">c3j6vE_</a>	 Alignment		36.0	18	<b>PDB header:</b> ribosome <b>Chain:</b> E; <b>PDB Molecule:</b> 28s ribosomal protein s5, mitochondrial; <b>PDBTitle:</b> cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
19	<a href="#">c2k8hA_</a>	 Alignment		34.8	6	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> small ubiquitin protein; <b>PDBTitle:</b> solution structure of sumo from trypanosoma brucei
20	<a href="#">c4ywjB_</a>	 Alignment		32.1	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate reductase; <b>PDBTitle:</b> crystal structure of 4-hydroxy-tetrahydrodipicolinate reductase (htpa2 reductase) from pseudomonas aeruginosa
21	<a href="#">c2ba0A_</a>	 Alignment	not modelled	29.5	13	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> archaeal exosome rna binding protein rrp4; <b>PDBTitle:</b> archaeal exosome core
22	<a href="#">c5us6L_</a>	 Alignment	not modelled	28.3	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> L; <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate reductase; <b>PDBTitle:</b> structure of dihydrodipicolinate reductase from vibrio vulnificus2 bound to nadh and 2,6 pyridine dicarboxylic acid with intact3 polyhistidine tag
23	<a href="#">c3nqwB_</a>	 Alignment	not modelled	27.6	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> cg11900; <b>PDBTitle:</b> a metazoan ortholog of spot hydrolyzes pppp and plays a role in2 starvation responses
24	<a href="#">d1itza2</a>	 Alignment	not modelled	24.4	23	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> TK-like Pyr module
25	<a href="#">c2nn6G_</a>	 Alignment	not modelled	24.0	15	<b>PDB header:</b> hydrolase/transferase <b>Chain:</b> G; <b>PDB Molecule:</b> exosome complex exonuclease rrp40; <b>PDBTitle:</b> structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
26	<a href="#">c2k4mA_</a>	 Alignment	not modelled	23.6	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> upf0146 protein mth_1000; <b>PDBTitle:</b> solution nmr structure of m. thermoautotrophicum protein mth_1000,2 northeast structural genomics consortium target tr8
27	<a href="#">c5knnG_</a>	 Alignment	not modelled	20.3	18	<b>PDB header:</b> ligase <b>Chain:</b> G; <b>PDB Molecule:</b> alanine--trna ligase, cytoplasmic; <b>PDBTitle:</b> evolutionary gain of alanine mischarging to non-cognate trnas with a2 g4:u69 base pair
						<b>PDB header:</b> transferase

28	<a href="#">c3d6kB_</a>	Alignment	not modelled	20.1	17	<b>Chain:</b> B; <b>PDB Molecule:</b> putative aminotransferase; <b>PDBTitle:</b> the crystal structure of a putative aminotransferase from <i>Corynebacterium diphtheriae</i>
29	<a href="#">d1c55a_</a>	Alignment	not modelled	19.3	40	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Scorpion toxin-like <b>Family:</b> Short-chain scorpion toxins
30	<a href="#">d2ed6a1</a>	Alignment	not modelled	18.9	17	<b>Fold:</b> WSSV envelope protein-like <b>Superfamily:</b> WSSV envelope protein-like <b>Family:</b> WSSV envelope protein-like
31	<a href="#">d2oc5a1</a>	Alignment	not modelled	18.1	25	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> PMT1231-like
32	<a href="#">d1sr9a3</a>	Alignment	not modelled	17.7	18	<b>Fold:</b> 2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain <b>Superfamily:</b> 2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain <b>Family:</b> 2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain
33	<a href="#">c2dnrA_</a>	Alignment	not modelled	16.9	9	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> synaptojanin-1; <b>PDBTitle:</b> solution structure of rna binding domain in synaptojanin 1
34	<a href="#">c2becB_</a>	Alignment	not modelled	15.3	56	<b>PDB header:</b> metal binding protein/transport protein <b>Chain:</b> B; <b>PDB Molecule:</b> sodium/hydrogen exchanger 1; <b>PDBTitle:</b> crystal structure of chp2 in complex with its binding2 region in nhe1 and insights into the mechanism of ph3 regulation
35	<a href="#">c5o5jl_</a>	Alignment	not modelled	14.9	18	<b>PDB header:</b> ribosome <b>Chain:</b> I; <b>PDB Molecule:</b> 30s ribosomal protein s9; <b>PDBTitle:</b> structure of the 30s small ribosomal subunit from <i>Mycobacterium smegmatis</i>
36	<a href="#">c3nr1A_</a>	Alignment	not modelled	14.9	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> hd domain-containing protein 3; <b>PDBTitle:</b> a metazoan ortholog of spot hydrolyzes ppGpp and plays a role in2 starvation responses
37	<a href="#">d1vj7a1</a>	Alignment	not modelled	14.1	28	<b>Fold:</b> HD-domain/PDEase-like <b>Superfamily:</b> HD-domain/PDEase-like <b>Family:</b> HD domain
38	<a href="#">c4a8jA_</a>	Alignment	not modelled	13.7	35	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> elongator complex protein 4; <b>PDBTitle:</b> crystal structure of the elongator subcomplex elp456
39	<a href="#">c4joiA_</a>	Alignment	not modelled	12.7	30	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> cst complex subunit stn1; <b>PDBTitle:</b> crystal structure of the human telomeric stn1-ten1 complex
40	<a href="#">c1drwA_</a>	Alignment	not modelled	12.6	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> dihydrodipicolinate reductase; <b>PDBTitle:</b> <i>Escherichia coli</i> dhpr/nhdh complex
41	<a href="#">c4xeoB_</a>	Alignment	not modelled	11.4	18	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> alanine--trna ligase, cytoplasmic; <b>PDBTitle:</b> crystal structure of human alars catalytic domain with r329h mutation
42	<a href="#">d2caza1</a>	Alignment	not modelled	11.4	22	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Endosomal sorting complex assembly domain <b>Family:</b> VPS23 C-terminal domain
43	<a href="#">c2cazD_</a>	Alignment	not modelled	10.5	22	<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
44	<a href="#">d2csba2</a>	Alignment	not modelled	10.4	33	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> RuvA domain 2-like <b>Family:</b> Topoisomerase V repeat domain
45	<a href="#">d2r4qa1</a>	Alignment	not modelled	10.4	16	<b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> PTS system IIB component-like <b>Family:</b> PTS system, Fructose specific IIB subunit-like
46	<a href="#">c3ne9B_</a>	Alignment	not modelled	10.3	16	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> phosphopantetheine protein transferase, ppt1p; <b>PDBTitle:</b> <i>Chromobacterium ammoniagenes</i> apo-acps structure
47	<a href="#">d2r48a1</a>	Alignment	not modelled	10.3	19	<b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> PTS system IIB component-like <b>Family:</b> PTS system, Fructose specific IIB subunit-like
48	<a href="#">c2kyrA_</a>	Alignment	not modelled	10.3	22	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> fructose-like phosphotransferase enzyme iib component 1; <b>PDBTitle:</b> solution structure of enzyme iib subunit of pts system from <i>Escherichia coli</i> K12. northeast structural genomics consortium target3 er315/ontario center for structural proteomics target ec0544
49	<a href="#">c2vxob_</a>	Alignment	not modelled	10.2	20	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing]; <b>PDBTitle:</b> human gmp synthetase in complex with xmp
50	<a href="#">c2nq5A_</a>	Alignment	not modelled	10.1	15	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> 5-methyltetrahydropteroyltriglutamate--homocysteine <b>PDBTitle:</b> crystal structure of methyltransferase from <i>Streptococcus mutans</i>
51	<a href="#">c2l36A_</a>	Alignment	not modelled	9.4	58	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A; <b>PDB Molecule:</b> msi594; <b>PDBTitle:</b> solution structure of msi-594 derived mutant peptide msi594f5a in2 lipopolysaccharide micelles
52	<a href="#">d1szpa2</a>	Alignment	not modelled	9.3	29	<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)
53	<a href="#">d1dha2</a>	Alignment	not modelled	9.2	24	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-

53	<a href="#">c1qumaz</a>	Alignment	not modelled	9.2	34	terminal domain <b>Family:</b> Dihydrodipicolinate reductase-like
54	<a href="#">c1itzC</a>	Alignment	not modelled	9.0	25	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> maize transketolase in complex with tpp
55	<a href="#">c5dleD</a>	Alignment	not modelled	9.0	19	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> pts system, fructose-specific iiabc component; <b>PDBTitle:</b> crystal structure from a domain (thr161-f265) from fructose-specific2 iiabc component (pts system) from borrelia burgdorferi
56	<a href="#">d1g99a1</a>	Alignment	not modelled	8.9	41	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Acetokinase-like
57	<a href="#">c4chhB</a>	Alignment	not modelled	8.7	13	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> protein interacting with hsp90 1; <b>PDBTitle:</b> n-terminal domain of yeast pih1p
58	<a href="#">c2m1zA</a>	Alignment	not modelled	8.7	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lmo0427 protein; <b>PDBTitle:</b> solution structure of uncharacterized protein lmo0427
59	<a href="#">d2r8oa1</a>	Alignment	not modelled	8.6	17	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> TK-like Pyr module
60	<a href="#">c5j43F</a>	Alignment	not modelled	8.4	20	<b>PDB header:</b> toxin <b>Chain:</b> F: <b>PDB Molecule:</b> trna nuclease cdia; <b>PDBTitle:</b> cdia-ct from uropathogenic escherichia coli in complex with cysk
61	<a href="#">d1yl7a2</a>	Alignment	not modelled	8.3	19	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> Dihydrodipicolinate reductase-like
62	<a href="#">c4quwA</a>	Alignment	not modelled	8.1	30	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> aldehyde decarboxylase; <b>PDBTitle:</b> crystal structure of the apo form of cyanobacterial aldehyde-2 deformylating oxygenase
63	<a href="#">c1s1hE</a>	Alignment	not modelled	8.0	16	<b>PDB header:</b> ribosome <b>Chain:</b> E: <b>PDB Molecule:</b> 40s ribosomal protein s2; <b>PDBTitle:</b> structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1h, contains 40s subunit. the 60s4 ribosomal subunit is in file 1s1i.
64	<a href="#">c4g5sZ</a>	Alignment	not modelled	7.9	33	<b>PDB header:</b> cell cycle/signaling protein <b>Chain:</b> Z: <b>PDB Molecule:</b> g-protein-signaling modulator 2; <b>PDBTitle:</b> structure of lgn g13/galpai3 complex
65	<a href="#">c1y88A</a>	Alignment	not modelled	7.9	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein af1548; <b>PDBTitle:</b> crystal structure of protein of unknown function af1548
66	<a href="#">c4ztxA</a>	Alignment	not modelled	7.8	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cobalamin-independent methionine synthase; <b>PDBTitle:</b> neurospora crassa cobalamin-independent methionine synthase complexed2 with zn2+
67	<a href="#">c3l7sA</a>	Alignment	not modelled	7.7	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-methyltetrahydropteroyltriglutamate--homocysteine <b>PDBTitle:</b> crystal structure of mete coordinated with zinc from streptococcus2 mutans
68	<a href="#">d1xp8a1</a>	Alignment	not modelled	7.6	38	<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)
69	<a href="#">c1vj7B</a>	Alignment	not modelled	7.5	29	<b>PDB header:</b> hydrolase, transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional rela/spot; <b>PDBTitle:</b> crystal structure of the bifunctional catalytic fragment of relseq,2 the rela/spot homolog from streptococcus equisimilis.
70	<a href="#">c3tvsA</a>	Alignment	not modelled	7.5	26	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> cryptochrome-1; <b>PDBTitle:</b> structure of full-length drosophila cryptochrome
71	<a href="#">d2e1za1</a>	Alignment	not modelled	7.5	29	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Acetokinase-like
72	<a href="#">c3so6A</a>	Alignment	not modelled	7.4	7	<b>PDB header:</b> protein binding/protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> ldl receptor adaptor protein; <b>PDBTitle:</b> crystal structure of the ldl receptor tail in complex with autosomal2 recessive hypercholesterolemia ptb domain
73	<a href="#">d2uube1</a>	Alignment	not modelled	7.4	21	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Translational machinery components
74	<a href="#">d1y88a2</a>	Alignment	not modelled	7.4	25	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> MRR-like
75	<a href="#">c2qzbB</a>	Alignment	not modelled	7.4	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein yfey; <b>PDBTitle:</b> crystal structure of the uncharacterized protein yfey from escherichia2 coli
76	<a href="#">d1u69a</a>	Alignment	not modelled	7.3	8	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> 3-demethylubiquinone-9 3-methyltransferase
77	<a href="#">d2f6ma1</a>	Alignment	not modelled	7.3	26	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Endosomal sorting complex assembly domain <b>Family:</b> VPS23 C-terminal domain
						<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fructose-like phosphotransferase enzyme

78	<a href="#">c4jxdA_</a>	Alignment	not modelled	7.2	19	iib component 3; <b>PDBTitle:</b> crystal structure of predicted fructose specific iib from escherichia2 coli
79	<a href="#">c3bs4A_</a>	Alignment	not modelled	7.2	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ph0321; <b>PDBTitle:</b> crystal structure of uncharacterized protein ph0321 from pyrococcus2 horikoshii in complex with an unknown peptide
80	<a href="#">c4psiA_</a>	Alignment	not modelled	6.8	17	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> pih1 domain-containing protein 1; <b>PDBTitle:</b> pih1d1/phospho-tel2 complex
81	<a href="#">c3dc1A_</a>	Alignment	not modelled	6.6	7	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> kynurenine/alpha-aminoadipate aminotransferase <b>PDBTitle:</b> crystal structure of kynurenine aminotransferase ii complex with2 alpha-ketoglutarate
82	<a href="#">d1ftha_</a>	Alignment	not modelled	6.6	50	<b>Fold:</b> 4'-phosphopantetheinyl transferase <b>Superfamily:</b> 4'-phosphopantetheinyl transferase <b>Family:</b> Holo-(acyl carrier protein) synthase ACPS
83	<a href="#">c3gzaB_</a>	Alignment	not modelled	6.5	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative alpha-l-fucosidase; <b>PDBTitle:</b> crystal structure of putative alpha-l-fucosidase (np_812709.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.60 a resolution
84	<a href="#">c5xumA_</a>	Alignment	not modelled	6.5	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> holo-[acyl-carrier-protein] synthase; <b>PDBTitle:</b> crystal structure of thermotoga maritima holo-[acyl-carrier-protein]2 synthase (acps)
85	<a href="#">c2lb0A_</a>	Alignment	not modelled	6.4	15	<b>PDB header:</b> signaling protein/transcription <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase smurf1; <b>PDBTitle:</b> structure of the first ww domain of human smurf1 in complex with a di-2 phosphorylated human smad1 derived peptide
86	<a href="#">c2lzaA_</a>	Alignment	not modelled	6.4	15	<b>PDB header:</b> signaling protein/transcription <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase smurf1; <b>PDBTitle:</b> structure of the first ww domain of human smurf1 in complex with a2 mono-phosphorylated human smad1 derived peptide
87	<a href="#">c2auhB_</a>	Alignment	not modelled	6.4	40	<b>PDB header:</b> transferase/signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> growth factor receptor-bound protein 14; <b>PDBTitle:</b> crystal structure of the grb14 bps region in complex with2 the insulin receptor tyrosine kinase
88	<a href="#">c2e30B_</a>	Alignment	not modelled	6.3	56	<b>PDB header:</b> metal binding protein/transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> sodium/hydrogen exchanger 1; <b>PDBTitle:</b> solution structure of the cytoplasmic region of na+/h+2 exchanger 1 complexed with essential cofactor calcineurin3 b homologous protein 1
89	<a href="#">d1n0wa_</a>	Alignment	not modelled	6.2	29	<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)
90	<a href="#">c3k2tA_</a>	Alignment	not modelled	6.2	33	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lmo2511 protein; <b>PDBTitle:</b> crystal structure of lmo2511 protein from listeria2 monocytogenes, northeast structural genomics consortium3 target lkr84a
91	<a href="#">c1yfsB_</a>	Alignment	not modelled	6.2	20	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> alanyl-trna synthetase; <b>PDBTitle:</b> the crystal structure of alanyl-trna synthetase in complex2 with l-alanine
92	<a href="#">d1v5wa_</a>	Alignment	not modelled	6.1	24	<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)
93	<a href="#">c2x1cA_</a>	Alignment	not modelled	5.9	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coenzyme <b>PDBTitle:</b> the crystal structure of precursor acyl coenzyme2 a:isopenicillin n acyltransferase from penicillium3 chrysogenum
94	<a href="#">d1r9ja1</a>	Alignment	not modelled	5.9	20	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> TK-like Pyr module
95	<a href="#">c1r9jB_</a>	Alignment	not modelled	5.9	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> transketolase; <b>PDBTitle:</b> transketolase from leishmania mexicana
96	<a href="#">c3io5B_</a>	Alignment	not modelled	5.9	31	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> recombination and repair protein; <b>PDBTitle:</b> crystal structure of a dimeric form of the uvx recombinase core2 domain from enterobacteria phage t4
97	<a href="#">c4p63A_</a>	Alignment	not modelled	5.8	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable deoxyhypusine synthase; <b>PDBTitle:</b> crystal structure of deoxyhypusine synthase from pyrococcus horikoshii
98	<a href="#">c3bbnl_</a>	Alignment	not modelled	5.8	15	<b>PDB header:</b> ribosome <b>Chain:</b> I: <b>PDB Molecule:</b> ribosomal protein s9; <b>PDBTitle:</b> homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
99	<a href="#">c4ht4A_</a>	Alignment	not modelled	5.8	8	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> nickening enzyme; <b>PDBTitle:</b> molecular basis of vancomycin resistance transfer in staphylococcus2 aureus