



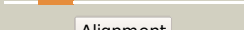




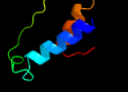




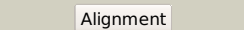

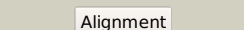

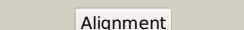
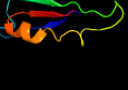
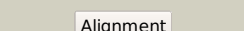



# Phyre2



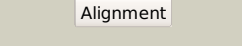
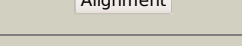




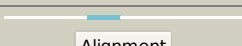
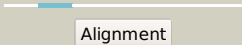

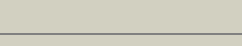
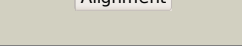
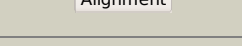
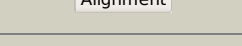

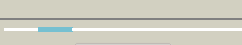
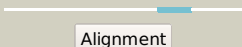

Email	mdejesus@rockefeller.edu
Description	RVBD2062c_cobN_2317177_2320761
Date	Mon Aug 5 13:25:17 BST 2019
Unique Job ID	f1f6d9be52418ded

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4zhjA_</a>	 Alignment		100.0	28	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> mg-chelatase subunit chlh; <b>PDBTitle:</b> crystal structure of the catalytic subunit of magnesium chelatase
2	<a href="#">c3g85A_</a>	 Alignment		88.9	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (laci family); <b>PDBTitle:</b> crystal structure of laci family transcription regulator from2 clostridium acetobutylicum
3	<a href="#">d2ajta2</a>	 Alignment		88.7	21	<b>Fold:</b> Fucl/AraA N-terminal and middle domains <b>Superfamily:</b> Fucl/AraA N-terminal and middle domains <b>Family:</b> AraA N-terminal and middle domain-like
4	<a href="#">c4r1oF_</a>	 Alignment		84.4	16	<b>PDB header:</b> isomerase <b>Chain:</b> F: <b>PDB Molecule:</b> l-arabinose isomerase; <b>PDBTitle:</b> crystal structure of thermophilic geobacillus kaustophilus l-arabinose2 isomerase
5	<a href="#">d2iafa1</a>	 Alignment		77.2	18	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Serine metabolism enzymes domain <b>Family:</b> Serine dehydratase beta chain-like
6	<a href="#">c1i9xA_</a>	 Alignment		74.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gamma-glutamyl hydrolase; <b>PDBTitle:</b> structure of gamma-glutamyl hydrolase
7	<a href="#">d1i9xA_</a>	 Alignment		74.8	17	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
8	<a href="#">c4lqlF_</a>	 Alignment		74.6	13	<b>PDB header:</b> isomerase <b>Chain:</b> F: <b>PDB Molecule:</b> l-arabinose isomerase; <b>PDBTitle:</b> crystal structure of l-arabinose isomerase from lactobacillus2 fermentum cgmmc2921
9	<a href="#">c2f59B_</a>	 Alignment		72.8	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 6,7-dimethyl-8-ribitylumazine synthase 1; <b>PDBTitle:</b> lumazine synthase ribh1 from brucella abortus (gene bruab1_0785,2 swiss-prot entry q57dy1) complexed with inhibitor 5-nitro-6-(d-3 ribitylamino)-2,4(1h,3h) pyrimidinedione
10	<a href="#">c4e14A_</a>	 Alignment		72.7	10	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> kynurenine formamidase; <b>PDBTitle:</b> crystal structure of kynurenine formamidase conjugated with2 phenylmethylsulfonyl fluoride
11	<a href="#">c5nn7A_</a>	 Alignment		69.2	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uracil-dna glycosylase; <b>PDBTitle:</b> kshv uracil-dna glycosylase, apo form

12	<a href="#">d3euga_</a>	Alignment		69.2	20	<b>Fold:</b> Uracil-DNA glycosylase-like <b>Superfamily:</b> Uracil-DNA glycosylase-like <b>Family:</b> Uracil-DNA glycosylase
13	<a href="#">c3aerC_</a>	Alignment		69.0	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase subunit n; <b>PDBTitle:</b> structure of the light-independent protochlorophyllide reductase2 catalyzing a key reduction for greening in the dark
14	<a href="#">c4plaA_</a>	Alignment		68.3	20	<b>PDB header:</b> transferase,hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chimera protein of phosphatidylinositol 4-kinase type 2- <b>PDBTitle:</b> crystal structure of phosphatidyl inositol 4-kinase ii alpha in2 complex with atp
15	<a href="#">c4l8fA_</a>	Alignment		68.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gamma-glutamyl hydrolase; <b>PDBTitle:</b> crystal structure of gamma-glutamyl hydrolase (c108a) complex with mtx
16	<a href="#">d1okba_</a>	Alignment		67.9	17	<b>Fold:</b> Uracil-DNA glycosylase-like <b>Superfamily:</b> Uracil-DNA glycosylase-like <b>Family:</b> Uracil-DNA glycosylase
17	<a href="#">d2hxma1</a>	Alignment		67.5	15	<b>Fold:</b> Uracil-DNA glycosylase-like <b>Superfamily:</b> Uracil-DNA glycosylase-like <b>Family:</b> Uracil-DNA glycosylase
18	<a href="#">c3fijD_</a>	Alignment		67.1	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> lin1909 protein; <b>PDBTitle:</b> crystal structure of a uncharacterized protein lin1909
19	<a href="#">c2booA_</a>	Alignment		67.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uracil-dna glycosylase; <b>PDBTitle:</b> the crystal structure of uracil-dna n-glycosylase (ung) from2 deinococcus radiodurans.
20	<a href="#">c4ggmX_</a>	Alignment		66.2	20	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> udp-2,3-diacylglucosamine pyrophosphatase lpxi; <b>PDBTitle:</b> structure of lpxi
21	<a href="#">c4rqoB_</a>	Alignment	not modelled	64.4	18	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> l-serine dehydratase; <b>PDBTitle:</b> crystal structure of l-serine dehydratase from legionella pneumophila
22	<a href="#">c3cxmA_</a>	Alignment	not modelled	63.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uracil-dna glycosylase; <b>PDBTitle:</b> leishmania naiffi uracil-dna glycosylase in complex with 5-bromouracil
23	<a href="#">d1jhfa1</a>	Alignment	not modelled	63.0	28	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> LexA repressor, N-terminal DNA-binding domain
24	<a href="#">d2pbla1</a>	Alignment	not modelled	62.2	11	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase
25	<a href="#">c3d54D_</a>	Alignment	not modelled	62.0	17	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphoribosylformylglycinamide synthase 1; <b>PDBTitle:</b> structure of purlqs from thermotoga maritima
26	<a href="#">d1laue_</a>	Alignment	not modelled	57.5	26	<b>Fold:</b> Uracil-DNA glycosylase-like <b>Superfamily:</b> Uracil-DNA glycosylase-like <b>Family:</b> Uracil-DNA glycosylase
27	<a href="#">d1stza1</a>	Alignment	not modelled	56.5	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Heat-inducible transcription repressor HrcA, N-terminal domain
28	<a href="#">c5x55A_</a>	Alignment	not modelled	56.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable uracil-dna glycosylase; <b>PDBTitle:</b> crystal structure of mimivirus uracil-dna glycosylase
						<b>PDB header:</b> hydrolase

29	<a href="#">c3tr7A_</a>	Alignment	not modelled	55.8	15	<b>Chain:</b> A: <b>PDB Molecule:</b> uracil-dna glycosylase; <b>PDBTitle:</b> structure of a uracil-dna glycosylase (ung) from coxiella burnetii
30	<a href="#">c2owrD_</a>	Alignment	not modelled	54.7	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> uracil-dna glycosylase; <b>PDBTitle:</b> crystal structure of vaccinia virus uracil-dna glycosylase
31	<a href="#">d1uc8a1</a>	Alignment	not modelled	54.3	19	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> Lysine biosynthesis enzyme LysX, N-terminal domain
32	<a href="#">d1m1na_</a>	Alignment	not modelled	53.9	12	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
33	<a href="#">c4n5iX_</a>	Alignment	not modelled	53.1	8	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> esterase/lipase; <b>PDBTitle:</b> crystal structure of a c8-c4 sn3 inhibited esterase b from2 lactobacillus rhamnosis
34	<a href="#">d2j8xa1</a>	Alignment	not modelled	52.9	21	<b>Fold:</b> Uracil-DNA glycosylase-like <b>Superfamily:</b> Uracil-DNA glycosylase-like <b>Family:</b> Uracil-DNA glycosylase
35	<a href="#">c3zoqA_</a>	Alignment	not modelled	52.7	16	<b>PDB header:</b> hydrolase/viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> uracil-dna glycosylase; <b>PDBTitle:</b> structure of bsudg-p56 complex
36	<a href="#">c3okaA_</a>	Alignment	not modelled	52.6	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> gdp-mannose-dependent alpha-(1-6)-phosphatidylinositol <b>PDBTitle:</b> crystal structure of corynebacterium glutamicum pimb' in complex with2 gdp-man (triclinic crystal form)
37	<a href="#">c2xdqB_</a>	Alignment	not modelled	51.6	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase subunit b; <b>PDBTitle:</b> dark operative protochlorophyllide oxidoreductase (chlnc-hlb)2 complex
38	<a href="#">c3uugB_</a>	Alignment	not modelled	51.3	15	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> multiple sugar-binding periplasmic receptor chve; <b>PDBTitle:</b> crystal structure of the periplasmic sugar binding protein chve
39	<a href="#">d1qvwa_</a>	Alignment	not modelled	51.0	24	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
40	<a href="#">c3aerB_</a>	Alignment	not modelled	48.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase subunit b; <b>PDBTitle:</b> structure of the light-independent protochlorophyllide reductase2 catalyzing a key reduction for greening in the dark
41	<a href="#">c4byfA_</a>	Alignment	not modelled	48.1	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> unconventional myosin-ic; <b>PDBTitle:</b> crystal structure of human myosin 1c in complex with2 calmodulin in the pre-power stroke state
42	<a href="#">d1iowa1</a>	Alignment	not modelled	46.6	21	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> D-Alanine ligase N-terminal domain
43	<a href="#">c5x3hA_</a>	Alignment	not modelled	46.0	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> uracil-dna glycosylase; <b>PDBTitle:</b> the y81g mutant of the ung crystal structure from nitratifactor2 salsuginis
44	<a href="#">c5hsgA_</a>	Alignment	not modelled	45.1	22	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative abc transporter, nucleotide binding/atpase <b>PDBTitle:</b> crystal structure of an abc transporter solute binding protein from2 klebsiella pneumoniae (kpn_01730, target efi-511059), apo open3 structure
45	<a href="#">d1qh8a_</a>	Alignment	not modelled	43.8	14	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
46	<a href="#">d2iw1a1</a>	Alignment	not modelled	42.4	25	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Glycosyl transferases group 1
47	<a href="#">c3h3mB_</a>	Alignment	not modelled	42.4	19	<b>PDB header:</b> structural genomics <b>Chain:</b> B: <b>PDB Molecule:</b> flagellar protein flit; <b>PDBTitle:</b> crystal structure of flagellar protein flit from bordetella2 bronchiseptica
48	<a href="#">c4pd3B_</a>	Alignment	not modelled	42.1	23	<b>PDB header:</b> contractile protein <b>Chain:</b> B: <b>PDB Molecule:</b> nonmuscle myosin heavy chain b, alpha-actinin a chimera <b>PDBTitle:</b> crystal structure of rigor-like human nonmuscle myosin-2b
49	<a href="#">c5kpaA_</a>	Alignment	not modelled	41.7	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> curd; <b>PDBTitle:</b> crystal structure of the curacin biosynthetic pathway hmg synthase in2 complex with acetyl donor-accp
50	<a href="#">d1q7ra_</a>	Alignment	not modelled	40.4	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
51	<a href="#">c3gv0A_</a>	Alignment	not modelled	40.0	12	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, lacI family; <b>PDBTitle:</b> crystal structure of lacI family transcription regulator from2 agrobacterium tumefaciens
52	<a href="#">c1br2C_</a>	Alignment	not modelled	39.9	21	<b>PDB header:</b> muscle protein <b>Chain:</b> C: <b>PDB Molecule:</b> myosin; <b>PDBTitle:</b> smooth muscle myosin motor domain complexed with mgadp.alf4
53	<a href="#">c5vzmB_</a>	Alignment	not modelled	39.8	42	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> dna repair protein rev1; <b>PDBTitle:</b> solution nmr structure of human rev1 (932-1039) in complex with2 ubiquitin

54	<a href="#">c3c4vB_</a>		Alignment	not modelled	39.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> predicted glycosyltransferases; <b>PDBTitle:</b> structure of the retaining glycosyltransferase msha:the2 first step in mycothiol biosynthesis. organism:3 corynebacterium glutamicum : complex with udp and 1l-ins-1-4 p.
55	<a href="#">d2isya1</a>		Alignment	not modelled	38.7	26	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
56	<a href="#">c3nkzD_</a>		Alignment	not modelled	38.4	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> flagellar protein flit; <b>PDBTitle:</b> the crystal structure of a flagella protein from yersinia2 enterocolitica subsp. enterocolitica 8081
57	<a href="#">c4nq3B_</a>		Alignment	not modelled	38.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cyanuric acid amidohydrolase; <b>PDBTitle:</b> crystal structure of cyanuric acid hydrolase from a. caulinodans
58	<a href="#">d1g3wa1</a>		Alignment	not modelled	37.7	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
59	<a href="#">c2qq1A_</a>		Alignment	not modelled	37.7	21	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> molybdenum cofactor biosynthesis mog; <b>PDBTitle:</b> crystal structure of molybdenum cofactor biosynthesis2 (aq_061) other form from aquifex aeolicus vf5
60	<a href="#">c3kkIA_</a>		Alignment	not modelled	37.1	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable chaperone protein hsp33; <b>PDBTitle:</b> crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae
61	<a href="#">d2f7wa1</a>		Alignment	not modelled	36.8	17	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
62	<a href="#">c4x0oG_</a>		Alignment	not modelled	36.8	12	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 3 protein 2; <b>PDBTitle:</b> beta-ketoacyl-(acyl carrier protein) synthase iii-2 (fabh2) from2 vibrio cholerae soaked with acetyl-coa
63	<a href="#">c3q9tB_</a>		Alignment	not modelled	36.8	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> choline dehydrogenase and related flavoproteins; <b>PDBTitle:</b> crystal structure analysis of formate oxidase
64	<a href="#">d1kk8a2</a>		Alignment	not modelled	36.4	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Motor proteins
65	<a href="#">c3bjrA_</a>		Alignment	not modelled	36.3	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative carboxylesterase; <b>PDBTitle:</b> crystal structure of a putative carboxylesterase (lp_1002) from2 lactobacillus plantarum wcf51 at 2.09 a resolution
66	<a href="#">c5tbyA_</a>		Alignment	not modelled	36.1	21	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> myosin-7; <b>PDBTitle:</b> human beta cardiac heavy meromyosin interacting-heads motif obtained2 by homology modeling (using swiss-model) of human sequence from3 aphonopelma homology model (pdb-3jhb), rigidly fitted to human beta-4 cardiac negatively stained thick filament 3d-reconstruction (emd-5 2240)
67	<a href="#">c3hxB_</a>		Alignment	not modelled	36.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> sugar hydrolase; <b>PDBTitle:</b> crystal structure of a sugar hydrolase (yeeb) from lactococcus lactis,2 northeast structural genomics consortium target kr108
68	<a href="#">c4h1hB_</a>		Alignment	not modelled	35.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lmo1638 protein; <b>PDBTitle:</b> crystal structure of mcf homolog from listeria monocytogenes egd-e
69	<a href="#">c5hw4C_</a>		Alignment	not modelled	35.6	16	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> ribosomal rna small subunit methyltransferase i; <b>PDBTitle:</b> crystal structure of escherichia coli 16s rrna methyltransferase rsmi2 in complex with adomet
70	<a href="#">d1mioa_</a>		Alignment	not modelled	35.1	13	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
71	<a href="#">c4I79A_</a>		Alignment	not modelled	35.1	27	<b>PDB header:</b> motor protein/metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> unconventional myosin-ib; <b>PDBTitle:</b> crystal structure of nucleotide-free myosin 1b residues 1-728 with2 bound calmodulin
72	<a href="#">c5tx7A_</a>		Alignment	not modelled	34.3	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-isomer specific 2-hydroxyacid dehydrogenase family <b>PDBTitle:</b> crystal structure of d-isomer specific 2-hydroxyacid dehydrogenase2 from desulfovibrio vulgaris
73	<a href="#">c3bbIA_</a>		Alignment	not modelled	34.1	12	<b>PDB header:</b> regulatory protein <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein of laci family; <b>PDBTitle:</b> crystal structure of a regulatory protein of laci family from2 chloroflexus aggregans
74	<a href="#">c5n6yD_</a>		Alignment	not modelled	34.1	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> nitrogenase vanadium-iron protein alpha chain; <b>PDBTitle:</b> azotobacter vinelandii vanadium nitrogenase
75	<a href="#">d1c41a_</a>		Alignment	not modelled	33.8	10	<b>Fold:</b> Lumazine synthase <b>Superfamily:</b> Lumazine synthase <b>Family:</b> Lumazine synthase
76	<a href="#">c1w9iA_</a>		Alignment	not modelled	33.5	20	<b>PDB header:</b> myosin <b>Chain:</b> A: <b>PDB Molecule:</b> myosin ii heavy chain; <b>PDBTitle:</b> myosin ii dictyostelium discoideum motor domain s456y bound2 with mgadp-befx
77	<a href="#">d1j0xo1</a>		Alignment	not modelled	33.3	20	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain <b>PDB header:</b> chaperone

78	<a href="#">c3sf5D_</a>	Alignment	not modelled	33.1	23	<b>Chain:</b> D: <b>PDB Molecule:</b> urease accessory protein ureh; <b>PDBTitle:</b> crystal structure of helicobacter pylori urease accessory protein2 uref/h complex
79	<a href="#">d1lkxa_</a>	Alignment	not modelled	32.8	27	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Motor proteins
80	<a href="#">c2fp3A_</a>	Alignment	not modelled	32.7	12	<b>PDB header:</b> hydrolysis/apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> caspase nc; <b>PDBTitle:</b> crystal structure of the drosophila initiator caspase dronc
81	<a href="#">d2c4va1</a>	Alignment	not modelled	32.6	5	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Type II 3-dehydroquinase dehydratase <b>Family:</b> Type II 3-dehydroquinase dehydratase
82	<a href="#">c5a4nB_</a>	Alignment	not modelled	32.5	5	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> bpsl1147; <b>PDBTitle:</b> crystal structure of bpsl1147, a pc4 homolog from burkholderia2 pseudomallei k96243 (tetragonal crystal form)
83	<a href="#">d1d0xa2</a>	Alignment	not modelled	32.5	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Motor proteins
84	<a href="#">c1x9eB_</a>	Alignment	not modelled	32.1	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> hmg-coa synthase; <b>PDBTitle:</b> crystal structure of hmg-coa synthase from enterococcus2 faecalis
85	<a href="#">c3gjzB_</a>	Alignment	not modelled	31.8	17	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> microcin immunity protein mccf; <b>PDBTitle:</b> crystal structure of microcin immunity protein mccf from bacillus2 anthracis str. ames
86	<a href="#">d1tifa_</a>	Alignment	not modelled	31.2	17	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
87	<a href="#">c5kp0A_</a>	Alignment	not modelled	31.1	25	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> flagellar protein flit,flagellum-specific atp synthase; <b>PDBTitle:</b> recognition and targeting mechanisms by chaperones in flagella2 assembly and operation
88	<a href="#">c3gg9C_</a>	Alignment	not modelled	31.1	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase oxidoreductase protein; <b>PDBTitle:</b> crystal structure of putative d-3-phosphoglycerate dehydrogenase2 oxidoreductase from ralstonia solanacearum
89	<a href="#">c4xkja_</a>	Alignment	not modelled	30.9	21	<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
90	<a href="#">c3pdiG_</a>	Alignment	not modelled	30.1	21	<b>PDB header:</b> protein binding <b>Chain:</b> G: <b>PDB Molecule:</b> nitrogenase mofe cofactor biosynthesis protein nife; <b>PDBTitle:</b> precursor bound nifen
91	<a href="#">c5dteD_</a>	Alignment	not modelled	30.0	12	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> monosaccharide-transporting atpase; <b>PDBTitle:</b> crystal structure of an abc transporter periplasmic solute binding2 protein (ipr025997) from actinobacillus succinogenes 130z(asuc_0081,3 target efi-511065) with bound d-allose
92	<a href="#">c6ch2E_</a>	Alignment	not modelled	30.0	26	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> flagellar hook-associated protein 2,flagellar protein flit; <b>PDBTitle:</b> crystal structure of the cytoplasmic domain of flha and flit-flid2 complex
93	<a href="#">d1nqua_</a>	Alignment	not modelled	29.9	20	<b>Fold:</b> Lumazine synthase <b>Superfamily:</b> Lumazine synthase <b>Family:</b> Lumazine synthase
94	<a href="#">d2a5la1</a>	Alignment	not modelled	29.8	27	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> WrbA-like
95	<a href="#">c5wb4H_</a>	Alignment	not modelled	29.8	14	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> n-acetylglucosaminylidiphosphoundecaprenol n-acetyl-beta-d-glycosyltransferase <b>PDBTitle:</b> crystal structure of the tara wall teichoic acid glycosyltransferase
96	<a href="#">d1u8fo1</a>	Alignment	not modelled	29.6	20	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
97	<a href="#">c2zkiH_</a>	Alignment	not modelled	29.5	16	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> 199aa long hypothetical trp repressor binding <b>PDBTitle:</b> crystal structure of hypothetical trp repressor binding2 protein from sul folobus tokodaii (st0872)
98	<a href="#">c4rxuA_</a>	Alignment	not modelled	28.9	8	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic sugar-binding protein; <b>PDBTitle:</b> crystal structure of carbohydrate transporter solute binding protein2 caur_1924 from chloroflexus aurantiacus, target efi-511158, in3 complex with d-glucose
99	<a href="#">d2dria_</a>	Alignment	not modelled	28.9	14	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
100	<a href="#">d1hdgo1</a>	Alignment	not modelled	28.9	30	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
101	<a href="#">c2q62A_</a>	Alignment	not modelled	28.7	13	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> arsh; <b>PDBTitle:</b> crystal structure of arsh from sinorhizobium meliloti
102	<a href="#">d1t92a_</a>	Alignment	not modelled	28.5	20	<b>Fold:</b> Pili subunits <b>Superfamily:</b> Pili subunits <b>Family:</b> Pseudopilin

103	<a href="#">c3av0A_</a>	Alignment	not modelled	28.2	11	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> dna double-strand break repair protein mre11; <b>PDBTitle:</b> crystal structure of mre11-rad50 bound to atp s
104	<a href="#">c2kwuA_</a>	Alignment	not modelled	27.9	38	<b>PDB header:</b> protein binding/signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iota; <b>PDBTitle:</b> solution structure of ubm2 of murine polymerase iota in complex with2 ubiquitin
105	<a href="#">c4jenB_</a>	Alignment	not modelled	27.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cmp n-glycosidase; <b>PDBTitle:</b> structure of clostridium botulinum cmp n-glycosidase, bcmb
106	<a href="#">c5tkaA_</a>	Alignment	not modelled	27.8	12	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> oxsa protein; <b>PDBTitle:</b> structure of the hd-domain phosphohydrolase oxsa
107	<a href="#">d1t3ta2</a>	Alignment	not modelled	27.7	17	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
108	<a href="#">c3ahyD_</a>	Alignment	not modelled	27.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> crystal structure of beta-glucosidase 2 from fungus trichoderma reesei2 in complex with tris
109	<a href="#">c3jbhA_</a>	Alignment	not modelled	27.0	20	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> myosin 2 heavy chain striated muscle; <b>PDBTitle:</b> two heavy meromyosin interacting-heads motifs flexible docked into2 tarantula thick filament 3d-map allows in depth study of intra- and3 intermolecular interactions
110	<a href="#">d2paqa1</a>	Alignment	not modelled	26.9	20	<b>Fold:</b> HD-domain/PDEase-like <b>Superfamily:</b> HD-domain/PDEase-like <b>Family:</b> HD domain
111	<a href="#">c3il3A_</a>	Alignment	not modelled	26.8	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase 3; <b>PDBTitle:</b> structure of haemophilus influenzae fabh
112	<a href="#">c3sipC_</a>	Alignment	not modelled	26.6	22	<b>PDB header:</b> hydrolase/ligase/hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> caspase; <b>PDBTitle:</b> crystal structure of drice and diap1-bir1 complex
113	<a href="#">c3h5oB_</a>	Alignment	not modelled	26.6	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator gntr; <b>PDBTitle:</b> the crystal structure of transcription regulator gntr from2 chromobacterium violaceum
114	<a href="#">d1qfma2</a>	Alignment	not modelled	26.4	10	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Prolyl oligopeptidase, C-terminal domain
115	<a href="#">d1ggaa1</a>	Alignment	not modelled	26.3	20	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
116	<a href="#">c3huuC_</a>	Alignment	not modelled	26.3	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> transcription regulator like protein; <b>PDBTitle:</b> crystal structure of transcription regulator like protein from2 staphylococcus haemolyticus
117	<a href="#">c2kepA_</a>	Alignment	not modelled	26.0	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> general secretion pathway protein g; <b>PDBTitle:</b> solution structure of xcpt, the main component of the type 22 secretion system of pseudomonas aeruginosa
118	<a href="#">c4fi0A_</a>	Alignment	not modelled	26.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase ald1; <b>PDBTitle:</b> crystal structure of ald1 from arabidopsis thaliana
119	<a href="#">d1gado1</a>	Alignment	not modelled	25.8	30	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
120	<a href="#">c4gxhC_</a>	Alignment	not modelled	25.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> pyrrolidone-carboxylate peptidase; <b>PDBTitle:</b> crystal structure of a pyrrolidone-carboxylate peptidase 1 (target id2 nysgrc-012831) from xenorhabdus bovienii ss-2004