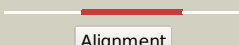



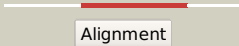



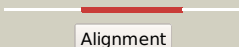



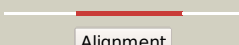



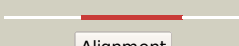





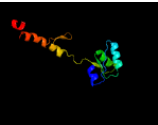





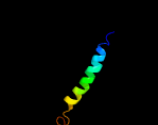
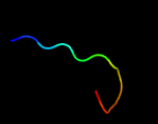
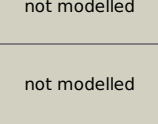


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0822c_(-)_914260_916314
Date	Fri Jul 26 01:50:41 BST 2019
Unique Job ID	2926cdd7e48d350d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3pe5B_</a>	 Alignment		100.0	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> three-dimensional structure of protein a7vv38_9clot from clostridium2 leptum dsm 753, northeast structural genomics consortium target3 qlr103
2	<a href="#">c5v8cA_</a>	 Alignment		100.0	25	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> lytr-csp2a-psr enzyme from actinomyces oris
3	<a href="#">c3okzB_</a>	 Alignment		100.0	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein gbs0355; <b>PDBTitle:</b> crystal structure of protein gbs0355 from streptococcus agalactiae,2 northeast structural genomics consortium target sar127
4	<a href="#">c4de8A_</a>	 Alignment		100.0	23	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> cps2a; <b>PDBTitle:</b> lytr-cps2a-psr family protein with bound octaprenyl monophosphate2 lipid
5	<a href="#">c3qfiA_</a>	 Alignment		100.0	24	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> x-ray crystal structure of transcriptional regulator (ef0465) from2 enterococcus faecalis, northeast structural genomics consortium3 target efr190
6	<a href="#">c3owqB_</a>	 Alignment		100.0	30	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> lin1025 protein; <b>PDBTitle:</b> x-ray structure of lin1025 protein from listeria innocua, northeast2 structural genomics consortium target lkr164
7	<a href="#">c3mejA_</a>	 Alignment		100.0	26	<b>PDB header:</b> transcriptional regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator ywtf; <b>PDBTitle:</b> crystal structure of putative transcriptional regulator ywtf from2 bacillus subtilis, northeast structural genomics consortium target3 sr736
8	<a href="#">c3nroA_</a>	 Alignment		100.0	30	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lmo1026 protein; <b>PDBTitle:</b> crystal structure of putative transcriptional factor lmo1026 from2 listeria monocytogenes (fragment 52-321), northeast structural3 genomics consortium target lmr194
9	<a href="#">c4obmA_</a>	 Alignment		100.0	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative transcription regulator (eubsir_01389)2 from eubacterium siraeum dsm 15702 at 2.15 a resolution
10	<a href="#">c3nxhA_</a>	 Alignment		100.0	22	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator yvhj; <b>PDBTitle:</b> crystal structure of the transcriptional regulator yvhj from bacillus2 subtilis. northeast structural genomics consortium target sr735.
11	<a href="#">c2m5yA_</a>	 Alignment		99.7	22	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative tuberculin related peptide; <b>PDBTitle:</b> solution structure of the c-terminal domain of rv0431

12	<a href="#">c2pjuD</a>	Alignment		87.2	15	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> propionate catabolism operon regulatory protein; <b>PDBTitle:</b> crystal structure of propionate catabolism operon regulatory protein2 prpr
13	<a href="#">c3txsC</a>	Alignment		67.5	18	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> terminase dna packaging enzyme small subunit; <b>PDBTitle:</b> crystal structure of phage 44rr small terminase gp16
14	<a href="#">d1y81a1</a>	Alignment		24.0	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
15	<a href="#">c1oheA</a>	Alignment		22.4	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cdc14b2 phosphatase; <b>PDBTitle:</b> structure of cdc14b phosphatase with a peptide ligand
16	<a href="#">c5j5vC</a>	Alignment		18.1	29	<b>PDB header:</b> toxin <b>Chain:</b> C: <b>PDB Molecule:</b> immunity protein cdii; <b>PDBTitle:</b> cdia-ct from uropathogenic escherichia coli in complex with cognate2 immunity protein and cysk
17	<a href="#">c4ddpA</a>	Alignment		17.3	18	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> beclin-1; <b>PDBTitle:</b> crystal structure of beclin 1 evolutionarily conserved domain(ecd)
18	<a href="#">d1ny8a</a>	Alignment		16.7	24	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> BolA-like <b>Family:</b> BolA-like
19	<a href="#">c6f0kA</a>	Alignment		16.5	9	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c family protein; <b>PDBTitle:</b> alternative complex iii
20	<a href="#">d1gsoa2</a>	Alignment		16.2	25	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
21	<a href="#">d1xjca</a>	Alignment	not modelled	16.1	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
22	<a href="#">c2ppwA</a>	Alignment	not modelled	16.0	11	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> conserved domain protein; <b>PDBTitle:</b> the crystal structure of uncharacterized ribose 5-phosphate isomerase2 rpib from streptococcus pneumoniae
23	<a href="#">d1vkza2</a>	Alignment	not modelled	14.3	17	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
24	<a href="#">d1ohea2</a>	Alignment	not modelled	13.4	20	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Dual specificity phosphatase-like
25	<a href="#">c5iiqA</a>	Alignment	not modelled	12.7	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar transporter chaperone 4; <b>PDBTitle:</b> structure of the spx-ttm domain fragment of the yeast inorganic2 polyphosphate polymerase vtc4 (form b).
26	<a href="#">c5z5bA</a>	Alignment	not modelled	12.7	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-tyrosine phosphatase; <b>PDBTitle:</b> crystal structure of tk-tp in the g95a mutant form
27	<a href="#">c3bnuA</a>	Alignment	not modelled	11.9	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> polyamine oxidase fms1; <b>PDBTitle:</b> crystal structure of polyamine oxidase fms1 from2 saccharomyces cerevisiae in complex with bis-(3s,3's)-3 methylated spermine
28	<a href="#">c4qn9A</a>	Alignment	not modelled	11.7	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acyl-phosphatidylethanolamine-hydrolyzing phospholipase <b>PDBTitle:</b> structure of human nape-pld
						<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar protein sorting-associated

29	<a href="#">c3vp7A_</a>	Alignment	not modelled	11.4	18	protein 30; <b>PDBTitle:</b> crystal structure of the beta-alpha repeated, autophagy-specific2 (bara) domain of vps30/atg6
30	<a href="#">d1tf4a2</a>	Alignment	not modelled	11.3	30	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Carbohydrate-binding domain <b>Family:</b> Cellulose-binding domain family III
31	<a href="#">d2cdqa3</a>	Alignment	not modelled	11.2	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> Aspartokinase allosteric domain-like
32	<a href="#">c4b96A_</a>	Alignment	not modelled	11.1	10	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cellulose binding domain-containing protein; <b>PDBTitle:</b> family 3b carbohydrate-binding module from the biomass2 sensing system of clostridium clariflavum
33	<a href="#">c2duwA_</a>	Alignment	not modelled	10.8	14	<b>PDB header:</b> ligand binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative coa-binding protein; <b>PDBTitle:</b> solution structure of putative coa-binding protein of2 klebsiella pneumoniae
34	<a href="#">c4eccgA_</a>	Alignment	not modelled	10.7	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative iron-regulated protein a; <b>PDBTitle:</b> crystal structure of a putative iron-regulated protein a precursor2 (bdi_2603) from parabacteroides distasonis atcc 8503 at 2.30 a3 resolution
35	<a href="#">c4alnE_</a>	Alignment	not modelled	10.7	13	<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)
36	<a href="#">d2d59a1</a>	Alignment	not modelled	10.0	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
37	<a href="#">c4puiA_</a>	Alignment	not modelled	9.8	24	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> sufe-like protein, chloroplastic; <b>PDBTitle:</b> bola domain of sufe1 from arabidopsis thaliana
38	<a href="#">c3k31B_</a>	Alignment	not modelled	9.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-(acyl-carrier-protein) reductase; <b>PDBTitle:</b> crystal structure of enoyl-(acyl-carrier-protein) reductase from2 anaplasma phagocytophilum in complex with nad at 1.9a resolution
39	<a href="#">c4nk4E_</a>	Alignment	not modelled	9.7	9	<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
40	<a href="#">c4b9cA_</a>	Alignment	not modelled	9.5	30	<b>PDB header:</b> carbohydrate-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> type 3a cellulose-binding domain protein; <b>PDBTitle:</b> biomass sensing modules from putative rsgj-like proteins2 of clostridium thermocellum resemble family 3 carbohydrate-3 binding module of cellulosome
41	<a href="#">c3ff4A_</a>	Alignment	not modelled	9.5	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterized protein chu_1412
42	<a href="#">d1nbca_</a>	Alignment	not modelled	9.4	30	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Carbohydrate-binding domain <b>Family:</b> Cellulose-binding domain family III
43	<a href="#">c3o2eA_</a>	Alignment	not modelled	9.4	29	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> bola-like protein; <b>PDBTitle:</b> crystal structure of a bol-like protein from babesia bovis
44	<a href="#">c3grkE_</a>	Alignment	not modelled	9.4	6	<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
45	<a href="#">c2fgyA_</a>	Alignment	not modelled	9.2	39	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxysome shell polypeptide; <b>PDBTitle:</b> beta carbonic anhydrase from the carboxysomal shell of2 halothiobacillus neapolitanus (csosca)
46	<a href="#">c2dhmA_</a>	Alignment	not modelled	9.2	14	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> protein bola; <b>PDBTitle:</b> solution structure of the bola protein from escherichia coli
47	<a href="#">c2xfgB_</a>	Alignment	not modelled	9.1	20	<b>PDB header:</b> hydrolase/sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> endoglucanase 1; <b>PDBTitle:</b> reassembly and co-crystallization of a family 9 processive2 endoglucanase from separately expressed gh9 and cbm3c3 modules
48	<a href="#">c1u8sB_</a>	Alignment	not modelled	8.9	13	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> glycine cleavage system transcriptional <b>PDBTitle:</b> crystal structure of putative glycine cleavage system2 transcriptional repressor
49	<a href="#">d2hmfa2</a>	Alignment	not modelled	8.8	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> Aspartokinase allosteric domain-like
50	<a href="#">c5ijpA_</a>	Alignment	not modelled	8.8	13	<b>PDB header:</b> inositol phosphate binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of the spx domain of chaetomium thermophilum vtc4 in2 complex with inositol hexakisphosphate (insp6).
51	<a href="#">d1t70a_</a>	Alignment	not modelled	8.8	21	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> DR1281-like
52	<a href="#">c5iitC_</a>	Alignment	not modelled	8.8	13	<b>PDB header:</b> inositol phosphate binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> vacuolar transporter chaperone 4,core histone macro-h2a.1; <b>PDBTitle:</b> structure of spx domain of the yeast inorganic polyphosphate polymerase2 vtc4 crystallized by carrier-driven

						crystallization in fusion with3 the macro domain of human histone macroh2a1.1
53	<a href="#">c1wv9B_</a>	Alignment	not modelled	8.7	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> rhodanese homolog tt1651; <b>PDBTitle:</b> crystal structure of rhodanese homolog tt1651 from an2 extremely thermophilic bacterium thermus thermophilus hb8
54	<a href="#">c5ijjB_</a>	Alignment	not modelled	8.7	24	<b>PDB header:</b> inositol polyphosphate binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> spx domain; <b>PDBTitle:</b> structure of the spx domain of chaetomium thermophilum2 glycerophosphodiester phosphodiesterase 1 in complex with inositol3 hexakisphosphate (insp6)
55	<a href="#">d2z06a1</a>	Alignment	not modelled	8.7	18	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> TTHA0625-like
56	<a href="#">c3i7aA_</a>	Alignment	not modelled	8.7	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative metal-dependent phosphohydrolase; <b>PDBTitle:</b> crystal structure of putative metal-dependent phosphohydrolase2 (yp_926882.1) from shewanella amazonensis sb2b at 2.06 a resolution
57	<a href="#">c6d5bL_</a>	Alignment	not modelled	8.4	20	<b>PDB header:</b> sugar binding protein <b>Chain:</b> L: <b>PDB Molecule:</b> glycoside hydrolase wp_045175321; <b>PDBTitle:</b> structure of caldicellulosiruptor danielii cbm3 module of glycoside2 hydrolase wp_045175321
58	<a href="#">d1iaza_</a>	Alignment	not modelled	8.4	22	<b>Fold:</b> Cytolysin/lectin <b>Superfamily:</b> Cytolysin/lectin <b>Family:</b> Anemone pore-forming cytolysin
59	<a href="#">c2nclA_</a>	Alignment	not modelled	8.4	10	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> bola-like protein 3; <b>PDBTitle:</b> solution structure of bola3 from homo sapiens
60	<a href="#">c2l8aA_</a>	Alignment	not modelled	8.4	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endoglucanase; <b>PDBTitle:</b> structure of a novel cbm3 lacking the calcium-binding site
61	<a href="#">c4pugA_</a>	Alignment	not modelled	8.4	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> bola like protein; <b>PDBTitle:</b> bola1 from arabidopsis thaliana
62	<a href="#">d1g87a2</a>	Alignment	not modelled	8.3	20	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Carbohydrate-binding domain <b>Family:</b> Cellulose-binding domain family III
63	<a href="#">c2o8sA_</a>	Alignment	not modelled	8.3	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> agr_c_984p; <b>PDBTitle:</b> x-ray crystal structure of protein agr_c_984 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr120.
64	<a href="#">c2jb1B_</a>	Alignment	not modelled	8.1	35	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> l-amino acid oxidase; <b>PDBTitle:</b> the l-amino acid oxidase from rhodococcus opacus in complex2 with l-alanine
65	<a href="#">c2xbtA_</a>	Alignment	not modelled	8.0	30	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cellulosomal scaffoldin; <b>PDBTitle:</b> structure of a scaffoldin carbohydrate-binding module family 3b from2 the cellulosome of bacteroides cellulosolvens: structural diversity3 and implications for carbohydrate binding
66	<a href="#">d1vqon1</a>	Alignment	not modelled	8.0	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Translational machinery components <b>Family:</b> Ribosomal protein L18 and S11
67	<a href="#">c4q9nD_</a>	Alignment	not modelled	7.9	9	<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-acyl reductase (fabI)2 in complex with nadh and afn-1252
68	<a href="#">d1fnna1</a>	Alignment	not modelled	7.9	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Helicase DNA-binding domain
69	<a href="#">c2ozeA_</a>	Alignment	not modelled	7.9	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> orf delta'; <b>PDBTitle:</b> the crystal structure of delta protein of psm19035 from2 streptococcus pyogenes
70	<a href="#">c3l76B_</a>	Alignment	not modelled	7.9	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartokinase; <b>PDBTitle:</b> crystal structure of aspartate kinase from synechocystis
71	<a href="#">c2e1mA_</a>	Alignment	not modelled	7.7	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-glutamate oxidase; <b>PDBTitle:</b> crystal structure of l-glutamate oxidase from streptomyces sp. x-119-6
72	<a href="#">c2n5iA_</a>	Alignment	not modelled	7.6	19	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> peptidyl carrier protein pltI; <b>PDBTitle:</b> pltI-pyrrolyl
73	<a href="#">d1v86a_</a>	Alignment	not modelled	7.4	31	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
74	<a href="#">c5xw4A_</a>	Alignment	not modelled	7.3	11	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein phosphatase cdc14; <b>PDBTitle:</b> crystal structure of budding yeast cdc14p (wild type) in the apo state
75	<a href="#">c5nfmA_</a>	Alignment	not modelled	7.3	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> yrba; <b>PDBTitle:</b> crystal structure of yrba from sinorhizobium melliloti in complex with2 copper.
76	<a href="#">c2qnwA_</a>	Alignment	not modelled	7.2	19	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> toxoplasma gondii apicoplast-targeted acyl carrier protein
77	<a href="#">d1iuKa_</a>	Alignment	not modelled	7.0	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains

						<b>Family:</b> CoA-binding domain
78	<a href="#">c2yIkD_</a>	Alignment	not modelled	6.9	10	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> cellulose 1,4-beta-cellobiosidase; <b>PDBTitle:</b> carbohydrate-binding module cbm3b from the cellulosomal2 cellobiohydrolase 9a from clostridium thermocellum
79	<a href="#">c2yg4B_</a>	Alignment	not modelled	6.9	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putrescine oxidase; <b>PDBTitle:</b> structure-based redesign of cofactor binding in putrescine2 oxidase: wild type bound to putrescine
80	<a href="#">c3gdfA_</a>	Alignment	not modelled	6.9	22	<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 cladospirium herbarum.
81	<a href="#">c1b22A_</a>	Alignment	not modelled	6.8	31	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair protein rad51; <b>PDBTitle:</b> rad51 (n-terminal domain)
82	<a href="#">d1b22a_</a>	Alignment	not modelled	6.8	31	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> Rad51 N-terminal domain-like <b>Family:</b> DNA repair protein Rad51, N-terminal domain
83	<a href="#">d1f80d_</a>	Alignment	not modelled	6.8	16	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> ACP-like <b>Family:</b> Acyl-carrier protein (ACP)
84	<a href="#">d1e6ya2</a>	Alignment	not modelled	6.7	23	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Methyl-coenzyme M reductase subunits <b>Family:</b> Methyl-coenzyme M reductase alpha and beta chain N-terminal domain
85	<a href="#">c3ce7A_</a>	Alignment	not modelled	6.6	10	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> specific mitochondrial acyl carrier protein; <b>PDBTitle:</b> crystal structure of toxoplasma specific mitochondrial acyl carrier2 protein, 59.m03510
86	<a href="#">c2mm9A_</a>	Alignment	not modelled	6.6	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> bola2; <b>PDBTitle:</b> solution structure of reduced bola2 from arabidopsis thaliana
87	<a href="#">c2f06B_</a>	Alignment	not modelled	6.6	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> crystal structure of protein bt0572 from bacteroides thetaiotaomicron
88	<a href="#">c4m87B_</a>	Alignment	not modelled	6.6	6	<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+
89	<a href="#">c1n7sB_</a>	Alignment	not modelled	6.5	17	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> syntaxin 1a; <b>PDBTitle:</b> high resolution structure of a truncated neuronal snare complex
90	<a href="#">c3un1D_</a>	Alignment	not modelled	6.5	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> probable oxidoreductase; <b>PDBTitle:</b> crystal structure of an oxidoreductase from sinorhizobium meliloti2 1021
91	<a href="#">d2voua1</a>	Alignment	not modelled	6.5	24	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
92	<a href="#">c2zuaA_</a>	Alignment	not modelled	6.5	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lacto-n-biose phosphorylase; <b>PDBTitle:</b> crystal structure of galacto-n-biose/lacto-n-biose i phosphorylase in2 complex with glcnaC
93	<a href="#">c4iyrB_</a>	Alignment	not modelled	6.4	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> caspase-6; <b>PDBTitle:</b> crystal structure of full-length caspase-6 zymogen
94	<a href="#">c2lfvA_</a>	Alignment	not modelled	6.4	8	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> protein damx; <b>PDBTitle:</b> solution structure of the spor domain from e. coli damx
95	<a href="#">c1v60A_</a>	Alignment	not modelled	6.4	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> riken cdna 1810037g04; <b>PDBTitle:</b> solution structure of bola1 protein from mus musculus
96	<a href="#">c5ldgA_</a>	Alignment	not modelled	6.4	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> (-)-isopiperitenone reductase; <b>PDBTitle:</b> isopiperitenone reductase from mentha piperita in complex with2 isopiperitenone and nadp
97	<a href="#">c3gr6A_</a>	Alignment	not modelled	6.3	13	<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
98	<a href="#">c5y4bA_</a>	Alignment	not modelled	6.3	5	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> bola-like protein 2; <b>PDBTitle:</b> solution structure of yeast fra2
99	<a href="#">c4ne4A_</a>	Alignment	not modelled	6.3	19	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter, substrate binding protein <b>PDBTitle:</b> crystal structure of abc transporter substrate binding protein prox2 from agrobacterium tumefaciens cocrystallized with btb