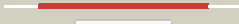



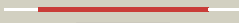

















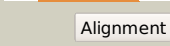

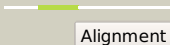
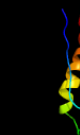
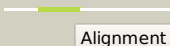
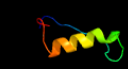

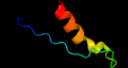

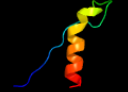
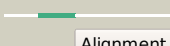
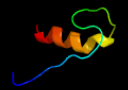
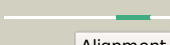
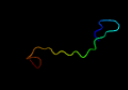
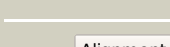

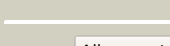

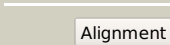
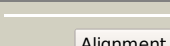
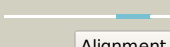



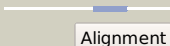
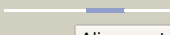


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1014c_(pth)_1133337_1133912
Date	Wed Jul 31 22:05:08 BST 2019
Unique Job ID	5a09030df92dc694

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2mj1A_</a>	 Alignment		100.0	37	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidyl-trna hydrolase; <b>PDBTitle:</b> solution structure of peptidyl-trna hydrolase from vibrio cholerae
2	<a href="#">c4dhwA_</a>	 Alignment		100.0	36	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidyl-trna hydrolase; <b>PDBTitle:</b> crystal structure of peptidyl-trna hydrolase from pseudomonas2 aeruginosa with adipic acid at 2.4 angstrom resolution
3	<a href="#">d2ptha_</a>	 Alignment		100.0	40	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Peptidyl-tRNA hydrolase-like <b>Family:</b> Peptidyl-tRNA hydrolase-like
4	<a href="#">c4fopA_</a>	 Alignment		100.0	39	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidyl-trna hydrolase; <b>PDBTitle:</b> crystal structure of peptidyl-trna hydrolase from acinetobacter2 baumannii at 1.86 a resolution
5	<a href="#">c2z2jA_</a>	 Alignment		100.0	100	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidyl-trna hydrolase; <b>PDBTitle:</b> crystal structure of peptidyl-trna hydrolase from mycobacterium2 tuberculosis
6	<a href="#">c4q55B_</a>	 Alignment		100.0	31	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> peptidyl-trna hydrolase; <b>PDBTitle:</b> crystal structure of peptidyl-trna hydrolase from a gram-positive2 bacterium, streptococcus pyogenes at 2.19a resolution shows the3 closed structure of the substrate binding cleft
7	<a href="#">c3neaA_</a>	 Alignment		100.0	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidyl-trna hydrolase; <b>PDBTitle:</b> crystal structure of peptidyl-trna hydrolase from francisella2 tularensis
8	<a href="#">c3v2iA_</a>	 Alignment		100.0	40	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidyl-trna hydrolase; <b>PDBTitle:</b> structure of a peptidyl-trna hydrolase (pth) from burkholderia2 thailandensis
9	<a href="#">c4lylB_</a>	 Alignment		100.0	37	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> peptidyl-trna hydrolase; <b>PDBTitle:</b> crystal structure of peptidyl-trna hydrolase from a gram-positive2 bacterium, staphylococcus aureus at 2.25 angstrom resolution
10	<a href="#">d1ryba_</a>	 Alignment		100.0	43	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Peptidyl-tRNA hydrolase-like <b>Family:</b> Peptidyl-tRNA hydrolase-like
11	<a href="#">c5zx8A_</a>	 Alignment		100.0	44	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidyl-trna hydrolase; <b>PDBTitle:</b> crystal structure of peptidyl-trna hydrolase from thermus thermophilus

12	<a href="#">d1c8ba_</a>	 Alignment		81.6	25	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> HybD-like <b>Family:</b> Germination protease
13	<a href="#">d1cfza_</a>	 Alignment		67.8	27	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> HybD-like <b>Family:</b> Hydrogenase maturing endopeptidase HybD
14	<a href="#">c2e85B_</a>	 Alignment		67.7	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hydrogenase 3 maturation protease; <b>PDBTitle:</b> crystal structure of the hydrogenase 3 maturation protease
15	<a href="#">c5zbyA_</a>	 Alignment		65.1	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase maturation protease hyci; <b>PDBTitle:</b> crystal structure of a [nife] hydrogenase maturation protease hyci2 from thermococcus kodakarensis kod1
16	<a href="#">c5ijaB_</a>	 Alignment		52.2	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hydrogenase-specific maturation endopeptidase; <b>PDBTitle:</b> [nife] hydrogenase maturation protease hybd from thermococcus2 kodakarensis
17	<a href="#">c5ttxB_</a>	 Alignment		48.5	36	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hydrogenase 2 maturation peptidase; <b>PDBTitle:</b> crystal structure of hydrogenase 2 maturation peptidase from2 thaumarchaeota archaeon scgc_ab-539-e09
18	<a href="#">c2jvaA_</a>	 Alignment		41.1	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidyl-trna hydrolase domain protein; <b>PDBTitle:</b> nmr solution structure of peptidyl-trna hydrolase domain protein from2 pseudomonas syringae pv. tomato. northeast structural genomics3 consortium target psr211
19	<a href="#">d2ea9a1</a>	 Alignment		41.1	17	<b>Fold:</b> Profilin-like <b>Superfamily:</b> YeeU-like <b>Family:</b> YagB/YeeU/YfjZ-like
20	<a href="#">d2inwa1</a>	 Alignment		38.0	14	<b>Fold:</b> Profilin-like <b>Superfamily:</b> YeeU-like <b>Family:</b> YagB/YeeU/YfjZ-like
21	<a href="#">d2h28a1</a>	 Alignment	not modelled	36.6	17	<b>Fold:</b> Profilin-like <b>Superfamily:</b> YeeU-like <b>Family:</b> YagB/YeeU/YfjZ-like
22	<a href="#">c3tgnA_</a>	 Alignment	not modelled	34.9	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> adc operon repressor adcr; <b>PDBTitle:</b> crystal structure of the zinc-dependent marr family transcriptional2 regulator adcr in the zn(ii)-bound state
23	<a href="#">c2jy9A_</a>	 Alignment	not modelled	33.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative trna hydrolase domain; <b>PDBTitle:</b> nmr structure of putative trna hydrolase domain from2 salmonella typhimurium. northeast structural genomics3 consortium target str220
24	<a href="#">c3mpoD_</a>	 Alignment	not modelled	28.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> predicted hydrolase of the had superfamily; <b>PDBTitle:</b> the crystal structure of a hydrolase from lactobacillus brevis
25	<a href="#">c6ar6A_</a>	 Alignment	not modelled	28.2	25	<b>PDB header:</b> toxin/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> toxin b; <b>PDBTitle:</b> clostridioides difficile toxinb with dld-4 darpin
26	<a href="#">c3ippA_</a>	 Alignment	not modelled	27.2	6	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative thiosulfate sulfurtransferase ynje; <b>PDBTitle:</b> crystal structure of sulfur-free ynje
27	<a href="#">c3gygA_</a>	 Alignment	not modelled	26.4	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ntd biosynthesis operon putative hydrolase ntdb; <b>PDBTitle:</b> crystal structure of yhjk (haloacid dehalogenase-like hydrolase2 protein) from bacillus subtilis
28	<a href="#">c6h98A</a>	 Alignment	not modelled	23.9	6	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfurtransferase;

28	<a href="#">c1h26A_</a>	Alignment	not modelled	23.9	0	<b>PDBTitle:</b> native crystal structure of anaerobic ergothioneine biosynthesis2 enzyme from chlorobium limicola. <b>PDB header:</b> transferase
29	<a href="#">c2bb3B_</a>	Alignment	not modelled	23.7	23	<b>Chain:</b> B; <b>PDB Molecule:</b> cobalamin biosynthesis precorrin-6y methylase (cbie); <b>PDBTitle:</b> crystal structure of cobalamin biosynthesis precorrin-6y methylase2 (cbie) from archaeoglobus fulgidus
30	<a href="#">d2nqra3</a>	Alignment	not modelled	20.9	18	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like
31	<a href="#">c1ujjA_</a>	Alignment	not modelled	20.8	18	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> potassium voltage-gated channel subfamily h <b>PDBTitle:</b> solution structure of the herg k+ channel s5-p2 extracellular linker
32	<a href="#">c3ktdC_</a>	Alignment	not modelled	20.5	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> prephenate dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative prephenate dehydrogenase (cg10226)2 from corynebacterium glutamicum atcc 13032 at 2.60 a resolution
33	<a href="#">c6fc1B_</a>	Alignment	not modelled	19.9	32	<b>PDB header:</b> translation <b>Chain:</b> B; <b>PDB Molecule:</b> protein eap1; <b>PDBTitle:</b> crystal structure of the eif4e-eap1p complex from saccharomyces2 cerevisiae in the cap-bound state
34	<a href="#">c5yhxH_</a>	Alignment	not modelled	19.7	12	<b>PDB header:</b> metal binding protein <b>Chain:</b> H; <b>PDB Molecule:</b> zinc transport transcriptional regulator; <b>PDBTitle:</b> structure of lactococcus lactis zittr, wild type
35	<a href="#">c1ynmA_</a>	Alignment	not modelled	19.5	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> r.hinp1i restriction endonuclease; <b>PDBTitle:</b> crystal structure of restriction endonuclease hinp1i
36	<a href="#">c3hzuA_</a>	Alignment	not modelled	19.5	27	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> thiosulfate sulfurtransferase ssea; <b>PDBTitle:</b> crystal structure of probable thiosulfate sulfurtransferase ssea2 (rhodanese) from mycobacterium tuberculosis
37	<a href="#">c3bj6B_</a>	Alignment	not modelled	18.3	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> B; <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of marr family transcription regulator sp03579
38	<a href="#">d3eeqa2</a>	Alignment	not modelled	17.6	20	<b>Fold:</b> CbiG N-terminal domain-like <b>Superfamily:</b> CbiG N-terminal domain-like <b>Family:</b> CbiG N-terminal domain-like
39	<a href="#">c4aq2l_</a>	Alignment	not modelled	17.0	14	<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
40	<a href="#">c5g2rA_</a>	Alignment	not modelled	16.3	18	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> molybdopterin biosynthesis protein cnx1; <b>PDBTitle:</b> crystal structure of the mo-insertase domain cnx1e from2 arabidopsis thaliana
41	<a href="#">c3utnX_</a>	Alignment	not modelled	16.2	19	<b>PDB header:</b> transferase <b>Chain:</b> X; <b>PDB Molecule:</b> thiosulfate sulfurtransferase tum1; <b>PDBTitle:</b> crystal structure of tum1 protein from saccharomyces cerevisiae
42	<a href="#">c3kp3B_</a>	Alignment	not modelled	16.0	14	<b>PDB header:</b> transcription regulator/antibiotic <b>Chain:</b> B; <b>PDB Molecule:</b> transcriptional regulator tcar; <b>PDBTitle:</b> staphylococcus epidermidis in complex with ampicillin
43	<a href="#">d1am7a_</a>	Alignment	not modelled	15.1	17	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> Lambda lysozyme
44	<a href="#">d2bb3a1</a>	Alignment	not modelled	14.8	29	<b>Fold:</b> Tetrapyrrole methylase <b>Superfamily:</b> Tetrapyrrole methylase <b>Family:</b> Tetrapyrrole methylase
45	<a href="#">c3e8mD_</a>	Alignment	not modelled	14.6	19	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> acylneuraminate cytidylyltransferase; <b>PDBTitle:</b> structure-function analysis of 2-keto-3-deoxy-d-glycero-d-galacto-2 nononate-9-phosphate (kdn) phosphatase defines a new clad within the3 type c0 had subfamily
46	<a href="#">c5jlsA_</a>	Alignment	not modelled	14.3	24	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> adhesin competence repressor; <b>PDBTitle:</b> crystal structure of adhesin competence repressor (adcr) from2 streptococcus pyogenes (c-terminally his tagged)
47	<a href="#">c4uz2D_</a>	Alignment	not modelled	14.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> cell wall-binding endopeptidase-related protein; <b>PDBTitle:</b> crystal structure of the n-terminal lysm domains from the putative2 nlp/p60 d,l endopeptidase from t. thermophilus
48	<a href="#">c3wz2C_</a>	Alignment	not modelled	13.7	23	<b>PDB header:</b> chaperone <b>Chain:</b> C; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of pyrococcus furiosus pbaa, an archaeal homolog of2 proteasome-assembly chaperone
49	<a href="#">d1lama2</a>	Alignment	not modelled	13.7	30	<b>Fold:</b> Macro domain-like <b>Superfamily:</b> Macro domain-like <b>Family:</b> Leucine aminopeptidase (Aminopeptidase A), N-terminal domain
50	<a href="#">c3n1uA_</a>	Alignment	not modelled	13.5	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> hydrolase, had superfamily, subfamily iii a; <b>PDBTitle:</b> structure of putative had superfamily (subfamily iii a) hydrolase from2 legionella pneumophila
51	<a href="#">d2bgxa2</a>	Alignment	not modelled	13.4	27	<b>Fold:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Superfamily:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Family:</b> N-acetylmuramoyl-L-alanine amidase-like
52	<a href="#">d1s2oa1</a>	Alignment	not modelled	13.2	19	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
53	<a href="#">c3s2wB_</a>	Alignment	not modelled	13.1	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> B; <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> the crystal structure of a marr transcriptional regulator

						from2 methanosarcina mazei go1
54	<a href="#">c3vdoB_</a>	Alignment	not modelled	13.0	11	<b>PDB header:</b> dna binding protein/protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> anti-sigma-k factor rskA; <b>PDBTitle:</b> structure of extra-cytoplasmic function(ecf) sigma factor sigk in2 complex with its negative regulator rskA from mycobacterium3 tuberculosis
55	<a href="#">d1bofa2</a>	Alignment	not modelled	12.7	38	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
56	<a href="#">c3bpgD_</a>	Alignment	not modelled	12.6	36	<b>PDB header:</b> toxin <b>Chain:</b> D: <b>PDB Molecule:</b> toxin rele3; <b>PDBTitle:</b> crystal structure of relb-rele antitoxin-toxin complex from2 methanococcus jannaschii
57	<a href="#">c3av6A_</a>	Alignment	not modelled	12.2	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna (cytosine-5)-methyltransferase 1; <b>PDBTitle:</b> crystal structure of mouse dna methyltransferase 1 with adomet
58	<a href="#">c1uarA_</a>	Alignment	not modelled	11.9	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rhodanese; <b>PDBTitle:</b> crystal structure of rhodanese from thermus thermophilus hb8
59	<a href="#">c3ecoB_</a>	Alignment	not modelled	11.3	3	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> mepr; <b>PDBTitle:</b> crystal structure of mepr, a transcription regulator of the2 staphylococcus aureus multidrug efflux pump mepa
60	<a href="#">c2jcyA_</a>	Alignment	not modelled	11.3	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 1-deoxy-d-xylulose 5-phosphate reductoisomerase; <b>PDBTitle:</b> x-ray structure of mutant 1-deoxy-d-xylulose 5-phosphate2 reductoisomerase, dxr, rv2870c, from mycobacterium tuberculosis
61	<a href="#">c6alyA_</a>	Alignment	not modelled	11.1	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> mediator of rna polymerase ii transcription subunit 15; <b>PDBTitle:</b> solution structure of yeast med15 abd2 residues 277-368
62	<a href="#">d2al3a1</a>	Alignment	not modelled	11.0	9	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> UBX domain
63	<a href="#">c4ol9A_</a>	Alignment	not modelled	10.7	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative 2-dehydropantoate 2-reductase; <b>PDBTitle:</b> crystal structure of putative 2-dehydropantoate 2-reductase pane from2 mycobacterium tuberculosis complexed with nadp and oxamate
64	<a href="#">c2p9jH_</a>	Alignment	not modelled	10.5	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> H: <b>PDB Molecule:</b> hypothetical protein aq2171; <b>PDBTitle:</b> crystal structure of aq2171 from aquifex aeolicus
65	<a href="#">c1uz5A_</a>	Alignment	not modelled	10.3	23	<b>PDB header:</b> molybdopterin biosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> 402aa long hypothetical molybdopterin <b>PDBTitle:</b> the crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikoshii
66	<a href="#">c5t57A_</a>	Alignment	not modelled	10.3	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> semialdehyde dehydrogenase nad-binding protein; <b>PDBTitle:</b> crystal structure of a semialdehyde dehydrogenase nad-binding protein2 from cupriavidus necator in complex with calcium and nad
67	<a href="#">d2etha1</a>	Alignment	not modelled	10.2	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
68	<a href="#">c2bh7A_</a>	Alignment	not modelled	9.9	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylmuramoyl-l-alanine amidase; <b>PDBTitle:</b> crystal structure of a semet derivative of amid at 2.22 angstroms
69	<a href="#">d1k47a2</a>	Alignment	not modelled	9.8	7	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GHMP Kinase, C-terminal domain <b>Family:</b> Phosphomevalonate kinase (PMK)
70	<a href="#">c6oq5A_</a>	Alignment	not modelled	9.8	25	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> toxin b; <b>PDBTitle:</b> structure of the full-length clostridium difficile toxin b in complex2 with 3 vhhs
71	<a href="#">c3mn1B_</a>	Alignment	not modelled	9.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable yrbi family phosphatase; <b>PDBTitle:</b> crystal structure of probable yrbi family phosphatase from pseudomonas2 syringae pv.phaseolica 1448a
72	<a href="#">c4r04A_</a>	Alignment	not modelled	9.4	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> toxin a; <b>PDBTitle:</b> clostridium difficile toxin a (tcda)
73	<a href="#">d1s3ja_</a>	Alignment	not modelled	9.2	28	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
74	<a href="#">c3fzqA_</a>	Alignment	not modelled	9.1	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative hydrolase; <b>PDBTitle:</b> crystal structure of putative haloacid dehalogenase-like hydrolase2 (yp_001086940.1) from clostridium difficile 630 at 2.10 a resolution
75	<a href="#">d1k1ea_</a>	Alignment	not modelled	9.0	23	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Probable phosphatase Yrbl
76	<a href="#">c1okqA_</a>	Alignment	not modelled	8.7	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> possible 3-mercaptopyruvate sulfurtransferase; <b>PDBTitle:</b> 3-mercaptopyruvate sulfurtransferase from leishmania major
77	<a href="#">c3rfqC_</a>	Alignment	not modelled	8.6	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> C: <b>PDB Molecule:</b> pterin-4-alpha-carbinolamine dehydratase moab2; <b>PDBTitle:</b> crystal structure of pterin-4-alpha-carbinolamine

						dehydratase moab22 from mycobacterium marinum <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glycerol-3-phosphate dehydrogenase [nad(p)+]; <b>PDBTitle:</b> 2.1 angstrom resolution crystal structure of glycerol-3-phosphate2 dehydrogenase (gpsa) from coxiella burnetii
78	<a href="#">c3k96B_</a>	Alignment	not modelled	8.6	28	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase subunit gamma-1; <b>PDBTitle:</b> structural basis for processivity and antiviral drug toxicity in human2 mitochondrial dna replicase
79	<a href="#">c4ztuA_</a>	Alignment	not modelled	8.5	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> pcav transcriptional regulator; <b>PDBTitle:</b> crystal structure of the pcav transcriptional regulator from2 streptomyces coelicolor in complex with its natural ligand
80	<a href="#">c4fhtA_</a>	Alignment	not modelled	8.5	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein xcc279; <b>PDBTitle:</b> crystal structure of hypothetical protein xcc2798 from xanthomonas2 campestris, target efi-508608
81	<a href="#">c4navB_</a>	Alignment	not modelled	8.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ampdh2; <b>PDBTitle:</b> crystal structure of ampdh2 from pseudomonas aeruginosa in2 complex with pentapeptide
82	<a href="#">c4bolA_</a>	Alignment	not modelled	8.3	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ampdh2; <b>PDBTitle:</b> crystal structure of ampdh2 from pseudomonas aeruginosa in2 complex with pentapeptide
83	<a href="#">d3broa1</a>	Alignment	not modelled	8.2	7	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
84	<a href="#">c5cvoA_</a>	Alignment	not modelled	8.1	23	<b>PDB header:</b> hydrolase/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> wd repeat-containing protein 48; <b>PDBTitle:</b> wdr48:usp46~ubiquitin ternary complex
85	<a href="#">c4bndB_</a>	Alignment	not modelled	8.1	16	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-phosphoglucomutase; <b>PDBTitle:</b> structure of an atypical alpha-phosphoglucomutase similar to2 eukaryotic phosphomannomutases
86	<a href="#">c6czlA_</a>	Alignment	not modelled	8.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> atp phosphoribosyltransferase catalytic subunit; <b>PDBTitle:</b> crystal structure of medicago truncatula atp-phosphoribosyltransferase2 in relaxed form
87	<a href="#">d1fima_</a>	Alignment	not modelled	7.9	17	<b>Fold:</b> Tautomerase/MIF <b>Superfamily:</b> Tautomerase/MIF <b>Family:</b> MIF-related
88	<a href="#">c6jbxB_</a>	Alignment	not modelled	7.8	13	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid biosynthesis transcriptional regulator; <b>PDBTitle:</b> crystal structure of streptococcus pneumoniae fabt in complex with dna
89	<a href="#">c3oopA_</a>	Alignment	not modelled	7.8	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin2960 protein; <b>PDBTitle:</b> the structure of a protein with unknown function from listeria innocua2 clip11262
90	<a href="#">d1kmma1</a>	Alignment	not modelled	7.7	15	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> Class II aaRS ABD-related <b>Family:</b> Anticodon-binding domain of Class II aaRS
91	<a href="#">d1wdea_</a>	Alignment	not modelled	7.6	40	<b>Fold:</b> Tetrapyrrole methylase <b>Superfamily:</b> Tetrapyrrole methylase <b>Family:</b> Tetrapyrrole methylase
92	<a href="#">c3ikmD_</a>	Alignment	not modelled	7.4	22	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> dna polymerase subunit gamma-1; <b>PDBTitle:</b> crystal structure of human mitochondrial dna polymerase holoenzyme
93	<a href="#">c3boqB_</a>	Alignment	not modelled	7.4	10	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of marr family transcriptional regulator from2 silicibacter pomeroyi
94	<a href="#">c2r8zC_</a>	Alignment	not modelled	7.4	27	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> 3-deoxy-d-manno-octulosonate 8-phosphate phosphatase; <b>PDBTitle:</b> crystal structure of yrbi phosphatase from escherichia coli in complex2 with a phosphate and a calcium ion
95	<a href="#">c3kbqA_</a>	Alignment	not modelled	7.4	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein ta0487; <b>PDBTitle:</b> the crystal structure of the protein cina with unknown function from2 thermoplasma acidophilum
96	<a href="#">c3ihtB_</a>	Alignment	not modelled	7.3	40	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> s-adenosyl-l-methionine methyl transferase; <b>PDBTitle:</b> crystal structure of s-adenosyl-l-methionine methyl transferase2 (yp_165822.1) from silicibacter pomeroyi dss-3 at 1.80 a resolution
97	<a href="#">c2avxA_</a>	Alignment	not modelled	7.3	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein sdia; <b>PDBTitle:</b> solution structure of e coli sdia1-171
98	<a href="#">c2abyA_</a>	Alignment	not modelled	7.2	22	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ta0743; <b>PDBTitle:</b> solution structure of ta0743 from thermoplasma acidophilum
99	<a href="#">c2cukC_</a>	Alignment	not modelled	7.2	35	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glycerate dehydrogenase/glyoxylate reductase; <b>PDBTitle:</b> crystal structure of tt0316 protein from thermus thermophilus hb8