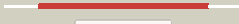



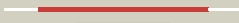


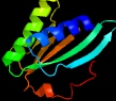



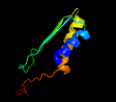







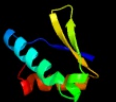


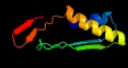
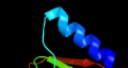

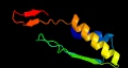
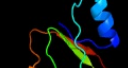






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2420c (- )_2717806_2718186
Date	Wed Aug 7 12:50:04 BST 2019
Unique Job ID	4855e2830b864732

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4wcvB_</a>	 Alignment		100.0	99	<b>PDB header:</b> translation <b>Chain:</b> B; <b>PDB Molecule:</b> ribosomal silencing factor rsfs; <b>PDBTitle:</b> ribosomal silencing factor during starvation or stationary phase2 (rsfs) from mycobacterium tuberculosis
2	<a href="#">d2id1a1</a>	 Alignment		100.0	28	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> lojap/YbeB-like
3	<a href="#">c3upsA_</a>	 Alignment		100.0	29	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> iojap-like protein; <b>PDBTitle:</b> crystal structure of iojap-like protein from zymomonas mobilis
4	<a href="#">d2o5aa1</a>	 Alignment		100.0	34	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> lojap/YbeB-like
5	<a href="#">c5oomu_</a>	 Alignment		100.0	25	<b>PDB header:</b> ribosome <b>Chain:</b> U; <b>PDB Molecule:</b> 39s ribosomal protein l23, mitochondrial; <b>PDBTitle:</b> structure of a native assembly intermediate of the human mitochondrial l2 ribosome with unfolded interfacial rrna
6	<a href="#">c2omdB_</a>	 Alignment		66.0	15	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> molybdopterin-converting factor subunit 2; <b>PDBTitle:</b> crystal structure of molybdopterin converting factor subunit 22 (aq_2181) from aquifex aeolicus vf5
7	<a href="#">d1n0ua4</a>	 Alignment		47.2	11	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> EF-G C-terminal domain-like <b>Family:</b> EF-G/eEF-2 domains III and V
8	<a href="#">d1ex9a_</a>	 Alignment		43.6	25	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Bacterial lipase
9	<a href="#">d2dy1a4</a>	 Alignment		37.0	8	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> EF-G C-terminal domain-like <b>Family:</b> EF-G/eEF-2 domains III and V
10	<a href="#">d2bm0a4</a>	 Alignment		33.8	8	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> EF-G C-terminal domain-like <b>Family:</b> EF-G/eEF-2 domains III and V
11	<a href="#">c5z58C_</a>	 Alignment		32.9	14	<b>PDB header:</b> splicing <b>Chain:</b> C; <b>PDB Molecule:</b> 116 kda u5 small nuclear ribonucleoprotein component; <b>PDBTitle:</b> cryo-em structure of a human activated spliceosome (early bact) at 4.92 angstrom.

12	<a href="#">c2qieA_</a>	Alignment		26.7	11	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> molybdopterin-converting factor subunit 2; <b>PDBTitle:</b> staphylococcus aureus molybdopterin synthase in complex with precursor2 z
13	<a href="#">c3fniA_</a>	Alignment		25.1	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> putative diflavin flavoprotein a 3; <b>PDBTitle:</b> crystal structure of a diflavin flavoprotein a3 (all3895) from nostoc2 sp., northeast structural genomics consortium target nsr431a
14	<a href="#">c3b8hA_</a>	Alignment		24.8	11	<b>PDB header:</b> biosynthetic protein/transferase <b>Chain:</b> A; <b>PDB Molecule:</b> elongation factor 2; <b>PDBTitle:</b> structure of the eef2-exoa(e546a)-nad+ complex
15	<a href="#">d1fm0e_</a>	Alignment		24.5	17	<b>Fold:</b> alpha/beta-Hammerhead <b>Superfamily:</b> Molybdopterin synthase subunit MoaE <b>Family:</b> Molybdopterin synthase subunit MoaE
16	<a href="#">c3hlyA_</a>	Alignment		24.1	11	<b>PDB header:</b> flavoprotein <b>Chain:</b> A; <b>PDB Molecule:</b> flavodoxin-like domain; <b>PDBTitle:</b> crystal structure of the flavodoxin-like domain from synechococcus sp2 q5mzp6_syp6 protein. northeast structural genomics consortium target3 snr135d.
17	<a href="#">d1lk5a2</a>	Alignment		23.7	8	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> D-ribose-5-phosphate isomerase (RpiA), lid domain <b>Family:</b> D-ribose-5-phosphate isomerase (RpiA), lid domain
18	<a href="#">c6jc0D_</a>	Alignment		23.4	16	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> putative molybdenum cofactor biosynthesis protein; <b>PDBTitle:</b> structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
19	<a href="#">c5mqfB_</a>	Alignment		22.9	14	<b>PDB header:</b> splicing <b>Chain:</b> B; <b>PDB Molecule:</b> 116 kda u5 small nuclear ribonucleoprotein component; <b>PDBTitle:</b> cryo-em structure of a human spliceosome activated for step 2 of2 splicing (c* complex)
20	<a href="#">c3jb9B_</a>	Alignment		22.3	14	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> B; <b>PDB Molecule:</b> pre-mrna-splicing factor cwf10; <b>PDBTitle:</b> cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution
21	<a href="#">d1vmea1</a>	Alignment	not modelled	22.1	9	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
22	<a href="#">c2xexA_</a>	Alignment	not modelled	21.8	3	<b>PDB header:</b> translation <b>Chain:</b> A; <b>PDB Molecule:</b> elongation factor g; <b>PDBTitle:</b> crystal structure of staphylococcus aureus elongation factor2 g
23	<a href="#">c6jbcC_</a>	Alignment	not modelled	21.2	15	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> molybdenum cofactor biosynthesis protein e; <b>PDBTitle:</b> structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
24	<a href="#">c3j38z_</a>	Alignment	not modelled	20.7	11	<b>PDB header:</b> ribosome <b>Chain:</b> Z; <b>PDB Molecule:</b> 40s ribosomal protein s25; <b>PDBTitle:</b> structure of the d. melanogaster 40s ribosomal proteins
25	<a href="#">d1e4ea1</a>	Alignment	not modelled	18.5	16	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> D-Alanine ligase N-terminal domain
26	<a href="#">c2pjmA_</a>	Alignment	not modelled	17.6	14	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> structure of ribose 5-phosphate isomerase a from2 methanocaldococcus jannaschii
27	<a href="#">d1xpja_</a>	Alignment	not modelled	17.5	16	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Hypothetical protein VC0232
28	<a href="#">d2arka1</a>	Alignment	not modelled	16.1	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> WrbA-like

29	<a href="#">d1e5da1</a>	Alignment	not modelled	16.1	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
30	<a href="#">c6h0cA</a>	Alignment	not modelled	16.1	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative diflavin flavoprotein a 3; <b>PDBTitle:</b> flv1 flavodiiron core from synechocystis sp. pcc6803
31	<a href="#">c4gmkB</a>	Alignment	not modelled	16.1	16	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> crystal structure of ribose 5-phosphate isomerase from the probiotic2 bacterium lactobacillus salivarius ucc118
32	<a href="#">c3dnpA</a>	Alignment	not modelled	15.7	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> stress response protein yhax; <b>PDBTitle:</b> crystal structure of stress response protein yhax from bacillus2 subtilis
33	<a href="#">c3jcrB</a>	Alignment	not modelled	14.9	14	<b>PDB header:</b> splicing <b>Chain:</b> B: <b>PDB Molecule:</b> hsnu114; <b>PDBTitle:</b> 3d structure determination of the human*u4/u6.u5* tri-snrrnp complex
34	<a href="#">d1kqfa1</a>	Alignment	not modelled	14.6	10	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
35	<a href="#">d1mp9a1</a>	Alignment	not modelled	14.5	11	<b>Fold:</b> TBP-like <b>Superfamily:</b> TATA-box binding protein-like <b>Family:</b> TATA-box binding protein (TBP), C-terminal domain
36	<a href="#">c1k5C</a>	Alignment	not modelled	14.4	8	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> d-ribose-5-phosphate isomerase; <b>PDBTitle:</b> structure of the d-ribose-5-phosphate isomerase from2 pyrococcus horikoshii
37	<a href="#">c2rdo7</a>	Alignment	not modelled	14.1	3	<b>PDB header:</b> ribosome <b>Chain:</b> 7: <b>PDB Molecule:</b> elongation factor g; <b>PDBTitle:</b> 50s subunit with ef-g(gdnpn) and rrf bound
38	<a href="#">d2bfdb2</a>	Alignment	not modelled	14.0	25	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
39	<a href="#">c5dxlA</a>	Alignment	not modelled	14.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> trehalose-6-phosphate phosphatase; <b>PDBTitle:</b> structure of aspergillus fumigatus trehalose-6-phosphate phosphatase2 crystal form 1
40	<a href="#">c4fn5A</a>	Alignment	not modelled	13.9	6	<b>PDB header:</b> translation/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor g 1; <b>PDBTitle:</b> elongation factor g 1 (pseudomonas aeruginosa) in complex with argyris2 b
41	<a href="#">c6notB</a>	Alignment	not modelled	13.9	6	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> elongation factor g; <b>PDBTitle:</b> crystal structure of a full length elongation factor g (ef-g) from2 rickettsia prowazekii
42	<a href="#">d2obba1</a>	Alignment	not modelled	13.8	20	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> BT0820-like
43	<a href="#">d1w4xa1</a>	Alignment	not modelled	13.5	20	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
44	<a href="#">c5lj3C</a>	Alignment	not modelled	13.3	13	<b>PDB header:</b> splicing <b>Chain:</b> C: <b>PDB Molecule:</b> pre-mrna-splicing factor snu114; <b>PDBTitle:</b> structure of the core of the yeast spliceosome immediately after2 branching
45	<a href="#">c3b6iB</a>	Alignment	not modelled	12.7	35	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> flavoprotein wrba; <b>PDBTitle:</b> wrba from escherichia coli, native structure
46	<a href="#">d2hd3a1</a>	Alignment	not modelled	12.7	28	<b>Fold:</b> OB-fold <b>Superfamily:</b> EutN/CcmL-like <b>Family:</b> EutN/CcmL-like
47	<a href="#">d1wzca1</a>	Alignment	not modelled	12.3	10	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
48	<a href="#">c1olsB</a>	Alignment	not modelled	12.1	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-oxoisovalerate dehydrogenase beta subunit; <b>PDBTitle:</b> roles of his291-alpha and his146-beta' in the reductive acylation2 reaction catalyzed by human branched-chain alpha-ketoacid3 dehydrogenase
49	<a href="#">d1ycga1</a>	Alignment	not modelled	12.0	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
50	<a href="#">c3w7aD</a>	Alignment	not modelled	11.3	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> fmn-dependent nadh-azoreductase; <b>PDBTitle:</b> crystal structure of azoreductase azrc fin complex with sulfone-2 modified azo dye acid red 88
51	<a href="#">c6jy5B</a>	Alignment	not modelled	11.0	23	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> unidentified carboxysome polypeptide; <b>PDBTitle:</b> structure of csos4b from halothiobacillus neapolitanus
52	<a href="#">c3hheA</a>	Alignment	not modelled	10.7	9	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> crystal structure of ribose-5-phosphate isomerase a from bartonella2 henselae
53	<a href="#">c2bm0A</a>	Alignment	not modelled	10.6	6	<b>PDB header:</b> elongation factor <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor g; <b>PDBTitle:</b> ribosomal elongation factor g (ef-g) fusidic acid resistant mutant2 t84a
54	<a href="#">c3tr5C</a>	Alignment	not modelled	10.6	9	<b>PDB header:</b> translation <b>Chain:</b> C: <b>PDB Molecule:</b> peptide chain release factor 3; <b>PDBTitle:</b> structure of a peptide chain release factor 3 (prfc) from coxiella2 burnetii
						<b>PDB header:</b> electron transport

55	<a href="#">c5b3kA</a>	Alignment	not modelled	10.6	10	<b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein pa3435; <b>PDBTitle:</b> c101a mutant of flavodoxin from pseudomonas aeruginosa
56	<a href="#">c1zn0B</a>	Alignment	not modelled	10.5	6	<b>PDB header:</b> translation/biosynthetic protein/rna <b>Chain:</b> B: <b>PDB Molecule:</b> elongation factor g; <b>PDBTitle:</b> coordinates of rrf and ef-g fitted into cryo-em map of the 2 50s subunit bound with both ef-g (gdpnp) and rrf
57	<a href="#">d1llda1</a>	Alignment	not modelled	10.3	10	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
58	<a href="#">d2z1ca1</a>	Alignment	not modelled	10.1	6	<b>Fold:</b> OB-fold <b>Superfamily:</b> HupF/HypC-like <b>Family:</b> HupF/HypC-like
59	<a href="#">c5h7lB</a>	Alignment	not modelled	10.0	8	<b>PDB header:</b> translation/ribosomal protein <b>Chain:</b> B: <b>PDB Molecule:</b> elongation factor 2; <b>PDBTitle:</b> complex of elongation factor 2-50s ribosomal protein l12
60	<a href="#">c2c5iP</a>	Alignment	not modelled	10.0	67	<b>PDB header:</b> protein transport <b>Chain:</b> P: <b>PDB Molecule:</b> vacuolar protein sorting protein 51; <b>PDBTitle:</b> n-terminal domain of tlg1 complexed with n-terminus of 2 vps51 in distorted conformation
61	<a href="#">c4hg1C</a>	Alignment	not modelled	9.5	31	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> putative cytoplasmic protein; <b>PDBTitle:</b> crystal structure of uncharacterized protein from salmonella enterica2 subsp. enterica serovar typhimurium str. 14028s
62	<a href="#">c2c5kP</a>	Alignment	not modelled	9.5	67	<b>PDB header:</b> protein transport <b>Chain:</b> P: <b>PDB Molecule:</b> vacuolar protein sorting protein 51; <b>PDBTitle:</b> n-terminal domain of tlg1 complexed with n-terminus of 2 vps51
63	<a href="#">c5zbyA</a>	Alignment	not modelled	9.4	13	<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
64	<a href="#">c5c0vA</a>	Alignment	not modelled	9.4	30	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> la-related protein 1; <b>PDBTitle:</b> structure of the larp1-unique domain dm15
65	<a href="#">d2qw7a1</a>	Alignment	not modelled	9.0	29	<b>Fold:</b> OB-fold <b>Superfamily:</b> EutN/CcmL-like <b>Family:</b> EutN/CcmL-like
66	<a href="#">c3vr1B</a>	Alignment	not modelled	8.9	11	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> peptide chain release factor 3; <b>PDBTitle:</b> crystal structure analysis of the translation factor rf3
67	<a href="#">c3zupB</a>	Alignment	not modelled	8.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mannosyl-3-phosphoglycerate phosphatase; <b>PDBTitle:</b> the 3-dimensional structure of mpgp from thermus2 thermophilus hb27, in complex with the alpha-3 mannosylglycerate and orthophosphate reaction products.
68	<a href="#">c3niwA</a>	Alignment	not modelled	8.7	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> haloacid dehalogenase-like hydrolase; <b>PDBTitle:</b> crystal structure of a haloacid dehalogenase-like hydrolase from2 bacteroides thetaiotaomicron
69	<a href="#">d2fz5a1</a>	Alignment	not modelled	8.6	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
70	<a href="#">d1nrwa</a>	Alignment	not modelled	8.6	21	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
71	<a href="#">d1qnaa1</a>	Alignment	not modelled	8.5	7	<b>Fold:</b> TBP-like <b>Superfamily:</b> TATA-box binding protein-like <b>Family:</b> TATA-box binding protein (TBP), C-terminal domain
72	<a href="#">d1uj4a2</a>	Alignment	not modelled	8.4	13	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> D-ribose-5-phosphate isomerase (RpiA), lid domain <b>Family:</b> D-ribose-5-phosphate isomerase (RpiA), lid domain
73	<a href="#">d1a5za1</a>	Alignment	not modelled	8.4	7	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
74	<a href="#">c5i37E</a>	Alignment	not modelled	8.4	24	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> msm0273; <b>PDBTitle:</b> the structure of the pentameric shell protein msm0273 from the rmm2 microcompartment
75	<a href="#">d2ot2a1</a>	Alignment	not modelled	8.3	19	<b>Fold:</b> OB-fold <b>Superfamily:</b> HupF/HypC-like <b>Family:</b> HupF/HypC-like
76	<a href="#">c5ancK</a>	Alignment	not modelled	8.2	8	<b>PDB header:</b> translation <b>Chain:</b> K: <b>PDB Molecule:</b> elongation factor tu gtp-binding domain-containing protein <b>PDBTitle:</b> mechanism of eif6 release from the nascent 60s ribosomal subunit
77	<a href="#">c3l7oB</a>	Alignment	not modelled	8.2	17	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> crystal structure of ribose-5-phosphate isomerase a from streptococcus2 mutans ua159
78	<a href="#">c5ganC</a>	Alignment	not modelled	8.1	13	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> pre-mrna-splicing factor snu114; <b>PDBTitle:</b> the overall structure of the yeast spliceosomal u4/u6.u5 tri-snrnp at2 3.7 angstrom
79	<a href="#">c1xjqA</a>	Alignment	not modelled	8.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional 3'-phosphoadenosine 5'-phosphosulfate <b>PDBTitle:</b> adp complex of human paps synthetase 1
80	<a href="#">c3pgvB</a>	Alignment	not modelled	7.9	37	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> haloacid dehalogenase-like hydrolase; <b>PDBTitle:</b> crystal structure of a haloacid dehalogenase-like hydrolase2 (kpn_04322) from klebsiella pneumoniae subsp.

						pneumoniae mgh 78578 at3 2.39 a resolution
81	<a href="#">c6j1kA_</a>	Alignment	not modelled	7.9	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> crystal structure of ribose-5-phosphate isomerase a from ochrobactrum2 sp. csl1
82	<a href="#">c6cl4A_</a>	Alignment	not modelled	7.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipase c12; <b>PDBTitle:</b> lipc12 - lipase from metagenomics
83	<a href="#">c5mp4C_</a>	Alignment	not modelled	7.7	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> protoplast secreted protein 2; <b>PDBTitle:</b> the structure of pst2p from saccharomyces cerevisiae
84	<a href="#">d1nf2a_</a>	Alignment	not modelled	7.7	21	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
85	<a href="#">d1nh2a1</a>	Alignment	not modelled	7.6	6	<b>Fold:</b> TBP-like <b>Superfamily:</b> TATA-box binding protein-like <b>Family:</b> TATA-box binding protein (TBP), C-terminal domain
86	<a href="#">c2mmvA_</a>	Alignment	not modelled	7.6	12	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein zapa; <b>PDBTitle:</b> zapa mutant dimer from geobacillus stearothermophilus
87	<a href="#">d1aisa1</a>	Alignment	not modelled	7.5	11	<b>Fold:</b> TBP-like <b>Superfamily:</b> TATA-box binding protein-like <b>Family:</b> TATA-box binding protein (TBP), C-terminal domain
88	<a href="#">d1xvia_</a>	Alignment	not modelled	7.5	5	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
89	<a href="#">c1xviA_</a>	Alignment	not modelled	7.5	5	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative mannosyl-3-phosphoglycerate phosphatase; <b>PDBTitle:</b> crystal structure of yedp, phosphatase-like domain protein2 from escherichia coli k12
90	<a href="#">d3d3ra1</a>	Alignment	not modelled	7.4	19	<b>Fold:</b> OB-fold <b>Superfamily:</b> HupF/HypC-like <b>Family:</b> HupF/HypC-like
91	<a href="#">d1k8kd1</a>	Alignment	not modelled	7.3	18	<b>Fold:</b> Secretion chaperone-like <b>Superfamily:</b> Arp2/3 complex subunits <b>Family:</b> Arp2/3 complex subunits
92	<a href="#">c4jw0A_</a>	Alignment	not modelled	7.3	26	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> carbon dioxide concentrating mechanism protein; <b>PDBTitle:</b> structure of gloeobacter violaceus ccml
93	<a href="#">c4q86B_</a>	Alignment	not modelled	7.2	9	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> ribosomal protein s12 methylthiotransferase accessory <b>PDBTitle:</b> ycao with amp bound
94	<a href="#">c2zf8A_</a>	Alignment	not modelled	7.2	11	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> component of sodium-driven polar flagellar motor; <b>PDBTitle:</b> crystal structure of moty
95	<a href="#">c3e5nA_</a>	Alignment	not modelled	7.2	13	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> d-alanine-d-alanine ligase a; <b>PDBTitle:</b> crystal structure of d-alanine-d-alanine ligase from2 xanthomonas oryzae pv. oryzae kacc10331
96	<a href="#">d2fi9a1</a>	Alignment	not modelled	7.1	11	<b>Fold:</b> MTH938-like <b>Superfamily:</b> MTH938-like <b>Family:</b> MTH938-like
97	<a href="#">d1pj3a2</a>	Alignment	not modelled	7.0	20	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Malic enzyme N-domain
98	<a href="#">d1o0sa2</a>	Alignment	not modelled	7.0	20	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Malic enzyme N-domain
99	<a href="#">c3gygA_</a>	Alignment	not modelled	7.0	10	<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