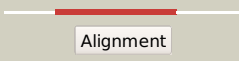



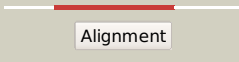





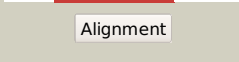
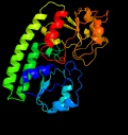
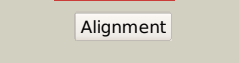

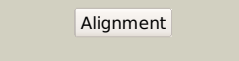

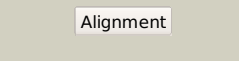

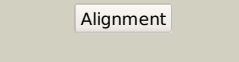

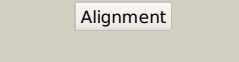



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2059_(-)_2315182_2316717
Date	Mon Aug 5 13:25:17 BST 2019
Unique Job ID	9c1ff12d3f262319

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2ps3A_</a>			100.0	19	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> high-affinity zinc uptake system protein znua; <b>PDBTitle:</b> structure and metal binding properties of znua, a periplasmic zinc2 transporter from escherichia coli
2	<a href="#">c2ogwB_</a>			100.0	18	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> high-affinity zinc uptake system protein znua <b>PDBTitle:</b> structure of abc type zinc transporter from e. coli
3	<a href="#">c6r6kB_</a>			100.0	22	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter substrate-binding protein; <b>PDBTitle:</b> structure of a fpvc mutant from pseudomonas aeruginosa
4	<a href="#">c2o1eB_</a>			100.0	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> ycdh; <b>PDBTitle:</b> crystal structure of the metal-dependent lipoprotein ycdh2 from bacillus subtilis, northeast structural genomics3 target sr583
5	<a href="#">c3hjtB_</a>			100.0	21	<b>PDB header:</b> cell adhesion, transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> lmb; <b>PDBTitle:</b> structure of laminin binding protein (lmb) of streptococcus agalactiae2 a bifunctional protein with adhesion and metal transporting activity
6	<a href="#">c4xrvB_</a>			100.0	21	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> periplasmic solute binding protein; <b>PDBTitle:</b> structure of a zn abc transporter substrate binding protein from2 paracoccus denitrificans
7	<a href="#">c5uyvA_</a>			100.0	18	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic chelated iron-binding protein yfea; <b>PDBTitle:</b> yfea ancillary sites that do not co-load with site 2
8	<a href="#">d1xvla1</a>			100.0	24	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> TroA-like
9	<a href="#">d1toaa_</a>			100.0	16	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> TroA-like
10	<a href="#">c1toaA_</a>			100.0	16	<b>PDB header:</b> binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein (periplasmic binding protein troa); <b>PDBTitle:</b> periplasmic zinc binding protein troa from treponema pallidum
11	<a href="#">c2ov3A_</a>			100.0	22	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic binding protein component of an abc type zinc <b>PDBTitle:</b> crystal structure of 138-173 znua deletion mutant plus zinc bound

12	<a href="#">c4cl2A_</a>	Alignment		100.0	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic solute binding protein; <b>PDBTitle:</b> structure of periplasmic metal binding protein from candidatus2 liberibacter asiaticus
13	<a href="#">d1pq4a_</a>	Alignment		100.0	21	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> TroA-like
14	<a href="#">c5hx7A_</a>	Alignment		100.0	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> manganese-binding lipoprotein mnta; <b>PDBTitle:</b> metal abc transporter from listeria monocytogenes
15	<a href="#">c3cx3A_</a>	Alignment		100.0	19	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> lipoprotein; <b>PDBTitle:</b> crystal structure analysis of the streptococcus pneumoniae2 adcaii protein
16	<a href="#">c3mfqB_</a>	Alignment		100.0	16	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> high-affinity zinc uptake system protein znua; <b>PDBTitle:</b> a glance into the metal binding specificity of troa: where elaborate2 behaviors occur in the active center
17	<a href="#">d1psza_</a>	Alignment		100.0	18	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> TroA-like
18	<a href="#">c4oxqB_</a>	Alignment		100.0	17	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> manganese abc transporter, periplasmic-binding protein <b>PDBTitle:</b> structure of staphylococcus pseudintermedius metal-binding protein2 sita in complex with zinc
19	<a href="#">c4k3vA_</a>	Alignment		100.0	19	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc superfamily atp binding cassette transporter, binding <b>PDBTitle:</b> structure of staphylococcus aureus mntc
20	<a href="#">c1xvlC_</a>	Alignment		100.0	28	<b>PDB header:</b> metal transport <b>Chain:</b> C: <b>PDB Molecule:</b> mn transporter; <b>PDBTitle:</b> the three-dimensional structure of mntc from synechocystis2 6803
21	<a href="#">c5jg7A_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> fur regulated salmonella iron transporter; <b>PDBTitle:</b> crystal structure of putative periplasmic binding protein from2 salmonella typhimurium lt2
22	<a href="#">c5n6yD_</a>	Alignment	not modelled	97.3	14	<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
23	<a href="#">d1qh8a_</a>	Alignment	not modelled	97.0	15	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
24	<a href="#">c3pdiB_</a>	Alignment	not modelled	96.6	18	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> nitrogenase mofe cofactor biosynthesis protein nifn; <b>PDBTitle:</b> precursor bound nifen
25	<a href="#">d1m1na_</a>	Alignment	not modelled	96.4	9	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
26	<a href="#">c5kojD_</a>	Alignment	not modelled	96.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> nitrogenase femo beta subunit protein nifk; <b>PDBTitle:</b> nitrogenase mofep protein in the ids oxidized state
27	<a href="#">d1wo8a1</a>	Alignment	not modelled	96.3	19	<b>Fold:</b> Methylglyoxal synthase-like <b>Superfamily:</b> Methylglyoxal synthase-like <b>Family:</b> Methylglyoxal synthase, MgsA
28	<a href="#">d2ay1a_</a>	Alignment	not modelled	96.3	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
						<b>Fold:</b> Chelatase-like

29	<a href="#">d1mioa_</a>	Alignment	not modelled	96.2	10	<b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
30	<a href="#">c6f2cK_</a>	Alignment	not modelled	96.0	15	<b>PDB header:</b> lyase <b>Chain:</b> K: <b>PDB Molecule:</b> methylglyoxal synthase; <b>PDBTitle:</b> methylglyoxal synthase mgsa from bacillus subtilis
31	<a href="#">c2xdqB_</a>	Alignment	not modelled	95.7	14	<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
32	<a href="#">d1m1nb_</a>	Alignment	not modelled	95.4	10	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
33	<a href="#">c3pdiG_</a>	Alignment	not modelled	95.3	14	<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
34	<a href="#">c4effA_</a>	Alignment	not modelled	95.3	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aromatic-amino-acid aminotransferase; <b>PDBTitle:</b> crystal structure of aromatic-amino-acid aminotransferase from2 burkholderia pseudomallei
35	<a href="#">c3trjC_</a>	Alignment	not modelled	95.0	9	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphoheptose isomerase; <b>PDBTitle:</b> structure of a phosphoheptose isomerase from francisella tularensis
36	<a href="#">c4rkdA_</a>	Alignment	not modelled	94.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aromatic amino acid aminotransferase; <b>PDBTitle:</b> psychrophilic aromatic amino acids aminotransferase from psychrobacter2 sp. b6 cocrystalized with aspartic acid
37	<a href="#">c3aerB_</a>	Alignment	not modelled	94.6	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
38	<a href="#">c4wd2A_</a>	Alignment	not modelled	94.5	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aromatic-amino-acid transaminase tyrb; <b>PDBTitle:</b> crystal structure of an aromatic amino acid aminotransferase from2 burkholderia cenocepacia j2315
39	<a href="#">d7aata_</a>	Alignment	not modelled	94.4	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
40	<a href="#">d1qh8b_</a>	Alignment	not modelled	94.4	12	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
41	<a href="#">c3mebB_</a>	Alignment	not modelled	94.2	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartate aminotransferase; <b>PDBTitle:</b> structure of cytoplasmic aspartate aminotransferase from giardia2 lamblia
42	<a href="#">c2yvqA_</a>	Alignment	not modelled	94.0	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> carbamoyl-phosphate synthase; <b>PDBTitle:</b> crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens
43	<a href="#">d1vmda_</a>	Alignment	not modelled	94.0	20	<b>Fold:</b> Methylglyoxal synthase-like <b>Superfamily:</b> Methylglyoxal synthase-like <b>Family:</b> Methylglyoxal synthase, MgsA
44	<a href="#">c5n6yE_</a>	Alignment	not modelled	93.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> nitrogenase vanadium-iron protein beta chain; <b>PDBTitle:</b> azotobacter vinelandii vanadium nitrogenase
45	<a href="#">c3h75A_</a>	Alignment	not modelled	93.9	6	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic sugar-binding domain protein; <b>PDBTitle:</b> crystal structure of a periplasmic sugar-binding protein from the2 pseudomonas fluorescens
46	<a href="#">c3j21Z_</a>	Alignment	not modelled	93.6	15	<b>PDB header:</b> ribosome <b>Chain:</b> Z: <b>PDB Molecule:</b> 50s ribosomal protein l30e; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
47	<a href="#">c3zf7g_</a>	Alignment	not modelled	93.4	11	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 Brucei ribosome
48	<a href="#">c5i01B_</a>	Alignment	not modelled	93.4	13	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoheptose isomerase; <b>PDBTitle:</b> structure of phosphoheptose isomerase gmha from neisseria gonorrhoeae
49	<a href="#">c3tcmB_</a>	Alignment	not modelled	93.3	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> alanine aminotransferase 2; <b>PDBTitle:</b> crystal structure of alanine aminotransferase from hordeum vulgare
50	<a href="#">c3s99A_</a>	Alignment	not modelled	93.3	17	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> basic membrane lipoprotein; <b>PDBTitle:</b> crystal structure of a basic membrane lipoprotein from brucella2 melitensis, iodide soak
51	<a href="#">d2csta_</a>	Alignment	not modelled	93.3	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
52	<a href="#">d1w41a1</a>	Alignment	not modelled	93.2	14	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> L30e-like <b>Family:</b> L30e/L7ae ribosomal proteins
53	<a href="#">c3cpqB_</a>	Alignment	not modelled	93.2	11	<b>PDB header:</b> ribosomal protein <b>Chain:</b> B: <b>PDB Molecule:</b> 50s ribosomal protein l30e; <b>PDBTitle:</b> crystal structure of l30e a ribosomal protein from2 methanocaldococcus jannaschii dsm2661 (mj1044)
54	<a href="#">d1t0kb_</a>	Alignment	not modelled	93.2	11	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> L30e-like <b>Family:</b> L30e/L7ae ribosomal proteins

55	<a href="#">c2zy4F_</a>	Alignment	not modelled	93.1	17	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> l-aspartate beta-decarboxylase; <b>PDBTitle:</b> dodecameric l-aspartate beta-decarboxylase
56	<a href="#">c4a1dG_</a>	Alignment	not modelled	93.1	16	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> rpl30; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rna and proteins of3 molecule 4.
57	<a href="#">d2bo1a1</a>	Alignment	not modelled	93.0	16	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> L30e-like <b>Family:</b> L30e/L7ae ribosomal proteins
58	<a href="#">d1yaaa_</a>	Alignment	not modelled	92.9	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
59	<a href="#">d1a9xa2</a>	Alignment	not modelled	92.8	19	<b>Fold:</b> Methylglyoxal synthase-like <b>Superfamily:</b> Methylglyoxal synthase-like <b>Family:</b> Carbamoyl phosphate synthetase, large subunit allosteric, C-terminal domain
60	<a href="#">d1miob_</a>	Alignment	not modelled	92.7	12	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
61	<a href="#">d2ez9a1</a>	Alignment	not modelled	92.6	18	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
62	<a href="#">c5by2A_</a>	Alignment	not modelled	92.4	8	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoheptose isomerase; <b>PDBTitle:</b> sedoheptulose 7-phosphate isomerase from colwellia psychrerythraea2 strain 34h
63	<a href="#">c6btmB_</a>	Alignment	not modelled	92.3	13	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> alternative complex iii subunit b; <b>PDBTitle:</b> structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
64	<a href="#">c4eu1A_</a>	Alignment	not modelled	92.2	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mitochondrial aspartate aminotransferase; <b>PDBTitle:</b> structure of a mitochondrial aspartate aminotransferase from2 trypanosoma brucei
65	<a href="#">c6hnuA_</a>	Alignment	not modelled	92.2	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aromatic amino acid aminotransferase i; <b>PDBTitle:</b> crystal structure of the aminotransferase aro8 from c. albicans with2 ligands
66	<a href="#">c4mlcA_</a>	Alignment	not modelled	92.0	17	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> extracellular ligand-binding receptor; <b>PDBTitle:</b> abc transporter substrate-binding protein fromdesulfitobacterium2 hafniense
67	<a href="#">c6dspB_</a>	Alignment	not modelled	92.0	18	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> autoinducer 2-binding protein lsrb; <b>PDBTitle:</b> lsrb from clostridium saccharobutylicum in complex with ai-2
68	<a href="#">c5braA_</a>	Alignment	not modelled	91.9	14	<b>PDB header:</b> solute-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative periplasmic binding protein with substrate ribose; <b>PDBTitle:</b> crystal structure of a putative periplasmic solute binding protein2 (ipr025997) from ochrobactrum anthropi atcc49188 (oant_2843, target3 efi-511085)
69	<a href="#">c3v7qB_</a>	Alignment	not modelled	91.7	11	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable ribosomal protein ylqx; <b>PDBTitle:</b> crystal structure of b. subtilis ylqx at 1.55 a resolution
70	<a href="#">c3k7yA_</a>	Alignment	not modelled	91.5	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate aminotransferase; <b>PDBTitle:</b> aspartate aminotransferase of plasmodium falciparum
71	<a href="#">c2ynmD_</a>	Alignment	not modelled	91.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase subunit b; <b>PDBTitle:</b> structure of the adpxalf3-stabilized transition state of the2 nitrogenase-like dark-operative protochlorophyllide oxidoreductase3 complex from prochlorococcus marinus with its substrate4 protochlorophyllide a
72	<a href="#">c4rxuA_</a>	Alignment	not modelled	91.3	18	<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
73	<a href="#">c4wzzA_</a>	Alignment	not modelled	91.3	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative sugar abc transporter, substrate-binding protein; <b>PDBTitle:</b> crystal structure of an abc transporter solute binding protein2 (ipr025997) from clostridium phytofermentas (cphy_0583, target efi-3 511148) with bound l-rhamnose
74	<a href="#">c3zeyF_</a>	Alignment	not modelled	91.2	7	<b>PDB header:</b> ribosome <b>Chain:</b> F: <b>PDB Molecule:</b> 40s ribosomal protein s12; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
75	<a href="#">c4wwhA_</a>	Alignment	not modelled	91.2	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter; <b>PDBTitle:</b> crystal structure of an abc transporter solute binding protein2 (ipr025997) from mycobacterium smegmatis (msmeg_1704, target efi-3 510967) with bound d-galactose
76	<a href="#">d1ajsa_</a>	Alignment	not modelled	91.2	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
77	<a href="#">c2yvaB_</a>	Alignment	not modelled	91.0	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dnaa initiator-associating protein diaa; <b>PDBTitle:</b> crystal structure of escherichia coli diaa
78	<a href="#">d2ji7a1</a>	Alignment	not modelled	90.8	17	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain

79	<a href="#">c3on1A</a>	Alignment	not modelled	90.7	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> bh2414 protein; <b>PDBTitle:</b> the structure of a protein with unknown function from bacillus2 halodurans c
80	<a href="#">c4kzkA</a>	Alignment	not modelled	90.7	15	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> l-arabinose abc transporter, periplasmic l-arabinose- <b>PDBTitle:</b> the structure of the periplasmic l-arabinose binding protein from2 burkholderia thailandensis
81	<a href="#">d2dja1</a>	Alignment	not modelled	90.6	17	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
82	<a href="#">c6ezbB</a>	Alignment	not modelled	90.4	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartate aminotransferase; <b>PDBTitle:</b> crystal structure of aspartate aminotransferase from trypanosoma cruzi2 at 2.07 angstrom resolution
83	<a href="#">c3g7qA</a>	Alignment	not modelled	90.4	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> valine-pyruvate aminotransferase; <b>PDBTitle:</b> crystal structure of valine-pyruvate aminotransferase avta2 (np_462565.1) from salmonella typhimurium lt2 at 1.80 a resolution
84	<a href="#">d1ybha1</a>	Alignment	not modelled	89.9	19	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
85	<a href="#">c1ynuA</a>	Alignment	not modelled	89.8	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 1-aminocyclopropane-1-carboxylate synthase; <b>PDBTitle:</b> crystal structure of apple acc synthase in complex with l-vinylglycine
86	<a href="#">c6hndA</a>	Alignment	not modelled	89.7	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aromatic-amino-acid:2-oxoglutarate transaminase; <b>PDBTitle:</b> crystal structure of the aromatic aminotransferase aro9 from c.2 albicans
87	<a href="#">d3tata</a>	Alignment	not modelled	89.7	17	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
88	<a href="#">c6c3aB</a>	Alignment	not modelled	89.6	13	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> o2-, plp-dependent l-arginine hydroxylase rohp 4-hydroxy-2-2 ketoarginine complex
89	<a href="#">c2zkr6</a>	Alignment	not modelled	89.4	15	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> 6: <b>PDB Molecule:</b> 60s ribosomal protein l30e; <b>PDBTitle:</b> structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
90	<a href="#">c4a0rB</a>	Alignment	not modelled	89.2	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> adenosylmethionine-8-amino-7-oxononoate <b>PDBTitle:</b> structure of bifunctional dapa aminotransferase-dtb synthetase from2 arabidopsis thaliana bound to dethiobiotin (dtb).
91	<a href="#">c3uugB</a>	Alignment	not modelled	89.0	16	<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
92	<a href="#">c2lbwA</a>	Alignment	not modelled	88.9	14	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> h/aca ribonucleoprotein complex subunit 2; <b>PDBTitle:</b> solution structure of the s. cerevisiae h/aca rnp protein nhp2p-s82w2 mutant
93	<a href="#">d1iaya</a>	Alignment	not modelled	88.7	12	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
94	<a href="#">c3f6tA</a>	Alignment	not modelled	88.5	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate aminotransferase; <b>PDBTitle:</b> crystal structure of aspartate aminotransferase (e.c. 2.6.1.1)2 (yp_194538.1) from lactobacillus acidophilus ncfm at 2.15 a3 resolution
95	<a href="#">d1tjya</a>	Alignment	not modelled	88.4	15	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
96	<a href="#">c3jtbB</a>	Alignment	not modelled	88.3	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminotransferase; <b>PDBTitle:</b> crystal structure of aminotransferase (np_283882.1) from neisseria2 meningitidis z2491 at 1.91 a resolution
97	<a href="#">d2q7wa1</a>	Alignment	not modelled	88.3	10	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
98	<a href="#">c1p1hD</a>	Alignment	not modelled	88.2	22	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> inositol-3-phosphate synthase; <b>PDBTitle:</b> crystal structure of the 1l-myo-inositol/nad+ complex
99	<a href="#">c2xznU</a>	Alignment	not modelled	88.2	9	<b>PDB header:</b> ribosome <b>Chain:</b> U: <b>PDB Molecule:</b> ribosomal protein l7ae containing protein; <b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
100	<a href="#">c2zy3A</a>	Alignment	not modelled	88.0	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> l-aspartate beta-decarboxylase; <b>PDBTitle:</b> dodecameric l-aspartate beta-decarboxylase
101	<a href="#">d1vkoa1</a>	Alignment	not modelled	88.0	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
102	<a href="#">c3nraA</a>	Alignment	not modelled	87.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate aminotransferase; <b>PDBTitle:</b> crystal structure of an aspartate aminotransferase



						(yp_354942.1) from2 rhodobacter sphaeroides 2.4.1 at 2.15 a resolution
103	<a href="#">c3hmuA_</a>	Alignment	not modelled	87.8	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase, class iii; <b>PDBTitle:</b> crystal structure of a class iii aminotransferase from silicibacter2 pomeroyi
104	<a href="#">c4h51B_</a>	Alignment	not modelled	87.8	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartate aminotransferase; <b>PDBTitle:</b> crystal structure of a putative aspartate aminotransferase from2 leishmania major friedlin
105	<a href="#">c4je5C_</a>	Alignment	not modelled	87.7	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> aromatic/aminoadipate aminotransferase 1; <b>PDBTitle:</b> crystal structure of the aromatic aminotransferase aro8, a putative2 alpha-aminoadipate aminotransferase in saccharomyces cerevisiae
106	<a href="#">d2byla1</a>	Alignment	not modelled	87.4	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
107	<a href="#">c4pz0A_</a>	Alignment	not modelled	87.3	9	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar abc transporter, sugar-binding protein; <b>PDBTitle:</b> the crystal structure of a solute binding protein from bacillus2 anthracis str. ames in complex with quorum-sensing signal3 autoinducer-2 (ai-2)
108	<a href="#">c3o1hB_</a>	Alignment	not modelled	87.3	13	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> periplasmic protein tort; <b>PDBTitle:</b> crystal structure of the tors sensor domain - tort complex in the2 presence of tmao
109	<a href="#">c5ewrA_</a>	Alignment	not modelled	87.3	16	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> box c/d snorpp and u4 snrnp component snu13p; <b>PDBTitle:</b> c merolae u4 snrnp protein snu13
110	<a href="#">c5uowB_</a>	Alignment	not modelled	86.9	17	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> n-methyl-d-aspartate receptor subunit nr2a; <b>PDBTitle:</b> triheteromeric nmda receptor glun1/glun2a/glun2b in complex with2 glycine, glutamate, mk-801 and a glun2b-specific fab, at ph 6.5
111	<a href="#">c5xyiM_</a>	Alignment	not modelled	86.8	7	<b>PDB header:</b> ribosome <b>Chain:</b> M: <b>PDB Molecule:</b> ribosomal protein l7ae, putative; <b>PDBTitle:</b> small subunit of trichomonas vaginalis ribosome
112	<a href="#">c6irfD_</a>	Alignment	not modelled	86.6	19	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> glutamate receptor ionotropic, nmda 2a; <b>PDBTitle:</b> structure of the human glun1/glun2a nmda receptor in the2 glutamate/glycine-bound state at ph 6.3, class i
113	<a href="#">d1ozha1</a>	Alignment	not modelled	86.1	14	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
114	<a href="#">d2cc0a1</a>	Alignment	not modelled	86.0	11	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> Glycoside hydrolase/deacetylase <b>Family:</b> NodB-like polysaccharide deacetylase
115	<a href="#">c4y9tA_</a>	Alignment	not modelled	85.8	19	<b>PDB header:</b> solute-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter, solute binding protein; <b>PDBTitle:</b> crystal structure of an abc transporter solute binding protein2 (ipr025997) from agrobacterium vitis s4 (avi_5305, target efi-511224)3 with bound alpha-d-glucosamine
116	<a href="#">c4pe6B_</a>	Alignment	not modelled	85.7	21	<b>PDB header:</b> solute-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative abc transporter; <b>PDBTitle:</b> crystal structure of abc transporter solute binding protein from2 thermobispora bispora dsm 43833
117	<a href="#">d1vqof1</a>	Alignment	not modelled	85.5	16	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> L30e-like <b>Family:</b> L30e/L7ae ribosomal proteins
118	<a href="#">c5xxuM_</a>	Alignment	not modelled	85.3	11	<b>PDB header:</b> ribosome <b>Chain:</b> M: <b>PDB Molecule:</b> ribosomal protein es12; <b>PDBTitle:</b> small subunit of toxoplasma gondii ribosome
119	<a href="#">c5c4nD_</a>	Alignment	not modelled	85.1	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> precorrin-6a reductase; <b>PDBTitle:</b> cobk precorrin-6a reductase
120	<a href="#">d1bw0a_</a>	Alignment	not modelled	85.0	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like