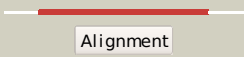

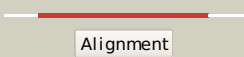

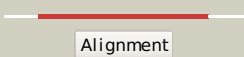

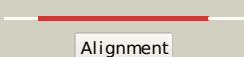

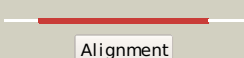

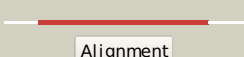

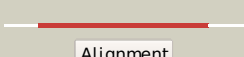

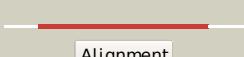

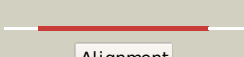

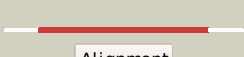











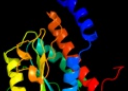


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2yvaB_</a>	 Alignment		100.0	100	<b>PDB header:</b> dna binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> dnaa initiator-associating protein diaa; <b>PDBTitle:</b> crystal structure of escherichia coli diaa
2	<a href="#">d1x92a_</a>	 Alignment		100.0	58	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
3	<a href="#">d1tk9a_</a>	 Alignment		100.0	40	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
4	<a href="#">c2x3yA_</a>	 Alignment		100.0	40	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> phosphoheptose isomerase; <b>PDBTitle:</b> crystal structure of gmha from burkholderia pseudomallei
5	<a href="#">c3trjC_</a>	 Alignment		100.0	46	<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
6	<a href="#">d1x94a_</a>	 Alignment		100.0	42	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
7	<a href="#">c3cvjB_</a>	 Alignment		99.9	17	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> putative phosphoheptose isomerase; <b>PDBTitle:</b> crystal structure of a putative phosphoheptose isomerase (bh3325) from <i>Bacillus halodurans</i> c-125 at 2.00 Å resolution
8	<a href="#">d1nria_</a>	 Alignment		99.9	16	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
9	<a href="#">c1nriA_</a>	 Alignment		99.9	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein hi0754; <b>PDBTitle:</b> crystal structure of putative phosphosugar isomerase hi0754 from <i>Haemophilus influenzae</i>
10	<a href="#">c3fxaA_</a>	 Alignment		99.9	20	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> sis domain protein; <b>PDBTitle:</b> crystal structure of a putative sugar-phosphate isomerase2 (lmof2365_0531) from <i>Listeria monocytogenes</i> str. 4b f2365 at 1.60 Å resolution
11	<a href="#">c3etnD_</a>	 Alignment		99.9	18	<b>PDB header:</b> isomerase <b>Chain:</b> D; <b>PDB Molecule:</b> putative phosphosugar isomerase involved in capsule <b>PDBTitle:</b> crystal structure of putative phosphosugar isomerase involved in capsule formation (yp_209877.1) from <i>Bacteroides fragilis</i> nctc 93433 at 1.70 Å resolution

12	<a href="#">c2xhzC_</a>	Alignment		99.8	14	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> arabinose 5-phosphate isomerase; <b>PDBTitle:</b> probing the active site of the sugar isomerase domain from e. coli2 arabinose-5-phosphate isomerase via x-ray crystallography
13	<a href="#">d1m3sa_</a>	Alignment		99.8	17	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
14	<a href="#">c3shoA_</a>	Alignment		99.8	22	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, rpir family; <b>PDBTitle:</b> crystal structure of rpir transcription factor from spharobacter2 thermophilus (sugar isomerase domain)
15	<a href="#">d1vima_</a>	Alignment		99.8	19	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
16	<a href="#">d1jeoa_</a>	Alignment		99.7	16	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
17	<a href="#">c3hbaA_</a>	Alignment		99.7	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphosugar isomerase; <b>PDBTitle:</b> crystal structure of a putative phosphosugar isomerase (sden_2705)2 from shewanella denitrificans os217 at 2.00 a resolution
18	<a href="#">c2a3nA_</a>	Alignment		99.7	15	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative glucosamine-fructose-6-phosphate aminotransferase; <b>PDBTitle:</b> crystal structure of a putative glucosamine-fructose-6-phosphate2 aminotransferase (stm4540.s) from salmonella typhimurium lt2 at 1.353 a resolution
19	<a href="#">c3fj1A_</a>	Alignment		99.7	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphosugar isomerase; <b>PDBTitle:</b> crystal structure of putative phosphosugar isomerase (yp_167080.1)2 from silicibacter pomeroyi dss-3 at 1.75 a resolution
20	<a href="#">c3knzA_</a>	Alignment		99.7	15	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative sugar binding protein; <b>PDBTitle:</b> crystal structure of putative sugar binding protein (np_459565.1) from2 salmonella typhimurium lt2 at 2.50 a resolution
21	<a href="#">c2puwA_</a>	Alignment	not modelled	99.6	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> isomerase domain of glutamine-fructose-6-phosphate <b>PDBTitle:</b> the crystal structure of isomerase domain of glucosamine-6-phosphate2 synthase from candida albicans
22	<a href="#">d1j5xa_</a>	Alignment	not modelled	99.6	19	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> double-SIS domain
23	<a href="#">c2amlB_</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sis domain protein; <b>PDBTitle:</b> crystal structure of lmo0035 protein (46906266) from listeria2 monocytogenes 4b f2365 at 1.50 a resolution
24	<a href="#">c2zj3A_</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucosamine--fructose-6-phosphate <b>PDBTitle:</b> isomerase domain of human glucose:fructose-6-phosphate2 amidotransferase
25	<a href="#">c3g68A_</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphosugar isomerase; <b>PDBTitle:</b> crystal structure of a putative phosphosugar isomerase (cd3275) from2 clostridium difficile 630 at 1.80 a resolution
26	<a href="#">c3euaD_</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> putative fructose-aminoacid-6-phosphate deglycase; <b>PDBTitle:</b> crystal structure of a putative phosphosugar isomerase (bsu32610) from2 bacillus subtilis at 1.90 a resolution
27	<a href="#">c3tbfA_</a>	Alignment	not modelled	99.6	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucosamine--fructose-6-phosphate aminotransferase <b>PDBTitle:</b> c-terminal domain of glucosamine-fructose-6-phosphate aminotransferase2 from francisella tularensis.
28	<a href="#">d1moqa_</a>	Alignment	not modelled	99.6	13	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> double-SIS domain

29	<a href="#">d1x9ia_</a>	Alignment	not modelled	99.5	24	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> double-SIS domain
30	<a href="#">c3fkjA_</a>	Alignment	not modelled	99.5	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphosugar isomerases; <b>PDBTitle:</b> crystal structure of a putative phosphosugar isomerase (stm_0572) from2 salmonella typhimurium lt2 at 2.12 a resolution
31	<a href="#">c2decA_</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> 325aa long hypothetical protein; <b>PDBTitle:</b> crystal structure of the ph0510 protein from pyrococcus horikoshii ot3
32	<a href="#">c3i0zB_</a>	Alignment	not modelled	99.4	22	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative tagatose-6-phosphate ketose/al dose isomerase; <b>PDBTitle:</b> crystal structure of putative putative tagatose-6-phosphate2 ketose/al dose isomerase (np_344614.1) from streptococcus pneumoniae3 tigr4 at 1.70 a resolution
33	<a href="#">c3odpA_</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative tagatose-6-phosphate ketose/al dose isomerase; <b>PDBTitle:</b> crystal structure of a putative tagatose-6-phosphate ketose/al dose2 isomerase (nt01cx_0292) from clostridium novyi nt at 2.35 a3 resolution
34	<a href="#">c3c3jA_</a>	Alignment	not modelled	99.3	24	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative tagatose-6-phosphate ketose/al dose isomerase; <b>PDBTitle:</b> crystal structure of tagatose-6-phosphate ketose/al dose isomerase from2 escherichia coli
35	<a href="#">c1jxaA_</a>	Alignment	not modelled	99.3	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucosamine 6-phosphate synthase; <b>PDBTitle:</b> glucosamine 6-phosphate synthase with glucose 6-phosphate
36	<a href="#">c2q8nB_</a>	Alignment	not modelled	98.4	14	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> crystal structure of glucose-6-phosphate isomerase (ec2_5.3.1.9) (tm1385) from thermotoga maritima at 1.82 a3 resolution
37	<a href="#">c3ff1B_</a>	Alignment	not modelled	98.3	19	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> structure of glucose 6-phosphate isomerase from staphylococcus aureus
38	<a href="#">d1c7qa_</a>	Alignment	not modelled	98.1	16	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI
39	<a href="#">c3jx9B_</a>	Alignment	not modelled	98.0	13	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative phosphoheptose isomerase; <b>PDBTitle:</b> crystal structure of putative phosphoheptose isomerase2 (yp_001815198.1) from exiguobacterium sp. 255-15 at 1.95 a resolution
40	<a href="#">c1zzgB_</a>	Alignment	not modelled	97.9	16	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> crystal structure of hypothetical protein tt0462 from thermus2 thermophilus hb8
41	<a href="#">c3ljkA_</a>	Alignment	not modelled	97.6	12	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> glucose-6-phosphate isomerase from francisella tularensis.
42	<a href="#">d1gzda_</a>	Alignment	not modelled	97.4	15	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI
43	<a href="#">c2wu8A_</a>	Alignment	not modelled	97.4	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> structural studies of phosphoglucose isomerase from2 mycobacterium tuberculosis h37rv
44	<a href="#">d1u0fa_</a>	Alignment	not modelled	97.4	16	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI
45	<a href="#">d1iata_</a>	Alignment	not modelled	97.4	14	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI
46	<a href="#">d1hm5a_</a>	Alignment	not modelled	97.3	14	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI
47	<a href="#">c3hjbA_</a>	Alignment	not modelled	97.3	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> 1.5 angstrom crystal structure of glucose-6-phosphate isomerase from2 vibrio cholerae.
48	<a href="#">c1t10A_</a>	Alignment	not modelled	97.2	12	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> phosphoglucose isomerase from leishmania mexicana in complex with2 substrate d-fructose-6-phosphate
49	<a href="#">c2o2cB_</a>	Alignment	not modelled	97.2	15	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate isomerase, glycosomal; <b>PDBTitle:</b> crystal structure of phosphoglucose isomerase from t. brucei2 containing glucose-6-phosphate in the active site
50	<a href="#">d1q50a_</a>	Alignment	not modelled	97.1	14	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI
51	<a href="#">c3nbuC_</a>	Alignment	not modelled	97.1	12	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> crystal structure of pgi glucosephosphate isomerase
52	<a href="#">c3ujhB_</a>	Alignment	not modelled	96.8	13	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> crystal structure of substrate-bound glucose-6-phosphate isomerase2 from toxoplasma gondii
53	<a href="#">c3hbnB_</a>	Alignment	not modelled	96.3	17	<b>PDB header:</b> ribosome <b>Chain:</b> B: <b>PDB Molecule:</b> ribosomal protein s2;

53	<a href="#">c3ubnB_</a>	Alignment	not modelled	96.3	17	<b>PDBTitle:</b> homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome. <b>PDB header:</b> isomerase
54	<a href="#">c3pr3B_</a>	Alignment	not modelled	96.3	19	<b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> crystal structure of plasmodium falciparum glucose-6-phosphate2 isomerase (pf14_0341) in complex with fructose-6-phosphate
55	<a href="#">c2zkqb_</a>	Alignment	not modelled	96.2	20	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> B: <b>PDB Molecule:</b> rna expansion segment es3; <b>PDBTitle:</b> structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
56	<a href="#">c3iz6A_</a>	Alignment	not modelled	96.1	15	<b>PDB header:</b> ribosome <b>Chain:</b> A: <b>PDB Molecule:</b> 40s ribosomal protein sa (s2p); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
57	<a href="#">c3bchA_</a>	Alignment	not modelled	95.8	20	<b>PDB header:</b> cell adhesion, ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> 40s ribosomal protein sa; <b>PDBTitle:</b> crystal structure of the human laminin receptor precursor
58	<a href="#">d1y5ia2</a>	Alignment	not modelled	95.7	8	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3
59	<a href="#">c1h0hA_</a>	Alignment	not modelled	95.7	11	<b>PDB header:</b> dehydrogenase <b>Chain:</b> A: <b>PDB Molecule:</b> formate dehydrogenase (large subunit); <b>PDBTitle:</b> tungsten containing formate dehydrogenase from2 desulfovibrio gigas
60	<a href="#">d2jioa2</a>	Alignment	not modelled	95.7	13	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3
61	<a href="#">c3izbA_</a>	Alignment	not modelled	95.7	15	<b>PDB header:</b> ribosome <b>Chain:</b> A: <b>PDB Molecule:</b> 40s ribosomal protein rps0 (s2p); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
62	<a href="#">c1s1hB_</a>	Alignment	not modelled	95.6	14	<b>PDB header:</b> ribosome <b>Chain:</b> B: <b>PDB Molecule:</b> 40s ribosomal protein s0-a; <b>PDBTitle:</b> structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
63	<a href="#">c1y5iA_</a>	Alignment	not modelled	95.5	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> respiratory nitrate reductase 1 alpha chain; <b>PDBTitle:</b> the crystal structure of the narghi mutant nari-k86a
64	<a href="#">c2v45A_</a>	Alignment	not modelled	95.5	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic nitrate reductase; <b>PDBTitle:</b> a new catalytic mechanism of periplasmic nitrate reductase2 from desulfovibrio desulfuricans atcc 27774 from3 crystallographic and epr data and based on detailed4 analysis of the sixth ligand
65	<a href="#">d1logya2</a>	Alignment	not modelled	95.4	10	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3
66	<a href="#">c2xznB_</a>	Alignment	not modelled	95.4	19	<b>PDB header:</b> ribosome <b>Chain:</b> B: <b>PDB Molecule:</b> rps0e; <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
67	<a href="#">d1h0ha2</a>	Alignment	not modelled	95.3	12	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3
68	<a href="#">c2ivfA_</a>	Alignment	not modelled	95.3	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ethylbenzene dehydrogenase alpha-subunit; <b>PDBTitle:</b> ethylbenzene dehydrogenase from aromatoleum aromaticum
69	<a href="#">d2uubb1</a>	Alignment	not modelled	95.2	23	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Ribosomal protein S2 <b>Family:</b> Ribosomal protein S2
70	<a href="#">d2iv2x2</a>	Alignment	not modelled	95.2	9	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3
71	<a href="#">c2e7zA_</a>	Alignment	not modelled	95.1	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> acetylene hydratase ahγ; <b>PDBTitle:</b> acetylene hydratase from pelobacter acetylenicus
72	<a href="#">c1kqgA_</a>	Alignment	not modelled	95.0	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> formate dehydrogenase, nitrate-inducible, major subunit; <b>PDBTitle:</b> formate dehydrogenase n from e. coli
73	<a href="#">d2gy9b1</a>	Alignment	not modelled	94.9	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Ribosomal protein S2 <b>Family:</b> Ribosomal protein S2
74	<a href="#">c2nyaF_</a>	Alignment	not modelled	94.8	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> periplasmic nitrate reductase; <b>PDBTitle:</b> crystal structure of the periplasmic nitrate reductase2 (nap) from escherichia coli
75	<a href="#">d1kqfa2</a>	Alignment	not modelled	94.7	9	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3
76	<a href="#">c1ogyA_</a>	Alignment	not modelled	94.7	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic nitrate reductase; <b>PDBTitle:</b> crystal structure of the heterodimeric nitrate reductase2 from rhodobacter sphaeroides
						<b>PDB header:</b> oxidoreductase

77	<a href="#">c2vpyE_</a>	Alignment	not modelled	94.6	11	<b>Chain:</b> E: <b>PDB Molecule:</b> thiosulfate reductase; <b>PDBTitle:</b> polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
78	<a href="#">c2iv2X_</a>	Alignment	not modelled	94.4	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> X: <b>PDB Molecule:</b> formate dehydrogenase h; <b>PDBTitle:</b> reinterpretation of reduced form of formate dehydrogenase h2 from e. coli
79	<a href="#">d1vi6a_</a>	Alignment	not modelled	93.8	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Ribosomal protein S2 <b>Family:</b> Ribosomal protein S2
80	<a href="#">d1vlfm2</a>	Alignment	not modelled	92.8	5	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3
81	<a href="#">c1tmoA_</a>	Alignment	not modelled	92.1	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trimethylamine n-oxide reductase; <b>PDBTitle:</b> trimethylamine n-oxide reductase from shewanella massilia
82	<a href="#">d1dmra2</a>	Alignment	not modelled	92.1	11	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3
83	<a href="#">d1p3da1</a>	Alignment	not modelled	91.5	11	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
84	<a href="#">c1vlfQ_</a>	Alignment	not modelled	91.5	5	<b>PDB header:</b> oxidoreductase <b>Chain:</b> Q: <b>PDB Molecule:</b> pyrogallol hydroxytransferase large subunit; <b>PDBTitle:</b> crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici complexed3 with inhibitor 1,2,4,5-tetrahydroxy-benzene
85	<a href="#">c3jwpA_</a>	Alignment	not modelled	90.8	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein sir2 homologue; <b>PDBTitle:</b> crystal structure of plasmodium falciparum sir2a (pf13_0152) in2 complex with amp
86	<a href="#">c3uagA_</a>	Alignment	not modelled	90.3	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (udp-n-acetylmuramoyl-l-alanine:d- <b>PDBTitle:</b> udp-n-acetylmuramoyl-l-alanine:d-glutamate ligase
87	<a href="#">c2axqA_</a>	Alignment	not modelled	90.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine dehydrogenase; <b>PDBTitle:</b> apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
88	<a href="#">d1tmoa2</a>	Alignment	not modelled	89.7	9	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3
89	<a href="#">c1h5nC_</a>	Alignment	not modelled	89.5	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> dmsO reductase; <b>PDBTitle:</b> dmsO reductase modified by the presence of dms and air
90	<a href="#">d2ax3a2</a>	Alignment	not modelled	89.0	12	<b>Fold:</b> YjeF N-terminal domain-like <b>Superfamily:</b> YjeF N-terminal domain-like <b>Family:</b> YjeF N-terminal domain-like
91	<a href="#">d1j6ua1</a>	Alignment	not modelled	88.6	17	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
92	<a href="#">c3lk7A_</a>	Alignment	not modelled	88.5	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramoylalanine--d-glutamate ligase; <b>PDBTitle:</b> the crystal structure of udp-n-acetylmuramoylalanine-d-2 glutamate (murd) ligase from streptococcus agalactiae to3 1.5a
93	<a href="#">d2jfga1</a>	Alignment	not modelled	88.5	14	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
94	<a href="#">c2q1yB_</a>	Alignment	not modelled	88.2	22	<b>PDB header:</b> cell cycle, signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsz; <b>PDBTitle:</b> crystal structure of cell division protein ftsz from mycobacterium2 tuberculosis in complex with gtp-gamma-s
95	<a href="#">d1ma3a_</a>	Alignment	not modelled	88.0	7	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Sir2 family of transcriptional regulators
96	<a href="#">c1j6uA_</a>	Alignment	not modelled	86.9	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate-alanine ligase murc; <b>PDBTitle:</b> crystal structure of udp-n-acetylmuramate-alanine ligase2 murc (tm0231) from thermotoga maritima at 2.3 a resolution
97	<a href="#">c2f00A_</a>	Alignment	not modelled	86.8	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate--l-alanine ligase; <b>PDBTitle:</b> escherichia coli murc
98	<a href="#">d2b4ya1</a>	Alignment	not modelled	86.7	9	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Sir2 family of transcriptional regulators
99	<a href="#">c1w59B_</a>	Alignment	not modelled	86.2	19	<b>PDB header:</b> cell division <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsz homolog 1; <b>PDBTitle:</b> ftsz dimer, empty (m. jannaschii)
100	<a href="#">c3k35D_</a>	Alignment	not modelled	85.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> nad-dependent deacetylase sirtuin-6; <b>PDBTitle:</b> crystal structure of human sir6
101	<a href="#">d1m2ka_</a>	Alignment	not modelled	85.8	11	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Sir2 family of transcriptional regulators
102	<a href="#">d1yc5a1</a>	Alignment	not modelled	85.7	5	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain



					<b>Family:</b> Sir2 family of transcriptional regulators
103	<a href="#">c3d3jA_</a>	Alignment	not modelled	85.3	11 <b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> enhancer of mrna-decapping protein 3; <b>PDBTitle:</b> crystal structure of human edc3p
104	<a href="#">c3pkiF_</a>	Alignment	not modelled	85.0	12 <b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> nad-dependent deacetylase sirtuin-6; <b>PDBTitle:</b> human sirt6 crystal structure in complex with adp ribose
105	<a href="#">c2ax3A_</a>	Alignment	not modelled	84.2	12 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein tm0922; <b>PDBTitle:</b> crystal structure of a putative carbohydrate kinase (tm0922) from2 thermotoga maritima msb8 at 2.25 a resolution
106	<a href="#">c2rhoB_</a>	Alignment	not modelled	83.2	22 <b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsz; <b>PDBTitle:</b> synthetic gene encoded bacillus subtilis ftsz ncs dimer with2 bound gdp and gtp-gamma-s
107	<a href="#">c1ir6A_</a>	Alignment	not modelled	82.9	14 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> exonuclease recj; <b>PDBTitle:</b> crystal structure of exonuclease recj bound to manganese
108	<a href="#">d1ir6a_</a>	Alignment	not modelled	82.9	14 <b>Fold:</b> DHH phosphoesterases <b>Superfamily:</b> DHH phosphoesterases <b>Family:</b> Exonuclease Recj
109	<a href="#">d1pjqa1</a>	Alignment	not modelled	81.5	21 <b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Siroheme synthase N-terminal domain-like
110	<a href="#">d1rq2a1</a>	Alignment	not modelled	80.4	25 <b>Fold:</b> Tubulin nucleotide-binding domain-like <b>Superfamily:</b> Tubulin nucleotide-binding domain-like <b>Family:</b> Tubulin, GTPase domain
111	<a href="#">c1e5lA_</a>	Alignment	not modelled	78.5	15 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine reductase; <b>PDBTitle:</b> apo saccharopine reductase from magnaporthe grisea
112	<a href="#">d1s5pa_</a>	Alignment	not modelled	78.4	21 <b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Sir2 family of transcriptional regulators
113	<a href="#">c2dg2D_</a>	Alignment	not modelled	77.2	11 <b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> apolipoprotein a-i binding protein; <b>PDBTitle:</b> crystal structure of mouse apolipoprotein a-i binding2 protein
114	<a href="#">c3eagA_</a>	Alignment	not modelled	77.2	23 <b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate:l-alanyl-gamma-d-glutamyl-meso- <b>PDBTitle:</b> the crystal structure of udp-n-acetylmuramate:l-alanyl-gamma-d-2 glutamyl-meso-diaminopimelate ligase (mpl) from neisseria3 meningitides
115	<a href="#">c3d3kD_</a>	Alignment	not modelled	77.1	12 <b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> enhancer of mrna-decapping protein 3; <b>PDBTitle:</b> crystal structure of human edc3p
116	<a href="#">c2vawA_</a>	Alignment	not modelled	76.9	22 <b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsz; <b>PDBTitle:</b> ftsz pseudomonas aeruginosa gdp
117	<a href="#">c3q2oB_</a>	Alignment	not modelled	76.8	21 <b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase, atpase subunit; <b>PDBTitle:</b> crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase
118	<a href="#">c3ijpA_</a>	Alignment	not modelled	76.7	14 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate reductase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate reductase from2 bartonella henselae at 2.0a resolution
119	<a href="#">d1libja_</a>	Alignment	not modelled	74.2	17 <b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
120	<a href="#">d1kjqa2</a>	Alignment	not modelled	74.2	8 <b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like