







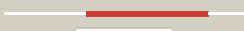





















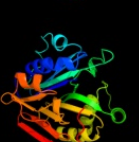


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1jxaA_</a>	 Alignment		100.0	100	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucosamine 6-phosphate synthase; <b>PDBTitle:</b> glucosamine 6-phosphate synthase with glucose 6-phosphate
2	<a href="#">d1moqa_</a>	 Alignment		100.0	100	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> double-SIS domain
3	<a href="#">c2zj3A_</a>	 Alignment		100.0	42	<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
4	<a href="#">c3tbfA_</a>	 Alignment		100.0	54	<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.
5	<a href="#">c3odpA_</a>	 Alignment		100.0	18	<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
6	<a href="#">c3i0zB_</a>	 Alignment		100.0	19	<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
7	<a href="#">c2amlB_</a>	 Alignment		100.0	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
8	<a href="#">c2puwA_</a>	 Alignment		100.0	40	<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
9	<a href="#">c3c3jA_</a>	 Alignment		100.0	19	<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
10	<a href="#">c3g68A_</a>	 Alignment		100.0	20	<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
11	<a href="#">c3fj1A_</a>	 Alignment		100.0	24	<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

12	<a href="#">d1j5xa_</a>	Alignment		100.0	27	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> double-SIS domain
13	<a href="#">c2decA_</a>	Alignment		100.0	27	<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
14	<a href="#">c3fkjA_</a>	Alignment		100.0	18	<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
15	<a href="#">c2a3nA_</a>	Alignment		100.0	18	<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
16	<a href="#">c3euaD_</a>	Alignment		100.0	23	<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
17	<a href="#">c3hbaA_</a>	Alignment		100.0	29	<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="#">c3knzA_</a>	Alignment		100.0	20	<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
19	<a href="#">d1xffa_</a>	Alignment		100.0	100	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
20	<a href="#">c1gph1_</a>	Alignment		100.0	27	<b>PDB header:</b> transferase(glutamine amidotransferase) <b>Chain:</b> 1: <b>PDB Molecule:</b> glutamine phosphoribosyl-pyrophosphate amidotransferase; <b>PDBTitle:</b> structure of the allosteric regulatory enzyme of purine biosynthesis
21	<a href="#">c1ecjB_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glutamine phosphoribosylpyrophosphate <b>PDBTitle:</b> escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
22	<a href="#">d1ecfa2</a>	Alignment	not modelled	100.0	29	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
23	<a href="#">d1gph12</a>	Alignment	not modelled	100.0	28	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
24	<a href="#">d1x9ia_</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> double-SIS domain
25	<a href="#">c1ct9D_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> asparagine synthetase b; <b>PDBTitle:</b> crystal structure of asparagine synthetase b from2 escherichia coli
26	<a href="#">d1ct9a2</a>	Alignment	not modelled	100.0	29	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
27	<a href="#">d1ofda3</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
28	<a href="#">d1ea0a3</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases

29	<a href="#">d1te5a_</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
30	<a href="#">c3mdnD_</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> glutamine aminotransferase class-ii domain protein; <b>PDBTitle:</b> structure of glutamine aminotransferase class-ii domain protein2 (spo2029) from silicibacter pomeroyi
31	<a href="#">c1m1zB_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactam synthetase; <b>PDBTitle:</b> beta-lactam synthetase apo enzyme
32	<a href="#">c1q15A_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> cara; <b>PDBTitle:</b> carbapenam synthetase
33	<a href="#">d1jgta2_</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
34	<a href="#">d1q15a2_</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
35	<a href="#">c2xhzC_</a>	Alignment	not modelled	99.9	20	<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
36	<a href="#">c3etnD_</a>	Alignment	not modelled	99.9	22	<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 in2 capsule formation (yp_209877.1) from bacteroides fragilis nctc 93433 at 1.70 a resolution
37	<a href="#">c1nriA_</a>	Alignment	not modelled	99.8	24	<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 from2 haemophilus influenzae
38	<a href="#">d1nria_</a>	Alignment	not modelled	99.8	24	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
39	<a href="#">d1vima_</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
40	<a href="#">c3fxaA_</a>	Alignment	not modelled	99.8	16	<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 listeria monocytogenes str. 4b f2365 at 1.60 a3 resolution
41	<a href="#">c3shoA_</a>	Alignment	not modelled	99.8	18	<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)
42	<a href="#">d1x94a_</a>	Alignment	not modelled	99.8	13	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
43	<a href="#">c2x3yA_</a>	Alignment	not modelled	99.7	15	<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
44	<a href="#">c1lm1A_</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin-dependent glutamate synthase; <b>PDBTitle:</b> structural studies on the synchronization of catalytic centers in2 glutamate synthase: native enzyme
45	<a href="#">d1tk9a_</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
46	<a href="#">c2vdcF_</a>	Alignment	not modelled	99.7	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> glutamate synthase [nadph] large chain; <b>PDBTitle:</b> the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications.
47	<a href="#">d1m3sa_</a>	Alignment	not modelled	99.7	19	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
48	<a href="#">c3cvjB_</a>	Alignment	not modelled	99.7	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) from2 bacillus halodurans c-125 at 2.00 a resolution
49	<a href="#">d1x92a_</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
50	<a href="#">d1jeoa_</a>	Alignment	not modelled	99.6	20	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
51	<a href="#">c3trjC_</a>	Alignment	not modelled	99.6	10	<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
52	<a href="#">c2yvaB_</a>	Alignment	not modelled	99.6	13	<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
53	<a href="#">d1wiwa_</a>	Alignment	not modelled	99.0	15	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> double-SIS domain

54	<a href="#">c2q8nB</a>	Alignment	not modelled	98.4	15	<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
55	<a href="#">c3ff1B</a>	Alignment	not modelled	98.3	16	<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
56	<a href="#">d1c7qa</a>	Alignment	not modelled	98.3	15	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI
57	<a href="#">d1gzda</a>	Alignment	not modelled	98.2	13	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI
58	<a href="#">d1q50a</a>	Alignment	not modelled	98.2	13	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI
59	<a href="#">c1zzgB</a>	Alignment	not modelled	98.2	23	<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
60	<a href="#">c1t10A</a>	Alignment	not modelled	98.1	13	<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
61	<a href="#">c3hjbA</a>	Alignment	not modelled	98.1	11	<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.
62	<a href="#">c2wu8A</a>	Alignment	not modelled	98.1	11	<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
63	<a href="#">d1hm5a</a>	Alignment	not modelled	98.0	12	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI
64	<a href="#">d1iata</a>	Alignment	not modelled	98.0	14	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI
65	<a href="#">d1u0fa</a>	Alignment	not modelled	98.0	14	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI
66	<a href="#">c3ljkA</a>	Alignment	not modelled	98.0	14	<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.
67	<a href="#">c3pr3B</a>	Alignment	not modelled	98.0	13	<b>PDB header:</b> isomerase <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
68	<a href="#">c3nbuC</a>	Alignment	not modelled	98.0	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
69	<a href="#">c2o2cB</a>	Alignment	not modelled	97.9	10	<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
70	<a href="#">c3ujhB</a>	Alignment	not modelled	97.9	14	<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
71	<a href="#">d1tmoa2</a>	Alignment	not modelled	92.9	16	<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
72	<a href="#">c1tmoA</a>	Alignment	not modelled	91.1	16	<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
73	<a href="#">d1dmra2</a>	Alignment	not modelled	88.3	18	<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
74	<a href="#">d1p3da1</a>	Alignment	not modelled	88.1	20	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
75	<a href="#">c2zkqb</a>	Alignment	not modelled	85.3	12	<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
76	<a href="#">c3iz6A</a>	Alignment	not modelled	85.1	13	<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
77	<a href="#">c1h5nC</a>	Alignment	not modelled	85.1	19	<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
78	<a href="#">c2vpyE</a>	Alignment	not modelled	84.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> thiosulfate reductase; <b>PDBTitle:</b> polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
79	<a href="#">d1ou1a2</a>	Alignment	not modelled	82.8	14	<b>Fold:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <b>Superfamily:</b> Formate dehydrogenase/DMSO reductase, domains 1-

79	<a href="#">c1e0ia2</a>	Alignment	not modelled	83.8	14	3 <b>Family:</b> Formate dehydrogenase/DMSO reductase, domains 1-3 <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
80	<a href="#">c2ivfA</a>	Alignment	not modelled	82.8	17	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
81	<a href="#">d1j6ua1</a>	Alignment	not modelled	80.9	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> acetylene hydratase ahy; <b>PDBTitle:</b> acetylene hydratase from pelobacter acetylenicus
82	<a href="#">c2e7zA</a>	Alignment	not modelled	80.5	15	<b>PDB header:</b> biosynthetic protein, flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophan halogenase; <b>PDBTitle:</b> rebh with bound l-trp
83	<a href="#">c2e4gB</a>	Alignment	not modelled	80.2	19	<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
84	<a href="#">d2iv2x2</a>	Alignment	not modelled	79.9	14	<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
85	<a href="#">c2f00A</a>	Alignment	not modelled	79.6	18	<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
86	<a href="#">c2iv2X</a>	Alignment	not modelled	79.3	13	<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
87	<a href="#">c1vlfQ</a>	Alignment	not modelled	79.1	18	<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
88	<a href="#">c2xznB</a>	Alignment	not modelled	77.3	7	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-galactopyranose mutase; <b>PDBTitle:</b> udp-galactopyranose mutase from mycobacterium tuberculosis
89	<a href="#">c1v0jB</a>	Alignment	not modelled	74.8	9	<b>PDB header:</b> biosynthetic protein, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of e81q mutant of mtnas in complex with s-2 adenosylmethionine
90	<a href="#">c3fpjA</a>	Alignment	not modelled	74.8	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
91	<a href="#">d1vlfm2</a>	Alignment	not modelled	74.6	17	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
92	<a href="#">d2dw4a2</a>	Alignment	not modelled	74.5	25	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-galactopyranose mutase; <b>PDBTitle:</b> udp-galactopyranose mutase from klebsiella pneumoniae with2 reduced fad
93	<a href="#">c2bi8A</a>	Alignment	not modelled	74.4	26	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan halogenase prna; <b>PDBTitle:</b> the structure of tryptophan 7-halogenase (prna) suggests a mechanism2 for regioselective chlorination
94	<a href="#">c2ardA</a>	Alignment	not modelled	72.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> l-amino acid oxidase; <b>PDBTitle:</b> the l-amino acid oxidase from rhodococcus opacus in complex2 with l-alanine
95	<a href="#">c2jb1B</a>	Alignment	not modelled	72.2	22	<b>Fold:</b> Pyruvate kinase C-terminal domain-like <b>Superfamily:</b> PK C-terminal domain-like <b>Family:</b> Pyruvate kinase, C-terminal domain
96	<a href="#">d1pkla3</a>	Alignment	not modelled	71.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protoporphyrinogen oxidase, mitochondrial; <b>PDBTitle:</b> crystal structure of protoporphyrinogen ix oxidase
97	<a href="#">c1sezA</a>	Alignment	not modelled	71.6	24	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan halogenase; <b>PDBTitle:</b> crystal structure of tryptophan halogenase (yp_750003.1) from2 shewanella frigidimarina ncimb 400 at 1.50 a resolution
98	<a href="#">c2pyxA</a>	Alignment	not modelled	71.5	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-glutamate oxidase; <b>PDBTitle:</b> crystal structure of l-glutamate oxidase from streptomyces sp. x-119-6
99	<a href="#">c2e1mA</a>	Alignment	not modelled	71.3	26	<b>Fold:</b> Pyruvate kinase C-terminal domain-like <b>Superfamily:</b> PK C-terminal domain-like <b>Family:</b> Pyruvate kinase, C-terminal domain
100	<a href="#">d1e0ta3</a>	Alignment	not modelled	70.9	19	<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
101	<a href="#">c3bchA</a>	Alignment	not modelled	70.1	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dimethyl sulfoxide reductase; <b>PDBTitle:</b> the crystal structure of rhodobacter sphaeroides dimethylsulfoxide2 reductase reveals two distinct molybdenum coordination environments.
102	<a href="#">c1eu1A</a>	Alignment	not modelled	70.0	19	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
103	<a href="#">d2jfga1</a>	Alignment	not modelled	68.5	17	<b>PDB header:</b> oxidoreductase/repressor <b>Chain:</b> A: <b>PDB Molecule:</b> lysine-specific histone demethylase 1; <b>PDBTitle:</b> structural basis of lsd1-corest selectivity in histone h32
104	<a href="#">c2v1dA</a>	Alignment	not modelled	67.6	17	



					recognition
105	<a href="#">c2xagA_</a>	Alignment	not modelled	67.5	17 <b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> lysine-specific histone demethylase 1; <b>PDBTitle:</b> crystal structure of lsd1-corest in complex with para-bromo-2 (-)-trans-2-phenylcyclopropyl-1-amine
106	<a href="#">d1reoa1</a>	Alignment	not modelled	67.2	36 <b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
107	<a href="#">c2weuD_</a>	Alignment	not modelled	66.5	15 <b>PDB header:</b> antifungal protein <b>Chain:</b> D: <b>PDB Molecule:</b> tryptophan 5-halogenase; <b>PDBTitle:</b> crystal structure of tryptophan 5-halogenase (pyrh) complex2 with substrate tryptophan
108	<a href="#">c2hkoA_</a>	Alignment	not modelled	66.5	17 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> lysine-specific histone demethylase 1; <b>PDBTitle:</b> crystal structure of lsd1
109	<a href="#">c3jwpA_</a>	Alignment	not modelled	66.1	7 <b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulatory protein sir2 homologue; <b>PDBTitle:</b> crystal structure of plasmodium falciparum sir2a (pf13_0152) in2 complex with amp
110	<a href="#">c2fymA_</a>	Alignment	not modelled	64.8	20 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enolase; <b>PDBTitle:</b> crystal structure of e. coli enolase complexed with the2 minimal binding segment of rnae e.
111	<a href="#">c3k35D_</a>	Alignment	not modelled	64.3	25 <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 sirt6
112	<a href="#">c1f8sA_</a>	Alignment	not modelled	63.8	31 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-amino acid oxidase; <b>PDBTitle:</b> crystal structure of l-amino acid oxidase from calloselasma2 rhodostoma, complexed with three molecules of o-aminobenzoate.
113	<a href="#">d1w6ta1</a>	Alignment	not modelled	63.5	20 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> Enolase
114	<a href="#">c3pkiF_</a>	Alignment	not modelled	63.2	25 <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
115	<a href="#">d1pdza1</a>	Alignment	not modelled	62.1	16 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> Enolase
116	<a href="#">d2iida1</a>	Alignment	not modelled	61.9	33 <b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
117	<a href="#">d1yc5a1</a>	Alignment	not modelled	61.3	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
118	<a href="#">c1y5iA_</a>	Alignment	not modelled	61.3	6 <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
119	<a href="#">c3a1lA_</a>	Alignment	not modelled	60.2	14 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-methyl-3-hydroxypyridine-5-carboxylic acid oxygenase; <b>PDBTitle:</b> crystal structure of 2-methyl-3-hydroxypyridine-5-carboxylic acid2 oxygenase, mutant y270a
120	<a href="#">d1liua3</a>	Alignment	not modelled	59.9	19 <b>Fold:</b> Pyruvate kinase C-terminal domain-like <b>Superfamily:</b> PK C-terminal domain-like <b>Family:</b> Pyruvate kinase, C-terminal domain