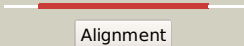

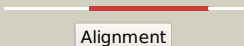

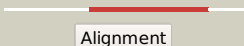







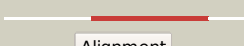











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3436c_glmS_3855195_3857069
Date	Fri Aug 9 18:20:11 BST 2019
Unique Job ID	6632c6015ba32ce5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1xaA_</a>	 Alignment		100.0	45	<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="#">c2zj3A_</a>	 Alignment		100.0	40	<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
3	<a href="#">d1moqa_</a>	 Alignment		100.0	46	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> double-SIS domain
4	<a href="#">c3tbfA_</a>	 Alignment		100.0	40	<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	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative tagatose-6-phosphate ketose/aldehyde isomerase; <b>PDBTitle:</b> crystal structure of a putative tagatose-6-phosphate ketose/aldehyde2 isomerase (nt01cx_0292) from clostridium novyi nt at 2.35 a3 resolution
6	<a href="#">c3i0zB_</a>	 Alignment		100.0	18	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative tagatose-6-phosphate ketose/aldehyde isomerase; <b>PDBTitle:</b> crystal structure of putative putative tagatose-6- phosphate2 ketose/aldehyde isomerase (np_344614.1) from streptococcus pneumoniae3 tigr4 at 1.70 a resolution
7	<a href="#">c4s1wA_</a>	 Alignment		100.0	39	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine--fructose-6-phosphate aminotransferase <b>PDBTitle:</b> structure of a putative glutamine--fructose-6-phosphate2 aminotransferase from staphylococcus aureus subsp. aureus mu50
8	<a href="#">c2amlB_</a>	 Alignment		100.0	20	<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
9	<a href="#">c3g68A_</a>	 Alignment		100.0	19	<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
10	<a href="#">c2puwA_</a>	 Alignment		100.0	36	<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
11	<a href="#">c3c3jA_</a>	 Alignment		100.0	20	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative tagatose-6-phosphate ketose/aldehyde isomerase; <b>PDBTitle:</b> crystal structure of tagatose-6-phosphate ketose/aldehyde isomerase from2 escherichia coli

12	<a href="#">c3fj1A</a>	Alignment		100.0	28	<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
13	<a href="#">d1j5xa</a>	Alignment		100.0	26	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> double-SIS domain
14	<a href="#">c2decA</a>	Alignment		100.0	24	<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
15	<a href="#">c3fkjA</a>	Alignment		100.0	20	<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
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="#">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
18	<a href="#">c3knzA</a>	Alignment		100.0	21	<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="#">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
20	<a href="#">c1gph1</a>	Alignment		100.0	25	<b>PDB header:</b> transferase <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	25	<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="#">d1xffa</a>	Alignment	not modelled	100.0	45	<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	27	<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="#">d1ecfa2</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
25	<a href="#">d1x9ia</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> double-SIS domain
26	<a href="#">c1ct9D</a>	Alignment	not modelled	100.0	27	<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
27	<a href="#">d1ct9a2</a>	Alignment	not modelled	100.0	27	<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="#">d1ofda3</a>	Alignment	not modelled	100.0	25	<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="#">c4zfb_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> amidohydrolase egtc; <b>PDBTitle:</b> ergothioneine-biosynthetic ntn hydrolase egtc, apo form
30	<a href="#">d1ea0a3</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
31	<a href="#">d1te5a_</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
32	<a href="#">c3mdnD_</a>	Alignment	not modelled	99.9	26	<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
33	<a href="#">c4s12C_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> n-acetylmuramic acid 6-phosphate etherase; <b>PDBTitle:</b> 1.55 angstrom crystal structure of n-acetylmuramic acid 6-phosphate2 etherase from yersinia enterocolitica.
34	<a href="#">c1m1zB_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactam synthetase; <b>PDBTitle:</b> beta-lactam synthetase apo enzyme
35	<a href="#">c1q15A_</a>	Alignment	not modelled	99.9	25	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> cara; <b>PDBTitle:</b> carbapenam synthetase
36	<a href="#">d1jgta2</a>	Alignment	not modelled	99.9	22	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
37	<a href="#">d1q15a2</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
38	<a href="#">c4lzd_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> lyase/lyase inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> n-acetylmuramic acid 6-phosphate etherase; <b>PDBTitle:</b> crystal structure of murq from h.influenzae with bound inhibitor
39	<a href="#">c2xhzC_</a>	Alignment	not modelled	99.9	21	<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
40	<a href="#">c5uqiA_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphosugar isomerase; <b>PDBTitle:</b> e. coli cft073 c3406 in complex with a5p
41	<a href="#">c3etnD_</a>	Alignment	not modelled	99.8	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 in2 capsule formation (yp_209877.1) from bacteroides fragilis nctc 93433 at 1.70 a resolution
42	<a href="#">d1nria_</a>	Alignment	not modelled	99.8	22	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
43	<a href="#">c1nriA_</a>	Alignment	not modelled	99.8	22	<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
44	<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
45	<a href="#">c3shoA_</a>	Alignment	not modelled	99.8	19	<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 sphaerobacter2 thermophilus (sugar isomerase domain)
46	<a href="#">d1vima_</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
47	<a href="#">d1x94a_</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
48	<a href="#">d1tk9a_</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
49	<a href="#">c4ivnB_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> the vibrio vulnificus nanr protein complexed with mannac-6p
50	<a href="#">d1m3sa_</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
51	<a href="#">c2x3yA_</a>	Alignment	not modelled	99.6	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
52	<a href="#">c3cvjB_</a>	Alignment	not modelled	99.6	16	<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
53	<a href="#">c2vdcF_</a>	Alignment	not modelled	99.6	22	<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 from

						cryo-2 electron microscopy and its oligomerization behavior in solution:3 functional implications.
54	<a href="#">d1jeoa_</a>	Alignment	not modelled	99.6	17	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
55	<a href="#">c5by2A_</a>	Alignment	not modelled	99.5	17	<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
56	<a href="#">d1x92a_</a>	Alignment	not modelled	99.5	15	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
57	<a href="#">c3trjC_</a>	Alignment	not modelled	99.5	14	<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
58	<a href="#">c1lm1A_</a>	Alignment	not modelled	99.5	17	<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
59	<a href="#">c5i01B_</a>	Alignment	not modelled	99.4	16	<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
60	<a href="#">c2yvaB_</a>	Alignment	not modelled	99.4	16	<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
61	<a href="#">c4bbaA_</a>	Alignment	not modelled	99.3	12	<b>PDB header:</b> protein-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> glucokinase regulatory protein; <b>PDBTitle:</b> crystal structure of glucokinase regulatory protein complexed to2 phosphate
62	<a href="#">c4lc9A_</a>	Alignment	not modelled	99.3	13	<b>PDB header:</b> transferase/transferase regulator <b>Chain:</b> A: <b>PDB Molecule:</b> glucokinase regulatory protein; <b>PDBTitle:</b> structural basis for regulation of human glucokinase by glucokinase2 regulatory protein
63	<a href="#">c3w0ID_</a>	Alignment	not modelled	99.2	15	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> glucokinase regulatory protein; <b>PDBTitle:</b> the crystal structure of xenopus glucokinase and glucokinase2 regulatory protein complex
64	<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
65	<a href="#">c2q8nB_</a>	Alignment	not modelled	98.4	19	<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 (ec 5.3.1.9)2 (tm1385) from thermotoga maritima at 1.82 a resolution
66	<a href="#">d1c7qa_</a>	Alignment	not modelled	98.1	17	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI
67	<a href="#">c1zzgB_</a>	Alignment	not modelled	98.1	18	<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
68	<a href="#">c6otuA_</a>	Alignment	not modelled	98.1	10	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> crystal structure of a glucose-6-phosphate isomerase from chlamydia2 trachomatis d/uv-3/cx
69	<a href="#">c3ff1B_</a>	Alignment	not modelled	98.1	23	<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
70	<a href="#">d1gzda_</a>	Alignment	not modelled	98.0	17	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI
71	<a href="#">c3hjbA_</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> 1.5 angstrom crystal structure of glucose-6-phosphate isomerase from2 vibrio cholerae.
72	<a href="#">d1q50a_</a>	Alignment	not modelled	98.0	14	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI
73	<a href="#">c4em6D_</a>	Alignment	not modelled	98.0	17	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> the structure of glucose-6-phosphate isomerase (gpi) from brucella2 melitensis
74	<a href="#">c2wu8A_</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> structural studies of phosphoglucose isomerase from2 mycobacterium tuberculosis h37rv
75	<a href="#">c3ljkA_</a>	Alignment	not modelled	97.9	18	<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.
76	<a href="#">d1iata_</a>	Alignment	not modelled	97.9	16	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI
77	<a href="#">c1t10A_</a>	Alignment	not modelled	97.9	14	<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
78	<a href="#">d1hm5a_</a>	Alignment	not modelled	97.9	15	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI
79	<a href="#">d1u0fa_</a>	Alignment	not modelled	97.9	15	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> Phosphoglucose isomerase, PGI

80	<a href="#">c3ujhB</a>	Alignment	not modelled	97.8	18	<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
81	<a href="#">c6bzcA</a>	Alignment	not modelled	97.8	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> crystal structure of glucose-6-phosphate isomerase from2 elizabethkingia anophelis with bound glucose-6-phosphate
82	<a href="#">c3pr3B</a>	Alignment	not modelled	97.8	17	<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
83	<a href="#">c2o2cB</a>	Alignment	not modelled	97.8	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
84	<a href="#">c3nbuC</a>	Alignment	not modelled	97.7	15	<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
85	<a href="#">c4qfA</a>	Alignment	not modelled	97.7	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> structure of a glucose-6-phosphate isomerase from trypanosoma cruzi
86	<a href="#">d2iv2x2</a>	Alignment	not modelled	94.8	17	<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
87	<a href="#">d1tmoa2</a>	Alignment	not modelled	94.6	14	<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
88	<a href="#">c1tmoA</a>	Alignment	not modelled	94.1	14	<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
89	<a href="#">c2iv2X</a>	Alignment	not modelled	93.9	16	<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 h from e.2 coli
90	<a href="#">c2ivfA</a>	Alignment	not modelled	93.0	21	<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
91	<a href="#">c2e7zA</a>	Alignment	not modelled	91.8	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> acetylene hydratase ahy; <b>PDBTitle:</b> acetylene hydratase from pelobacter acetylenicus
92	<a href="#">d1dmra2</a>	Alignment	not modelled	90.1	14	<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
93	<a href="#">d2jioa2</a>	Alignment	not modelled	90.0	17	<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
94	<a href="#">d1eu1a2</a>	Alignment	not modelled	89.9	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
95	<a href="#">c3fpjA</a>	Alignment	not modelled	89.5	11	<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 mtas in complex with s-2 adenosylmethionine
96	<a href="#">c3iz6A</a>	Alignment	not modelled	89.1	14	<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
97	<a href="#">c1h5nC</a>	Alignment	not modelled	88.7	14	<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
98	<a href="#">c1vifQ</a>	Alignment	not modelled	88.6	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-phloroglucinol transhydroxylase from2 pelobacter acidigallici complexed with inhibitor 1,2,4,5-3 tetrahydroxy-benzene
99	<a href="#">d1p3da1</a>	Alignment	not modelled	88.4	17	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
100	<a href="#">c5ucgE</a>	Alignment	not modelled	87.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> stage ii sporulation protein e; <b>PDBTitle:</b> structure of the pp2c phosphatase domain and a fragment of the2 regulatory domain of the cell fate determinant spoIie from bacillus3 subtilis
101	<a href="#">c2f00A</a>	Alignment	not modelled	84.7	19	<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
102	<a href="#">d1vlfm2</a>	Alignment	not modelled	83.6	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
103	<a href="#">c2vpyE</a>	Alignment	not modelled	82.8	15	<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) <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dimethyl sulfoxide reductase;

104	<a href="#">c1eu1A_</a>	Alignment	not modelled	80.5	17	<b>PDBTitle:</b> the crystal structure of rhodobacter sphaeroides dimethylsulfoxide2 reductase reveals two distinct molybdenum coordination environments.
105	<a href="#">c1h0hA_</a>	Alignment	not modelled	78.1	18	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> formate dehydrogenase subunit alpha; <b>PDBTitle:</b> tungsten containing formate dehydrogenase from desulfovibrio gigas
106	<a href="#">c4ffnA_</a>	Alignment	not modelled	77.7	19	<b>PDB header:</b> ligase/substrate <b>Chain:</b> A: <b>PDB Molecule:</b> pylc; <b>PDBTitle:</b> pylc in complex with d-ornithine and amppnp
107	<a href="#">c6cz7C_</a>	Alignment	not modelled	77.5	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> arra; <b>PDBTitle:</b> the arsenate respiratory reductase (arr) complex from shewanella sp.2 ana-3
108	<a href="#">c2e4gB_</a>	Alignment	not modelled	77.0	27	<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
109	<a href="#">c6ib5B_</a>	Alignment	not modelled	76.8	21	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophan 6-halogenase; <b>PDBTitle:</b> mutant of flavin-dependent tryptophan halogenase thal with altered2 regioselectivity (thal-rebh5)
110	<a href="#">c3zt9A_</a>	Alignment	not modelled	73.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> serine phosphatase; <b>PDBTitle:</b> the bacterial stressosome: a modular system that has been adapted to2 control secondary messenger signaling
111	<a href="#">c3jx9B_</a>	Alignment	not modelled	71.3	14	<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
112	<a href="#">c5fn0C_</a>	Alignment	not modelled	71.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> kynurenine 3-monooxygenase; <b>PDBTitle:</b> crystal structure of pseudomonas fluorescens kynurenine-3-2 monooxygenase (kmo) in complex with gsk180
113	<a href="#">c2xznB_</a>	Alignment	not modelled	70.8	14	<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
114	<a href="#">d1g8ka2</a>	Alignment	not modelled	69.1	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
115	<a href="#">d1h0ha2</a>	Alignment	not modelled	68.9	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
116	<a href="#">c2pyxA_</a>	Alignment	not modelled	68.8	18	<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
117	<a href="#">c3x0vA_</a>	Alignment	not modelled	68.5	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-lysine oxidase; <b>PDBTitle:</b> structure of l-lysine oxidase
118	<a href="#">c6frlA_</a>	Alignment	not modelled	68.5	30	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan halogenase superfamily; <b>PDBTitle:</b> brvh, a flavin-dependent halogenase from brevundimonas sp. bal3
119	<a href="#">d1j6ua1</a>	Alignment	not modelled	68.5	16	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
120	<a href="#">d1yc5a1</a>	Alignment	not modelled	67.7	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