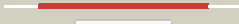



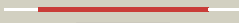



















Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0113_(gmhA)_137317_137907
 Date Tue Jul 23 14:50:15 BST 2019
 Unique Job ID df139f192c881beb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2x3yA_	 Alignment		100.0	41	PDB header: isomerase Chain: A: PDB Molecule: phosphoheptose isomerase; PDBTitle: crystal structure of gmha from burkholderia pseudomallei
2	d1x92a_	 Alignment		100.0	38	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
3	c2yvaB_	 Alignment		100.0	35	PDB header: dna binding protein Chain: B: PDB Molecule: dnaa initiator-associating protein diaa; PDBTitle: crystal structure of escherichia coli diaa
4	c5by2A_	 Alignment		100.0	36	PDB header: isomerase Chain: A: PDB Molecule: phosphoheptose isomerase; PDBTitle: sedoheptulose 7-phosphate isomerase from colwellia psychrerythraea2 strain 34h
5	d1tk9a_	 Alignment		100.0	37	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
6	c5i01B_	 Alignment		100.0	43	PDB header: isomerase Chain: B: PDB Molecule: phosphoheptose isomerase; PDBTitle: structure of phosphoheptose isomerase gmha from neisseria gonorrhoeae
7	c3trjC_	 Alignment		100.0	32	PDB header: isomerase Chain: C: PDB Molecule: phosphoheptose isomerase; PDBTitle: structure of a phosphoheptose isomerase from francisella tularensis
8	d1x94a_	 Alignment		100.0	39	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
9	d1nria_	 Alignment		99.9	16	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
10	c1nriA_	 Alignment		99.9	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein hi0754; PDBTitle: crystal structure of putative phosphosugar isomerase hi0754 from2 haemophilus influenzae
11	c4lzjD_	 Alignment		99.9	16	PDB header: lyase/lyase inhibitor Chain: D: PDB Molecule: n-acetylmuramic acid 6-phosphate etherase; PDBTitle: crystal structure of murq from h.influenzae with bound inhibitor

12	c4s12C_	Alignment		99.9	19	PDB header: lyase Chain: C: PDB Molecule: n-acetylmuramic acid 6-phosphate etherase; PDBTitle: 1.55 angstrom crystal structure of n-acetylmuramic acid 6-phosphate2 etherase from yersinia enterocolitica.
13	c3cvjB_	Alignment		99.9	19	PDB header: isomerase Chain: B: PDB Molecule: putative phosphoheptose isomerase; PDBTitle: crystal structure of a putative phosphoheptose isomerase (bh3325) from2 bacillus halodurans c-125 at 2.00 a resolution
14	c3fxaA_	Alignment		99.8	16	PDB header: sugar binding protein Chain: A: PDB Molecule: sis domain protein; PDBTitle: crystal structure of a putative sugar-phosphate isomerase2 (lmof2365_0531) from listeria monocytogenes str. 4b f2365 at 1.60 a3 resolution
15	c3etnD_	Alignment		99.8	14	PDB header: isomerase Chain: D: PDB Molecule: putative phosphosugar isomerase involved in capsule PDBTitle: crystal structure of putative phosphosugar isomerase involved in2 capsule formation (yp_209877.1) from bacteroides fragilis nctc 93433 at 1.70 a resolution
16	c2xhzC_	Alignment		99.8	18	PDB header: isomerase Chain: C: PDB Molecule: arabinose 5-phosphate isomerase; PDBTitle: probing the active site of the sugar isomerase domain from e. coli2 arabinose-5-phosphate isomerase via x-ray crystallography
17	c5uqiA_	Alignment		99.8	15	PDB header: isomerase Chain: A: PDB Molecule: phosphosugar isomerase; PDBTitle: e. coli cft073 c3406 in complex with a5p
18	d1m3sa_	Alignment		99.8	22	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
19	c3shoA_	Alignment		99.8	23	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, rpir family; PDBTitle: crystal structure of rpir transcription factor from spbaerobacter2 thermophilus (sugar isomerase domain)
20	d1vima_	Alignment		99.8	20	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
21	c4ivnB_	Alignment	not modelled	99.8	18	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: the vibrio vulnificus nanr protein complexed with mannac-6p
22	d1jeoa_	Alignment	not modelled	99.7	25	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
23	c3hbaA_	Alignment	not modelled	99.7	17	PDB header: isomerase Chain: A: PDB Molecule: putative phosphosugar isomerase; PDBTitle: crystal structure of a putative phosphosugar isomerase (sden_2705)2 from shewanella denitrificans os217 at 2.00 a resolution
24	c3fj1A_	Alignment	not modelled	99.7	17	PDB header: isomerase Chain: A: PDB Molecule: putative phosphosugar isomerase; PDBTitle: crystal structure of putative phosphosugar isomerase (yp_167080.1)2 from silicibacter pomeroyi dss-3 at 1.75 a resolution
25	c4s1wA_	Alignment	not modelled	99.7	19	PDB header: transferase Chain: A: PDB Molecule: glutamine--fructose-6-phosphate aminotransferase PDBTitle: structure of a putative glutamine--fructose-6-phosphate2 aminotransferase from staphylococcus aureus subsp. aureus mu50
26	c2a3nA_	Alignment	not modelled	99.7	16	PDB header: sugar binding protein Chain: A: PDB Molecule: putative glucosamine-fructose-6-phosphate aminotransferase; PDBTitle: crystal structure of a putative glucosamine-fructose-6-phosphate2 aminotransferase (stm4540.s) from salmonella typhimurium lt2 at 1.353 a resolution
27	c3knzA_	Alignment	not modelled	99.7	20	PDB header: sugar binding protein Chain: A: PDB Molecule: putative sugar binding protein; PDBTitle: crystal structure of putative sugar binding protein (np_459565.1) from2 salmonella typhimurium lt2 at 2.50 a resolution
						PDB header: transferase Chain: A: PDB Molecule: isomerase domain of glutamine-fructose-

28	c2puwA_	Alignment	not modelled	99.7	15	6-phosphate PDBTitle: the crystal structure of isomerase domain of glucosamine-6-phosphate2 synthase from candida albicans
29	c2zj3A_	Alignment	not modelled	99.6	18	PDB header: transferase Chain: A: PDB Molecule: glucosamine--fructose-6-phosphate PDBTitle: isomerase domain of human glucose:fructose-6-phosphate2 amidotransferase
30	c3g68A_	Alignment	not modelled	99.6	14	PDB header: isomerase Chain: A: PDB Molecule: putative phosphosugar isomerase; PDBTitle: crystal structure of a putative phosphosugar isomerase (cd3275) from2 clostridium difficile 630 at 1.80 a resolution
31	d1j5xa_	Alignment	not modelled	99.6	15	Fold: SIS domain Superfamily: SIS domain Family: double-SIS domain
32	c3euaD_	Alignment	not modelled	99.6	17	PDB header: isomerase Chain: D: PDB Molecule: putative fructose-aminoacid-6-phosphate deglycase; PDBTitle: crystal structure of a putative phosphosugar isomerase (bsu32610) from2 bacillus subtilis at 1.90 a resolution
33	c2am1B_	Alignment	not modelled	99.6	22	PDB header: transferase Chain: B: PDB Molecule: sis domain protein; PDBTitle: crystal structure of lmo0035 protein (46906266) from listeria2 monocytogenes 4b f2365 at 1.50 a resolution
34	d1moqa_	Alignment	not modelled	99.6	14	Fold: SIS domain Superfamily: SIS domain Family: double-SIS domain
35	c3tbfA_	Alignment	not modelled	99.6	12	PDB header: transferase Chain: A: PDB Molecule: glucosamine--fructose-6-phosphate aminotransferase PDBTitle: c-terminal domain of glucosamine-fructose-6-phosphate aminotransferase2 from francisella tularensis.
36	c3fkjA_	Alignment	not modelled	99.6	23	PDB header: isomerase Chain: A: PDB Molecule: putative phosphosugar isomerases; PDBTitle: crystal structure of a putative phosphosugar isomerase (stm_0572) from2 salmonella typhimurium lt2 at 2.12 a resolution
37	c2decA_	Alignment	not modelled	99.5	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: 325aa long hypothetical protein; PDBTitle: crystal structure of the ph0510 protein from pyrococcus horikoshii ot3
38	d1x9ia_	Alignment	not modelled	99.5	25	Fold: SIS domain Superfamily: SIS domain Family: double-SIS domain
39	c3i0zB_	Alignment	not modelled	99.5	23	PDB header: isomerase Chain: B: PDB Molecule: putative tagatose-6-phosphate ketose/aldose isomerase; PDBTitle: crystal structure of putative putative tagatose-6-phosphate ketose/aldose isomerase (np_344614.1) from streptococcus pneumoniae3 tigr4 at 1.70 a resolution
40	c1jxaA_	Alignment	not modelled	99.4	15	PDB header: transferase Chain: A: PDB Molecule: glucosamine 6-phosphate synthase; PDBTitle: glucosamine 6-phosphate synthase with glucose 6-phosphate
41	c3c3jA_	Alignment	not modelled	99.4	22	PDB header: isomerase Chain: A: PDB Molecule: putative tagatose-6-phosphate ketose/aldose isomerase; PDBTitle: crystal structure of tagatose-6-phosphate ketose/aldose isomerase from2 escherichia coli
42	c3odpA_	Alignment	not modelled	99.4	18	PDB header: isomerase Chain: A: PDB Molecule: putative tagatose-6-phosphate ketose/aldose isomerase; PDBTitle: crystal structure of a putative tagatose-6-phosphate ketose/aldose2 isomerase (nt01cx_0292) from clostridium novyi nt at 2.35 a3 resolution
43	c3w01D_	Alignment	not modelled	99.3	15	PDB header: transferase/transferase inhibitor Chain: D: PDB Molecule: glucokinase regulatory protein; PDBTitle: the crystal structure of xenopus glucokinase and glucokinase2 regulatory protein complex
44	c4bbaA_	Alignment	not modelled	99.2	11	PDB header: protein-binding protein Chain: A: PDB Molecule: glucokinase regulatory protein; PDBTitle: crystal structure of glucokinase regulatory protein complexed to2 phosphate
45	c4lc9A_	Alignment	not modelled	99.2	11	PDB header: transferase/transferase regulator Chain: A: PDB Molecule: glucokinase regulatory protein; PDBTitle: structural basis for regulation of human glucokinase by glucokinase2 regulatory protein
46	c3ff1B_	Alignment	not modelled	98.1	21	PDB header: isomerase Chain: B: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: structure of glucose 6-phosphate isomerase from staphylococcus aureus
47	c2q8nB_	Alignment	not modelled	98.1	16	PDB header: isomerase Chain: B: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: crystal structure of glucose-6-phosphate isomerase (ec 5.3.1.9)2 (tm1385) from thermotoga maritima at 1.82 a resolution
48	d1c7qa_	Alignment	not modelled	98.0	18	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
49	c1zzgB_	Alignment	not modelled	97.8	23	PDB header: isomerase Chain: B: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: crystal structure of hypothetical protein tt0462 from thermus2 thermophilus hb8
50	c3jx9B_	Alignment	not modelled	97.6	10	PDB header: isomerase Chain: B: PDB Molecule: putative phosphoheptose isomerase; PDBTitle: crystal structure of putative phosphoheptose isomerase2 (yp_001815198.1) from exiguobacterium sp. 255-15 at 1.95 a resolution
51	c3ljkA_	Alignment	not modelled	97.0	18	PDB header: isomerase Chain: A: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: glucose-6-phosphate isomerase from francisella tularensis.
						PDB header: isomerase

52	c6bzcA	Alignment	not modelled	96.8	16	Chain: A: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: crystal structure of glucose-6-phosphate isomerase from2 elizabethkingia anophelis with bound glucose-6-phosphate
53	c3hjbA	Alignment	not modelled	96.7	18	PDB header: isomerase Chain: A: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: 1.5 angstrom crystal structure of glucose-6-phosphate isomerase from2 vibrio cholerae.
54	d1gzda	Alignment	not modelled	96.7	16	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
55	d1iata	Alignment	not modelled	96.7	16	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
56	c4em6D	Alignment	not modelled	96.7	20	PDB header: isomerase Chain: D: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: the structure of glucose-6-phosphate isomerase (gpi) from brucella2 melitensis
57	c2wu8A	Alignment	not modelled	96.6	18	PDB header: isomerase Chain: A: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: structural studies of phosphoglucose isomerase from2 mycobacterium tuberculosis h37rv
58	d1hm5a	Alignment	not modelled	96.5	16	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
59	d1q50a	Alignment	not modelled	96.5	13	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
60	c6otuA	Alignment	not modelled	96.3	14	PDB header: isomerase Chain: A: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: crystal structure of a glucose-6-phosphate isomerase from chlamydia2 trachomatis d/uv-3/cx
61	d1u0fa	Alignment	not modelled	96.3	16	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
62	d1y5ia2	Alignment	not modelled	96.1	13	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
63	c2e7zA	Alignment	not modelled	96.1	13	PDB header: lyase Chain: A: PDB Molecule: acetylene hydratase ahy; PDBTitle: acetylene hydratase from pelobacter acetylenicus
64	c5ch7E	Alignment	not modelled	96.0	10	PDB header: oxidoreductase Chain: E: PDB Molecule: dms0 reductase family type ii enzyme, molybdopterin PDBTitle: crystal structure of the perchlorate reductase pcrab - phe164 gate2 switch intermediate - from azospira suillum ps
65	c3ujhB	Alignment	not modelled	95.9	18	PDB header: isomerase Chain: B: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: crystal structure of substrate-bound glucose-6-phosphate isomerase2 from toxoplasma gondii
66	c1y5ia	Alignment	not modelled	95.9	10	PDB header: oxidoreductase Chain: A: PDB Molecule: respiratory nitrate reductase 1 alpha chain; PDBTitle: the crystal structure of the narghi mutant nari-k86a
67	c4qfhA	Alignment	not modelled	95.7	14	PDB header: isomerase Chain: A: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: structure of a glucose-6-phosphate isomerase from trypanosoma cruzi
68	c3nbuC	Alignment	not modelled	95.4	16	PDB header: isomerase Chain: C: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: crystal structure of pgi glucosephosphate isomerase
69	c1t10A	Alignment	not modelled	95.4	11	PDB header: isomerase Chain: A: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: phosphoglucose isomerase from leishmania mexicana in complex with2 substrate d-fructose-6-phosphate
70	c1h0hA	Alignment	not modelled	95.3	10	PDB header: electron transport Chain: A: PDB Molecule: formate dehydrogenase subunit alpha; PDBTitle: tungsten containing formate dehydrogenase from desulfovibrio gigas
71	d1h0ha2	Alignment	not modelled	95.3	12	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
72	d2jioa2	Alignment	not modelled	95.2	14	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
73	c2ivfA	Alignment	not modelled	95.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: ethylbenzene dehydrogenase alpha-subunit; PDBTitle: ethylbenzene dehydrogenase from aromatoleum aromaticum
74	c1kqgA	Alignment	not modelled	94.9	12	PDB header: oxidoreductase Chain: A: PDB Molecule: formate dehydrogenase, nitrate-inducible, major subunit; PDBTitle: formate dehydrogenase n from e. coli
75	c2nyaF	Alignment	not modelled	94.8	14	PDB header: oxidoreductase Chain: F: PDB Molecule: periplasmic nitrate reductase; PDBTitle: crystal structure of the periplasmic nitrate reductase2 (nap) from escherichia coli
76	d1kqfa2	Alignment	not modelled	94.8	12	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
77	c2o2cB	Alignment	not modelled	94.7	20	PDB header: isomerase Chain: B: PDB Molecule: glucose-6-phosphate isomerase, glycosomal; PDBTitle: crystal structure of phosphoglucose isomerase from t.

						brucei2 containing glucose-6-phosphate in the active site Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
78	d2iv2x2	Alignment	not modelled	94.7	16	PDB header: ribosome Chain: A: PDB Molecule: 40s ribosomal protein sa (s2p); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
79	c3iz6A_	Alignment	not modelled	94.6	12	PDB header: oxidoreductase Chain: A: PDB Molecule: periplasmic nitrate reductase; PDBTitle: 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
80	c2v45A_	Alignment	not modelled	94.5	16	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
81	d1ogyA2	Alignment	not modelled	94.4	15	PDB header: oxidoreductase Chain: C: PDB Molecule: arra; PDBTitle: the arsenate respiratory reductase (arr) complex from shewanella sp.2 ana-3
82	c6cz7C_	Alignment	not modelled	94.3	12	PDB header: oxidoreductase Chain: A: PDB Molecule: periplasmic nitrate reductase; PDBTitle: crystal structure of the heterodimeric nitrate reductase2 from rhodobacter sphaeroides
83	c1ogyA_	Alignment	not modelled	94.0	15	PDB header: ribosome Chain: B: PDB Molecule: 28s ribosomal protein s2, mitochondrial; PDBTitle: cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
84	c3j6vB_	Alignment	not modelled	94.0	12	Fold: Flavodoxin-like Superfamily: Ribosomal protein S2 Family: Ribosomal protein S2
85	d2gy9b1	Alignment	not modelled	94.0	18	PDB header: isomerase Chain: B: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: crystal structure of plasmodium falciparum glucose-6-phosphate2 isomerase (pf14_0341) in complex with fructose-6-phosphate
86	c3pr3B_	Alignment	not modelled	93.5	17	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
87	d1vlfm2	Alignment	not modelled	93.4	10	PDB header: oxidoreductase Chain: E: PDB Molecule: thiosulfate reductase; PDBTitle: polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
88	c2vpyE_	Alignment	not modelled	93.4	14	PDB header: ribosome Chain: V: PDB Molecule: 30s ribosomal protein s2; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
89	c5o5jV_	Alignment	not modelled	93.3	16	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s2,ribosomal protein s1; PDBTitle: crystal structure of e.coli ribosomal protein s2 in complex with n-2 terminal domain of s1
90	c4toiA_	Alignment	not modelled	93.2	16	PDB header: hydrolase Chain: A: PDB Molecule: nad-dependent protein deacylase; PDBTitle: sirtuin 4 orthologue from xenopus tropicalis in complex with adp-2 ribose
91	c5oj7A_	Alignment	not modelled	93.0	15	PDB header: ribosome Chain: B: PDB Molecule: 40s ribosomal protein s0-a; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1h, contains 40s subunit. the 60s4 ribosomal subunit is in file 1s1i.
92	c1s1hB_	Alignment	not modelled	92.8	17	PDB header: cell cycle, signaling protein Chain: B: PDB Molecule: cell division protein ftsz; PDBTitle: crystal structure of cell division protein ftsz from mycobacterium2 tuberculosis in complex with gtp-gamma-s
93	c2q1yB_	Alignment	not modelled	92.8	22	PDB header: oxidoreductase Chain: X: PDB Molecule: formate dehydrogenase h; PDBTitle: reinterpretation of reduced form of formate dehydrogenase h from e.2 coli
94	c2iv2X_	Alignment	not modelled	92.6	16	PDB header: ribosome Chain: B: PDB Molecule: rps0e; PDBTitle: 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
95	c2xznB_	Alignment	not modelled	92.6	14	PDB header: oxidoreductase Chain: Q: PDB Molecule: pyrogallol hydroxytransferase large subunit; PDBTitle: crystal structure of pyrogallol-phloroglucinol transhydroxylase from2 pelobacter acidigallici complexed with inhibitor 1,2,4,5-3 tetrahydroxy-benzene
96	c1vlfQ_	Alignment	not modelled	92.5	10	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
97	d1tmoa2	Alignment	not modelled	92.3	12	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
98	d1m2ka_	Alignment	not modelled	92.2	12	PDB header: ligase/substrate Chain: A: PDB Molecule: pylc; PDBTitle: pylc in complex with d-ornithine and amppnp
99	c4ffnA_	Alignment	not modelled	92.2	18	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsz; PDBTitle: crystal structure of a putative cell division protein ftsz (tfu_1113)2 from thermobifida fusca yx-er1 at 2.22 a resolution (psi community3 target, van wezel g.p.)
100	c4e6eA_	Alignment	not modelled	92.2	21	PDB header: ribosome

101	c3zeyC_	Alignment	not modelled	91.8	18	Chain: C: PDB Molecule: 40s ribosomal protein sa, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
102	c3bbnB_	Alignment	not modelled	91.7	19	PDB header: ribosome Chain: B: PDB Molecule: ribosomal protein s2; PDBTitle: homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
103	d1kjq2	Alignment	not modelled	91.5	17	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
104	c1h5nC_	Alignment	not modelled	91.5	10	PDB header: oxidoreductase Chain: C: PDB Molecule: dms0 reductase; PDBTitle: dms0 reductase modified by the presence of dms and air
105	c3izbA_	Alignment	not modelled	91.4	15	PDB header: ribosome Chain: A: PDB Molecule: 40s ribosomal protein rps0 (s2p); PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
106	d1ma3a_	Alignment	not modelled	91.2	11	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
107	c3jwpA_	Alignment	not modelled	91.2	11	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein sir2 homologue; PDBTitle: crystal structure of plasmodium falciparum sir2a (pf13_0152) in2 complex with amp
108	c2zqgb_	Alignment	not modelled	91.2	13	PDB header: ribosomal protein/rna Chain: B: PDB Molecule: rna expansion segment es3; PDBTitle: structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
109	c3uvzB_	Alignment	not modelled	91.0	18	PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase, atpase2 subunit from burkholderia ambifaria
110	c3j20B_	Alignment	not modelled	90.9	16	PDB header: ribosome Chain: B: PDB Molecule: 30s ribosomal protein s2p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
111	d1dmra2	Alignment	not modelled	90.8	11	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
112	c1tmoA_	Alignment	not modelled	90.8	10	PDB header: oxidoreductase Chain: A: PDB Molecule: trimethylamine n-oxide reductase; PDBTitle: trimethylamine n-oxide reductase from shewanella massilia
113	c3ax6C_	Alignment	not modelled	90.6	19	PDB header: ligase Chain: C: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide2 synthetase from thermotoga maritima
114	c4dimA_	Alignment	not modelled	90.6	20	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylglycinamide synthetase; PDBTitle: crystal structure of phosphoribosylglycinamide synthetase from2 anaerococcus prevotii
115	c3q2oB_	Alignment	not modelled	90.4	23	PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase
116	d1p3da1	Alignment	not modelled	90.3	13	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
117	c5t5mB_	Alignment	not modelled	90.0	14	PDB header: oxidoreductase Chain: B: PDB Molecule: tungsten formylmethanofuran dehydrogenase subunit fwdb; PDBTitle: tungsten-containing formylmethanofuran dehydrogenase from2 methanothermobacter wolfeii, trigonal form at 2.5 a.
118	d1yc5a1	Alignment	not modelled	89.8	9	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
119	c1gpjA_	Alignment	not modelled	89.7	16	PDB header: reductase Chain: A: PDB Molecule: glutamyl-trna reductase; PDBTitle: glutamyl-trna reductase from methanopyrus kandleri
120	c2dwcB_	Alignment	not modelled	89.7	20	PDB header: transferase Chain: B: PDB Molecule: 433aa long hypothetical phosphoribosylglycinamide formyl PDBTitle: crystal structure of probable phosphoribosylglycinamide formyl2 transferase from pyrococcus horikoshii ot3 complexed with adp