
























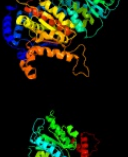
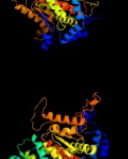
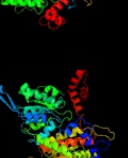


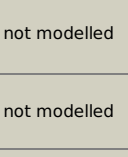


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0946c_(pgi)_1055028_1056689
Date	Fri Jul 26 01:50:54 BST 2019
Unique Job ID	0297f40250f74c3a

Detailed template information



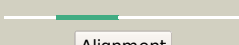

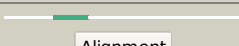
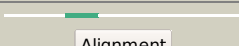






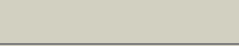
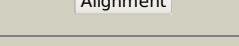
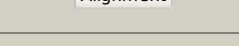
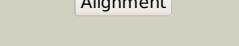

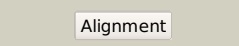
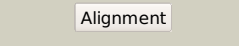
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2wu8A_	 Alignment		100.0	100	PDB header: isomerase Chain: A; PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: structural studies of phosphoglucose isomerase from2 mycobacterium tuberculosis h37rv
2	c3hjbA_	 Alignment		100.0	53	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.
3	c4qfhA_	 Alignment		100.0	48	PDB header: isomerase Chain: A; PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: structure of a glucose-6-phosphate isomerase from trypanosoma cruzi
4	d1q50a_	 Alignment		100.0	49	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
5	c2o2cB_	 Alignment		100.0	49	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
6	c1t10A_	 Alignment		100.0	49	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
7	d1iata_	 Alignment		100.0	48	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
8	c3nbuC_	 Alignment		100.0	53	PDB header: isomerase Chain: C; PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: crystal structure of pgi glucoselphosphate isomerase
9	d1lu0fa_	 Alignment		100.0	49	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
10	d1gzda_	 Alignment		100.0	50	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
11	d1hm5a_	 Alignment		100.0	51	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI

12	c6bzcA_	Alignment		100.0	49	PDB header: isomerase Chain: A: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: crystal structure of glucose-6-phosphate isomerase from2 elizabethkingia anophelis with bound glucose-6-phosphate
13	c4em6D_	Alignment		100.0	53	PDB header: isomerase Chain: D: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: the structure of glucose-6-phosphate isomerase (gpi) from brucella2 melitensis
14	c3pr3B_	Alignment		100.0	40	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
15	c3ujhB_	Alignment		100.0	46	PDB header: isomerase Chain: B: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: crystal structure of substrate-bound glucose-6-phosphate isomerase2 from toxoplasma gondii
16	c3ljkA_	Alignment		100.0	43	PDB header: isomerase Chain: A: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: glucose-6-phosphate isomerase from francisella tularensis.
17	c6otuA_	Alignment		100.0	35	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
18	d1c7qa_	Alignment		100.0	23	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
19	c3ff1B_	Alignment		100.0	21	PDB header: isomerase Chain: B: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: structure of glucose 6-phosphate isomerase from staphylococcus aureus
20	c2q8nB_	Alignment		100.0	28	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
21	c1zzgB_	Alignment	not modelled	100.0	27	PDB header: isomerase Chain: B: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: crystal structure of hypothetical protein tt0462 from thermus2 thermophilus hb8
22	d1x9ia_	Alignment	not modelled	99.1	14	Fold: SIS domain Superfamily: SIS domain Family: double-SIS domain
23	c2a3nA_	Alignment	not modelled	99.0	12	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
24	c3euaD_	Alignment	not modelled	98.9	15	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
25	c3hbaA_	Alignment	not modelled	98.8	16	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
26	d1j5xa_	Alignment	not modelled	98.8	11	Fold: SIS domain Superfamily: SIS domain Family: double-SIS domain
27	c3fkjA_	Alignment	not modelled	98.6	13	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
						PDB header: isomerase

28	c3g68A	Alignment	not modelled	98.6	14	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
29	c2puwA	Alignment	not modelled	98.6	11	PDB header: transferase Chain: A: PDB Molecule: isomerase domain of glutamine-fructose-6-phosphate PDBTitle: the crystal structure of isomerase domain of glucosamine-6-phosphate2 synthase from candida albicans
30	c3fj1A	Alignment	not modelled	98.6	14	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
31	c3knzA	Alignment	not modelled	98.6	12	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
32	c3c3jA	Alignment	not modelled	98.5	15	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
33	c2decA	Alignment	not modelled	98.5	12	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
34	c3odpA	Alignment	not modelled	98.5	16	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
35	c3i0zB	Alignment	not modelled	98.4	11	PDB header: isomerase Chain: B: PDB Molecule: putative tagatose-6-phosphate ketose/aldose isomerase; PDBTitle: crystal structure of putative putative tagatose-6-phosphate2 ketose/aldose isomerase (np_344614.1) from streptococcus pneumoniae3 tigr4 at 1.70 a resolution
36	c2zj3A	Alignment	not modelled	98.4	10	PDB header: transferase Chain: A: PDB Molecule: glucosamine--fructose-6-phosphate PDBTitle: isomerase domain of human glucose:fructose-6-phosphate2 amidotransferase
37	d1moqa	Alignment	not modelled	98.3	12	Fold: SIS domain Superfamily: SIS domain Family: double-SIS domain
38	c4s1wA	Alignment	not modelled	98.2	12	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
39	d1x92a	Alignment	not modelled	98.0	15	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
40	c1jxA	Alignment	not modelled	98.0	12	PDB header: transferase Chain: A: PDB Molecule: glucosamine 6-phosphate synthase; PDBTitle: glucosamine 6-phosphate synthase with glucose 6-phosphate
41	c2amIB	Alignment	not modelled	97.8	11	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
42	c3tbfA	Alignment	not modelled	97.8	9	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.
43	c4s12C	Alignment	not modelled	97.7	20	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.
44	c4ivnB	Alignment	not modelled	97.7	16	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: the vibrio vulnificus nanr protein complexed with mannac-6p
45	c5i01B	Alignment	not modelled	97.6	16	PDB header: isomerase Chain: B: PDB Molecule: phosphoheptose isomerase; PDBTitle: structure of phosphoheptose isomerase gmha from neisseria gonorrhoeae
46	d1tk9a	Alignment	not modelled	97.6	14	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
47	c1nriA	Alignment	not modelled	97.5	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein hi0754; PDBTitle: crystal structure of putative phosphosugar isomerase hi0754 from2 haemophilus influenzae
48	d1nria	Alignment	not modelled	97.5	15	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
49	c5by2A	Alignment	not modelled	97.5	13	PDB header: isomerase Chain: A: PDB Molecule: phosphoheptose isomerase; PDBTitle: sedoheptulose 7-phosphate isomerase from colwellia psycherythraea2 strain 34h
50	d1x94a	Alignment	not modelled	97.5	17	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
51	d1vima	Alignment	not modelled	97.5	13	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain

52	c2yvaB_	Alignment	not modelled	97.5	13	PDB header: dna binding protein Chain: B: PDB Molecule: dnaa initiator-associating protein diaa; PDBTitle: crystal structure of escherichia coli diaa
53	c3shoA_	Alignment	not modelled	97.4	21	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, rpir family; PDBTitle: crystal structure of rpir transcription factor from sphaerobacter2 thermophilus (sugar isomerase domain)
54	c4lzd_	Alignment	not modelled	97.3	13	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
55	d1m3sa_	Alignment	not modelled	97.2	20	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
56	c2x3yA_	Alignment	not modelled	97.1	17	PDB header: isomerase Chain: A: PDB Molecule: phosphoheptose isomerase; PDBTitle: crystal structure of gmha from burkholderia pseudomallei
57	c3etnD_	Alignment	not modelled	96.9	16	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
58	d1jeoa_	Alignment	not modelled	96.9	23	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
59	c3fxaA_	Alignment	not modelled	96.9	20	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
60	c2xhzC_	Alignment	not modelled	96.7	14	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
61	c3trjC_	Alignment	not modelled	96.7	16	PDB header: isomerase Chain: C: PDB Molecule: phosphoheptose isomerase; PDBTitle: structure of a phosphoheptose isomerase from francisella tularensis
62	c5uqiA_	Alignment	not modelled	96.4	19	PDB header: isomerase Chain: A: PDB Molecule: phosphosugar isomerase; PDBTitle: e. coli cft073 c3406 in complex with a5p
63	c3cvjB_	Alignment	not modelled	95.9	14	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
64	d1chda_	Alignment	not modelled	89.1	12	Fold: Methylesterase CheB, C-terminal domain Superfamily: Methylesterase CheB, C-terminal domain Family: Methylesterase CheB, C-terminal domain
65	d1p3da1	Alignment	not modelled	88.1	20	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
66	c2jkbB_	Alignment	not modelled	88.0	21	PDB header: transferase Chain: B: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: saccharomyces cerevisiae hypoxanthine-guanine2 phosphoribosyltransferase in complex with gmp (guanosine 5'-3' monophosphate) (orthorhombic crystal form)
67	c4pfgF_	Alignment	not modelled	87.2	13	PDB header: transferase Chain: F: PDB Molecule: hypoxanthine phosphoribosyltransferase; PDBTitle: crystal structure of hypoxanthine phosphoribosyltransferase from2 brachy bacterium faecium dsm 4810, nysgrc target 029763.
68	c4dxdA_	Alignment	not modelled	83.1	32	PDB header: cell cycle/inhibitor Chain: A: PDB Molecule: cell division protein ftsz; PDBTitle: staphylococcal aureus ftsz in complex with 723
69	c6cauA_	Alignment	not modelled	81.3	21	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate--l-alanine ligase; PDBTitle: udp-n-acetylmuramate--alanine ligase from acinetobacter baumannii2 ab5075-uw with amppnp
70	d1w5fa1	Alignment	not modelled	80.3	33	Fold: Tubulin nucleotide-binding domain-like Superfamily: Tubulin nucleotide-binding domain-like Family: Tubulin, GTPase domain
71	c3sftA_	Alignment	not modelled	80.0	15	PDB header: hydrolase Chain: A: PDB Molecule: chemotaxis response regulator protein-glutamate PDBTitle: crystal structure of thermotoga maritima cheb methylesterase catalytic2 domain
72	d1p17b_	Alignment	not modelled	79.2	18	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
73	c3hn7A_	Alignment	not modelled	79.0	17	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate-l-alanine ligase; PDBTitle: crystal structure of a murein peptide ligase mpl (psyc_0032) from2 psychrobacter arcticus 273-4 at 1.65 a resolution
74	c2vxyA_	Alignment	not modelled	78.8	33	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsz; PDBTitle: the structure of ftsz from bacillus subtilis at 1.7a2 resolution
75	d1hqxa_	Alignment	not modelled	77.8	10	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
						PDB header: cell cycle

76	c2r6r1_	Alignment	not modelled	75.6	34	Chain: 1: PDB Molecule: cell division protein ftsz; PDBTitle: aquifex aeolicus ftsz
77	c1w59B_	Alignment	not modelled	73.5	19	PDB header: cell division Chain: B: PDB Molecule: cell division protein ftsz homolog 1; PDBTitle: ftsz dimer, empty (m. jannaschii)
78	d2vapa1	Alignment	not modelled	72.8	23	Fold: Tubulin nucleotide-binding domain-like Superfamily: Tubulin nucleotide-binding domain-like Family: Tubulin, GTPase domain
79	c2f00A_	Alignment	not modelled	71.3	19	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate-l-alanine ligase; PDBTitle: escherichia coli murc
80	c3ezxA_	Alignment	not modelled	70.7	11	PDB header: transferase Chain: A: PDB Molecule: monomethylamine corrinoid protein 1; PDBTitle: structure of methanosarcina barkeri monomethylamine2 corrinoid protein
81	c2rhoB_	Alignment	not modelled	70.5	33	PDB header: cell cycle Chain: B: PDB Molecule: cell division protein ftsz; PDBTitle: synthetic gene encoded bacillus subtilis ftsz ncs dimer with bound gdp2 and gtp-gamma-s
82	c4e6eA_	Alignment	not modelled	70.4	32	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.)
83	d1ofua1	Alignment	not modelled	65.3	29	Fold: Tubulin nucleotide-binding domain-like Superfamily: Tubulin nucleotide-binding domain-like Family: Tubulin, GTPase domain
84	c1w5fA_	Alignment	not modelled	64.6	32	PDB header: cell division Chain: A: PDB Molecule: cell division protein ftsz; PDBTitle: ftsz, t7 mutated, domain swapped (t. maritima)
85	c3v3tA_	Alignment	not modelled	62.4	31	PDB header: structural protein Chain: A: PDB Molecule: cell division gtpase ftsz, diverged; PDBTitle: crystal structure of clostridium botulinum phage c-st tubz
86	d1zbsa2	Alignment	not modelled	61.9	27	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
87	c5husA_	Alignment	not modelled	59.8	27	PDB header: transferase Chain: A: PDB Molecule: trehalose synthase regulatory protein; PDBTitle: structure of candida albicans trehalose synthase regulatory protein c-2 terminal domain
88	d1q2la3	Alignment	not modelled	58.9	16	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: MPP-like
89	c1a2oB_	Alignment	not modelled	58.5	12	PDB header: bacterial chemotaxis Chain: B: PDB Molecule: cheb methyltransferase; PDBTitle: structural basis for methyltransferase cheb regulation by a2 phosphorylation-activated domain
90	c3ca8B_	Alignment	not modelled	56.6	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein ydcf; PDBTitle: crystal structure of escherichia coli ydcf, an s-adenosyl-l-methionine2 utilizing enzyme
91	c1ofuB_	Alignment	not modelled	56.1	27	PDB header: bacterial cell division inhibitor Chain: B: PDB Molecule: cell division protein ftsz; PDBTitle: crystal structure of sula:ftsiz from pseudomonas aeruginosa
92	d1liua3	Alignment	not modelled	55.7	15	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
93	d1j6ua1	Alignment	not modelled	55.4	16	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
94	c4lhsA_	Alignment	not modelled	54.8	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative gds1-like lipase (bacova_00914) from2 bacteroides ovatus atcc 8483 at 1.40 a resolution
95	c2eklA_	Alignment	not modelled	54.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: structure of st1218 protein from sulfobolus tokodaii
96	d1sc6a1	Alignment	not modelled	53.2	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
97	c4hh3C_	Alignment	not modelled	52.1	16	PDB header: flavoprotein/transcription Chain: C: PDB Molecule: appa protein; PDBTitle: structure of the appa-pps2 core complex from rb. sphaeroides
98	c4rqbB_	Alignment	not modelled	50.5	14	PDB header: transferase Chain: B: PDB Molecule: hypoxanthine phosphoribosyltransferase; PDBTitle: crystal structure of a hypoxanthine phosphoribosyltransferase (target2 id nysgrc-029686) from staphylococcus aureus (tetragonal space group)
99	c3zidB_	Alignment	not modelled	50.3	19	PDB header: gtp-binding protein Chain: B: PDB Molecule: tubulin/ftsiz, gtpase; PDBTitle: cetz from methanoseta thermophila strain dsm 6194
100	d1ufra_	Alignment	not modelled	50.2	13	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
101	c3eagA_	Alignment	not modelled	48.8	19	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate:l-alanyl-gamma-d-glutamyl-meso- PDBTitle: the crystal structure of udp-n-acetylmuramate:l-alanyl-gamma-d-2 glutamyl-meso-diaminopimelate ligase (mpl) from neisseria3 meningitides

102	c2ardA_	 Alignment	not modelled	44.7	22	PDB header: biosynthetic protein Chain: A: PDB Molecule: tryptophan halogenase prna; PDBTitle: the structure of tryptophan 7-halogenase (prna) suggests a mechanism2 for regioselective chlorination
103	c2q1yB_	 Alignment	not modelled	43.9	25	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
104	c3o7mD_	 Alignment	not modelled	42.6	10	PDB header: transferase Chain: D: PDB Molecule: hypoxanthine phosphoribosyltransferase; PDBTitle: 1.98 angstrom resolution crystal structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-2) from bacillus anthracis str. 'ames3 ancestor'
105	d1e0ta3	 Alignment	not modelled	42.1	11	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
106	c2pi1C_	 Alignment	not modelled	41.9	15	PDB header: oxidoreductase Chain: C: PDB Molecule: d-lactate dehydrogenase; PDBTitle: crystal structure of d-lactate dehydrogenase from aquifex2 aeolicus complexed with nad and lactic acid
107	c3ssmB_	 Alignment	not modelled	41.2	23	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: myce methyltransferase from the mycinamycin biosynthetic pathway in2 complex with mg and sah, crystal form 1
108	c3m8kA_	 Alignment	not modelled	40.5	14	PDB header: structural protein Chain: A: PDB Molecule: ftsz/tubulin-related protein; PDBTitle: protein structure of type iii plasmid segregation tubz
109	c1yfaA_	 Alignment	not modelled	40.0	17	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: novel imp binding in feedback inhibition of hypoxanthine-guanine2 phosphoribosyltransferase from thermoanaerobacter tengcongensis
110	d1yfa1	 Alignment	not modelled	40.0	17	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
111	d1rq2a1	 Alignment	not modelled	39.7	26	Fold: Tubulin nucleotide-binding domain-like Superfamily: Tubulin nucleotide-binding domain-like Family: Tubulin, GTPase domain
112	c4b87A_	 Alignment	not modelled	38.5	15	PDB header: hydrolase Chain: A: PDB Molecule: dna cross-link repair 1a protein; PDBTitle: crystal structure of human dna cross-link repair 1a
113	c4rhyC_	 Alignment	not modelled	38.4	14	PDB header: transferase/transferase inhibitor Chain: C: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: crystal structures of mycobacterium tuberculosis 6-oxopurine2 phosphoribosyltransferase which is a potential target for drug3 development against this disease
114	c4b46A_	 Alignment	not modelled	37.7	21	PDB header: structural protein Chain: A: PDB Molecule: cell division protein ftsz; PDBTitle: cetz1 from haloferax volcanii - gdp bound monomer
115	d1qx4a2	 Alignment	not modelled	37.4	12	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
116	c5eswB_	 Alignment	not modelled	37.0	20	PDB header: transferase Chain: B: PDB Molecule: purine/pyrimidine phosphoribosyltransferase; PDBTitle: crystal structure of apo hypoxanthine-guanine2 phosphoribosyltransferase from legionella pneumophila
117	c3louB_	 Alignment	not modelled	36.5	13	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
118	c2vawA_	 Alignment	not modelled	36.4	37	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsz; PDBTitle: ftsz pseudomonas aeruginosa gdp
119	d1j99a_	 Alignment	not modelled	36.0	10	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase
120	c6o9l6_	 Alignment	not modelled	35.6	18	PDB header: transcription/dna Chain: 6: PDB Molecule: general transcription factor iih subunit 2; PDBTitle: human holo-pic in the closed state