



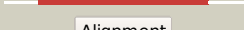

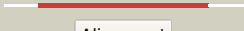









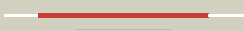







Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3256c_(-)_3636272_3637312
Date	Thu Aug 8 16:20:46 BST 2019
Unique Job ID	7d10d83a8afc45dd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1jxaA_	 Alignment		100.0	12	PDB header: transferase Chain: A; PDB Molecule: glucosamine 6-phosphate synthase; PDBTitle: glucosamine 6-phosphate synthase with glucose 6-phosphate
2	c3g68A_	 Alignment		100.0	10	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
3	c3fkjA_	 Alignment		100.0	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
4	c4s1wA_	 Alignment		100.0	13	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
5	d1moqa_	 Alignment		100.0	12	Fold: SIS domain Superfamily: SIS domain Family: double-SIS domain
6	c2amlB_	 Alignment		100.0	9	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
7	c3odpA_	 Alignment		100.0	13	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
8	c3fj1A_	 Alignment		100.0	12	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
9	c3i0zB_	 Alignment		100.0	12	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
10	c2zj3A_	 Alignment		100.0	12	PDB header: transferase Chain: A; PDB Molecule: glucosamine--fructose-6-phosphate PDBTitle: isomerase domain of human glucose:fructose-6-phosphate2 amidotransferase
11	c3tbfA_	 Alignment		100.0	10	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.

12	c3euaD_	Alignment		100.0	13	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
13	c2a3nA_	Alignment		100.0	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
14	c3hbaA_	Alignment		100.0	13	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
15	c2decA_	Alignment		100.0	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
16	c2puwA_	Alignment		100.0	13	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
17	c3c3jA_	Alignment		100.0	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
18	d1j5xa_	Alignment		100.0	9	Fold: SIS domain Superfamily: SIS domain Family: double-SIS domain
19	c3knzA_	Alignment		100.0	13	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
20	d1x9ia_	Alignment		100.0	15	Fold: SIS domain Superfamily: SIS domain Family: double-SIS domain
21	d1wiwa_	Alignment	not modelled	100.0	20	Fold: SIS domain Superfamily: SIS domain Family: double-SIS domain
22	c4s12C_	Alignment	not modelled	99.7	15	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.
23	c4lzjD_	Alignment	not modelled	99.7	14	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
24	d1nr1a_	Alignment	not modelled	99.6	14	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
25	c1nr1A_	Alignment	not modelled	99.6	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein hi0754; PDBTitle: crystal structure of putative phosphosugar isomerase hi0754 from2 haemophilus influenzae
26	c2xhzC_	Alignment	not modelled	99.5	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
27	c3shoA_	Alignment	not modelled	99.5	15	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)
28	c3pntD_	Alignment	not modelled	99.5	12	PDB header: isomerase Chain: D: PDB Molecule: putative phosphosugar isomerase involved in capsule

28	c2etnB	Alignment	not modelled	99.3	12	PDBTitle: crystal structure of putative phosphosugar isomerase involved in 2 capsule formation (yp_209877.1) from bacteroides fragilis nctc 93433 at 1.70 a resolution
29	c5uqiA	Alignment	not modelled	99.5	11	PDB header: isomerase Chain: A: PDB Molecule: phosphosugar isomerase; PDBTitle: e. coli cft073 c3406 in complex with a5p
30	c3fxaA	Alignment	not modelled	99.4	15	PDB header: sugar binding protein Chain: A: PDB Molecule: sis domain protein; PDBTitle: crystal structure of a putative sugar-phosphate isomerase2 (Imof2365_0531) from listeria monocytogenes str. 4b f2365 at 1.60 a3 resolution
31	d1x92a	Alignment	not modelled	99.4	15	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
32	d1vima	Alignment	not modelled	99.4	16	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
33	c4ivnB	Alignment	not modelled	99.4	16	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: the vibrio vulnificus nanr protein complexed with mannac-6p
34	c5by2A	Alignment	not modelled	99.4	14	PDB header: isomerase Chain: A: PDB Molecule: phosphoheptose isomerase; PDBTitle: sedoheptulose 7-phosphate isomerase from colwellia psychrerythraea2 strain 34h
35	c2yvaB	Alignment	not modelled	99.4	16	PDB header: dna binding protein Chain: B: PDB Molecule: dnaa initiator-associating protein diaa; PDBTitle: crystal structure of escherichia coli diaa
36	d1tk9a	Alignment	not modelled	99.3	12	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
37	c3trjC	Alignment	not modelled	99.3	11	PDB header: isomerase Chain: C: PDB Molecule: phosphoheptose isomerase; PDBTitle: structure of a phosphoheptose isomerase from francisella tularensis
38	d1m3sa	Alignment	not modelled	99.3	15	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
39	c3cvjB	Alignment	not modelled	99.2	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
40	d1x94a	Alignment	not modelled	99.2	14	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
41	c5i01B	Alignment	not modelled	99.2	15	PDB header: isomerase Chain: B: PDB Molecule: phosphoheptose isomerase; PDBTitle: structure of phosphoheptose isomerase gmha from neisseria gonorrhoeae
42	c2x3yA	Alignment	not modelled	99.2	13	PDB header: isomerase Chain: A: PDB Molecule: phosphoheptose isomerase; PDBTitle: crystal structure of gmha from burkholderia pseudomallei
43	d1jeoa	Alignment	not modelled	99.0	15	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
44	c3w0ID	Alignment	not modelled	98.9	14	PDB header: transferase/transferase inhibitor Chain: D: PDB Molecule: glucokinase regulatory protein; PDBTitle: the crystal structure of xenopus glucokinase and glucokinase2 regulatory protein complex
45	c2q8nB	Alignment	not modelled	98.8	14	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
46	c4lc9A	Alignment	not modelled	98.8	14	PDB header: transferase/transferase regulator Chain: A: PDB Molecule: glucokinase regulatory protein; PDBTitle: structural basis for regulation of human glucokinase by glucokinase2 regulatory protein
47	c3ff1B	Alignment	not modelled	98.7	11	PDB header: isomerase Chain: B: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: structure of glucose 6-phosphate isomerase from staphylococcus aureus
48	c1zzgB	Alignment	not modelled	98.7	12	PDB header: isomerase Chain: B: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: crystal structure of hypothetical protein tt0462 from thermus2 thermophilus hb8
49	c3hjbA	Alignment	not modelled	98.7	14	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.
50	d1c7qa	Alignment	not modelled	98.6	12	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
51	c2wu8A	Alignment	not modelled	98.6	12	PDB header: isomerase Chain: A: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: structural studies of phosphoglucose isomerase from2 mycobacterium tuberculosis h37rv
52	c4bbaA	Alignment	not modelled	98.6	11	PDB header: protein-binding protein Chain: A: PDB Molecule: glucokinase regulatory protein; PDBTitle: crystal structure of glucokinase regulatory protein complexed to2 phosphate
53	c4em6D	Alignment	not modelled	98.6	16	PDB header: isomerase Chain: D: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: the structure of glucose-6-phosphate isomerase (gpi) from brucella2 melitensis
						Fold: SIS domain

54	d1gzda_	Alignment	not modelled	98.6	13	Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
55	c3nbuC	Alignment	not modelled	98.6	12	PDB header: isomerase Chain: C: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: crystal structure of pgi glucosephosphate isomerase
56	c3ljka_	Alignment	not modelled	98.6	12	PDB header: isomerase Chain: A: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: glucose-6-phosphate isomerase from francisella tularensis.
57	d1q50a_	Alignment	not modelled	98.6	13	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
58	c6bzcA_	Alignment	not modelled	98.5	11	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
59	d1hm5a_	Alignment	not modelled	98.5	12	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
60	d1u0fa_	Alignment	not modelled	98.5	13	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
61	c1t10A_	Alignment	not modelled	98.5	13	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
62	c4qfha_	Alignment	not modelled	98.5	12	PDB header: isomerase Chain: A: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: structure of a glucose-6-phosphate isomerase from trypanosoma cruzi
63	c2o2cB_	Alignment	not modelled	98.5	15	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
64	c3ujhB_	Alignment	not modelled	98.4	14	PDB header: isomerase Chain: B: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: crystal structure of substrate-bound glucose-6-phosphate isomerase2 from toxoplasma gondii
65	d1iata_	Alignment	not modelled	98.4	12	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
66	c3pr3B_	Alignment	not modelled	98.3	11	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
67	c6otuA_	Alignment	not modelled	98.1	11	PDB header: isomerase Chain: A: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: crystal structure of a glucose-6-phosphate isomerase from chlamydia2 trachomatis d/uw-3/cx
68	c1tmoA_	Alignment	not modelled	92.9	10	PDB header: oxidoreductase Chain: A: PDB Molecule: trimethylamine n-oxide reductase; PDBTitle: trimethylamine n-oxide reductase from shewanella massilia
69	d1dmra2	Alignment	not modelled	92.2	15	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
70	c1h5nC_	Alignment	not modelled	92.0	14	PDB header: oxidoreductase Chain: C: PDB Molecule: dmsO reductase; PDBTitle: dmsO reductase modified by the presence of dms and air
71	d1tmoa2	Alignment	not modelled	89.8	9	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	c3jwpA_	Alignment	not modelled	89.0	10	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
73	d2iv2x2	Alignment	not modelled	82.0	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
74	d1yc5a1	Alignment	not modelled	82.0	27	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
75	c4yaja_	Alignment	not modelled	81.9	20	PDB header: ligase Chain: A: PDB Molecule: alpha subunit of acetyl-coenzyme a synthetase PDBTitle: ca. korarchaeum cryptofilum dinucleotide forming acetyl-coenzyme a2 synthetase 1 (apo form)
76	c2vpyE_	Alignment	not modelled	81.8	15	PDB header: oxidoreductase Chain: E: PDB Molecule: thiosulfate reductase; PDBTitle: polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
77	c1vlfO_	Alignment	not modelled	80.2	13	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
78	c2iv2X_	Alignment	not modelled	80.1	13	PDB header: oxidoreductase Chain: X: PDB Molecule: formate dehydrogenase h; PDBTitle: reinterpretation of reduced form of formate dehydrogenase h from e.2 coli PDB header: structural genomics, unknown function

79	c4jqsC_	Alignment	not modelled	79.6	16	Chain: C; PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative thua-like protein (bacuni_01602) from <i>Bacteroides uniformis</i> ATCC 8492 at 2.30 Å resolution
80	c3pkiF_	Alignment	not modelled	79.2	20	PDB header: hydrolase Chain: F; PDB Molecule: nad-dependent deacetylase sirtuin-6; PDBTitle: human sirt6 crystal structure in complex with adp ribose
81	c3k35D_	Alignment	not modelled	79.0	20	PDB header: hydrolase Chain: D; PDB Molecule: nad-dependent deacetylase sirtuin-6; PDBTitle: crystal structure of human sirt6
82	d2b4ya1	Alignment	not modelled	78.9	16	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
83	d1m2ka_	Alignment	not modelled	78.2	30	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
84	d1ma3a_	Alignment	not modelled	77.4	16	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
85	c3zg6A_	Alignment	not modelled	76.0	20	PDB header: hydrolase/inhibitor Chain: A; PDB Molecule: nad-dependent protein deacetylase sirtuin-6; PDBTitle: the novel de-long chain fatty acid function of human sirt6
86	d2csua1	Alignment	not modelled	74.4	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
87	c3jx9B_	Alignment	not modelled	73.8	12	PDB header: isomerase Chain: B; PDB Molecule: putative phosphoheptose isomerase; PDBTitle: crystal structure of putative phosphoheptose isomerase2 (yp_001815198.1) from <i>Exiguobacterium</i> sp. 255-15 at 1.95 Å resolution
88	d1s5pa_	Alignment	not modelled	73.5	18	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
89	c5oj7A_	Alignment	not modelled	71.5	6	PDB header: hydrolase Chain: A; PDB Molecule: nad-dependent protein deacetylase; PDBTitle: sirtuin 4 orthologue from <i>Xenopus tropicalis</i> in complex with adp-2 ribose
90	c2e7zA_	Alignment	not modelled	71.5	9	PDB header: lyase Chain: A; PDB Molecule: acetylene hydratase ahy; PDBTitle: acetylene hydratase from <i>Pelobacter acetylenicus</i>
91	d1g2oa_	Alignment	not modelled	70.7	25	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
92	d1vlfm2	Alignment	not modelled	70.7	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
93	d2ji7a1	Alignment	not modelled	70.1	17	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
94	d1eu1a2	Alignment	not modelled	69.7	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
95	d1euca1	Alignment	not modelled	67.0	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
96	c2ivfA_	Alignment	not modelled	64.5	17	PDB header: oxidoreductase Chain: A; PDB Molecule: ethylbenzene dehydrogenase alpha-subunit; PDBTitle: ethylbenzene dehydrogenase from <i>Aromatoleum aromaticum</i>
97	c5ch7E_	Alignment	not modelled	61.5	12	PDB header: oxidoreductase Chain: E; PDB Molecule: dmsO reductase family type ii enzyme, molybdopterin PDBTitle: crystal structure of the perchlorate reductase pcrab - phe164 gate2 switch intermediate - from <i>Azospira suillum</i> ps
98	c1pjtb_	Alignment	not modelled	60.0	11	PDB header: transferase/oxidoreductase/lyase Chain: B; PDB Molecule: siroheme synthase; PDBTitle: the structure of the ser128ala point-mutant variant of cysg, the2 multifunctional methyltransferase/dehydrogenase/ferrochelatase for3 siroheme synthesis
99	c3pdiG_	Alignment	not modelled	58.8	14	PDB header: protein binding Chain: G; PDB Molecule: nitrogenase mofe cofactor biosynthesis protein nife; PDBTitle: precursor bound nifen
100	d1qe5a_	Alignment	not modelled	57.2	16	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
101	c1h0hA_	Alignment	not modelled	55.2	24	PDB header: electron transport Chain: A; PDB Molecule: formate dehydrogenase subunit alpha; PDBTitle: tungsten containing formate dehydrogenase from <i>Desulfovibrio gigas</i>
102	d1ybha1	Alignment	not modelled	54.2	9	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
103	c5cxsa_	Alignment	not modelled	53.2	15	PDB header: transferase Chain: A; PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of isoform 2 of purine nucleoside phosphorylase2 complexed with mes
104	c2cpuB_	Alignment	not modelled	50.4	12	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: 457aa long hypothetical protein;

104	c2c5ub	Alignment	not modelled	39.4	12	PDBTitle: crystal structure of ph0766 from pyrococcus horikoshii ot3
105	d1pjqa3	Alignment	not modelled	49.5	11	Fold: Siroheme synthase middle domains-like Superfamily: Siroheme synthase middle domains-like Family: Siroheme synthase middle domains-like
106	c2qytA	Alignment	not modelled	48.1	12	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of 2-dehydropantoate 2-reductase from porphyromonas2 gingivalis w83
107	c2p4sA	Alignment	not modelled	46.0	16	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: structure of purine nucleoside phosphorylase from anopheles gambiae in2 complex with dadme-immh
108	d2a5la1	Alignment	not modelled	45.2	11	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
109	d1g8ka2	Alignment	not modelled	44.7	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
110	d2ez9a1	Alignment	not modelled	43.6	29	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
111	d1xx6a1	Alignment	not modelled	42.6	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Type II thymidine kinase
112	d5nula	Alignment	not modelled	42.4	8	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
113	c1kyqC	Alignment	not modelled	41.9	13	PDB header: oxidoreductase, lyase Chain: C: PDB Molecule: siroheme biosynthesis protein met8; PDBTitle: met8p: a bifunctional nad-dependent dehydrogenase and2 ferrochelatae involved in siroheme synthesis.
114	c3bbnB	Alignment	not modelled	40.8	11	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.
115	c2iy3A	Alignment	not modelled	40.5	17	PDB header: rna-binding Chain: A: PDB Molecule: signal recognition particle protein,signal recognition PDBTitle: structure of the e. coli signal regognition particle
116	d2gy9b1	Alignment	not modelled	38.7	20	Fold: Flavodoxin-like Superfamily: Ribosomal protein S2 Family: Ribosomal protein S2
117	d3bgsa1	Alignment	not modelled	38.4	16	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
118	d1yj5a1	Alignment	not modelled	38.0	18	Fold: HAD-like Superfamily: HAD-like Family: phosphatase domain of polynucleotide kinase
119	c2z2uA	Alignment	not modelled	38.0	19	PDB header: metal binding protein Chain: A: PDB Molecule: upf0026 protein mj0257; PDBTitle: crystal structure of archaeal tyw1
120	c3ghfA	Alignment	not modelled	37.5	16	PDB header: cell cycle Chain: A: PDB Molecule: septum site-determining protein minc; PDBTitle: crystal structure of the septum site-determining protein minc from2 salmonella typhimurium