



















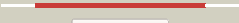
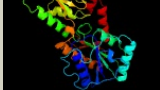


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3010c_(pfkA)_3368833_3369864
Date	Thu Aug 8 16:20:18 BST 2019
Unique Job ID	f676a05abb9b94b5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pfka_	 Alignment		100.0	40	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
2	d4pfka_	 Alignment		100.0	42	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
3	c1zxxA_	 Alignment		100.0	40	PDB header: transferase Chain: A: PDB Molecule: 6-phosphofructokinase; PDBTitle: the crystal structure of phosphofructokinase from lactobacillus2 delbrueckii
4	c3o8oB_	 Alignment		100.0	38	PDB header: transferase Chain: B: PDB Molecule: 6-phosphofructokinase subunit beta; PDBTitle: structure of phosphofructokinase from saccharomyces cerevisiae
5	c2higA_	 Alignment		100.0	33	PDB header: transferase Chain: A: PDB Molecule: 6-phospho-1-fructokinase; PDBTitle: crystal structure of phosphofructokinase apoenzyme from trypanosoma2 brucei.
6	c3opyH_	 Alignment		100.0	40	PDB header: transferase Chain: H: PDB Molecule: 6-phosphofructo-1-kinase beta-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state
7	c3o8oC_	 Alignment		100.0	39	PDB header: transferase Chain: C: PDB Molecule: 6-phosphofructokinase subunit alpha; PDBTitle: structure of phosphofructokinase from saccharomyces cerevisiae
8	c3opyB_	 Alignment		100.0	40	PDB header: transferase Chain: B: PDB Molecule: 6-phosphofructo-1-kinase beta-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state
9	c5xoeA_	 Alignment		100.0	41	PDB header: transferase Chain: A: PDB Molecule: atp-dependent 6-phosphofructokinase; PDBTitle: crystal structure of the apo staphylococcus aureus phosphofructokinase
10	c3o8nA_	 Alignment		100.0	40	PDB header: transferase Chain: A: PDB Molecule: 6-phosphofructokinase, muscle type; PDBTitle: structure of phosphofructokinase from rabbit skeletal muscle
11	c3opyG_	 Alignment		100.0	39	PDB header: transferase Chain: G: PDB Molecule: 6-phosphofructo-1-kinase alpha-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state

12	c3opyE_	Alignment		100.0	39	PDB header: transferase Chain: E: PDB Molecule: 6-phosphofructo-1-kinase alpha-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state
13	c3k2qA_	Alignment		100.0	30	PDB header: transferase Chain: A: PDB Molecule: pyrophosphate-dependent phosphofructokinase; PDBTitle: crystal structure of pyrophosphate-dependent2 phosphofructokinase from marinobacter aquaeolei, northeast3 structural genomics consortium target mqr88
14	d2f48a1	Alignment		100.0	26	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
15	d1vlja_	Alignment		96.0	14	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
16	d1rrma_	Alignment		96.0	24	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
17	c3ox4D_	Alignment		95.9	21	PDB header: oxidoreductase Chain: D: PDB Molecule: alcohol dehydrogenase 2; PDBTitle: structures of iron-dependent alcohol dehydrogenase 2 from zymomonas2 mobilis zm4 complexed with nad cofactor
18	c2an1D_	Alignment		95.7	23	PDB header: transferase Chain: D: PDB Molecule: putative kinase; PDBTitle: structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
19	c1xahA_	Alignment		95.5	21	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: crystal structure of staphylococcus aureus 3-dehydroquinase2 synthase (dhqs) in complex with zn2+ and nad+
20	d1u0ta_	Alignment		95.4	24	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like
21	c1yt5A_	Alignment	not modelled	95.4	21	PDB header: transferase Chain: A: PDB Molecule: inorganic polyphosphate/atp-nad kinase; PDBTitle: crystal structure of nad kinase from thermotoga maritima
22	d1z0sa1	Alignment	not modelled	95.4	22	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like
23	c6c76A_	Alignment	not modelled	95.4	14	PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase; PDBTitle: structure of iron containing alcohol dehydrogenase from thermococcus2 thioreducens in an orthorhombic crystal form
24	c5zx1D_	Alignment	not modelled	95.3	18	PDB header: oxidoreductase Chain: D: PDB Molecule: glycerol dehydrogenase; PDBTitle: structure of glda from e.coli
25	c1z0zC_	Alignment	not modelled	95.3	22	PDB header: transferase Chain: C: PDB Molecule: probable inorganic polyphosphate/atp-nad kinase; PDBTitle: crystal structure of a nad kinase from archaeoglobus2 fulgidus in complex with nad
26	d1o2da_	Alignment	not modelled	95.3	18	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
27	c3pfnB_	Alignment	not modelled	95.2	27	PDB header: transferase Chain: B: PDB Molecule: nad kinase; PDBTitle: crystal structure of human nad kinase
28	c6c5cA_	Alignment	not modelled	95.1	26	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: crystal structure of aro1p from candida albicans sc5314 in complex2 with nadh PDB header: lyase

29	c3okfA_	Alignment	not modelled	95.1	20	Chain: A: PDB Molecule: 3-dehydroquininate synthase; PDBTitle: 2.5 angstrom resolution crystal structure of 3-dehydroquininate synthase2 (arob) from vibrio cholerae
30	c3clhA_	Alignment	not modelled	95.1	18	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquininate synthase; PDBTitle: crystal structure of 3-dehydroquininate synthase (dhqs)from2 helicobacter pylori
31	c6jpkD_	Alignment	not modelled	95.0	16	PDB header: oxidoreductase Chain: D: PDB Molecule: methanol dehydrogenase; PDBTitle: crystal structure of sulfoacetaldehyde reductase from bifidobacterium2 kashiwanohense in complex with nad+
32	c3hl0B_	Alignment	not modelled	95.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: maleylacetate reductase; PDBTitle: crystal structure of maleylacetate reductase from agrobacterium2 tumefaciens
33	c5eksB_	Alignment	not modelled	94.8	27	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquininate synthase; PDBTitle: structure of 3-dehydroquininate synthase from acinetobacter baumannii in2 complex with nad
34	c3bfjK_	Alignment	not modelled	94.8	15	PDB header: oxidoreductase Chain: K: PDB Molecule: 1,3-propanediol oxidoreductase; PDBTitle: crystal structure analysis of 1,3-propanediol oxidoreductase
35	d1jq5a_	Alignment	not modelled	94.7	17	Fold: Dehydroquininate synthase-like Superfamily: Dehydroquininate synthase-like Family: Iron-containing alcohol dehydrogenase
36	c5yvmA_	Alignment	not modelled	94.7	23	PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase; PDBTitle: crystal structure of the archaeal halo-thermophilic red sea brine pool2 alcohol dehydrogenase adh/d1 bound to nzq
37	c3qbeA_	Alignment	not modelled	94.5	27	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquininate synthase; PDBTitle: crystal structure of the 3-dehydroquininate synthase (arob) from2 mycobacterium tuberculosis
38	c3afoB_	Alignment	not modelled	94.5	29	PDB header: transferase Chain: B: PDB Molecule: nadh kinase pos5; PDBTitle: crystal structure of yeast nadh kinase complexed with nadh
39	c4mcaB_	Alignment	not modelled	94.5	21	PDB header: oxidoreductase Chain: B: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase from serratia to 1.9a
40	c3jzdA_	Alignment	not modelled	94.5	21	PDB header: oxidoreductase Chain: A: PDB Molecule: iron-containing alcohol dehydrogenase; PDBTitle: crystal structure of putative alcohol dehydrogenase (yp_298327.1) from2 ralstonia eutropha jmp134 at 2.10 a resolution
41	c3uhjE_	Alignment	not modelled	94.4	17	PDB header: oxidoreductase Chain: E: PDB Molecule: probable glycerol dehydrogenase; PDBTitle: crystal structure of a probable glycerol dehydrogenase from2 sinorhizobium meliloti 1021
42	d1oj7a_	Alignment	not modelled	94.3	12	Fold: Dehydroquininate synthase-like Superfamily: Dehydroquininate synthase-like Family: Iron-containing alcohol dehydrogenase
43	c2gruB_	Alignment	not modelled	94.3	18	PDB header: lyase Chain: B: PDB Molecule: 2-deoxy-scylo-inosose synthase; PDBTitle: crystal structure of 2-deoxy-scylo-inosose synthase2 complexed with carbaglucose-6-phosphate, nad+ and co2+
44	c5tprB_	Alignment	not modelled	94.1	18	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquininate synthase; PDBTitle: desmethyl-4-deoxygadusol synthase from anabaena variabilis (ava_3858)2 with nad+ and zn2+ bound
45	c6csjD_	Alignment	not modelled	94.0	19	PDB header: oxidoreductase Chain: D: PDB Molecule: glycerol dehydrogenase; PDBTitle: structure of a bacillus coagulans polyol dehydrogenase double mutant2 with an acquired d-lactate dehydrogenase activity
46	c5hvnA_	Alignment	not modelled	93.9	24	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquininate synthase; PDBTitle: 3.0 angstrom crystal structure of 3-dehydroquininate synthase (arob)2 from francisella tularensis in complex with nad.
47	d1ujna_	Alignment	not modelled	93.9	18	Fold: Dehydroquininate synthase-like Superfamily: Dehydroquininate synthase-like Family: Dehydroquininate synthase, DHQS
48	c2i2aA_	Alignment	not modelled	93.8	24	PDB header: transferase Chain: A: PDB Molecule: probable inorganic polyphosphate/atp-nad kinase 1; PDBTitle: crystal structure of lmnadk1 from listeria monocytogenes
49	c3iv7B_	Alignment	not modelled	93.8	25	PDB header: oxidoreductase Chain: B: PDB Molecule: alcohol dehydrogenase iv; PDBTitle: crystal structure of iron-containing alcohol dehydrogenase2 (np_602249.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.07 a resolution
50	c4p53A_	Alignment	not modelled	93.8	20	PDB header: lyase Chain: A: PDB Molecule: cyclase; PDBTitle: vala (2-epi-5-epi-valiolone synthase) from streptomyces hygrosopicus2 subsp. jinggangensis 5008 with nad+ and zn2+ bound
51	c3rf7A_	Alignment	not modelled	93.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: iron-containing alcohol dehydrogenase; PDBTitle: crystal structure of an iron-containing alcohol dehydrogenase2 (sden_2133) from shewanella denitrificans os-217 at 2.12 a resolution
52	c3zdrA_	Alignment	not modelled	93.7	20	PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase domain of the bifunctional PDBTitle: structure of the alcohol dehydrogenase (adh) domain of a2 bifunctional adhe dehydrogenase from geobacillus3 thermoglucosidasius ncimb 11955
53	c3zokB_	Alignment	not modelled	93.5	18	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquininate synthase; PDBTitle: structure of 3-dehydroquininate synthase from actinidia chinensis in2 complex with nad

54	c4werA	Alignment	not modelled	93.0	16	PDB header: transferase Chain: A: PDB Molecule: diacylglycerol kinase catalytic domain protein; PDBTitle: crystal structure of diacylglycerol kinase catalytic domain protein2 from enterococcus faecalis v583
55	d2bona1	Alignment	not modelled	92.9	20	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
56	d1sg6a	Alignment	not modelled	92.7	25	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Dehydroquinase synthase, DHQS
57	d2jgra1	Alignment	not modelled	92.7	19	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
58	c2qv7A	Alignment	not modelled	91.8	21	PDB header: transferase Chain: A: PDB Molecule: diacylglycerol kinase dgkb; PDBTitle: crystal structure of diacylglycerol kinase dgkb in complex with adp2 and mg
59	c2bonB	Alignment	not modelled	91.7	20	PDB header: transferase Chain: B: PDB Molecule: lipid kinase; PDBTitle: structure of an escherichia coli lipid kinase (yegs)
60	c1ta9A	Alignment	not modelled	91.1	17	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase from schizosaccharomyces2 pombe
61	c4fr2A	Alignment	not modelled	91.0	16	PDB header: oxidoreductase, metal binding protein Chain: A: PDB Molecule: 1,3-propanediol dehydrogenase; PDBTitle: alcohol dehydrogenase from oenococcus oeni
62	c3h5oB	Alignment	not modelled	90.9	16	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator gntR; PDBTitle: the crystal structure of transcription regulator gntR from2 chromobacterium violaceum
63	d2p1ra1	Alignment	not modelled	90.7	18	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
64	d2qv7a1	Alignment	not modelled	90.4	21	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
65	c4ry8D	Alignment	not modelled	88.6	15	PDB header: transport protein Chain: D: PDB Molecule: periplasmic binding protein; PDBTitle: crystal structure of 5-methylthioribose transporter solute binding2 protein tlet_1677 from thermotoga lettingae tmo target efi-511109 in3 complex with 5-methylthioribose
66	c5utoB	Alignment	not modelled	88.4	16	PDB header: transport protein Chain: B: PDB Molecule: edd domain protein, degv family; PDBTitle: the crystal structure of the staphylococcus aureus fatty acid kinase2 (fak) b1 protein loaded with palmitic acid to 1.83 angstrom3 resolution
67	c3qk7C	Alignment	not modelled	87.7	10	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulators; PDBTitle: crystal structure of putative transcriptional regulator from yersinia2 pestis biovar microtus str. 91001
68	c2qh8A	Alignment	not modelled	87.3	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of conserved domain protein from vibrio2 cholerae o1 biovar eltor str. n16961
69	c3s40C	Alignment	not modelled	87.1	22	PDB header: transferase Chain: C: PDB Molecule: diacylglycerol kinase; PDBTitle: the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. Sterne
70	c3vzdB	Alignment	not modelled	86.9	18	PDB header: transferase/inhibitor Chain: B: PDB Molecule: sphingosine kinase 1; PDBTitle: crystal structure of sphingosine kinase 1 with inhibitor and adp
71	c5fb3C	Alignment	not modelled	84.8	27	PDB header: oxidoreductase Chain: C: PDB Molecule: glycerol-1-phosphate dehydrogenase [nad(p)+]; PDBTitle: structure of glycerophosphate dehydrogenase in complex with nadph
72	c3ce9A	Alignment	not modelled	84.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase (np_348253.1) from2 clostridium acetobutylicum at 2.37 a resolution
73	c3n8hA	Alignment	not modelled	84.4	15	PDB header: ligase Chain: A: PDB Molecule: pantothenate synthetase; PDBTitle: crystal structure of pantoate-beta-alanine ligase from francisella2 tularensis
74	c2yyaB	Alignment	not modelled	84.3	20	PDB header: ligase Chain: B: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of gar synthetase from aquifex aeolicus
75	c4rf1B	Alignment	not modelled	83.8	22	PDB header: oxidoreductase Chain: B: PDB Molecule: glycerol-1-phosphate dehydrogenase [nad(p)+]; PDBTitle: crystal structure of g1pdh with nadph from methanocaldococcus2 jannaschii
76	c6o55B	Alignment	not modelled	83.0	19	PDB header: isomerase Chain: B: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 (pure) from legionella pneumophila
77	c3g85A	Alignment	not modelled	82.9	10	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (laci family); PDBTitle: crystal structure of laci family transcription regulator from2 clostridium acetobutylicum
78	c2h31A	Alignment	not modelled	82.7	16	PDB header: ligase, lyase Chain: A: PDB Molecule: multifunctional protein ade2; PDBTitle: crystal structure of human paics, a bifunctional

						carboxylase and2 synthetase in purine biosynthesis
79	d1dbqa_	Alignment	not modelled	80.9	16	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
80	c3tqrA_	Alignment	not modelled	80.6	10	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: structure of the phosphoribosylglycinamide formyltransferase (purn) in2 complex with ches from coxiella burnetii
81	c4rweA_	Alignment	not modelled	80.6	11	PDB header: sugar binding protein Chain: A: PDB Molecule: sugar-binding transport protein; PDBTitle: the crystal structure of a sugar-binding transport protein from2 yersinia pestis co92
82	d1qcza_	Alignment	not modelled	80.4	26	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
83	c3lp6D_	Alignment	not modelled	79.9	19	PDB header: lyase Chain: D: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution
84	c2fw9A_	Alignment	not modelled	78.6	23	PDB header: lyase Chain: A: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: structure of pure (n5-carboxyaminoimidazole ribonucleotide mutase)2 h59f from the acidophilic bacterium acetobacter aceti, at ph 8
85	d1u11a_	Alignment	not modelled	78.3	23	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
86	c4grdA_	Alignment	not modelled	78.2	19	PDB header: lyase,isomerase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from burkholderia cenocepacia j2315
87	d1o4va_	Alignment	not modelled	78.2	23	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
88	c3hcbW_	Alignment	not modelled	78.1	11	PDB header: rna binding protein Chain: B: PDB Molecule: maltose operon transcriptional repressor; PDBTitle: crystal structure of probable maltose operon transcriptional repressor2 malr from staphylococcus aureus
89	d1kq3a_	Alignment	not modelled	75.4	29	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
90	c3uk2B_	Alignment	not modelled	74.6	21	PDB header: ligase Chain: B: PDB Molecule: pantothenate synthetase; PDBTitle: the structure of pantothenate synthetase from burkholderia2 thailandensis
91	d7reqa2	Alignment	not modelled	73.6	23	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
92	c3rggD_	Alignment	not modelled	73.2	11	PDB header: lyase Chain: D: PDB Molecule: phosphoribosylaminoimidazole carboxylase, pure protein; PDBTitle: crystal structure of treponema denticola pure bound to air
93	c3orsD_	Alignment	not modelled	72.5	22	PDB header: isomerase,biosynthetic protein Chain: D: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
94	d1ybha2	Alignment	not modelled	72.0	20	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
95	c3trhl_	Alignment	not modelled	70.5	19	PDB header: lyase Chain: I: PDB Molecule: phosphoribosylaminoimidazole carboxylase PDBTitle: structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
96	c5kwvA_	Alignment	not modelled	70.4	28	PDB header: ligase Chain: A: PDB Molecule: pantothenate synthetase; PDBTitle: crystal structure of a pantoate-beta-alanine ligase from neisseria2 gonorrhoeae with bound ampnp
97	d2a84a1	Alignment	not modelled	69.4	22	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
98	d1a9xa4	Alignment	not modelled	67.2	23	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
99	c2ejcA_	Alignment	not modelled	67.1	17	PDB header: ligase Chain: A: PDB Molecule: pantoate--beta-alanine ligase; PDBTitle: crystal structure of pantoate--beta-alanine ligase (panc)2 from thermotoga maritima
100	d1o6ca_	Alignment	not modelled	66.7	10	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
101	c5cijA_	Alignment	not modelled	66.5	13	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: the crystal structure of phosphoribosylglycinamide formyltransferase2 from campylobacter jejuni subsp. jejuni nctc

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102	d1ihoa_	Alignment	not modelled	66.3	21	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
103	c3innB_	Alignment	not modelled	66.2	21	PDB header: ligase Chain: B: PDB Molecule: pantothenate synthetase; PDBTitle: crystal structure of pantoate-beta-alanine-ligase in complex2 with atp at low occupancy at 2.1 a resolution
104	c4hwgA_	Alignment	not modelled	66.1	8	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: structure of udp-n-acetylglucosamine 2-epimerase from rickettsia2 bellii
105	c3bblA_	Alignment	not modelled	65.9	12	PDB header: regulatory protein Chain: A: PDB Molecule: regulatory protein of lacI family; PDBTitle: crystal structure of a regulatory protein of lacI family from2 chloroflexus aggregans
106	c3rotA_	Alignment	not modelled	65.8	12	PDB header: transport protein Chain: A: PDB Molecule: abc sugar transporter, periplasmic sugar binding protein; PDBTitle: crystal structure of abc sugar transporter (periplasmic sugar binding2 protein) from legionella pneumophila
107	c3tqtB_	Alignment	not modelled	63.7	23	PDB header: ligase Chain: B: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: structure of the d-alanine-d-alanine ligase from coxiella burnetii
108	c2ywrA_	Alignment	not modelled	62.2	17	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of gar transformylase from aquifex aeolicus
109	c1m6vE_	Alignment	not modelled	61.3	20	PDB header: ligase Chain: E: PDB Molecule: carbamoyl phosphate synthetase large chain; PDBTitle: crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
110	c3gv0A_	Alignment	not modelled	60.9	15	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of lacI family transcription regulator from2 agrobacterium tumefaciens
111	c5hsgA_	Alignment	not modelled	59.9	7	PDB header: transport protein Chain: A: PDB Molecule: putative abc transporter, nucleotide binding/atpase PDBTitle: crystal structure of an abc transporter solute binding protein from2 klebsiella pneumoniae (kpn_01730, target efi-511059), apo open3 structure
112	d3bula2	Alignment	not modelled	59.2	18	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
113	c4y9tA_	Alignment	not modelled	59.2	10	PDB header: solute-binding protein Chain: A: PDB Molecule: abc transporter, solute binding protein; PDBTitle: crystal structure of an abc transporter solute binding protein2 (ipr025997) from agrobacterium vitis s4 (avi_5305, target efi-511224)3 with bound alpha-d-glucosamine
114	c4yleA_	Alignment	not modelled	58.9	12	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein/lacI transcriptional regulator; PDBTitle: crystal structure of an abc transporter solute binding protein2 (ipr025997) from burkholderia multivorans (bmul_1631, target efi-3 511115) with an unknown ligand modelled as alpha-d-erythrofuranose
115	d1ozha2	Alignment	not modelled	58.7	13	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
116	c3lftA_	Alignment	not modelled	58.6	23	PDB header: structure genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of the abc domain in complex with l-trp from2 streptococcus pneumonia to 1.35a
117	d1w0ma_	Alignment	not modelled	58.5	22	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
118	c2pvpB_	Alignment	not modelled	58.1	23	PDB header: ligase Chain: B: PDB Molecule: d-alanine-d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase from helicobacter2 pylori
119	d1o6da_	Alignment	not modelled	57.9	19	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YbeA-like
120	c3ag5A_	Alignment	not modelled	57.5	17	PDB header: ligase Chain: A: PDB Molecule: pantothenate synthetase; PDBTitle: crystal structure of pantothenate synthetase from staphylococcus2 aureus