

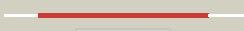
























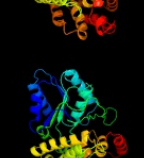


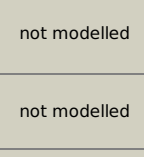


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2538c_ (aroB)_ 2861598_ 2862686
Date	Wed Aug 7 12:50:17 BST 2019
Unique Job ID	e81cbf7468b9393a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qbeA_	 Alignment		100.0	100	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinase; PDBTitle: crystal structure of the 3-dehydroquinase synthase (aroB) from2 mycobacterium tuberculosis
2	c3zokB_	 Alignment		100.0	37	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: structure of 3-dehydroquinase synthase from actinidia chinensis in2 complex with nad
3	c5tpkB_	 Alignment		100.0	26	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: desmethyl-4-deoxygadusol synthase from anabaena variabilis (ava_3858)2 with nad+ and zn2+ bound
4	c4p53A_	 Alignment		100.0	26	PDB header: lyase Chain: A: PDB Molecule: cyclase; PDBTitle: vala (2-epi-5-epi-valiolone synthase) from streptomyces hygroscopicus2 subsp. jinggangensis 5008 with nad+ and zn2+ bound
5	c5eksB_	 Alignment		100.0	37	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: structure of 3-dehydroquinase synthase from acinetobacter baumannii in2 complex with nad
6	c3okfA_	 Alignment		100.0	38	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: 2.5 angstrom resolution crystal structure of 3-dehydroquinase synthase2 (aroB) from vibrio cholerae
7	c6c5cA_	 Alignment		100.0	36	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: crystal structure of aro1p from candida albicans sc5314 in complex2 with nadh
8	c2gruB_	 Alignment		100.0	27	PDB header: lyase Chain: B: PDB Molecule: 2-deoxy-scylo-inosose synthase; PDBTitle: crystal structure of 2-deoxy-scylo-inosose synthase2 complexed with carbglucose-6-phosphate, nad+ and co2+
9	c5hvnA_	 Alignment		100.0	33	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: 3.0 angstrom crystal structure of 3-dehydroquinase synthase (aroB)2 from francisella tularensis in complex with nad.
10	d1ujna_	 Alignment		100.0	39	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Dehydroquinase synthase, DHQS
11	d1sg6a_	 Alignment		100.0	33	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Dehydroquinase synthase, DHQS

12	c1xahA	Alignment		100.0	31	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+
13	c3clhA	Alignment		100.0	33	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: crystal structure of 3-dehydroquinase synthase (dhqs)from2 helicobacter pylori
14	c3zdrA	Alignment		100.0	16	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
15	c3bfjK	Alignment		100.0	17	PDB header: oxidoreductase Chain: K: PDB Molecule: 1,3-propanediol oxidoreductase; PDBTitle: crystal structure analysis of 1,3-propanediol oxidoreductase
16	c6c76A	Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase; PDBTitle: structure of iron containing alcohol dehydrogenase from thermococcus2 thioireducens in an orthorhombic crystal form
17	c4fr2A	Alignment		100.0	17	PDB header: oxidoreductase, metal binding protein Chain: A: PDB Molecule: 1,3-propanediol dehydrogenase; PDBTitle: alcohol dehydrogenase from oenococcus oeni
18	c3ox4D	Alignment		100.0	16	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
19	d1jq5a	Alignment		100.0	18	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
20	d1vlja	Alignment		100.0	16	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
21	c5yvmA	Alignment	not modelled	100.0	17	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
22	d1rrma	Alignment	not modelled	100.0	17	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
23	c5zxlD	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: D: PDB Molecule: glycerol dehydrogenase; PDBTitle: structure of glda from e.coli
24	c6jkdD	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: D: PDB Molecule: methanol dehydrogenase; PDBTitle: crystal structure of sulfoacetaldehyde reductase from bifidobacterium2 kashiwanohense in complex with nad+
25	d1oj7a	Alignment	not modelled	100.0	15	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
26	c6csjD	Alignment	not modelled	100.0	17	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
27	c4mcaB	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase from serratia to 1.9a
28	c3jzdA	Alignment	not modelled	100.0	19	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
						Fold: Dehydroquinase synthase-like

29	d1o2da_	Alignment	not modelled	100.0	17	Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
30	c1ta9A_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase from schizosaccharomyces2 pombe
31	c3hl0B_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: maleylacetate reductase; PDBTitle: crystal structure of maleylacetate reductase from agrobacterium2 tumefaciens
32	c3iv7B_	Alignment	not modelled	100.0	17	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
33	c3uhjE_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: E: PDB Molecule: probable glycerol dehydrogenase; PDBTitle: crystal structure of a probable glycerol dehydrogenase from2 sinorhizobium melliloti 1021
34	c3rf7A_	Alignment	not modelled	100.0	13	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
35	c3ce9A_	Alignment	not modelled	100.0	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
36	d1kq3a_	Alignment	not modelled	100.0	20	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
37	c5fb3C_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: C: PDB Molecule: glycerol-1-phosphate dehydrogenase [nad(p+); PDBTitle: structure of glycerophosphate dehydrogenase in complex with nadph
38	c4rf1B_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: glycerol-1-phosphate dehydrogenase [nad(p+); PDBTitle: crystal structure of g1pdh with nadph from methanocaldococcus2 jannaschii
39	c3lp6D_	Alignment	not modelled	97.1	20	PDB header: lyase Chain: D: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution
40	d1o4va_	Alignment	not modelled	97.1	18	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
41	c3orsD_	Alignment	not modelled	97.0	19	PDB header: isomerase,biosynthetic protein Chain: D: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
42	d1qcza_	Alignment	not modelled	96.9	21	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
43	c3rggD_	Alignment	not modelled	96.9	17	PDB header: lyase Chain: D: PDB Molecule: phosphoribosylaminoimidazole carboxylase, pure protein; PDBTitle: crystal structure of treponema denticola pure bound to air
44	c4grdA_	Alignment	not modelled	96.9	21	PDB header: lyase,isomerase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from burkholderia cenocepacia j2315
45	d2bona1	Alignment	not modelled	96.9	16	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
46	d2jgra1	Alignment	not modelled	96.8	15	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
47	d2p1ra1	Alignment	not modelled	96.8	16	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
48	d1u11a_	Alignment	not modelled	96.8	17	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
49	c2fw9A_	Alignment	not modelled	96.8	17	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
50	c2h31A_	Alignment	not modelled	96.6	17	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
51	c6o55B_	Alignment	not modelled	96.6	16	PDB header: isomerase Chain: B: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 (pure) from legionella pneumophila

52	c4ja0A	Alignment	not modelled	96.5	13	PDB header: protein binding Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase; PDBTitle: crystal structure of the invertebrate bi-functional purine2 biosynthesis enzyme paics at 2.8 a resolution
53	c4b4kK	Alignment	not modelled	96.5	19	PDB header: isomerase Chain: K: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: crystal structure of bacillus anthracis pure
54	c3trhI	Alignment	not modelled	96.4	20	PDB header: lyase Chain: I: PDB Molecule: phosphoribosylaminoimidazole carboxylase PDBTitle: structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
55	d1xmpa	Alignment	not modelled	96.3	19	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
56	c4werA	Alignment	not modelled	96.2	13	PDB header: transferase Chain: A: PDB Molecule: diacylglycerol kinase catalytic domain protein2 PDBTitle: crystal structure of diacylglycerol kinase catalytic domain protein2 from enterococcus faecalis v583
57	c3s40C	Alignment	not modelled	95.9	19	PDB header: transferase Chain: C: PDB Molecule: diacylglycerol kinase; PDBTitle: the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. Sterne
58	c2ywxA	Alignment	not modelled	95.8	22	PDB header: lyase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from methanocaldococcus jannaschii
59	d2qv7a1	Alignment	not modelled	95.5	19	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
60	c2qv7A	Alignment	not modelled	95.4	17	PDB header: transferase Chain: A: PDB Molecule: diacylglycerol kinase dgkb; PDBTitle: crystal structure of diacylglycerol kinase dgkb in complex with adp2 and mg
61	c3vzdB	Alignment	not modelled	95.3	21	PDB header: transferase/inhibitor Chain: B: PDB Molecule: sphingosine kinase 1; PDBTitle: crystal structure of sphingosine kinase 1 with inhibitor and adp
62	c2bonB	Alignment	not modelled	95.3	17	PDB header: transferase Chain: B: PDB Molecule: lipid kinase; PDBTitle: structure of an escherichia coli lipid kinase (yegs)
63	d1u0ta	Alignment	not modelled	95.1	28	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like
64	d1pfka	Alignment	not modelled	93.6	31	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
65	d4pfka	Alignment	not modelled	93.1	26	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
66	c5xoeA	Alignment	not modelled	93.0	25	PDB header: transferase Chain: A: PDB Molecule: atp-dependent 6-phosphofructokinase; PDBTitle: crystal structure of the apo staphylococcus aureus phosphofructokinase
67	c3k2qA	Alignment	not modelled	91.6	24	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
68	d2f48a1	Alignment	not modelled	91.5	15	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
69	d2ez9a1	Alignment	not modelled	91.1	11	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
70	c3opyH	Alignment	not modelled	90.9	20	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
71	c3opyB	Alignment	not modelled	90.9	20	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
72	c1zxxA	Alignment	not modelled	90.6	27	PDB header: transferase Chain: A: PDB Molecule: 6-phosphofructokinase; PDBTitle: the crystal structure of phosphofructokinase from lactobacillus2 delbrueckii
73	d2djia1	Alignment	not modelled	89.2	8	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
74	d1ovma1	Alignment	not modelled	89.1	19	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
75	c2higA	Alignment	not modelled	88.9	25	PDB header: transferase Chain: A: PDB Molecule: 6-phospho-1-fructokinase; PDBTitle: crystal structure of phosphofructokinase apoenzyme from trypanosoma2 brucei.
76	c2q5cA	Alignment	not modelled	88.7	15	PDB header: transcription Chain: A: PDB Molecule: ntrc family transcriptional regulator; PDBTitle: crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum

77	c3o8nA	Alignment	not modelled	88.4	19	PDB header: transferase Chain: A: PDB Molecule: 6-phosphofructokinase, muscle type; PDBTitle: structure of phosphofructokinase from rabbit skeletal muscle
78	d1ybha1	Alignment	not modelled	88.4	13	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
79	d1pvdA1	Alignment	not modelled	88.1	17	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
80	d1zpdA1	Alignment	not modelled	88.0	28	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
81	c3opyG	Alignment	not modelled	87.5	18	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
82	c3opyE	Alignment	not modelled	87.2	19	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
83	c3o8oB	Alignment	not modelled	87.0	20	PDB header: transferase Chain: B: PDB Molecule: 6-phosphofructokinase subunit beta; PDBTitle: structure of phosphofructokinase from saccharomyces cerevisiae
84	c3o8oC	Alignment	not modelled	86.5	16	PDB header: transferase Chain: C: PDB Molecule: 6-phosphofructokinase subunit alpha; PDBTitle: structure of phosphofructokinase from saccharomyces cerevisiae
85	d2ji7a1	Alignment	not modelled	85.5	17	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
86	d1ozha1	Alignment	not modelled	85.0	14	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
87	d2ihtA1	Alignment	not modelled	83.8	13	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
88	d2pjuA1	Alignment	not modelled	83.7	18	Fold: Chelatase-like Superfamily: PrpR receptor domain-like Family: PrpR receptor domain-like
89	c3cf4G	Alignment	not modelled	83.3	11	PDB header: oxidoreductase Chain: G: PDB Molecule: acetyl-coa decarboxylase/synthase epsilon subunit; PDBTitle: structure of the codh component of the m. barkeri acds complex
90	d1q6za1	Alignment	not modelled	81.7	11	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
91	c3pfnB	Alignment	not modelled	80.9	18	PDB header: transferase Chain: B: PDB Molecule: nad kinase; PDBTitle: crystal structure of human nad kinase
92	c2an1D	Alignment	not modelled	78.4	16	PDB header: transferase Chain: D: PDB Molecule: putative kinase; PDBTitle: structural genomics, the crystal structure of a putative kinase from salmonella typhimurim lt2
93	c4nmlA	Alignment	not modelled	77.2	24	PDB header: isomerase Chain: A: PDB Molecule: ribulose 5-phosphate isomerase; PDBTitle: 2.60 angstrom resolution crystal structure of putative ribose 5-2 phosphate isomerase from toxoplasma gondii me49 in complex with dl-3 malic acid
94	d1v4va	Alignment	not modelled	76.7	19	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
95	c4q9dA	Alignment	not modelled	76.0	17	PDB header: lyase Chain: A: PDB Molecule: benzoylformate decarboxylase; PDBTitle: x-ray structure of a putative thiamin diphosphate-dependent enzyme2 isolated from mycobacterium smegmatis
96	d1t9ba1	Alignment	not modelled	74.6	13	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
97	c3wrwE	Alignment	not modelled	73.3	16	PDB header: transferase Chain: E: PDB Molecule: tm-1 protein; PDBTitle: crystal structure of the n-terminal domain of resistance protein
98	d1z0sa1	Alignment	not modelled	73.1	28	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like
99	c1z0zC	Alignment	not modelled	73.1	28	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
100	c2f59B	Alignment	not modelled	72.7	17	PDB header: transferase Chain: B: PDB Molecule: 6,7-dimethyl-8-ribityllumazine synthase 1; PDBTitle: lumazine synthase ribh1 from brucella abortus (gene bruab1_0785,2 swiss-prot entry q57dy1) complexed with inhibitor 5-nitro-6-(d-3 ribitylamino)-2,4(1h,3h) pyrimidinedione
101	c1sy7B	Alignment	not modelled	72.7	14	PDB header: oxidoreductase Chain: B: PDB Molecule: catalase 1; PDBTitle: crystal structure of the catalase-1 from neurospora crassa, native2 structure at 1.75a resolution.
102	c2i2aA	Alignment	not modelled	67.9	13	PDB header: transferase Chain: A: PDB Molecule: probable inorganic polyphosphate/atp-nad kinase 1;

						PDBTitle: crystal structure of lmnadk1 from listeria monocytogenes PDB header: transcription Chain: D: PDB Molecule: propionate catabolism operon regulatory protein; PDBTitle: crystal structure of propionate catabolism operon regulatory protein2 prpr
103	c2pjuD_	Alignment	not modelled	67.2	16	
104	c3d3jA_	Alignment	not modelled	66.2	13	PDB header: protein binding Chain: A: PDB Molecule: enhancer of mrna-decapping protein 3; PDBTitle: crystal structure of human edc3p
105	c2x7jA_	Alignment	not modelled	63.8	11	PDB header: transferase Chain: A: PDB Molecule: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene PDBTitle: structure of the menaquinone biosynthesis protein mend from2 bacillus subtilis
106	c4d9gA_	Alignment	not modelled	63.0	12	PDB header: lyase Chain: A: PDB Molecule: putative diaminopropionate ammonia-lyase; PDBTitle: crystal structure of selenomethionine incorporated holo2 diaminopropionate ammonia lyase from escherichia coli
107	c1powA_	Alignment	not modelled	62.8	10	PDB header: oxidoreductase(oxygen as acceptor) Chain: A: PDB Molecule: pyruvate oxidase; PDBTitle: the refined structures of a stabilized mutant and of wild-type2 pyruvate oxidase from lactobacillus plantarum
108	c1xtzA_	Alignment	not modelled	59.8	8	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase; PDBTitle: crystal structure of the s. cerevisiae d-ribose-5-phosphate isomerase:2 comparison with the archeal and bacterial enzymes
109	c3l4eA_	Alignment	not modelled	58.6	13	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized peptidase lmo0363; PDBTitle: 1.5a crystal structure of a putative peptidase e protein from listeria2 monocytogenes egd-e
110	c1yi1A_	Alignment	not modelled	57.9	14	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase; PDBTitle: crystal structure of arabidopsis thaliana acetohydroxyacid synthase in2 complex with a sulfonylurea herbicide, tribenuron methyl
111	c4xd9A_	Alignment	not modelled	57.7	8	PDB header: translation Chain: A: PDB Molecule: ribosome biogenesis protein, putative (afu_orthologue PDBTitle: structure of rpf2-rrs1 complex involved in ribosome biogenesis
112	c4xd9C_	Alignment	not modelled	57.7	8	PDB header: translation Chain: C: PDB Molecule: ribosome biogenesis protein, putative (afu_orthologue PDBTitle: structure of rpf2-rrs1 complex involved in ribosome biogenesis
113	c2j37W_	Alignment	not modelled	56.8	6	PDB header: ribosome Chain: W: PDB Molecule: signal recognition particle 54 kda protein (srp54); PDBTitle: model of mammalian srp bound to 80s rncs
114	c3ouzA_	Alignment	not modelled	55.1	16	PDB header: ligase Chain: A: PDB Molecule: biotin carboxylase; PDBTitle: crystal structure of biotin carboxylase-adp complex from campylobacter2 jejuni
115	d1c2ya_	Alignment	not modelled	53.4	19	Fold: Lumazine synthase Superfamily: Lumazine synthase Family: Lumazine synthase
116	c1uj6A_	Alignment	not modelled	53.3	15	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: crystal structure of thermus thermophilus ribose-5-phosphate isomerase2 complexed with arabinose-5-phosphate
117	d1nqua_	Alignment	not modelled	52.7	19	Fold: Lumazine synthase Superfamily: Lumazine synthase Family: Lumazine synthase
118	c4zhtB_	Alignment	not modelled	52.5	18	PDB header: isomerase Chain: B: PDB Molecule: bifunctional udp-n-acetylglucosamine 2-epimerase/n- PDBTitle: crystal structure of udp-glcna2-2-epimerase
119	d1sy7a1	Alignment	not modelled	52.3	12	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Catalase, C-terminal domain
120	c4e08B_	Alignment	not modelled	52.1	18	PDB header: motor protein Chain: B: PDB Molecule: dj-1 beta; PDBTitle: crystal structure of drosophila melanogaster dj-1beta