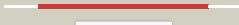
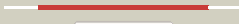
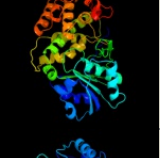
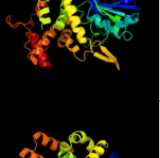
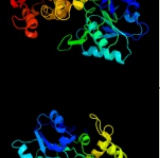
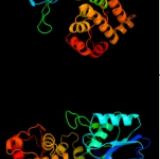
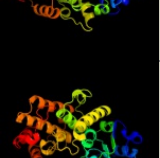
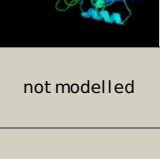
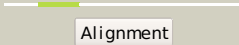
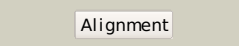
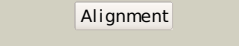
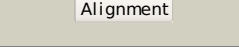
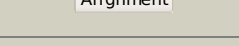
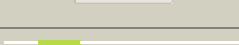
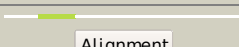
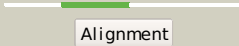
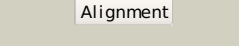
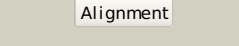
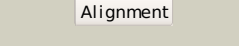
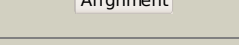
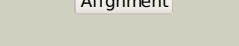
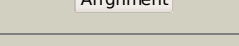
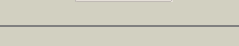
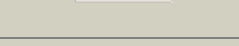
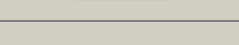
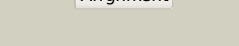
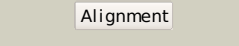


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1oj7a_	 Alignment		100.0	99	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
2	d1vlja_	 Alignment		100.0	36	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
3	c3bfjK_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: K: PDB Molecule: 1,3-propanediol oxidoreductase; PDBTitle: crystal structure analysis of 1,3-propanediol oxidoreductase
4	c3ox4D_	 Alignment		100.0	22	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
5	d1rrma_	 Alignment		100.0	23	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
6	d1o2da_	 Alignment		100.0	24	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
7	c3hl0B_	 Alignment		100.0	23	PDB header: oxidoreductase Chain: B: PDB Molecule: maleylacetate reductase; PDBTitle: crystal structure of maleylacetate reductase from agrobacterium2 tumefaciens
8	c3iv7B_	 Alignment		100.0	24	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
9	c3jzdA_	 Alignment		100.0	22	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
10	c3rf7A_	 Alignment		100.0	17	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
11	d1jq5a_	 Alignment		100.0	21	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase

12	c1ta9A_	Alignment		100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase from schizosaccharomyces2 pombe
13	c3uhjE_	Alignment		100.0	22	PDB header: oxidoreductase Chain: E: PDB Molecule: probable glycerol dehydrogenase; PDBTitle: crystal structure of a probable glycerol dehydrogenase from2 sinorhizobium meliloti 1021
14	d1kq3a_	Alignment		100.0	22	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
15	c3ce9A_	Alignment		100.0	15	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
16	c1xahA_	Alignment		100.0	20	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+
17	c3okfA_	Alignment		100.0	17	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
18	d1sg6a_	Alignment		100.0	18	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Dehydroquinase synthase, DHQS
19	d1ujna_	Alignment		100.0	18	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Dehydroquinase synthase, DHQS
20	c2gruB_	Alignment		100.0	15	PDB header: lyase Chain: B: PDB Molecule: 2-deoxy-scyllo-inosose synthase; PDBTitle: crystal structure of 2-deoxy-scyllo-inosose synthase2 complexed with carbamylglucose-6-phosphate, nad+ and co2+
21	c3clhA_	Alignment	not modelled	100.0	19	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: crystal structure of 3-dehydroquinase synthase (dhqs)from2 helicobacter pylori
22	c3orsD_	Alignment	not modelled	96.7	16	PDB header: isomerase,biosynthetic protein Chain: D: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
23	d1qcza_	Alignment	not modelled	96.6	20	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
24	c3lp6D_	Alignment	not modelled	96.5	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
25	d1u11a_	Alignment	not modelled	96.4	15	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
26	c2fw9A_	Alignment	not modelled	96.4	15	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
						Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole

27	d1o4va_	Alignment	not modelled	96.3	21	carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
28	d1xmpa_	Alignment	not modelled	95.8	17	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
29	c3trhl_	Alignment	not modelled	95.7	18	PDB header: lyase Chain: I: PDB Molecule: phosphoribosylaminoimidazole carboxylase PDBTitle: structure of a phosphoribosylaminoimidazole carboxylase catalytic subunit (pure) from coxiella burnetii
30	c3rggD_	Alignment	not modelled	95.6	12	PDB header: lyase Chain: D: PDB Molecule: phosphoribosylaminoimidazole carboxylase, pure protein; PDBTitle: crystal structure of treponema denticola pure bound to air
31	c2h31A_	Alignment	not modelled	95.0	19	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
32	d2p1ra1	Alignment	not modelled	94.9	17	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
33	d2jgra1	Alignment	not modelled	94.7	17	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
34	d1u0ta_	Alignment	not modelled	94.6	25	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like
35	d2bona1	Alignment	not modelled	94.1	18	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
36	d1pfka_	Alignment	not modelled	93.3	12	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
37	c1zxxA_	Alignment	not modelled	93.1	8	PDB header: transferase Chain: A: PDB Molecule: 6-phosphofructokinase; PDBTitle: the crystal structure of phosphofructokinase from lactobacillus2 delbrueckii
38	d4pfka_	Alignment	not modelled	92.8	13	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
39	c2bonB_	Alignment	not modelled	92.5	20	PDB header: transferase Chain: B: PDB Molecule: lipid kinase; PDBTitle: structure of an escherichia coli lipid kinase (yegs)
40	c3s40C_	Alignment	not modelled	91.9	19	PDB header: transferase Chain: C: PDB Molecule: diacylglycerol kinase; PDBTitle: the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. Sterne
41	c2ywxA_	Alignment	not modelled	91.8	19	PDB header: lyase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from methanocaldococcus jannaschii
42	d2f48a1	Alignment	not modelled	91.8	17	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
43	c3opyB_	Alignment	not modelled	90.9	12	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
44	c3opyH_	Alignment	not modelled	90.9	12	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
45	c2q5cA_	Alignment	not modelled	90.7	15	PDB header: transcription Chain: A: PDB Molecule: ntrc family transcriptional regulator; PDBTitle: crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
46	c2qv7A_	Alignment	not modelled	89.7	21	PDB header: transferase Chain: A: PDB Molecule: diacylglycerol kinase dgkb; PDBTitle: crystal structure of diacylglycerol kinase dgkb in complex with adp2 and mg
47	c3o8oB_	Alignment	not modelled	89.4	14	PDB header: transferase Chain: B: PDB Molecule: 6-phosphofructokinase subunit beta; PDBTitle: structure of phosphofructokinase from saccharomyces cerevisiae
48	c2an1D_	Alignment	not modelled	89.2	21	PDB header: transferase Chain: D: PDB Molecule: putative kinase; PDBTitle: structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
49	d2ez9a1	Alignment	not modelled	89.0	24	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
50	c3dm5A_	Alignment	not modelled	88.9	15	PDB header: rna binding protein, transport protein Chain: A: PDB Molecule: signal recognition 54 kda protein; PDBTitle: structures of srp54 and srp19, the two proteins assembling2 the ribonucleic core of the signal recognition particle3 from the archaeon pyrococcus furiosus.
51	c3k2qA_	Alignment	not modelled	88.6	13	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
52	d2pja1	Alignment	not modelled	88.6	12 Fold: Chelatase-like Superfamily: PrpR receptor domain-like Family: PrpR receptor domain-like
53	c2j37W	Alignment	not modelled	88.4	8 PDB header: ribosome Chain: W: PDB Molecule: signal recognition particle 54 kda protein PDBTitle: model of mammalian srp bound to 80s rncs
54	c2iy3A	Alignment	not modelled	87.9	11 PDB header: rna-binding Chain: A: PDB Molecule: signal recognition particle protein ffh; PDBTitle: structure of the e. coli signal recognition particle2 bound to a translating ribosome
55	c3opyE	Alignment	not modelled	87.8	15 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
56	c2higA	Alignment	not modelled	87.0	20 PDB header: transferase Chain: A: PDB Molecule: 6-phospho-1-fructokinase; PDBTitle: crystal structure of phosphofructokinase apoenzyme from trypanosoma2 brucei.
57	c3opyG	Alignment	not modelled	86.6	13 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
58	d2qv7a1	Alignment	not modelled	85.4	22 Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
59	c3o8oC	Alignment	not modelled	85.1	16 PDB header: transferase Chain: C: PDB Molecule: 6-phosphofructokinase subunit alpha; PDBTitle: structure of phosphofructokinase from saccharomyces cerevisiae
60	c3o8nA	Alignment	not modelled	83.6	10 PDB header: transferase Chain: A: PDB Molecule: 6-phosphofructokinase, muscle type; PDBTitle: structure of phosphofructokinase from rabbit skeletal muscle
61	c2yhsA	Alignment	not modelled	81.9	11 PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the e. coli srp receptor ftsy
62	d2djia1	Alignment	not modelled	79.0	15 Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
63	d1ybha1	Alignment	not modelled	78.8	21 Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
64	c1qzwC	Alignment	not modelled	78.4	15 PDB header: signaling protein/rna Chain: C: PDB Molecule: signal recognition 54 kda protein; PDBTitle: crystal structure of the complete core of archaeal srp and2 implications for inter-domain communication
65	c3dmdA	Alignment	not modelled	77.8	15 PDB header: transport protein Chain: A: PDB Molecule: signal recognition particle receptor; PDBTitle: structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus
66	c1vmaA	Alignment	not modelled	77.5	8 PDB header: protein transport Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: crystal structure of cell division protein ftsy (tm0570) from2 thermotoga maritima at 1.60 a resolution
67	c2j289	Alignment	not modelled	77.0	17 PDB header: ribosome Chain: 9: PDB Molecule: signal recognition particle 54; PDBTitle: model of e. coli srp bound to 70s rncs
68	c2jkzB	Alignment	not modelled	75.6	15 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)
69	c3cf4G	Alignment	not modelled	75.5	14 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
70	c3pfnB	Alignment	not modelled	75.3	17 PDB header: transferase Chain: B: PDB Molecule: nad kinase; PDBTitle: crystal structure of human nad kinase
71	c2qy9A	Alignment	not modelled	74.7	11 PDB header: protein transport Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the ng+1 construct of the e. coli srp receptor2 ftsy
72	c3rfqC	Alignment	not modelled	71.6	14 PDB header: biosynthetic protein Chain: C: PDB Molecule: pterin-4-alpha-carbinolamine dehydratase moab2; PDBTitle: crystal structure of pterin-4-alpha-carbinolamine dehydratase moab22 from mycobacterium marinum
73	c2cnwF	Alignment	not modelled	70.1	17 PDB header: signal recognition Chain: F: PDB Molecule: cell division protein ftsy; PDBTitle: gdpalf4 complex of the srp gtpases ffh and ftsy
74	c3mdqA	Alignment	not modelled	67.3	22 PDB header: hydrolase Chain: A: PDB Molecule: exopolyposphatase; PDBTitle: crystal structure of an exopolyposphatase (chu_0316) from cytophaga2 hutchinsonii atcc 33406 at 1.50 a resolution
75	d1t9ba1	Alignment	not modelled	67.2	19 Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
76	c3hbmA	Alignment	not modelled	66.6	16 PDB header: hydrolase Chain: A: PDB Molecule: udp-sugar hydrolase; PDBTitle: crystal structure of pseg from campylobacter jejuni

77	c2j7pA	 Alignment	not modelled	65.8	11	PDB header: signal recognition Chain: A: PDB Molecule: signal recognition particle protein; PDBTitle: gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and tsy
78	c3b9qA	 Alignment	not modelled	65.3	19	PDB header: protein transport Chain: A: PDB Molecule: chloroplast srp receptor homolog, alpha subunit PDBTitle: the crystal structure of cpfts from arabidopsis thaliana
79	c3n2bD	 Alignment	not modelled	64.0	12	PDB header: lyase Chain: D: PDB Molecule: diaminopimelate decarboxylase; PDBTitle: 1.8 angstrom resolution crystal structure of diaminopimelate2 decarboxylase (lysa) from vibrio cholerae.
80	c3sg0A	 Alignment	not modelled	63.1	10	PDB header: signaling protein Chain: A: PDB Molecule: extracellular ligand-binding receptor; PDBTitle: the crystal structure of an extracellular ligand-binding receptor from2 rhodospseudomonas palustris haa2
81	d1j8yf2	 Alignment	not modelled	63.0	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
82	c1j8yF	 Alignment	not modelled	62.2	14	PDB header: signaling protein Chain: F: PDB Molecule: signal recognition 54 kda protein; PDBTitle: signal recognition particle conserved gtpase domain from a.2 ambivalens t112a mutant
83	c3snrA	 Alignment	not modelled	61.8	9	PDB header: transport protein Chain: A: PDB Molecule: extracellular ligand-binding receptor; PDBTitle: rpd_1889 protein, an extracellular ligand-binding receptor from2 rhodospseudomonas palustris.
84	d2g2ca1	 Alignment	not modelled	61.5	15	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
85	d1di6a	 Alignment	not modelled	61.0	17	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
86	c3q41B	 Alignment	not modelled	59.5	11	PDB header: transport protein Chain: B: PDB Molecule: glutamate [nmda] receptor subunit zeta-1; PDBTitle: crystal structure of the glun1 n-terminal domain (ntd)
87	c2v36A	 Alignment	not modelled	59.1	17	PDB header: transferase Chain: A: PDB Molecule: gamma-glutamyltranspeptidase large chain; PDBTitle: crystal structure of gamma-glutamyl transferase from2 bacillus subtilis
88	c1yt5A	 Alignment	not modelled	58.8	24	PDB header: transferase Chain: A: PDB Molecule: inorganic polyphosphate/atp-nad kinase; PDBTitle: crystal structure of nad kinase from thermotoga maritima
89	c2floA	 Alignment	not modelled	57.5	13	PDB header: hydrolase Chain: A: PDB Molecule: exopolyphosphatase; PDBTitle: crystal structure of exopolyphosphatase (ppx) from e. coli o157:h7
90	c2i2aA	 Alignment	not modelled	55.9	20	PDB header: transferase Chain: A: PDB Molecule: probable inorganic polyphosphate/atp-nad kinase 1; PDBTitle: crystal structure of lmnadk1 from listeria monocytogenes
91	c2pjuD	 Alignment	not modelled	55.9	12	PDB header: transcription Chain: D: PDB Molecule: propionate catabolism operon regulatory protein; PDBTitle: crystal structure of propionate catabolism operon2 regulatory protein prpr
92	d1ovma1	 Alignment	not modelled	54.6	11	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
93	c3h5lB	 Alignment	not modelled	54.1	9	PDB header: transport protein Chain: B: PDB Molecule: putative branched-chain amino acid abc PDBTitle: crystal structure of a putative branched-chain amino acid2 abc transporter from silicibacter pomeroyi
94	c3eafA	 Alignment	not modelled	52.9	6	PDB header: transport protein Chain: A: PDB Molecule: abc transporter, substrate binding protein; PDBTitle: crystal structure of abc transporter, substrate binding protein2 aeropyrum pernix
95	d1pvdal	 Alignment	not modelled	52.9	17	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
96	c3lopA	 Alignment	not modelled	52.0	13	PDB header: substrate binding protein Chain: A: PDB Molecule: substrate binding periplasmic protein; PDBTitle: crystal structure of substrate-binding periplasmic protein2 (pbp) from ralstonia solanacearum
97	c2ek0B	 Alignment	not modelled	51.2	20	PDB header: metal binding protein Chain: B: PDB Molecule: stage v sporulation protein s (spovs) related protein; PDBTitle: stage v sporulation protein s (spovs) from thermus thermophilus zinc2 form
98	d1o8bb1	 Alignment	not modelled	51.1	24	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain
99	c3tqrA	 Alignment	not modelled	49.6	11	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: structure of the phosphoribosylglycinamide formyltransferase (purn) in2 complex with ches from coxiella burnetii
100	c3dcjA	 Alignment	not modelled	49.5	13	PDB header: transferase Chain: A: PDB Molecule: probable 5'-phosphoribosylglycinamide PDBTitle: crystal structure of glycinamide formyltransferase (purn)2 from mycobacterium tuberculosis in complex with 5-methyl-5,3 6,7,8-tetrahydrofolic acid derivative
101	c2ko8A	 Alignment	not modelled	47.6	10	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-enyl

101	c3ke6A_	Alignment	not modelled	47.9	10	diphosphate PDBTitle: crystal structure of isph:hmbpp-complex PDB header: transferase
102	c1yi1A_	Alignment	not modelled	47.4	21	Chain: A: PDB Molecule: acetolactate synthase; PDBTitle: crystal structure of arabidopsis thaliana acetoxyhydroxyacid synthase in2 complex with a sulfonylurea herbicide, tribenuron methyl
103	d2f7wa1	Alignment	not modelled	46.9	13	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
104	d2ptza1	Alignment	not modelled	46.2	16	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: Enolase
105	c3hi0B_	Alignment	not modelled	45.9	16	PDB header: hydrolase Chain: B: PDB Molecule: putative exopolyphosphatase; PDBTitle: crystal structure of putative exopolyphosphatase (17739545) from2 agrobacterium tumefaciens str. c58 (dupont) at 2.30 a resolution
106	d1v4va_	Alignment	not modelled	45.6	26	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
107	d1w6ta1	Alignment	not modelled	45.5	14	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: Enolase
108	d2eyqa5	Alignment	not modelled	44.2	9	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
109	d1s3ia2	Alignment	not modelled	43.2	9	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
110	c3i09A_	Alignment	not modelled	43.2	11	PDB header: transport protein Chain: A: PDB Molecule: periplasmic branched-chain amino acid-binding protein; PDBTitle: crystal structure of a periplasmic binding protein (bma2936) from2 burkholderia mallei at 1.80 a resolution
111	c2og2A_	Alignment	not modelled	43.0	18	PDB header: protein transport Chain: A: PDB Molecule: putative signal recognition particle receptor; PDBTitle: crystal structure of chloroplast ftsy from arabidopsis2 thaliana
112	c3u7jA_	Alignment	not modelled	42.8	24	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
113	c1powA_	Alignment	not modelled	42.7	27	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
114	d1jlja_	Alignment	not modelled	42.6	14	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
115	c2y69R_	Alignment	not modelled	41.8	27	PDB header: electron transport Chain: R: PDB Molecule: cytochrome c oxidase subunit 5a; PDBTitle: bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
116	c2z8jA_	Alignment	not modelled	41.6	20	PDB header: transferase Chain: A: PDB Molecule: gamma-glutamyltranspeptidase; PDBTitle: crystal structure of escherichia coli gamma-2 glutamyltranspeptidase in complex with azaserine prepared3 in the dark
117	d1v54e_	Alignment	not modelled	41.5	27	Fold: alpha-alpha superhelix Superfamily: Cytochrome c oxidase subunit E Family: Cytochrome c oxidase subunit E
118	c3mtqA_	Alignment	not modelled	41.5	17	PDB header: transferase Chain: A: PDB Molecule: putative phosphoenolpyruvate-dependent sugar PDBTitle: crystal structure of a putative phosphoenolpyruvate-dependent sugar2 phosphotransferase system (pts) permease (kpn_04802) from klebsiella3 pneumoniae subsp. pneumoniae mgh 78578 at 1.70 a resolution
119	d1fmta2	Alignment	not modelled	41.4	16	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
120	c1t6dB_	Alignment	not modelled	41.3	16	PDB header: hydrolase Chain: B: PDB Molecule: exopolyphosphatase; PDBTitle: miras phasing of the aquifex aeolicus ppx/gppa phosphatase: crystal2 structure of the type ii variant