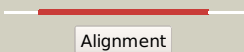
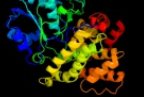
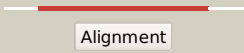
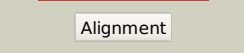
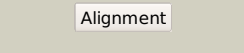
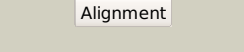
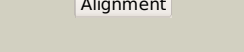
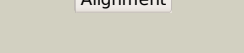
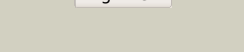
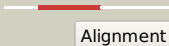
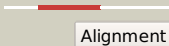
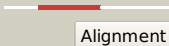
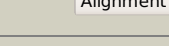
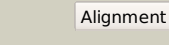
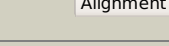
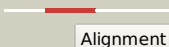
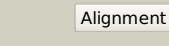
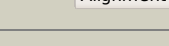


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ox4D_	 Alignment		100.0	34	PDB header: oxidoreductase Chain: D; PDB Molecule: alcohol dehydrogenase 2; PDBTitle: structures of iron-dependent alcohol dehydrogenase 2 from zymomonas2 mobilis zm4 complexed with nad cofactor
2	c3bfjK_	 Alignment		100.0	39	PDB header: oxidoreductase Chain: K; PDB Molecule: 1,3-propanediol oxidoreductase; PDBTitle: crystal structure analysis of 1,3-propanediol oxidoreductase
3	d1vlja_	 Alignment		100.0	24	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
4	d1oj7a_	 Alignment		100.0	24	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
5	d1rrma_	 Alignment		100.0	35	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
6	d1o2da_	 Alignment		100.0	32	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
7	c3hl0B_	 Alignment		100.0	26	PDB header: oxidoreductase Chain: B; PDB Molecule: maleylacetate reductase; PDBTitle: crystal structure of maleylacetate reductase from agrobacterium2 tumefaciens
8	c3iv7B_	 Alignment		100.0	27	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	29	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	24	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	25	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase

12	c1ta9A_	Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase from schizosaccharomyces2 pombe
13	d1kq3a_	Alignment		100.0	27	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
14	c3uhjE_	Alignment		100.0	20	PDB header: oxidoreductase Chain: E: PDB Molecule: probable glycerol dehydrogenase; PDBTitle: crystal structure of a probable glycerol dehydrogenase from2 sinorhizobium meliloti 1021
15	c3ce9A_	Alignment		100.0	18	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	c3okfA_	Alignment		100.0	18	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
17	d1sg6a_	Alignment		100.0	17	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Dehydroquinase synthase, DHQS
18	c1xahA_	Alignment		100.0	19	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+
19	c3qbeA_	Alignment		100.0	19	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: crystal structure of the 3-dehydroquinase synthase (arob) from2 mycobacterium tuberculosis
20	c2gruB_	Alignment		100.0	15	PDB header: lyase Chain: B: PDB Molecule: 2-deoxy-scylo-inosose synthase; PDBTitle: crystal structure of 2-deoxy-scylo-inosose synthase2 complexed with carbaglucoase-6-phosphate, nad+ and co2+
21	d1ujna_	Alignment	not modelled	100.0	20	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Dehydroquinase synthase, DHQS
22	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
23	d1qcza_	Alignment	not modelled	96.3	22	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
24	c3orsD_	Alignment	not modelled	96.2	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
25	d2p1ra1	Alignment	not modelled	96.2	17	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
26	c4grdA_	Alignment	not modelled	96.1	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
27	d2jgra1	Alignment	not modelled	96.1	16	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
28	d2bona1	Alignment	not modelled	96.0	14	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like

						Family: Diacylglycerol kinase-like
29	c3lp6D_	 Alignment	not modelled	96.0	22	PDB header: lyase Chain: D: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution
30	d1o4va_	 Alignment	not modelled	95.9	25	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
31	d1u11a_	 Alignment	not modelled	95.9	19	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
32	c2fw9A_	 Alignment	not modelled	95.9	19	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
33	c3trhl_	 Alignment	not modelled	95.4	21	PDB header: lyase Chain: I: PDB Molecule: phosphoribosylaminoimidazole carboxylase PDBTitle: structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
34	c2bonB_	 Alignment	not modelled	95.4	16	PDB header: transferase Chain: B: PDB Molecule: lipid kinase; PDBTitle: structure of an escherichia coli lipid kinase (yegs)
35	c4b4kK_	 Alignment	not modelled	95.3	23	PDB header: isomerase Chain: K: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: crystal structure of bacillus anthracis pure
36	d1xmpa_	 Alignment	not modelled	95.2	23	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
37	c4ja0A_	 Alignment	not modelled	95.0	18	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
38	c3rggD_	 Alignment	not modelled	94.9	16	PDB header: lyase Chain: D: PDB Molecule: phosphoribosylaminoimidazole carboxylase, pure protein; PDBTitle: crystal structure of treponema denticola pure bound to air
39	c2q5cA_	 Alignment	not modelled	94.3	14	PDB header: transcription Chain: A: PDB Molecule: ntrc family transcriptional regulator; PDBTitle: crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
40	c2h31A_	 Alignment	not modelled	94.2	15	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
41	d1u0ta_	 Alignment	not modelled	94.1	27	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like
42	c3s40C_	 Alignment	not modelled	93.6	21	PDB header: transferase Chain: C: PDB Molecule: diacylglycerol kinase; PDBTitle: the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. Sterne
43	d2qv7a1	 Alignment	not modelled	93.5	18	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
44	d1pfka_	 Alignment	not modelled	93.3	22	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
45	c2qv7A_	 Alignment	not modelled	93.3	16	PDB header: transferase Chain: A: PDB Molecule: diacylglycerol kinase dgkb; PDBTitle: crystal structure of diacylglycerol kinase dgkb in complex with adp2 and mg
46	c3vzdB_	 Alignment	not modelled	93.1	16	PDB header: transferase/inhibitor Chain: B: PDB Molecule: sphingosine kinase 1; PDBTitle: crystal structure of sphingosine kinase 1 with inhibitor and adp
47	c1zxxA_	 Alignment	not modelled	93.1	22	PDB header: transferase Chain: A: PDB Molecule: 6-phosphofructokinase; PDBTitle: the crystal structure of phosphofructokinase from lactobacillus2 delbrueckii
48	d4pfka_	 Alignment	not modelled	93.0	22	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
49	c3opyB_	 Alignment	not modelled	92.6	23	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
50	c3opyH_	 Alignment	not modelled	92.6	23	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
51	d2pjua1	Alignment	not modelled	90.9	13	Fold: Chelatase-like Superfamily: PrpR receptor domain-like Family: PrpR receptor domain-like
52	c3hi0B_	Alignment	not modelled	90.9	19	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
53	d2f48a1	Alignment	not modelled	90.8	21 Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
54	c3opyG	Alignment	not modelled	90.2	22 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
55	c3mdqA	Alignment	not modelled	90.1	23 PDB header: hydrolase Chain: A: PDB Molecule: exopolyphosphatase; PDBTitle: crystal structure of an exopolyphosphatase (chu_0316) from cytophaga2 hutchinsonii atcc 33406 at 1.50 a resolution
56	c3o8oB	Alignment	not modelled	89.7	23 PDB header: transferase Chain: B: PDB Molecule: 6-phosphofructokinase subunit beta; PDBTitle: structure of phosphofructokinase from saccharomyces cerevisiae
57	c3opyE	Alignment	not modelled	89.6	22 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
58	d1qo0a	Alignment	not modelled	89.3	21 Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
59	c3o8oC	Alignment	not modelled	89.1	22 PDB header: transferase Chain: C: PDB Molecule: 6-phosphofructokinase subunit alpha; PDBTitle: structure of phosphofructokinase from saccharomyces cerevisiae
60	c2higA	Alignment	not modelled	89.1	16 PDB header: transferase Chain: A: PDB Molecule: 6-phospho-1-fructokinase; PDBTitle: crystal structure of phosphofructokinase apoenzyme from trypanosoma2 brucei.
61	c1t6dB	Alignment	not modelled	88.8	19 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
62	c3k2qA	Alignment	not modelled	88.6	22 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
63	c3o8nA	Alignment	not modelled	87.2	18 PDB header: transferase Chain: A: PDB Molecule: 6-phosphofructokinase, muscle type; PDBTitle: structure of phosphofructokinase from rabbit skeletal muscle
64	c2j37W	Alignment	not modelled	86.3	11 PDB header: ribosome Chain: W: PDB Molecule: signal recognition particle 54 kda protein PDBTitle: model of mammalian srp bound to 80s rncs
65	c2floA	Alignment	not modelled	86.0	19 PDB header: hydrolase Chain: A: PDB Molecule: exopolyphosphatase; PDBTitle: crystal structure of exopolyphosphatase (ppx) from e. coli o157:h7
66	c2ywxA	Alignment	not modelled	85.7	30 PDB header: lyase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from methanocaldococcus jannaschii
67	c3b4uB	Alignment	not modelled	84.5	13 PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
68	c2j289	Alignment	not modelled	83.3	14 PDB header: ribosome Chain: 9: PDB Molecule: signal recognition particle 54; PDBTitle: model of e. coli srp bound to 70s rncs
69	c3aufA	Alignment	not modelled	83.3	20 PDB header: transferase Chain: A: PDB Molecule: glycinamide ribonucleotide transformylase 1; PDBTitle: crystal structure of glycinamide ribonucleotide transformylase 1 from2 symbiobacterium toebii
70	c2rfgB	Alignment	not modelled	83.0	23 PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
71	c2pjuD	Alignment	not modelled	82.9	13 PDB header: transcription Chain: D: PDB Molecule: propionate catabolism operon regulatory protein; PDBTitle: crystal structure of propionate catabolism operon2 regulatory protein prpr
72	c2i2aA	Alignment	not modelled	82.1	18 PDB header: transferase Chain: A: PDB Molecule: probable inorganic polyphosphate/atp-nad kinase 1; PDBTitle: crystal structure of Imnadk1 from listeria monocytogenes
73	c2iy3A	Alignment	not modelled	81.9	10 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
74	c3pfnB	Alignment	not modelled	81.8	22 PDB header: transferase Chain: B: PDB Molecule: nad kinase; PDBTitle: crystal structure of human nad kinase
75	c3h5lB	Alignment	not modelled	81.6	16 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
76	d1xi8a3	Alignment	not modelled	81.5	16 Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
					PDB header: lyase Chain: B: PDB Molecule: uncharacterized protein yage;

77	c3n2xB	Alignment	not modelled	81.1	22	PDBTitle: crystal structure of yage, a prophage protein belonging to the2 dihydrodipicolinic acid synthase family from e. coli k12 in complex3 with pyruvate
78	c3cerD	Alignment	not modelled	81.1	20	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: possible exopolyphosphatase-like protein; PDBTitle: crystal structure of the exopolyphosphatase-like protein2 q8g5j2. northeast structural genomics consortium target3 blr13
79	d1v4va	Alignment	not modelled	80.7	27	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
80	c3sg0A	Alignment	not modelled	80.3	13	PDB header: signaling protein Chain: A: PDB Molecule: extracellular ligand-binding receptor; PDBTitle: the crystal structure of an extracellular ligand-binding receptor from2 rhodopseudomonas palustris haa2
81	c2yxgD	Alignment	not modelled	80.0	18	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase (dapa)
82	c3lopA	Alignment	not modelled	79.4	12	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
83	c3snrA	Alignment	not modelled	79.2	13	PDB header: transport protein Chain: A: PDB Molecule: extracellular ligand-binding receptor; PDBTitle: rpd_1889 protein, an extracellular ligand-binding receptor from2 rhodopseudomonas palustris.
84	d1o5ka	Alignment	not modelled	79.1	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
85	c3i09A	Alignment	not modelled	78.9	10	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
86	c1yt5A	Alignment	not modelled	78.6	26	PDB header: transferase Chain: A: PDB Molecule: inorganic polyphosphate/atp-nad kinase; PDBTitle: crystal structure of nad kinase from thermotoga maritima
87	c3g0sA	Alignment	not modelled	78.0	16	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from salmonella typhimurium lt2
88	d2dx7a1	Alignment	not modelled	77.9	24	Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase
89	c3dm5A	Alignment	not modelled	77.9	13	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.
90	c2v9dB	Alignment	not modelled	77.1	21	PDB header: lyase Chain: B: PDB Molecule: yage; PDBTitle: crystal structure of yage, a prophage protein belonging to2 the dihydrodipicolinic acid synthase family from e. coli3 k12
91	c3av3A	Alignment	not modelled	76.3	14	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of glycinamide ribonucleotide transformylase 1 from2 geobacillus kaustophilus
92	c1qzwC	Alignment	not modelled	75.5	13	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
93	c2fmoA	Alignment	not modelled	75.2	17	PDB header: oxidoreductase Chain: A: PDB Molecule: 5,10-methylenetetrahydrofolate reductase; PDBTitle: ala177val mutant of e. coli methylenetetrahydrofolate2 reductase
94	c3s5oA	Alignment	not modelled	73.2	21	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-2-oxoglutarate aldolase, mitochondrial; PDBTitle: crystal structure of human 4-hydroxy-2-oxoglutarate aldolase bound to2 pyruvate
95	c3noeA	Alignment	not modelled	72.7	17	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
96	c1z0zC	Alignment	not modelled	71.7	19	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
97	d1z0sa1	Alignment	not modelled	71.7	19	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like
98	c3i45A	Alignment	not modelled	71.4	17	PDB header: signaling protein Chain: A: PDB Molecule: twin-arginine translocation pathway signal protein; PDBTitle: crystal structure of putative twin-arginine translocation pathway2 signal protein from rhodospirillum rubrum atcc 11170
99	c2yhsA	Alignment	not modelled	70.6	17	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the e. coli srp receptor ftsy
100	c3cf4G	Alignment	not modelled	70.1	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
101	c3eh2A	Alignment	not modelled	69.8	24	PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase;

101	c3e0zA	Alignment	not modelled	69.8	24	PDBTitle: crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution 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 PDB header: lyase Chain: B: PDB Molecule: agr_c_1641p; PDBTitle: the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58 PDB header: transport protein Chain: A: PDB Molecule: putative branched-chain amino acid abc PDBTitle: crystal structure of a putative branched-chain amino acid2 abc transporter from rhodospirillum rubrum
102	c3rfqC	Alignment	not modelled	69.3	19	PDB header: hydrolase Chain: A: PDB Molecule: low molecular weight protein-tyrosine- PDBTitle: structure of a protein tyrosine phosphatase
103	c2r8wB	Alignment	not modelled	69.3	20	PDB header: transferase Chain: D: PDB Molecule: putative kinase; PDBTitle: structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2 PDB header: protein transport Chain: A: PDB Molecule: chloroplast srp receptor homolog, alpha subunit PDBTitle: the crystal structure of cpfts from arabidopsis thaliana
104	c3hutA	Alignment	not modelled	69.0	8	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)
105	c2fekA	Alignment	not modelled	68.2	11	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
106	c2an1D	Alignment	not modelled	67.9	19	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of mosa from s. meliloti with pyruvate bound
107	c3b9qA	Alignment	not modelled	67.7	20	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
108	c2jkbB	Alignment	not modelled	67.4	26	PDB header: lyase Chain: E: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
109	d1xkya1	Alignment	not modelled	67.2	21	PDB header: lyase Chain: A: PDB Molecule: n-acetylneuraminate lyase; PDBTitle: the d-sialic acid aldolase mutant v251w
110	c2vc6A	Alignment	not modelled	67.2	20	PDB header: transport protein Chain: B: PDB Molecule: glutamate [nmda] receptor subunit zeta-1; PDBTitle: crystal structure of the glun1 n-terminal domain (ntd)
111	d2ez9a1	Alignment	not modelled	67.1	26	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
112	c2ehhE	Alignment	not modelled	66.7	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
113	c3lciA	Alignment	not modelled	65.9	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Putative alpha-L-fucosidase, catalytic domain
114	c3q41B	Alignment	not modelled	65.0	15	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
115	d1pvda1	Alignment	not modelled	65.0	17	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
116	d2a6na1	Alignment	not modelled	64.1	13	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
117	d1hl9a2	Alignment	not modelled	63.5	15	
118	c3fluD	Alignment	not modelled	62.5	15	
119	d1zesa1	Alignment	not modelled	62.4	19	
120	c1vmaA	Alignment	not modelled	62.4	13	