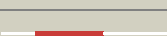
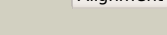
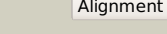
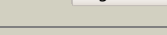
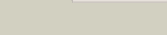
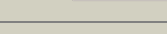
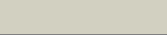
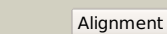


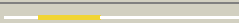
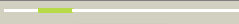
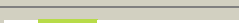
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bfjK_	 Alignment		100.0	39	PDB header: oxidoreductase Chain: K: PDB Molecule: 1,3-propanediol oxidoreductase; PDBTitle: crystal structure analysis of 1,3-propanediol oxidoreductase
2	c3ox4D_	 Alignment		100.0	33	PDB header: oxidoreductase Chain: D: PDB Molecule: alcohol dehydrogenase 2; PDBTitle: structures of iron-dependent alcohol dehydrogenase 2 from zymomonas2 mobilis zm4 complexed with nad cofactor
3	c4fr2A_	 Alignment		100.0	34	PDB header: oxidoreductase, metal binding protein Chain: A: PDB Molecule: 1,3-propanediol dehydrogenase; PDBTitle: alcohol dehydrogenase from oenococcus oeni
4	d1vlja_	 Alignment		100.0	26	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
5	c3zdrA_	 Alignment		100.0	33	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
6	d1oj7a_	 Alignment		100.0	24	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
7	d1rrma_	 Alignment		100.0	33	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
8	d1o2da_	 Alignment		100.0	32	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
9	c3hl0B_	 Alignment		100.0	26	PDB header: oxidoreductase Chain: B: PDB Molecule: maleylacetate reductase; PDBTitle: crystal structure of maleylacetate reductase from agrobacterium2 tumefaciens
10	c3iv7B_	 Alignment		100.0	28	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
11	c3jzdA_	 Alignment		100.0	31	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

12	c3rf7A_	Alignment		100.0	26	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
13	d1jq5a_	Alignment		100.0	24	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
14	c1ta9A_	Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase from schizosaccharomyces2 pombe
15	d1kq3a_	Alignment		100.0	27	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
16	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
17	c4mcaB_	Alignment		100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase from serratia to 1.9a
18	c3ce9A_	Alignment		100.0	17	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
19	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
20	c3zokB_	Alignment		100.0	15	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: structure of 3-dehydroquinase synthase from actinidia2 chinensis in complex with nad
21	c1xahA_	Alignment	not modelled	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+
22	d1sg6a_	Alignment	not modelled	100.0	16	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Dehydroquinase synthase, DHQS
23	c4p53A_	Alignment	not modelled	100.0	15	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
24	c3qbeA_	Alignment	not modelled	100.0	17	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: crystal structure of the 3-dehydroquinase synthase (arob) from2 mycobacterium tuberculosis
25	c2gruB_	Alignment	not modelled	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 carbagluco-6-phosphate, nad+ and co2+
26	c3clhA_	Alignment	not modelled	100.0	20	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: crystal structure of 3-dehydroquinase synthase (dhqs)from2 helicobacter pylori
27	d1ujna_	Alignment	not modelled	100.0	20	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Dehydroquinase synthase, DHQS
28	c3orsD_	Alignment	not modelled	96.8	15	PDB header: isomerase,biosynthetic protein Chain: D: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus

29	d1qcza_	 Alignment	not modelled	96.8	19	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
30	c4grdA_	 Alignment	not modelled	96.7	16	PDB header: lyase, isomerase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from burkholderia cenocepacia j2315
31	c3lp6D_	 Alignment	not modelled	96.7	18	PDB header: lyase Chain: D: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution
32	c3rggD_	 Alignment	not modelled	96.6	13	PDB header: lyase Chain: D: PDB Molecule: phosphoribosylaminoimidazole carboxylase, pure protein; PDBTitle: crystal structure of treponema denticola pure bound to air
33	d1o4va_	 Alignment	not modelled	96.6	21	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
34	d1u11a_	 Alignment	not modelled	96.5	17	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
35	c2fw9A_	 Alignment	not modelled	96.5	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
36	c4ja0A_	 Alignment	not modelled	96.3	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
37	c3trhl_	 Alignment	not modelled	96.3	17	PDB header: lyase Chain: I: PDB Molecule: phosphoribosylaminoimidazole carboxylase PDBTitle: structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
38	c4b4kK_	 Alignment	not modelled	96.3	19	PDB header: isomerase Chain: K: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: crystal structure of bacillus anthracis pure
39	d1xmpa_	 Alignment	not modelled	96.1	19	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
40	c2h31A_	 Alignment	not modelled	96.1	13	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	d2p1ra1	 Alignment	not modelled	95.6	17	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
42	d2jgra1	 Alignment	not modelled	95.3	17	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
43	d2bona1	 Alignment	not modelled	95.2	18	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
44	c4werA_	 Alignment	not modelled	94.8	19	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
45	d1u0ta_	 Alignment	not modelled	94.1	24	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like
46	c2ywxA_	 Alignment	not modelled	93.9	22	PDB header: lyase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from methanocaldococcus jannaschii
47	c2bonB_	 Alignment	not modelled	93.6	20	PDB header: transferase Chain: B: PDB Molecule: lipid kinase; PDBTitle: structure of an escherichia coli lipid kinase (yegs)
48	d4pfka_	 Alignment	not modelled	93.5	20	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
49	d1pfka_	 Alignment	not modelled	93.3	19	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
50	c1zxxA_	 Alignment	not modelled	93.1	20	PDB header: transferase Chain: A: PDB Molecule: 6-phosphofructokinase; PDBTitle: the crystal structure of phosphofructokinase from lactobacillus2 delbrueckii
51	c1t6dB_	 Alignment	not modelled	92.3	17	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 PDB header: hydrolase

52	c3hi0B_	Alignment	not modelled	92.2	19	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	c2qv7A_	Alignment	not modelled	92.0	16	PDB header: transferase Chain: A: PDB Molecule: diacylglycerol kinase dgkb; PDBTitle: crystal structure of diacylglycerol kinase dgkb in complex with adp2 and mg
54	c3s40C_	Alignment	not modelled	92.0	23	PDB header: transferase Chain: C: PDB Molecule: diacylglycerol kinase; PDBTitle: the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. Sterne
55	c2q5cA_	Alignment	not modelled	91.8	21	PDB header: transcription Chain: A: PDB Molecule: ntrc family transcriptional regulator; PDBTitle: crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
56	c3opyH_	Alignment	not modelled	91.7	22	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
57	c3opyB_	Alignment	not modelled	91.7	22	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
58	c3mdqA_	Alignment	not modelled	91.5	16	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
59	d2qv7a1	Alignment	not modelled	91.0	16	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
60	c3vzdB_	Alignment	not modelled	90.9	11	PDB header: transferase/inhibitor Chain: B: PDB Molecule: sphingosine kinase 1; PDBTitle: crystal structure of sphingosine kinase 1 with inhibitor and adp
61	d2pjua1	Alignment	not modelled	90.9	14	Fold: Chelatase-like Superfamily: PrpR receptor domain-like Family: PrpR receptor domain-like
62	d2f48a1	Alignment	not modelled	90.8	21	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
63	c3cerD_	Alignment	not modelled	90.2	29	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
64	c3o8oB_	Alignment	not modelled	89.9	23	PDB header: transferase Chain: B: PDB Molecule: 6-phosphofructokinase subunit beta; PDBTitle: structure of phosphofructokinase from saccharomyces cerevisiae
65	c2floA_	Alignment	not modelled	89.3	16	PDB header: hydrolase Chain: A: PDB Molecule: exopolyphosphatase; PDBTitle: crystal structure of exopolyphosphatase (ppx) from e. coli o157:h7
66	d1qo0a_	Alignment	not modelled	88.9	16	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
67	c3opyG_	Alignment	not modelled	88.9	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
68	c3k2qA_	Alignment	not modelled	88.9	29	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
69	c2higA_	Alignment	not modelled	88.8	18	PDB header: transferase Chain: A: PDB Molecule: 6-phospho-1-fructokinase; PDBTitle: crystal structure of phosphofructokinase apoenzyme from trypanosoma2 brucei.
70	c4m88A_	Alignment	not modelled	88.7	16	PDB header: transport protein Chain: A: PDB Molecule: extracellular ligand-binding receptor; PDBTitle: crystal structure of extracellular ligand-binding receptor from2 verminephrobacter eiseniae ef01-2
71	c3o8oC_	Alignment	not modelled	88.5	21	PDB header: transferase Chain: C: PDB Molecule: 6-phosphofructokinase subunit alpha; PDBTitle: structure of phosphofructokinase from saccharomyces cerevisiae
72	c3opyE_	Alignment	not modelled	88.3	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
73	c3aufA_	Alignment	not modelled	87.9	17	PDB header: transferase Chain: A: PDB Molecule: glycinamide ribonucleotide transformylase 1; PDBTitle: crystal structure of glycinamide ribonucleotide transformylase 1 from2 symbiobacterium toebii
74	c3o8nA_	Alignment	not modelled	87.7	12	PDB header: transferase Chain: A: PDB Molecule: 6-phosphofructokinase, muscle type; PDBTitle: structure of phosphofructokinase from rabbit skeletal muscle
75	d1v4va_	Alignment	not modelled	87.2	22	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
76	d1xi8a3	Alignment	not modelled	85.0	15	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
						PDB header: ribosome

77	c2j37W_	Alignment	not modelled	84.0	17	Chain: W: PDB Molecule: signal recognition particle 54 kda protein PDBTitle: model of mammalian srp bound to 80s rncs
78	c2pjuD_	Alignment	not modelled	83.9	14	PDB header: transcription Chain: D: PDB Molecule: propionate catabolism operon regulatory protein; PDBTitle: crystal structure of propionate catabolism operon2 regulatory protein prpr
79	d2dx7a1	Alignment	not modelled	83.6	24	Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase
80	c3pfnB_	Alignment	not modelled	83.5	20	PDB header: transferase Chain: B: PDB Molecule: nad kinase; PDBTitle: crystal structure of human nad kinase
81	c3khtA_	Alignment	not modelled	81.9	17	PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator from hahella chejuensis
82	d2g2ca1	Alignment	not modelled	81.4	16	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
83	d2ez9a1	Alignment	not modelled	80.9	24	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
84	d2djia1	Alignment	not modelled	79.0	13	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
85	c3av3A_	Alignment	not modelled	78.8	12	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of glycinamide ribonucleotide transformylase 1 from2 geobacillus kaustophilus
86	c3a0rB_	Alignment	not modelled	78.8	23	PDB header: transferase Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
87	c3rfqC_	Alignment	not modelled	78.8	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
88	c2iy3A_	Alignment	not modelled	78.7	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
89	c3sg0A_	Alignment	not modelled	78.2	19	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
90	c2zwmA_	Alignment	not modelled	77.8	20	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein yycf; PDBTitle: crystal structure of yycf receiver domain from bacillus2 subtilis
91	d1ybha1	Alignment	not modelled	77.5	21	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
92	d1peya_	Alignment	not modelled	77.5	19	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
93	c2i2aA_	Alignment	not modelled	77.3	15	PDB header: transferase Chain: A: PDB Molecule: probable inorganic polyphosphate/atp-nad kinase 1; PDBTitle: crystal structure of lmnadk1 from listeria monocytogenes
94	c1yt5A_	Alignment	not modelled	76.9	29	PDB header: transferase Chain: A: PDB Molecule: inorganic polyphosphate/atp-nad kinase; PDBTitle: crystal structure of nad kinase from thermotoga maritima
95	c3h5lB_	Alignment	not modelled	76.6	20	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
96	c2fmoA_	Alignment	not modelled	76.5	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 5,10-methylenetetrahydrofolate reductase; PDBTitle: ala177val mutant of e. coli methylenetetrahydrofolate2 reductase
97	c3wrwE_	Alignment	not modelled	75.9	24	PDB header: transferase Chain: E: PDB Molecule: tm-1 protein; PDBTitle: crystal structure of the n-terminal domain of resistance protein
98	c2g4rB_	Alignment	not modelled	75.5	16	PDB header: biosynthetic protein Chain: B: PDB Molecule: molybdopterin biosynthesis mog protein; PDBTitle: anomalous substructure of moga
99	c3snrA_	Alignment	not modelled	75.4	16	PDB header: transport protein Chain: A: PDB Molecule: extracellular ligand-binding receptor; PDBTitle: rpd_1889 protein, an extracellular ligand-binding receptor from2 rhodopseudomonas palustris.
100	d1m1na_	Alignment	not modelled	75.4	14	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
101	c3cf4G_	Alignment	not modelled	74.3	18	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
102	d1zesa1	Alignment	not modelled	74.0	19	Fold: Flavodoxin-like Superfamily: CheY-like

						Family: CheY-related
103	c3dm5A_	 Alignment	not modelled	73.9	17	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.
104	c2j289_	 Alignment	not modelled	73.9	16	PDB header: ribosome Chain: 9: PDB Molecule: signal recognition particle 54; PDBTitle: model of e. coli srp bound to 70s rncs
105	c2jkzB_	 Alignment	not modelled	72.5	23	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)
106	c3dcjA_	 Alignment	not modelled	72.3	12	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
107	c2fekA_	 Alignment	not modelled	72.1	4	PDB header: hydrolase Chain: A: PDB Molecule: low molecular weight protein-tyrosine- PDBTitle: structure of a protein tyrosine phosphatase
108	c3i45A_	 Alignment	not modelled	71.8	16	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
109	c2mswA_	 Alignment	not modelled	71.1	19	PDB header: transferase Chain: A: PDB Molecule: response regulator/sensor histidine kinase; PDBTitle: ligand-induced folding of a receiver domain
110	c4fq5B_	 Alignment	not modelled	70.3	17	PDB header: isomerase Chain: B: PDB Molecule: maleate cis-trans isomerase; PDBTitle: crytal structure of the maleate isomerase iso(c200a) from pseudomonas2 putida s16 with maleate
111	c3tqrA_	 Alignment	not modelled	70.3	15	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: structure of the phosphoribosylglycinamide formyltransferase (purn) in2 complex with ches from coxiella burnetii
112	d1qh8a_	 Alignment	not modelled	70.3	15	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
113	c3s99A_	 Alignment	not modelled	70.0	18	PDB header: lipid binding protein Chain: A: PDB Molecule: basic membrane lipoprotein; PDBTitle: crystal structure of a basic membrane lipoprotein from brucella2 melitensis, iodide soak
114	c2is8A_	 Alignment	not modelled	69.9	12	PDB header: structural protein Chain: A: PDB Molecule: molybdopterin biosynthesis enzyme, moab; PDBTitle: crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus thermophilus hb8
115	d1mvoa_	 Alignment	not modelled	69.4	21	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
116	d1y5ea1	 Alignment	not modelled	69.1	14	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
117	c3i09A_	 Alignment	not modelled	68.8	13	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
118	c4pyrA_	 Alignment	not modelled	68.5	9	PDB header: transport protein Chain: A: PDB Molecule: putative branched-chain amino acid abc transporter; PDBTitle: structure of a putative branched-chain amino acid abc transporter from2 chromobacterium violaceum atcc 12472
119	c2hqbA_	 Alignment	not modelled	67.9	21	PDB header: transcription Chain: A: PDB Molecule: transcriptional activator of comk gene; PDBTitle: crystal structure of a transcriptional activator of comk2 gene from bacillus halodurans
120	c1qzwC_	 Alignment	not modelled	67.8	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