
































#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ox4D_	 Alignment		100.0	64	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	49	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	d1rrma_	 Alignment		100.0	41	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
5	d1oj7a_	 Alignment		100.0	23	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
6	d1o2da_	 Alignment		100.0	29	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	26	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	22	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	22	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase

12	c1ta9A_	Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase from schizosaccharomyces2 pombe
13	d1kq3a_	Alignment		100.0	23	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
14	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
15	c3ce9A_	Alignment		100.0	19	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	19	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	c1xahA_	Alignment		100.0	16	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+
18	d1sg6a_	Alignment		100.0	17	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Dehydroquinase synthase, DHQS
19	c3clhA_	Alignment		100.0	18	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: crystal structure of 3-dehydroquinase synthase (dhqs)from2 helicobacter pylori
20	d1ujna_	Alignment		100.0	18	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Dehydroquinase synthase, DHQS
21	c2gruB_	Alignment	not modelled	100.0	12	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+
22	c3orsD_	Alignment	not modelled	97.1	12	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	d1o4va_	Alignment	not modelled	97.1	21	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
24	d1qcza_	Alignment	not modelled	97.0	16	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
25	c3lp6D_	Alignment	not modelled	96.9	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
26	d1u11a_	Alignment	not modelled	96.9	14	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
27	c3fu9A_	Alignment	not modelled	96.9	14	PDB header: lyase Chain: A: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase;

27	c21w3A	Alignment	not modelled	96.9	14	PDBTitle: structure of pure (n5-carboxyaminoimidazole ribonucleotide mutase)2 h59f from the acidophilic bacterium acetobacter aceti, at ph 8
28	d2p1ra1	Alignment	not modelled	96.9	15	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
29	c3rggD	Alignment	not modelled	96.9	19	PDB header: lyase Chain: D: PDB Molecule: phosphoribosylaminoimidazole carboxylase, pure protein; PDBTitle: crystal structure of treponema denticola pure bound to air
30	d2bona1	Alignment	not modelled	96.8	16	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
31	d2jgra1	Alignment	not modelled	96.8	14	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
32	c3trhl	Alignment	not modelled	96.5	16	PDB header: lyase Chain: I: PDB Molecule: phosphoribosylaminoimidazole carboxylase PDBTitle: structure of a phosphoribosylaminoimidazole carboxylase catalytic c2 subunit (pure) from coxiella burnetii
33	d1xmpa	Alignment	not modelled	96.5	14	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
34	c2bonB	Alignment	not modelled	96.4	14	PDB header: transferase Chain: B: PDB Molecule: lipid kinase; PDBTitle: structure of an escherichia coli lipid kinase (yegs)
35	d1u0ta	Alignment	not modelled	96.1	29	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like
36	d1qo0a	Alignment	not modelled	95.5	9	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
37	c2h31A	Alignment	not modelled	95.5	14	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
38	c2qv7A	Alignment	not modelled	95.4	20	PDB header: transferase Chain: A: PDB Molecule: diacylglycerol kinase dgkb; PDBTitle: crystal structure of diacylglycerol kinase dgkb in complex with adp2 and mg
39	c2ywxA	Alignment	not modelled	94.7	21	PDB header: lyase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from methanocaldococcus jannaschii
40	c3s40C	Alignment	not modelled	94.2	16	PDB header: transferase Chain: C: PDB Molecule: diacylglycerol kinase; PDBTitle: the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. sterne
41	d2qv7a1	Alignment	not modelled	94.0	19	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
42	c1zxxA	Alignment	not modelled	93.6	23	PDB header: transferase Chain: A: PDB Molecule: 6-phosphofructokinase; PDBTitle: the crystal structure of phosphofructokinase from lactobacillus2 delbrueckii
43	d1pfka	Alignment	not modelled	93.5	20	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
44	d4pfka	Alignment	not modelled	93.4	22	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
45	c3sg0A	Alignment	not modelled	93.3	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
46	c2an1D	Alignment	not modelled	93.2	24	PDB header: transferase Chain: D: PDB Molecule: putative kinase; PDBTitle: structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
47	d2f48a1	Alignment	not modelled	92.9	25	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
48	c3snrA	Alignment	not modelled	92.8	15	PDB header: transport protein Chain: A: PDB Molecule: extracellular ligand-binding receptor; PDBTitle: rpd_1889 protein, an extracellular ligand-binding receptor from2 rhodospseudomonas palustris.
49	d1ewka	Alignment	not modelled	92.4	10	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
50	c3pfnB	Alignment	not modelled	92.4	19	PDB header: transferase Chain: B: PDB Molecule: nad kinase; PDBTitle: crystal structure of human nad kinase
51	c3i09A	Alignment	not modelled	91.9	7	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
						PDB header: transferase

52	c3opyB_	Alignment	not modelled	91.7	13	Chain: B: PDB Molecule: 6-phosphofructo-1-kinase beta-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state
53	c3opyH_	Alignment	not modelled	91.7	13	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
54	c3mdqA_	Alignment	not modelled	91.4	12	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
55	dlv4va_	Alignment	not modelled	91.0	18	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
56	c3hi0B_	Alignment	not modelled	90.4	14	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
57	c1t6dB_	Alignment	not modelled	90.4	13	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
58	c3i45A_	Alignment	not modelled	90.1	11	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
59	c3k2qA_	Alignment	not modelled	90.0	16	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
60	d2ez9a1	Alignment	not modelled	89.9	18	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
61	c3eafA_	Alignment	not modelled	89.7	13	PDB header: transport protein Chain: A: PDB Molecule: abc transporter, substrate binding protein; PDBTitle: crystal structure of abc transporter, substrate binding protein2 aeropyrum pernix
62	c3o8oB_	Alignment	not modelled	89.5	14	PDB header: transferase Chain: B: PDB Molecule: 6-phosphofructokinase subunit beta; PDBTitle: structure of phosphofructokinase from saccharomyces cerevisiae
63	c2q5cA_	Alignment	not modelled	89.4	15	PDB header: transcription Chain: A: PDB Molecule: ntrc family transcriptional regulator; PDBTitle: crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
64	c2higA_	Alignment	not modelled	89.2	15	PDB header: transferase Chain: A: PDB Molecule: 6-phospho-1-fructokinase; PDBTitle: crystal structure of phosphofructokinase apoenzyme from trypanosoma2 brucei.
65	c3n0wA_	Alignment	not modelled	89.0	9	PDB header: transport protein Chain: A: PDB Molecule: abc branched chain amino acid family transporter, PDBTitle: crystal structure of a branched chain amino acid abc transporter2 periplasmic ligand-binding protein (bx_e_c0949) from burkholderia3 xenovorans lb400 at 1.88 a resolution
66	c3lopA_	Alignment	not modelled	89.0	14	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
67	c3cf4G_	Alignment	not modelled	88.9	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
68	c3opyG_	Alignment	not modelled	88.9	16	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
69	dlpvda1	Alignment	not modelled	87.6	17	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
70	c3q41B_	Alignment	not modelled	87.3	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)
71	c3h5lB_	Alignment	not modelled	87.2	11	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
72	c2floA_	Alignment	not modelled	87.1	21	PDB header: hydrolase Chain: A: PDB Molecule: exopolyphosphatase; PDBTitle: crystal structure of exopolyphosphatase (ppx) from e. coli o157:h7
73	c3o8nA_	Alignment	not modelled	86.6	10	PDB header: transferase Chain: A: PDB Molecule: 6-phosphofructokinase, muscle type; PDBTitle: structure of phosphofructokinase from rabbit skeletal muscle
74	c3tqrA_	Alignment	not modelled	86.6	13	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: structure of the phosphoribosylglycinamide formyltransferase (purn) in2 complex with ches from coxiella burnetii
75	c3opyE_	Alignment	not modelled	86.5	16	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
76	c3cerD_	Alignment	not modelled	86.0	21	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
77	d2ji7a1	Alignment	not modelled	86.0	12	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
78	d2pjuA1	Alignment	not modelled	85.5	20	Fold: Chelatase-like Superfamily: PrpR receptor domain-like Family: PrpR receptor domain-like
79	c1qzwC_	Alignment	not modelled	85.4	14	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
80	c3o8oC_	Alignment	not modelled	85.4	23	PDB header: transferase Chain: C: PDB Molecule: 6-phosphofructokinase subunit alpha; PDBTitle: structure of phosphofructokinase from saccharomyces cerevisiae
81	d1q6za1	Alignment	not modelled	85.0	16	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
82	c2i2aA_	Alignment	not modelled	84.9	22	PDB header: transferase Chain: A: PDB Molecule: probable inorganic polyphosphate/atp-nad kinase 1; PDBTitle: crystal structure of lmnadk1 from listeria monocytogenes
83	c2j37W_	Alignment	not modelled	84.0	16	PDB header: ribosome Chain: W: PDB Molecule: signal recognition particle 54 kda protein PDBTitle: model of mammalian srp bound to 80s rncs
84	d1fma2	Alignment	not modelled	84.0	15	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
85	c2e4wA_	Alignment	not modelled	84.0	12	PDB header: signaling protein Chain: A: PDB Molecule: metabotropic glutamate receptor 3; PDBTitle: crystal structure of the extracellular region of the group ii2 metabotropic glutamate receptor complexed with 1s,3s-acpd
86	c2hqba_	Alignment	not modelled	83.8	12	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
87	c2j289_	Alignment	not modelled	83.8	17	PDB header: ribosome Chain: 9: PDB Molecule: signal recognition particle 54; PDBTitle: model of e. coli srp bound to 70s rncs
88	c2xecD_	Alignment	not modelled	83.7	16	PDB header: isomerase Chain: D: PDB Molecule: putative maleate isomerase; PDBTitle: nocardia farcinica maleate cis-trans isomerase bound to2 tris
89	c3lkbB_	Alignment	not modelled	83.3	13	PDB header: transport protein Chain: B: PDB Molecule: probable branched-chain amino acid abc PDBTitle: crystal structure of a branched chain amino acid abc2 transporter from thermus thermophilus with bound valine
90	c3kg2A_	Alignment	not modelled	82.6	13	PDB header: membrane protein, transport protein Chain: A: PDB Molecule: glutamate receptor 2; PDBTitle: ampa subtype ionotropic glutamate receptor in complex with competitive2 antagonist zk 200775
91	c3dm5A_	Alignment	not modelled	81.5	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.
92	d2ihta1	Alignment	not modelled	81.0	14	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
93	c3rfqC_	Alignment	not modelled	81.0	16	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
94	d1ovma1	Alignment	not modelled	80.7	26	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
95	c2o6lA_	Alignment	not modelled	80.5	14	PDB header: transferase Chain: A: PDB Molecule: udp-glucuronosyltransferase 2b7; PDBTitle: crystal structure of the udp-glucuronic acid binding domain2 of the human drug metabolizing udp-glucuronosyltransferase3 2b7
96	c2iy3A_	Alignment	not modelled	80.0	9	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
97	d1xi8a3	Alignment	not modelled	79.9	19	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
98	c3huta_	Alignment	not modelled	79.0	16	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
99	c3ip5A_	Alignment	not modelled	78.3	18	PDB header: transport protein Chain: A: PDB Molecule: abc transporter, substrate binding protein (amino acid); PDBTitle: structure of atu2422-gaba receptor in complex with alanine
100	c3t0nA_	Alignment	not modelled	78.2	10	PDB header: signaling protein Chain: A: PDB Molecule: twin-arginine translocation pathway signal;

						PDBTitle: crystal structure of twin-arginine translocation pathway signal from2 rhodospseudomonas palustris bisb5
101	c3dcjA_	Alignment	not modelled	78.1	10	PDB header: transferase Chain: A: PDB Molecule: probable 5'-phosphoribosylglycinamide PDBTitle: crystal structure of glycylamide formyltransferase (purn)2 from mycobacterium tuberculosis in complex with 5-methyl-5,3 6,7,8-tetrahydrofolic acid derivative
102	c2dwcB_	Alignment	not modelled	77.5	9	PDB header: transferase Chain: B: PDB Molecule: 433aa long hypothetical phosphoribosylglycinamide formyl PDBTitle: crystal structure of probable phosphoribosylglycinamide formyl2 transferase from pyrococcus horikoshii ot3 complexed with adp
103	c1kjjA_	Alignment	not modelled	77.3	11	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase 2; PDBTitle: crystal structure of glycylamide ribonucleotide2 transformylase in complex with mg-atp-gamma-s
104	dlzpdal	Alignment	not modelled	76.9	17	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
105	c2wjxA_	Alignment	not modelled	76.9	13	PDB header: transport protein Chain: A: PDB Molecule: glutamate receptor 2; PDBTitle: crystal structure of the human ionotropic glutamate2 receptor glur2 atd region at 4.1 a resolution
106	c3khtA_	Alignment	not modelled	76.8	21	PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator from hahella chejuensis
107	c2jkzB_	Alignment	not modelled	76.6	18	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)
108	d2g2ca1	Alignment	not modelled	76.5	10	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
109	d2bw0a2	Alignment	not modelled	76.1	12	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
110	c1m6vE_	Alignment	not modelled	75.8	22	PDB header: ligase Chain: E: PDB Molecule: carbamoyl phosphate synthetase large chain; PDBTitle: crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
111	c1z0zC_	Alignment	not modelled	74.7	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
112	dlz0sa1	Alignment	not modelled	74.7	28	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like
113	c3p9xB_	Alignment	not modelled	74.1	19	PDB header: transferase Chain: B: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of phosphoribosylglycinamide formyltransferase from2 bacillus halodurans
114	c3dnfB_	Alignment	not modelled	73.8	16	PDB header: oxidoreductase Chain: B: PDB Molecule: 4-hydroxy-3-methylbut-2-enyl diphosphate reductase; PDBTitle: structure of (e)-4-hydroxy-3-methyl-but-2-enyl diphosphate reductase,2 the terminal enzyme of the non-mevalonate pathway
115	d1t9ba1	Alignment	not modelled	73.3	10	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
116	c2pjuD_	Alignment	not modelled	72.7	19	PDB header: transcription Chain: D: PDB Molecule: propionate catabolism operon regulatory protein; PDBTitle: crystal structure of propionate catabolism operon2 regulatory protein prpr
117	c2zwmA_	Alignment	not modelled	71.5	16	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein yycf; PDBTitle: crystal structure of yycf receiver domain from bacillus2 subtilis
118	dlusga_	Alignment	not modelled	71.3	25	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
119	dlvh3a_	Alignment	not modelled	71.2	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: Cytidylyltransferase
120	d3ckma1	Alignment	not modelled	71.0	10	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like