























#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3kbqA_	 Alignment		100.0	31	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein ta0487; PDBTitle: the crystal structure of the protein cina with unknown function from <i>Thermoplasma acidophilum</i>
2	d1mkza_	 Alignment		100.0	20	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
3	c2pjka_	 Alignment		100.0	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: 178aa long hypothetical molybdenum cofactor PDBTitle: structure of hypothetical molybdenum cofactor biosynthesis2 protein b from <i>Sulfolobus tokodaii</i>
4	d2ftsa3	 Alignment		100.0	28	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
5	c2is8A_	 Alignment		100.0	22	PDB header: structural protein Chain: A: PDB Molecule: molybdopterin biosynthesis enzyme, moab; PDBTitle: crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from <i>Thermus thermophilus</i> hb8
6	d1y5ea1	 Alignment		100.0	18	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
7	d2a9sa1	 Alignment		100.0	20	Fold: Anticodon-binding domain-like Superfamily: CinA-like Family: CinA-like
8	d2nqra3	 Alignment		100.0	23	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
9	c3rfqC_	 Alignment		100.0	15	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 <i>Mycobacterium marinum</i>
10	d1uuya_	 Alignment		100.0	22	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
11	d1jlja_	 Alignment		99.9	17	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like

12	c2g4rB_	Alignment		99.9	16	PDB header: biosynthetic protein Chain: B: PDB Molecule: molybdopterin biosynthesis mog protein; PDBTitle: anomalous substructure of moga
13	d2f7wa1	Alignment		99.9	17	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
14	d2g2ca1	Alignment		99.9	16	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
15	c2nqqA_	Alignment		99.9	24	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin biosynthesis protein moea; PDBTitle: moea r137q
16	c2fu3A_	Alignment		99.9	30	PDB header: biosynthetic protein/structural protein Chain: A: PDB Molecule: gephyrin; PDBTitle: crystal structure of gephyrin e-domain
17	d1uz5a3	Alignment		99.9	25	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
18	c1uz5A_	Alignment		99.9	25	PDB header: molybdopterin biosynthesis Chain: A: PDB Molecule: 402aa long hypothetical molybdopterin PDBTitle: the crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikoshii
19	d1di6a_	Alignment		99.9	20	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
20	d1wu2a3	Alignment		99.9	17	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
21	c1wu2B_	Alignment	not modelled	99.8	18	PDB header: structural genomics,biosynthetic protein Chain: B: PDB Molecule: molybdopterin biosynthesis moea protein; PDBTitle: crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikoshii ot3
22	d1xi8a3	Alignment	not modelled	99.7	20	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
23	d1wl8a1	Alignment	not modelled	93.9	8	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
24	d1l7da1	Alignment	not modelled	93.7	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
25	d2nv0a1	Alignment	not modelled	92.0	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
26	d2a9va1	Alignment	not modelled	91.4	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
27	d1pjca1	Alignment	not modelled	90.2	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
28	c3l3ba_	Alignment	not modelled	89.5	17	PDB header: biosynthetic protein Chain: A: PDB Molecule: es1 family protein; PDBTitle: crystal structure of isoprenoid biosynthesis protein with2 amidotransferase-like domain from ehrlichia chaffeensis at 1.90a3 resolution

29	d1ka9h_	Alignment	not modelled	89.0	23	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
30	c3p2yA_	Alignment	not modelled	88.5	15	PDB header: oxidoreductase Chain: A: PDB Molecule: alanine dehydrogenase/pyridine nucleotide transhydrogenase; PDBTitle: crystal structure of alanine dehydrogenase/pyridine nucleotide2 transhydrogenase from mycobacterium smegmatis
31	c3dojA_	Alignment	not modelled	87.6	21	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase-like protein; PDBTitle: structure of glyoxylate reductase 1 from arabidopsis2 (atglyr1)
32	c2rirA_	Alignment	not modelled	86.6	18	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase, a chain; PDBTitle: crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
33	c1z0zC_	Alignment	not modelled	85.4	17	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
34	d1gpma2	Alignment	not modelled	85.4	14	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
35	d1z0sa1	Alignment	not modelled	84.9	17	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like
36	c2issF_	Alignment	not modelled	84.3	22	PDB header: lyase, transferase Chain: F: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: structure of the plp synthase holoenzyme from thermotoga maritima
37	d1n1ea2	Alignment	not modelled	83.6	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
38	d1k9vf_	Alignment	not modelled	82.7	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
39	c3c1nA_	Alignment	not modelled	82.5	15	PDB header: transferase Chain: A: PDB Molecule: probable aspartokinase; PDBTitle: crystal structure of allosteric inhibition threonine-sensitive2 aspartokinase from methanococcus jannaschii with l-threonine
40	d1vhqa_	Alignment	not modelled	81.8	23	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
41	c3s40C_	Alignment	not modelled	81.1	18	PDB header: transferase Chain: C: PDB Molecule: diacylglycerol kinase; PDBTitle: the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. Sterne
42	c2f1kD_	Alignment	not modelled	80.4	20	PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of synechocystis aroenate dehydrogenase
43	d1i36a2	Alignment	not modelled	78.9	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
44	c3ckyA_	Alignment	not modelled	78.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-hydroxymethyl glutarate dehydrogenase; PDBTitle: structural and kinetic properties of a beta-hydroxyacid dehydrogenase2 involved in nicotinate fermentation
45	c3d4oA_	Alignment	not modelled	76.4	24	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase subunit a; PDBTitle: crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from bacillus halodurans at 2.10 a resolution
46	c3en0A_	Alignment	not modelled	75.6	10	PDB header: hydrolase Chain: A: PDB Molecule: cyanophycinase; PDBTitle: the structure of cyanophycinase
47	d2cdqa1	Alignment	not modelled	74.9	20	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
48	c2v6bB_	Alignment	not modelled	74.6	24	PDB header: oxidoreductase Chain: B: PDB Molecule: l-lactate dehydrogenase; PDBTitle: crystal structure of lactate dehydrogenase from deinococcus2 radiodurans (apo form)
49	d1qdlb_	Alignment	not modelled	74.4	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
50	c3k94A_	Alignment	not modelled	74.3	14	PDB header: transferase Chain: A: PDB Molecule: thiamin pyrophosphokinase; PDBTitle: crystal structure of thiamin pyrophosphokinase from geobacillus2 thermodenitrificans, northeast structural genomics consortium target3 gtr2
51	c2qhpA_	Alignment	not modelled	72.5	19	PDB header: transferase Chain: A: PDB Molecule: fructokinase; PDBTitle: crystal structure of fructokinase (np_810670.1) from bacteroides2 thetaiotaomicron vpi-5482 at 1.80 a resolution
52	c2ywjA_	Alignment	not modelled	72.4	26	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii
53	d2hmfal	Alignment	not modelled	70.9	15	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
						PDB header: oxidoreductase

54	c3plnA	Alignment	not modelled	70.5	18	Chain: A: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: crystal structure of klebsiella pneumoniae udp-glucose 6-dehydrogenase2 complexed with udp-glucose
55	c1a5zA	Alignment	not modelled	70.5	15	PDB header: oxidoreductase Chain: A: PDB Molecule: l-lactate dehydrogenase; PDBTitle: lactate dehydrogenase from thermotoga maritima (tml dh)
56	d1vcoa1	Alignment	not modelled	69.3	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
57	c1l7eC	Alignment	not modelled	68.7	13	PDB header: oxidoreductase Chain: C: PDB Molecule: nicotinamide nucleotide transhydrogenase, PDBTitle: crystal structure of r. rubrum transhydrogenase domain i2 with bound nadh
58	c2v4uA	Alignment	not modelled	68.2	16	PDB header: ligase Chain: A: PDB Molecule: ctp synthase 2; PDBTitle: human ctp synthetase 2 - glutaminase domain in complex with2 5-oxo-l-norleucine
59	d1q7ra	Alignment	not modelled	67.9	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
60	c3c7cB	Alignment	not modelled	67.7	25	PDB header: oxidoreductase Chain: B: PDB Molecule: octopine dehydrogenase; PDBTitle: a structural basis for substrate and stereo selectivity in2 octopine dehydrogenase (odh-nadh-l-arginine)
61	c1np3B	Alignment	not modelled	67.5	13	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of class i acetohydroxy acid isomeroreductase from2 pseudomonas aeruginosa
62	d2naca2	Alignment	not modelled	66.9	23	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
63	c3l4eA	Alignment	not modelled	66.7	25	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized peptidase lmo0363; PDBTitle: 1.5a crystal structure of a putative peptidase e protein from listeria2 monocytogenes egd-e
64	d1jvna2	Alignment	not modelled	65.9	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
65	d1i7qb	Alignment	not modelled	65.8	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
66	d1v19a	Alignment	not modelled	63.7	19	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
67	d1fmfa	Alignment	not modelled	63.6	19	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
68	d1u7za	Alignment	not modelled	62.5	12	Fold: Ribokinase-like Superfamily: CoaB-like Family: CoaB-like
69	d1java	Alignment	not modelled	62.4	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
70	c1i36A	Alignment	not modelled	61.7	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein mth1747; PDBTitle: structure of conserved protein mth1747 of unknown function2 reveals structural similarity with 3-hydroxyacid3 dehydrogenases
71	c3qfnA	Alignment	not modelled	61.7	37	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of streptococcal asymmetric ap4a hydrolase and2 phosphodiesterase spr1479/saph in complex with inorganic phosphate
72	c3kklA	Alignment	not modelled	61.3	13	PDB header: hydrolase Chain: A: PDB Molecule: probable chaperone protein hsp33; PDBTitle: crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae
73	d1ccwa	Alignment	not modelled	61.3	14	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
74	c2cukC	Alignment	not modelled	60.8	24	PDB header: oxidoreductase Chain: C: PDB Molecule: glycerate dehydrogenase/glyoxylate reductase; PDBTitle: crystal structure of tt0316 protein from thermus thermophilus hb8
75	c2z04A	Alignment	not modelled	60.7	13	PDB header: lyase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase atpase PDBTitle: crystal structure of phosphoribosylaminoimidazole2 carboxylase atpase subunit from aquifex aeolicus
76	d1a9xb2	Alignment	not modelled	60.0	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
77	d3bula2	Alignment	not modelled	59.4	14	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
78	c3cq9C	Alignment	not modelled	59.0	16	PDB header: transferase Chain: C: PDB Molecule: uncharacterized protein lp_1622; PDBTitle: crystal structure of the lp_1622 protein from lactobacillus2 plantarum. northeast structural genomics consortium target3 lpr114

79	d1mv8a2	Alignment	not modelled	59.0	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
80	c2e85B	Alignment	not modelled	58.9	17	PDB header: hydrolase Chain: B: PDB Molecule: hydrogenase 3 maturation protease; PDBTitle: crystal structure of the hydrogenase 3 maturation protease
81	c1mv8A	Alignment	not modelled	58.4	14	PDB header: oxidoreductase Chain: A: PDB Molecule: gdp-mannose 6-dehydrogenase; PDBTitle: 1.55 a crystal structure of a ternary complex of gdp-mannose2 dehydrogenase from psuedomonas aeruginosa
82	c3iq0B	Alignment	not modelled	58.4	17	PDB header: transferase Chain: B: PDB Molecule: putative ribokinase ii; PDBTitle: crystal structure of a putative ribokinase ii in complex2 with atp and mg+2 from e.coli
83	c3l76B	Alignment	not modelled	57.7	21	PDB header: transferase Chain: B: PDB Molecule: aspartokinase; PDBTitle: crystal structure of aspartate kinase from synechocystis
84	d1i1qb	Alignment	not modelled	56.7	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
85	c1ta9A	Alignment	not modelled	56.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase from schizosaccharomyces2 pombe
86	c1su1A	Alignment	not modelled	55.5	31	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein yfce; PDBTitle: structural and biochemical characterization of yfce, a2 phosphoesterase from e. coli
87	d1su1a	Alignment	not modelled	55.5	31	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfCE-like
88	d1s1ma1	Alignment	not modelled	55.4	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
89	c3l6dB	Alignment	not modelled	55.4	16	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
90	d1fyea	Alignment	not modelled	55.3	29	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Aspartyl dipeptidase PepE
91	c3ghyA	Alignment	not modelled	54.5	23	PDB header: oxidoreductase Chain: A: PDB Molecule: ketopantoate reductase protein; PDBTitle: crystal structure of a putative ketopantoate reductase from ralstonia2 solanacearum molk2
92	d1a5za1	Alignment	not modelled	54.3	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
93	c2gk4A	Alignment	not modelled	54.3	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: the crystal structure of the dna/pantothenate metabolism flavoprotein2 from streptococcus pneumoniae
94	c1rcuB	Alignment	not modelled	53.2	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved hypothetical protein vt76; PDBTitle: x-ray structure of tm1055 northeast structural genomics2 consortium target vt76
95	c3ihkC	Alignment	not modelled	52.6	19	PDB header: transferase Chain: C: PDB Molecule: thiamin pyrophosphokinase; PDBTitle: crystal structure of thiamin pyrophosphokinase from2 s.mutans, northeast structural genomics consortium target3 smr83
96	c2y0dB	Alignment	not modelled	52.4	9	PDB header: oxidoreductase Chain: B: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: bcec mutation y10k
97	c3lkiA	Alignment	not modelled	52.1	18	PDB header: transferase Chain: A: PDB Molecule: fructokinase; PDBTitle: crystal structure of fructokinase with bound atp from2 xylella fastidiosa
98	d1civa1	Alignment	not modelled	51.3	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
99	c3pu6A	Alignment	not modelled	50.8	31	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of an uncharacterized protein from wolinella2 succinogenes
100	d1o1ya	Alignment	not modelled	50.2	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
101	c2an1D	Alignment	not modelled	49.8	27	PDB header: transferase Chain: D: PDB Molecule: putative kinase; PDBTitle: structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
102	d9lata1	Alignment	not modelled	49.6	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
103	c2dc1A	Alignment	not modelled	49.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: l-aspartate dehydrogenase; PDBTitle: crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus
104	c1y80A	Alignment	not modelled	49.4	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted cobalamin binding protein; PDBTitle: structure of a corrinoid (factor iiii)-binding protein from2 moorella thermoacetica
						PDB header: oxidoreductase

105	c1ks9A_	Alignment	not modelled	49.3	20	Chain: A: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: ketopantoate reductase from escherichia coli
106	d1tyya_	Alignment	not modelled	49.0	13	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
107	d1qf6a1	Alignment	not modelled	48.7	18	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
108	c2q3eH_	Alignment	not modelled	48.5	13	PDB header: oxidoreductase Chain: H: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of human udp-glucose dehydrogenase complexed with nadh and2 udp-glucose
109	c2yxbA_	Alignment	not modelled	48.5	19	PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
110	c2gf2B_	Alignment	not modelled	47.7	20	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of human hydroxyisobutyrate dehydrogenase
111	d1rcua_	Alignment	not modelled	46.9	15	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: MoCo carrier protein-like
112	d1e8ca2	Alignment	not modelled	46.0	11	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
113	c2pkkA_	Alignment	not modelled	45.8	17	PDB header: transferase Chain: A: PDB Molecule: adenosine kinase; PDBTitle: crystal structure of m tuberculosis adenosine kinase complexed with 2-2 fluoro adenosine
114	c3cumA_	Alignment	not modelled	45.8	31	PDB header: oxidoreductase Chain: A: PDB Molecule: probable 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of a possible 3-hydroxyisobutyrate dehydrogenase2 from pseudomonas aeruginosa pao1
115	c3etjB_	Alignment	not modelled	44.9	10	PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase atpase PDBTitle: crystal structure e. coli purk in complex with mg, adp, and2 pi
116	c3prjB_	Alignment	not modelled	44.8	12	PDB header: oxidoreductase Chain: B: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: role of packing defects in the evolution of allostery and induced fit2 in human udp-glucose dehydrogenase.
117	c2uyyD_	Alignment	not modelled	44.8	16	PDB header: cytokine Chain: D: PDB Molecule: n-pac protein; PDBTitle: structure of the cytokine-like nuclear factor n-pac
118	c1m67A_	Alignment	not modelled	44.7	11	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol-3-phosphate dehydrogenase; PDBTitle: crystal structure of leishmania mexicana gpdh complexed with inhibitor2 2-bromo-6-hydroxy-purine
119	d1txga2	Alignment	not modelled	44.4	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
120	c1ibjC_	Alignment	not modelled	43.7	16	PDB header: lyase Chain: C: PDB Molecule: cystathionine beta-lyase; PDBTitle: crystal structure of cystathionine beta-lyase from arabidopsis2 thaliana