























Phyre2

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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5zi9B_	 Alignment		100.0	27	PDB header: hydrolase Chain: B: PDB Molecule: cytokinin riboside 5'-monophosphate phosphoribohydrolase; PDBTitle: crystal strcuture of type-ii log from streptomyces coelicolor a3
2	d1weka_	 Alignment		100.0	28	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: MoCo carrier protein-like
3	c3sxbC_	 Alignment		100.0	26	PDB header: unknown function Chain: C: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from2 mycobacterium marinum bound to adenosine 5'-monophosphate amp
4	c5wq3A_	 Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: cytokinin riboside 5'-monophosphate phosphoribohydrolase; PDBTitle: crystal strcuture of type-ii log from corynebacterium glutamicum
5	c5zbjA_	 Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: putative cytokinin riboside 5'-monophosphate PDBTitle: crystal strcuture of type-i log from pseudomonas aeruginosa pao1
6	d1t35a_	 Alignment		100.0	21	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: MoCo carrier protein-like
7	c2iz6A_	 Alignment		100.0	34	PDB header: metal transport Chain: A: PDB Molecule: molybdenum cofactor carrier protein; PDBTitle: structure of the chlamydomonas reinhardtii moco carrier2 protein
8	d1ydha_	 Alignment		100.0	20	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: MoCo carrier protein-like
9	c2q4dB_	 Alignment		100.0	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: lysine decarboxylase-like protein at5g11950; PDBTitle: ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at5g11950
10	c5itsD_	 Alignment		100.0	18	PDB header: hydrolase Chain: D: PDB Molecule: cytokinin riboside 5'-monophosphate phosphoribohydrolase; PDBTitle: crystal strcuture of log from corynebacterium glutamicum
11	c3quaA_	 Alignment		100.0	23	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein and possible2 molybdenum cofactor protein from mycobacterium smegmatis

12	d1rcua_	Alignment		100.0	25	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: MoCo carrier protein-like
13	c1rcuB_	Alignment		100.0	25	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
14	d2q4oa1	Alignment		100.0	22	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: MoCo carrier protein-like
15	c2q4oA_	Alignment		100.0	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein at2g37210/t2n18.3; PDBTitle: ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at2g37210
16	c5ajtA_	Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: phosphoribohydrolase lonely guy; PDBTitle: crystal structure of ligand-free phosphoribohydrolase lonely guy from2 claviceps purpurea
17	d1weha_	Alignment		100.0	25	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: MoCo carrier protein-like
18	c3uqzB_	Alignment		100.0	21	PDB header: dna binding protein Chain: B: PDB Molecule: dna processing protein dpra; PDBTitle: x-ray structure of dna processing protein a (dpra) from streptococcus2 pneumoniae
19	c3majA_	Alignment		100.0	23	PDB header: dna binding protein Chain: A: PDB Molecule: dna processing chain a; PDBTitle: crystal structure of putative dna processing protein dpra from2 rhodospseudomonas palustris cga009
20	c3bq9A_	Alignment		100.0	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted rossmann fold nucleotide-binding domain- PDBTitle: crystal structure of predicted nucleotide-binding protein from2 idiomarina baltica os145
21	c6gfmA_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: pyrimidine/purine nucleotide 5'-monophosphate nucleosidase; PDBTitle: crystal structure of the escherichia coli nucleosidase ppnn (ppp-gpp-2 form)
22	c4ljkA_	Alignment	not modelled	100.0	19	PDB header: dna binding protein Chain: A: PDB Molecule: dna processing chain a (dpra); PDBTitle: structural insights into the unique single-stranded dna binding mode2 of dna processing protein a from helicobacter pylori
23	c3gh1A_	Alignment	not modelled	100.0	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted nucleotide-binding protein; PDBTitle: crystal structure of predicted nucleotide-binding protein from vibrio2 cholerae
24	d2nx2a1	Alignment	not modelled	99.2	14	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: YpsA-like
25	c6mizC_	Alignment	not modelled	98.4	19	PDB header: membrane protein Chain: C: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: human trpm2 ion channel in an adpr-bound state
26	c6d73C_	Alignment	not modelled	98.2	20	PDB header: transport protein Chain: C: PDB Molecule: transient receptor potential cation channel, subfamily m; PDBTitle: cryo-em structure of the zebrafish trpm2 channel in the presence of2 ca2+
27	c3imkA_	Alignment	not modelled	98.2	18	PDB header: metal binding protein Chain: A: PDB Molecule: putative molybdenum carrier protein; PDBTitle: crystal structure of putative molybdenum carrier protein (yp_461806.1)2 from syntrophus aciditrophicus sb at 1.45 a resolution
						PDB header: membrane protein

28	c6co7C_	Alignment	not modelled	98.2	20	Chain: C: PDB Molecule: predicted protein; PDBTitle: structure of the nvtrpm2 channel in complex with ca2+
29	c6bcoD_	Alignment	not modelled	98.2	16	PDB header: transport protein Chain: D: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of trpm4 in atp bound state with short coiled coil2 at 2.9 angstrom resolution
30	c6drkD_	Alignment	not modelled	98.2	21	PDB header: transport protein Chain: D: PDB Molecule: transient receptor potential cation channel, subfamily m, PDBTitle: structure of trpm2 ion channel receptor by single particle electron2 cryo-microscopy, apo state
31	c6bccqB_	Alignment	not modelled	98.1	16	PDB header: transport protein Chain: B: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of trpm4 in atp bound state with long coiled coil at2 3.3 angstrom resolution
32	c6d73B_	Alignment	not modelled	98.1	23	PDB header: transport protein Chain: B: PDB Molecule: transient receptor potential cation channel, subfamily m; PDBTitle: cryo-em structure of the zebrafish trpm2 channel in the presence of2 ca2+
33	c6nr3D_	Alignment	not modelled	97.9	17	PDB header: transport protein Chain: D: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of the trpm8 ion channel in complex with high2 occupancy icilin, pi(4,5)p2, and calcium
34	c6nr3C_	Alignment	not modelled	97.9	17	PDB header: transport protein Chain: C: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of the trpm8 ion channel in complex with high2 occupancy icilin, pi(4,5)p2, and calcium
35	c6nr3A_	Alignment	not modelled	97.9	17	PDB header: transport protein Chain: A: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of the trpm8 ion channel in complex with high2 occupancy icilin, pi(4,5)p2, and calcium
36	c6nr3B_	Alignment	not modelled	97.9	17	PDB header: transport protein Chain: B: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of the trpm8 ion channel in complex with high2 occupancy icilin, pi(4,5)p2, and calcium
37	c6nr2A_	Alignment	not modelled	97.7	15	PDB header: transport protein Chain: A: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of the trpm8 ion channel in complex with the menthol2 analog ws-12 and pi(4,5)p2
38	c6nr2C_	Alignment	not modelled	97.7	15	PDB header: transport protein Chain: C: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of the trpm8 ion channel in complex with the menthol2 analog ws-12 and pi(4,5)p2
39	c6nr2B_	Alignment	not modelled	97.7	15	PDB header: transport protein Chain: B: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of the trpm8 ion channel in complex with the menthol2 analog ws-12 and pi(4,5)p2
40	c6nr2D_	Alignment	not modelled	97.7	15	PDB header: transport protein Chain: D: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of the trpm8 ion channel in complex with the menthol2 analog ws-12 and pi(4,5)p2
41	c4jemA_	Alignment	not modelled	96.9	16	PDB header: hydrolase Chain: A: PDB Molecule: cmp/hydroxymethyl cmp hydrolase; PDBTitle: crystal structure of milb complexed with cytidine 5'-monophosphate
42	c5vtoA_	Alignment	not modelled	96.9	16	PDB header: hydrolase Chain: A: PDB Molecule: blasticidin m; PDBTitle: solution structure of blsm
43	c2khzB_	Alignment	not modelled	96.7	14	PDB header: nuclear protein Chain: B: PDB Molecule: cc-myc-responsive protein rcl; PDBTitle: solution structure of rcl
44	c4jenB_	Alignment	not modelled	96.6	14	PDB header: hydrolase Chain: B: PDB Molecule: cmp n-glycosidase; PDBTitle: structure of clostridium botulinum cmp n-glycosidase, bcmb
45	c6evsA_	Alignment	not modelled	96.5	10	PDB header: transferase Chain: A: PDB Molecule: n-deoxyribosyltransferase; PDBTitle: characterization of 2-deoxyribosyltransferase from psychrotolerant2 bacterium bacillus psychrosaccharolyticus: a suitable biocatalyst for3 the industrial synthesis of antiviral and antitumoral nucleosides
46	c6bpqA_	Alignment	not modelled	96.4	15	PDB header: transport protein Chain: A: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: structure of the cold- and menthol-sensing ion channel trpm8
47	c6bpqB_	Alignment	not modelled	96.4	15	PDB header: transport protein Chain: B: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: structure of the cold- and menthol-sensing ion channel trpm8
48	c6bpqC_	Alignment	not modelled	96.4	15	PDB header: transport protein Chain: C: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: structure of the cold- and menthol-sensing ion channel trpm8
49	c6bpqD_	Alignment	not modelled	96.4	15	PDB header: transport protein Chain: D: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: structure of the cold- and menthol-sensing ion channel

						trpm8
50	c5nbrB	Alignment	not modelled	95.4	13	PDB header: transferase Chain: B: PDB Molecule: deoxyribosyltransferase; PDBTitle: 2-desoxiribosyltransferase from leishmania mexicana
51	d1f8ya	Alignment	not modelled	95.3	9	Fold: Flavodoxin-like Superfamily: N-(deoxy)ribosyltransferase-like Family: N-deoxyribosyltransferase
52	d2f62a1	Alignment	not modelled	95.0	13	Fold: Flavodoxin-like Superfamily: N-(deoxy)ribosyltransferase-like Family: N-deoxyribosyltransferase
53	c3ehdA	Alignment	not modelled	93.7	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized conserved protein; PDBTitle: crystal structure of conserved protein from enterococcus faecalis v583
54	c6eoaA	Alignment	not modelled	92.9	15	PDB header: flavoprotein Chain: A: PDB Molecule: phosphopantothenoilcysteine decarboxylase; PDBTitle: crystal structure of hal3 from cryptococcus neoformans
55	c6hcyA	Alignment	not modelled	89.7	17	PDB header: membrane protein Chain: A: PDB Molecule: metalloreductase steap4; PDBTitle: human steap4 bound to nadp, fad, heme and fe(iii)-nta.
56	c2bonB	Alignment	not modelled	87.3	27	PDB header: transferase Chain: B: PDB Molecule: lipid kinase; PDBTitle: structure of an escherichia coli lipid kinase (yegs)
57	d1s2da	Alignment	not modelled	86.7	9	Fold: Flavodoxin-like Superfamily: N-(deoxy)ribosyltransferase-like Family: N-deoxyribosyltransferase
58	c1mv1A	Alignment	not modelled	85.5	14	PDB header: lyase Chain: A: PDB Molecule: ppc decarboxylase athal3a; PDBTitle: ppc decarboxylase mutant c175s
59	d1mv1a	Alignment	not modelled	85.5	14	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
60	c5v2kA	Alignment	not modelled	83.7	10	PDB header: transferase Chain: A: PDB Molecule: udp-glycosyltransferase 74f2; PDBTitle: crystal structure of udp-glucosyltransferase, ugt74f2 (t15a), with udp2 and 2-bromobenzoic acid
61	c2ejbA	Alignment	not modelled	81.9	16	PDB header: lyase Chain: A: PDB Molecule: probable aromatic acid decarboxylase; PDBTitle: crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
62	d1iuka	Alignment	not modelled	80.7	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
63	d1sbza	Alignment	not modelled	80.0	19	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
64	c2jzcA	Alignment	not modelled	79.6	13	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine transferase subunit PDBTitle: nmr solution structure of alg13: the sugar donor subunit of2 a yeast n-acetylglucosamine transferase. northeast3 structural genomics consortium target yg1
65	c1r01D	Alignment	not modelled	79.1	10	PDB header: oxidoreductase Chain: D: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: 1-deoxy-d-xylulose 5-phosphate reductoisomerase from zymomonas mobilis2 in complex with nadph
66	c2duwA	Alignment	not modelled	78.9	19	PDB header: ligand binding protein Chain: A: PDB Molecule: putative coa-binding protein; PDBTitle: solution structure of putative coa-binding protein of2 klebsiella pneumoniae
67	d1g5qa	Alignment	not modelled	78.6	11	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
68	d2d59a1	Alignment	not modelled	78.5	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
69	c6jtdB	Alignment	not modelled	78.3	16	PDB header: transferase Chain: B: PDB Molecule: c-glycosyltransferase; PDBTitle: crystal structure of tccg1 in complex with udp
70	c6qlgD	Alignment	not modelled	76.9	18	PDB header: transferase Chain: D: PDB Molecule: flavin prenyltransferase pad1, mitochondrial; PDBTitle: crystal structure of anubix (pada1) in complex with fmn and2 dimethylallyl pyrophosphate
71	c4rheB	Alignment	not modelled	74.7	17	PDB header: lyase Chain: B: PDB Molecule: 3-octaprenyl-4-hydroxybenzoate carboxylase; PDBTitle: crystal structure of ubix, an aromatic acid decarboxylase from the2 colwellia psychrerythraea 34h
72	d1p3y1	Alignment	not modelled	74.1	8	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
73	d1r0ka2	Alignment	not modelled	70.7	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain

74	c3zquA	Alignment	not modelled	70.3	13	PDB header: lyase Chain: A: PDB Molecule: probable aromatic acid decarboxylase; PDBTitle: structure of a probable aromatic acid decarboxylase
75	c3afoB	Alignment	not modelled	68.8	11	PDB header: transferase Chain: B: PDB Molecule: nadh kinase pos5; PDBTitle: crystal structure of yeast nadh kinase complexed with nadh
76	d2acva1	Alignment	not modelled	68.6	10	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
77	d2jgra1	Alignment	not modelled	68.6	27	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
78	d1e3ia2	Alignment	not modelled	67.5	6	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
79	c3nywD	Alignment	not modelled	66.9	22	PDB header: oxidoreductase Chain: D: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a betaketoacyl-[acp] reductase (fabg) from2 bacteroides thetaiotaomicron
80	c3pfnB	Alignment	not modelled	66.5	13	PDB header: transferase Chain: B: PDB Molecule: nad kinase; PDBTitle: crystal structure of human nad kinase
81	c1qzuB	Alignment	not modelled	64.3	14	PDB header: lyase Chain: B: PDB Molecule: hypothetical protein mds018; PDBTitle: crystal structure of human phosphopantothenoylcysteine decarboxylase
82	d2bona1	Alignment	not modelled	62.6	27	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
83	c4yxfB	Alignment	not modelled	61.5	29	PDB header: oxidoreductase Chain: B: PDB Molecule: mups; PDBTitle: mups, a 3-oxoacyl (acp) reductase involved in mupirocin biosynthesis
84	c3wisA	Alignment	not modelled	61.4	12	PDB header: oxidoreductase Chain: A: PDB Molecule: putative dihydromethanopterin reductase (afpa); PDBTitle: crystal structure of burkholderia xenovorans dmrB in complex with fmN:2 a cubic protein cage for redox transfer
85	d1o89a2	Alignment	not modelled	61.2	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
86	c3hbjA	Alignment	not modelled	60.5	12	PDB header: transferase Chain: A: PDB Molecule: flavonoid 3-o-glucosyltransferase; PDBTitle: structure of ugt78g1 complexed with udp
87	c6jlsA	Alignment	not modelled	60.5	11	PDB header: biosynthetic protein Chain: A: PDB Molecule: putative flavoprotein decarboxylase; PDBTitle: crystal structure of fmN-dependent cysteine decarboxylases tvaf from2 thioviridamide biosynthesis
88	c3urkA	Alignment	not modelled	60.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-enyl diphosphate reductase; PDBTitle: isph in complex with propynyl diphosphate (1061)
89	c3ke8A	Alignment	not modelled	60.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-enyl diphosphate reductase; PDBTitle: crystal structure of isph:hmbpp-complex
90	d2p1ra1	Alignment	not modelled	59.7	27	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
91	c5nlmB	Alignment	not modelled	59.0	11	PDB header: transferase Chain: B: PDB Molecule: indoxyl udp-glucosyltransferase; PDBTitle: complex between a udp-glucosyltransferase from polygonum tinctorium2 capable of glucosylating indoxyl and indoxyl sulfate
92	c3ftpD	Alignment	not modelled	58.9	16	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-oxoacyl-[acyl-carrier protein] reductase; PDBTitle: crystal structure of 3-ketoacyl-(acyl-carrier-protein) reductase from2 burkholderia pseudomallei at 2.05 a resolution
93	c6m9uA	Alignment	not modelled	58.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase family PDBTitle: structure of the apo-form of 20beta-hydroxysteroid dehydrogenase from2 bifidobacterium adolescentis strain I2-32
94	c3gafF	Alignment	not modelled	58.1	19	PDB header: oxidoreductase Chain: F: PDB Molecule: 7-alpha-hydroxysteroid dehydrogenase; PDBTitle: 2.2a crystal structure of 7-alpha-hydroxysteroid dehydrogenase from2 brucella melitensis
95	c3p19A	Alignment	not modelled	57.2	23	PDB header: oxidoreductase Chain: A: PDB Molecule: putative blue fluorescent protein; PDBTitle: improved nadph-dependent blue fluorescent protein
96	d1qora2	Alignment	not modelled	56.8	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
97	c2xcuC	Alignment	not modelled	56.0	17	PDB header: transferase Chain: C: PDB Molecule: 3-deoxy-d-manno-2-octulosonic acid transferase; PDBTitle: membrane-embedded monofunctional glycosyltransferase waaa of aquifex2 aeolicus, complex with cmp
98	c4n7bA	Alignment	not modelled	55.6	24	PDB header: oxidoreductase Chain: A: PDB Molecule: lytb; PDBTitle: structure of the e-1-hydroxy-2-methyl-but-2-enyl-4-diphosphate2 reductase from plasmodium falciparum
99	d2vcha1	Alignment	not modelled	55.6	8	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase

						Family: UDPGT-like
100	c3imfA_	Alignment	not modelled	54.7	22	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: 1.99 angstrom resolution crystal structure of a short chain2 dehydrogenase from bacillus anthracis str. 'ames ancestor'
101	c3upyB_	Alignment	not modelled	54.5	13	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of the brucella abortus enzyme catalyzing the first2 committed step of the methylethyltritol 4-phosphate pathway.
102	d1lpfa2	Alignment	not modelled	54.5	26	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
103	c3ff4A_	Alignment	not modelled	54.2	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein chu_1412
104	c4kmsB_	Alignment	not modelled	54.1	21	PDB header: oxidoreductase Chain: B: PDB Molecule: acetoacetyl-coa reductase; PDBTitle: crystal structure of acetoacetyl-coa reductase from rickettsia felis
105	c2vq3B_	Alignment	not modelled	54.0	30	PDB header: oxidoreductase Chain: B: PDB Molecule: metalloreductase steap3; PDBTitle: crystal structure of the membrane proximal oxidoreductase2 domain of human steap3, the dominant ferric reductase of3 the erythroid transferrin cycle
106	c4zu3D_	Alignment	not modelled	53.9	14	PDB header: lyase Chain: D: PDB Molecule: halohydrin epoxidase b; PDBTitle: halohydrin hydrogen-halide-lyases, hheb
107	d1h6va2	Alignment	not modelled	53.8	22	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
108	c2q5cA_	Alignment	not modelled	53.6	15	PDB header: transcription Chain: A: PDB Molecule: ntrc family transcriptional regulator; PDBTitle: crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
109	c2q62A_	Alignment	not modelled	53.2	15	PDB header: flavoprotein Chain: A: PDB Molecule: arsh; PDBTitle: crystal structure of arsh from sinorhizobium meliloti
110	d3grsa2	Alignment	not modelled	52.5	19	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
111	c5iz4A_	Alignment	not modelled	52.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: putative short-chain dehydrogenase/reductase; PDBTitle: crystal structure of a putative short-chain dehydrogenase/reductase2 from burkholderia xenovorans
112	d1qzua_	Alignment	not modelled	51.5	11	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
113	c5b1yB_	Alignment	not modelled	51.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: crystal structure of nadph bound carbonyl reductase from aeropyrum2 pernix
114	d1e7wa_	Alignment	not modelled	50.9	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
115	d1f8fa2	Alignment	not modelled	50.6	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
116	c3a14B_	Alignment	not modelled	50.5	15	PDB header: oxidoreductase Chain: B: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: crystal structure of dxr from thermotoga maritima, in complex with2 nadph
117	c2dknA_	Alignment	not modelled	50.4	29	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-alpha-hydroxysteroid dehydrogenase; PDBTitle: crystal structure of the 3-alpha-hydroxysteroid dehydrogenase from2 pseudomonas sp. b-0831 complexed with nadh
118	c3t4xA_	Alignment	not modelled	50.3	19	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase family; PDBTitle: short chain dehydrogenase/reductase family oxidoreductase from2 bacillus anthracis str. ames ancestor
119	c3nvaB_	Alignment	not modelled	50.2	25	PDB header: ligase Chain: B: PDB Molecule: ctp synthase; PDBTitle: dimeric form of ctp synthase from sulfolobus solfataricus
120	c3a28H_	Alignment	not modelled	49.7	13	PDB header: oxidoreductase Chain: H: PDB Molecule: l-2,3-butanediol dehydrogenase; PDBTitle: crystal structure of l-2,3-butanediol dehydrogenase