
































#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3mt5A_</a>	 Alignment		100.0	15	<b>PDB header:</b> membrane protein, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> potassium large conductance calcium-activated channel, <b>PDBTitle:</b> crystal structure of the human bk gating apparatus
2	<a href="#">c3u6nC_</a>	 Alignment		100.0	15	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> high-conductance ca2+-activated k+ channel protein; <b>PDBTitle:</b> open structure of the bk channel gating ring
3	<a href="#">c3l4bG_</a>	 Alignment		100.0	22	<b>PDB header:</b> transport protein <b>Chain:</b> G: <b>PDB Molecule:</b> trka k+ channel protien tm1088b; <b>PDBTitle:</b> crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
4	<a href="#">c2fy8A_</a>	 Alignment		100.0	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> calcium-gated potassium channel mthk; <b>PDBTitle:</b> crystal structure of mthk rck domain in its ligand-free gating-ring2 form
5	<a href="#">c3nafA_</a>	 Alignment		100.0	15	<b>PDB header:</b> ion transport <b>Chain:</b> A: <b>PDB Molecule:</b> calcium-activated potassium channel subunit alpha-1; <b>PDBTitle:</b> structure of the intracellular gating ring from the human high-2 conductance ca2+ gated k+ channel (bk channel)
6	<a href="#">c1lnqC_</a>	 Alignment		100.0	15	<b>PDB header:</b> metal transport <b>Chain:</b> C: <b>PDB Molecule:</b> potassium channel related protein; <b>PDBTitle:</b> crystal structure of mthk at 3.3 a
7	<a href="#">c3eywA_</a>	 Alignment		100.0	23	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> c-terminal domain of glutathione-regulated potassium-efflux <b>PDBTitle:</b> crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
8	<a href="#">d1lssa_</a>	 Alignment		100.0	35	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Potassium channel NAD-binding domain
9	<a href="#">c3fwzA_</a>	 Alignment		99.9	21	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> inner membrane protein ybal; <b>PDBTitle:</b> crystal structure of trka-n domain of inner membrane protein ybal from2 escherichia coli
10	<a href="#">d1ld1a_</a>	 Alignment		99.9	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Potassium channel NAD-binding domain
11	<a href="#">c2g1uA_</a>	 Alignment		99.9	30	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein tm1088a; <b>PDBTitle:</b> crystal structure of a putative transport protein (tm1088a) from2 thermotoga maritima at 1.50 a resolution

12	<a href="#">d2hmva1</a>	Alignment		99.9	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Potassium channel NAD-binding domain
13	<a href="#">c3llva_</a>	Alignment		99.9	18	<b>PDB header:</b> nad(p) binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> exopolysphatase-related protein; <b>PDBTitle:</b> the crystal structure of the nad(p)-binding domain of an2 exopolysphatase-related protein from archaeoglobus fulgidus to3 1.7a
14	<a href="#">d2fy8a1</a>	Alignment		99.9	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Potassium channel NAD-binding domain
15	<a href="#">c3c85A_</a>	Alignment		99.9	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative glutathione-regulated potassium-efflux system <b>PDBTitle:</b> crystal structure of trka domain of putative glutathione-regulated2 potassium-efflux kefb from vibrio parahaemolyticus
16	<a href="#">d1e5qa1</a>	Alignment		99.7	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
17	<a href="#">c3jxoB_</a>	Alignment		99.3	28	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> trka-n domain protein; <b>PDBTitle:</b> crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
18	<a href="#">d2fy8a2</a>	Alignment		99.1	16	<b>Fold:</b> TrkA C-terminal domain-like <b>Superfamily:</b> TrkA C-terminal domain-like <b>Family:</b> TrkA C-terminal domain-like
19	<a href="#">c2bknA_</a>	Alignment		99.0	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ph0236; <b>PDBTitle:</b> structure analysis of unknown function protein
20	<a href="#">d1vcta2</a>	Alignment		99.0	13	<b>Fold:</b> TrkA C-terminal domain-like <b>Superfamily:</b> TrkA C-terminal domain-like <b>Family:</b> TrkA C-terminal domain-like
21	<a href="#">d1pjqal</a>	Alignment	not modelled	98.9	24	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Siroheme synthase N-terminal domain-like
22	<a href="#">c3ic5A_</a>	Alignment	not modelled	98.7	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative saccharopine dehydrogenase; <b>PDBTitle:</b> n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
23	<a href="#">c1e5lA_</a>	Alignment	not modelled	98.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine reductase; <b>PDBTitle:</b> apo saccharopine reductase from magnaporthe grisea
24	<a href="#">c2axqA_</a>	Alignment	not modelled	98.6	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine dehydrogenase; <b>PDBTitle:</b> apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
25	<a href="#">c1z7eC_</a>	Alignment	not modelled	98.5	16	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> protein arna; <b>PDBTitle:</b> crystal structure of full length arna
26	<a href="#">d2f1ka2</a>	Alignment	not modelled	98.5	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
27	<a href="#">c2f1kD_</a>	Alignment	not modelled	98.5	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> prephenate dehydrogenase; <b>PDBTitle:</b> crystal structure of synechocystis arogenate dehydrogenase
28	<a href="#">c2x4gA_</a>	Alignment	not modelled	98.4	14	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoside-diphosphate-sugar epimerase; <b>PDBTitle:</b> crystal structure of pa4631, a nucleoside-diphosphate-sugar2 epimerase from pseudomonas aeruginosa

29	<a href="#">d2pgda2</a>	Alignment	not modelled	98.4	7	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
30	<a href="#">c2z2vA</a>	Alignment	not modelled	98.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ph1688; <b>PDBTitle:</b> crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
31	<a href="#">c3fwnB</a>	Alignment	not modelled	98.4	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase, decarboxylating; <b>PDBTitle:</b> dimeric 6-phosphogluconate dehydrogenase complexed with 6-2 phosphogluconate and 2'-monophosphoadenosine-5'-diphosphate
32	<a href="#">c2vrcD</a>	Alignment	not modelled	98.4	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> triphenylmethane reductase; <b>PDBTitle:</b> crystal structure of the citrobacter sp. triphenylmethane2 reductase complexed with nadp(h)
33	<a href="#">d1pgja2</a>	Alignment	not modelled	98.4	9	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
34	<a href="#">c3l6dB</a>	Alignment	not modelled	98.3	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
35	<a href="#">d1pjca1</a>	Alignment	not modelled	98.3	26	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
36	<a href="#">c3ckyA</a>	Alignment	not modelled	98.3	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-hydroxymethyl glutarate dehydrogenase; <b>PDBTitle:</b> structural and kinetic properties of a beta-hydroxyacid dehydrogenase2 involved in nicotinate fermentation
37	<a href="#">c2qx7A</a>	Alignment	not modelled	98.3	18	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> eugenol synthase 1; <b>PDBTitle:</b> structure of eugenol synthase from ocimum basilicum
38	<a href="#">c3qhaB</a>	Alignment	not modelled	98.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative oxidoreductase from mycobacterium2 avium 104
39	<a href="#">d2blia1</a>	Alignment	not modelled	98.3	22	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
40	<a href="#">c1pgjA</a>	Alignment	not modelled	98.3	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase; <b>PDBTitle:</b> x-ray structure of 6-phosphogluconate dehydrogenase from the protozoan2 parasite t. brucei
41	<a href="#">c2y0dB</a>	Alignment	not modelled	98.2	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-glucose dehydrogenase; <b>PDBTitle:</b> bcec mutation y10k
42	<a href="#">c2p5uC</a>	Alignment	not modelled	98.2	18	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> udp-glucose 4-epimerase; <b>PDBTitle:</b> crystal structure of thermus thermophilus hb8 udp-glucose 4-2 epimerase complex with nad
43	<a href="#">c3gg2B</a>	Alignment	not modelled	98.2	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> sugar dehydrogenase, udp-glucose/gdp-mannose <b>PDBTitle:</b> crystal structure of udp-glucose 6-dehydrogenase from2 porphyromonas gingivalis bound to product udp-glucuronate
44	<a href="#">d2c5aa1</a>	Alignment	not modelled	98.2	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
45	<a href="#">c3ktdC</a>	Alignment	not modelled	98.2	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> prephenate dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative prephenate dehydrogenase (cgl0226)2 from corynebacterium glutamicum atcc 13032 at 2.60 a resolution
46	<a href="#">c3g0oA</a>	Alignment	not modelled	98.2	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxyisobutyrate dehydrogenase; <b>PDBTitle:</b> crystal structure of 3-hydroxyisobutyrate dehydrogenase2 (ygbj) from salmonella typhimurium
47	<a href="#">d1udca</a>	Alignment	not modelled	98.2	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
48	<a href="#">c2zcuA</a>	Alignment	not modelled	98.2	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized oxidoreductase ytfq; <b>PDBTitle:</b> crystal structure of a new type of nadph-dependent quinone2 oxidoreductase (qor2) from escherichia coli
49	<a href="#">c3plnA</a>	Alignment	not modelled	98.2	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-glucose 6-dehydrogenase; <b>PDBTitle:</b> crystal structure of klebsiella pneumoniae udp-glucose 6-dehydrogenase2 complexed with udp-glucose
50	<a href="#">c2pk3B</a>	Alignment	not modelled	98.2	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> gdp-6-deoxy-d-lyxo-4-hexulose reductase; <b>PDBTitle:</b> crystal structure of a gdp-4-keto-6-deoxy-d-mannose reductase
51	<a href="#">c2pzlB</a>	Alignment	not modelled	98.2	26	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative nucleotide sugar epimerase/dehydratase; <b>PDBTitle:</b> crystal structure of the bordetella bronchiseptica enzyme2 wbmj in complex with nad and udp
52	<a href="#">c2gf2B</a>	Alignment	not modelled	98.2	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-hydroxyisobutyrate dehydrogenase; <b>PDBTitle:</b> crystal structure of human hydroxyisobutyrate dehydrogenase
53	<a href="#">c2iz1C</a>	Alignment	not modelled	98.1	6	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase,

53	<a href="#">c2t2tC_</a>	Alignment	not modelled	98.1	0	decarboxylating; <b>PDBTitle:</b> 6pdh complexed with pex inhibitor synchrotron data
54	<a href="#">d1mv8a2</a>	Alignment	not modelled	98.1	24	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphoglucuronate dehydrogenase-like, N-terminal domain
55	<a href="#">c3dttA_</a>	Alignment	not modelled	98.1	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadp oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative f420 dependent nadp-reductase2 (arth_0613) from arthrobacter sp. fb24 at 1.70 a resolution
56	<a href="#">c2p4qA_</a>	Alignment	not modelled	98.1	6	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphoglucuronate dehydrogenase, decarboxylating 1; <b>PDBTitle:</b> crystal structure analysis of gnd1 in saccharomyces cerevisiae
57	<a href="#">c3triB_</a>	Alignment	not modelled	98.1	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> pyrroline-5-carboxylate reductase; <b>PDBTitle:</b> structure of a pyrroline-5-carboxylate reductase (proc) from coxiella2 burnetii
58	<a href="#">d1dlja2</a>	Alignment	not modelled	98.1	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphoglucuronate dehydrogenase-like, N-terminal domain
59	<a href="#">d1jaya_</a>	Alignment	not modelled	98.1	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphoglucuronate dehydrogenase-like, N-terminal domain
60	<a href="#">c1vpdA_</a>	Alignment	not modelled	98.1	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> tartronate semialdehyde reductase; <b>PDBTitle:</b> x-ray crystal structure of tartronate semialdehyde reductase2 [salmonella typhimurium lt2]
61	<a href="#">c1mv8A_</a>	Alignment	not modelled	98.1	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> gdp-mannose 6-dehydrogenase; <b>PDBTitle:</b> 1.55 a crystal structure of a ternary complex of gdp-mannose2 dehydrogenase from pseudomonas aeruginosa
62	<a href="#">c3icpA_</a>	Alignment	not modelled	98.1	22	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent epimerase/dehydratase; <b>PDBTitle:</b> crystal structure of udp-galactose 4-epimerase
63	<a href="#">c3cumA_</a>	Alignment	not modelled	98.1	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable 3-hydroxyisobutyrate dehydrogenase; <b>PDBTitle:</b> crystal structure of a possible 3-hydroxyisobutyrate dehydrogenase2 from pseudomonas aeruginosa pao1
64	<a href="#">c3dhyC_</a>	Alignment	not modelled	98.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> adenosylhomocysteinease; <b>PDBTitle:</b> crystal structures of mycobacterium tuberculosis s-adenosyl-l-2 homocysteine hydrolase in ternary complex with substrate and3 inhibitors
65	<a href="#">c3d1lB_</a>	Alignment	not modelled	98.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative nadp oxidoreductase bf3122; <b>PDBTitle:</b> crystal structure of putative nadp oxidoreductase bf3122 from2 bacteroides fragilis
66	<a href="#">c2ew2B_</a>	Alignment	not modelled	98.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-dehydropantoate 2-reductase, putative; <b>PDBTitle:</b> crystal structure of the putative 2-dehydropantoate 2-reductase from2 enterococcus faecalis
67	<a href="#">c2q1wC_</a>	Alignment	not modelled	98.0	26	<b>PDB header:</b> sugar binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> putative nucleotide sugar epimerase/dehydratase; <b>PDBTitle:</b> crystal structure of the bordetella bronchiseptica enzyme wbmh in2 complex with nad+
68	<a href="#">c3c1oA_</a>	Alignment	not modelled	98.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> eugenol synthase; <b>PDBTitle:</b> the multiple phenylpropene synthases in both clarkia2 breweri and petunia hybrida represent two distinct lineages
69	<a href="#">c1dliA_</a>	Alignment	not modelled	98.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-glucose dehydrogenase; <b>PDBTitle:</b> the first structure of udp-glucose dehydrogenase (udpgdh) reveals the2 catalytic residues necessary for the two-fold oxidation
70	<a href="#">d1xgka_</a>	Alignment	not modelled	98.0	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
71	<a href="#">c2ahrB_</a>	Alignment	not modelled	98.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative pyrroline carboxylate reductase; <b>PDBTitle:</b> crystal structures of 1-pyrroline-5-carboxylate reductase from human2 pathogen streptococcus pyogenes
72	<a href="#">c3b1fA_</a>	Alignment	not modelled	98.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative prephenate dehydrogenase; <b>PDBTitle:</b> crystal structure of prephenate dehydrogenase from streptococcus2 mutans
73	<a href="#">c3m2pD_</a>	Alignment	not modelled	98.0	15	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> udp-n-acetylglucosamine 4-epimerase; <b>PDBTitle:</b> the crystal structure of udp-n-acetylglucosamine 4-epimerase2 from bacillus cereus
74	<a href="#">c2g5cD_</a>	Alignment	not modelled	98.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> prephenate dehydrogenase; <b>PDBTitle:</b> crystal structure of prephenate dehydrogenase from aquifex aeolicus
75	<a href="#">c2o3jC_</a>	Alignment	not modelled	98.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> udp-glucose 6-dehydrogenase; <b>PDBTitle:</b> structure of caenorhabditis elegans udp-glucose dehydrogenase
76	<a href="#">c3dojA_</a>	Alignment	not modelled	98.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dehydrogenase-like protein; <b>PDBTitle:</b> structure of glyoxylate reductase 1 from arabidopsis2 (atglyr1)
77	<a href="#">c3gpiA_</a>	Alignment	not modelled	98.0	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent epimerase/dehydratase; <b>PDBTitle:</b> structure of putative nad-dependent epimerase/dehydratase2 from methylobacillus flagellatus

78	<a href="#">c3n58D_</a>	Alignment	not modelled	98.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> adenosylhomocysteine; <b>PDBTitle:</b> crystal structure of s-adenosyl-l-homocysteine hydrolase from brucella2 melitensis in ternary complex with nad and adenosine, orthorhombic3 form
79	<a href="#">d1kewa_</a>	Alignment	not modelled	97.9	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
80	<a href="#">d1bg6a2</a>	Alignment	not modelled	97.9	22	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
81	<a href="#">c1ks9A_</a>	Alignment	not modelled	97.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydropantoate 2-reductase; <b>PDBTitle:</b> ketopantoate reductase from escherichia coli
82	<a href="#">c3ggpA_</a>	Alignment	not modelled	97.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> prephenate dehydrogenase; <b>PDBTitle:</b> crystal structure of prephenate dehydrogenase from a. aeolicus in2 complex with hydroxyphenyl propionate and nad+
83	<a href="#">c1bg6A_</a>	Alignment	not modelled	97.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> n-(1-d-carboxylethyl)-l-norvaline dehydrogenase; <b>PDBTitle:</b> crystal structure of the n-(1-d-carboxylethyl)-l-norvaline2 dehydrogenase from arthrobacter sp. strain 1c
84	<a href="#">d1bxka_</a>	Alignment	not modelled	97.9	25	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
85	<a href="#">c3e48B_</a>	Alignment	not modelled	97.9	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative nucleoside-diphosphate-sugar epimerase; <b>PDBTitle:</b> crystal structure of a nucleoside-diphosphate-sugar epimerase2 (sav0421) from staphylococcus aureus, northeast structural genomics3 consortium target zr319
86	<a href="#">c3dqpA_</a>	Alignment	not modelled	97.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase ylbe; <b>PDBTitle:</b> crystal structure of the oxidoreductase ylbe from2 lactococcus lactis, northeast structural genomics3 consortium target kr121.
87	<a href="#">d1txga2</a>	Alignment	not modelled	97.9	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
88	<a href="#">c2vhyB_</a>	Alignment	not modelled	97.9	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alanine dehydrogenase; <b>PDBTitle:</b> crystal structure of apo l-alanine dehydrogenase from2 mycobacterium tuberculosis
89	<a href="#">c3egoB_</a>	Alignment	not modelled	97.9	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable 2-dehydropantoate 2-reductase; <b>PDBTitle:</b> crystal structure of probable 2-dehydropantoate 2-reductase2 pane from bacillus subtilis
90	<a href="#">c2graA_</a>	Alignment	not modelled	97.9	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrroline-5-carboxylate reductase 1; <b>PDBTitle:</b> crystal structure of human pyrroline-5-carboxylate reductase complexed2 with nadp
91	<a href="#">c2ofpB_</a>	Alignment	not modelled	97.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ketopantoate reductase; <b>PDBTitle:</b> crystal structure of escherichia coli ketopantoate2 reductase in a ternary complex with nadp+ and pantoate
92	<a href="#">c1gpiA_</a>	Alignment	not modelled	97.9	24	<b>PDB header:</b> reductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna reductase; <b>PDBTitle:</b> glutamyl-trna reductase from methanopyrus kandleri
93	<a href="#">cli36A_</a>	Alignment	not modelled	97.9	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein mth1747; <b>PDBTitle:</b> structure of conserved protein mth1747 of unknown function2 reveals structural similarity with 3-hydroxyacid3 dehydrogenases
94	<a href="#">d2jfga1</a>	Alignment	not modelled	97.8	16	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
95	<a href="#">c2c20D_</a>	Alignment	not modelled	97.8	22	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> udp-glucose 4-epimerase; <b>PDBTitle:</b> crystal structure of udp-glucose 4-epimerase
96	<a href="#">c3slgB_</a>	Alignment	not modelled	97.8	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pbgp3 protein; <b>PDBTitle:</b> crystal structure of pbgp3 protein from burkholderia pseudomallei
97	<a href="#">c2uyyD_</a>	Alignment	not modelled	97.8	23	<b>PDB header:</b> cytokine <b>Chain:</b> D: <b>PDB Molecule:</b> n-pac protein; <b>PDBTitle:</b> structure of the cytokine-like nuclear factor n-pac
98	<a href="#">c2pv7B_</a>	Alignment	not modelled	97.8	17	<b>PDB header:</b> isomerase, oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> t-protein [includes: chorismate mutase (ec 5.4.99.5) (cm) <b>PDBTitle:</b> crystal structure of chorismate mutase / prephenate dehydrogenase2 (tyra) (1574749) from haemophilus influenzae rd at 2.00 a resolution
99	<a href="#">c1pggA_</a>	Alignment	not modelled	97.8	7	<b>PDB header:</b> oxidoreductase (choh(d)-nadp+(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase; <b>PDBTitle:</b> crystallographic study of coenzyme, coenzyme analogue and substrate2 binding in 6-phosphogluconate dehydrogenase: implications for nadp3 specificity and the enzyme mechanism
100	<a href="#">c2izzE_</a>	Alignment	not modelled	97.8	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> pyrroline-5-carboxylate reductase 1; <b>PDBTitle:</b> crystal structure of human pyrroline-5-carboxylate2 reductase
101	<a href="#">c3c7cB_</a>	Alignment	not modelled	97.8	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> octopine dehydrogenase; <b>PDBTitle:</b> a structural basis for substrate and stereo selectivity in2 octopine dehydrogenase (odh-nadh-l-arginine)



102	<a href="#">c3ghyA</a>	Alignment	not modelled	97.8	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ketopantoate reductase protein; <b>PDBTitle:</b> crystal structure of a putative ketopantoate reductase from ralstonia2 solanacearum molk2
103	<a href="#">c2eezG</a>	Alignment	not modelled	97.8	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> alanine dehydrogenase; <b>PDBTitle:</b> crystal structure of alanine dehydrogenase from themus thermophilus
104	<a href="#">c1v8bA</a>	Alignment	not modelled	97.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structure of a hydrolase
105	<a href="#">c3k96B</a>	Alignment	not modelled	97.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glycerol-3-phosphate dehydrogenase [nad(p)+]; <b>PDBTitle:</b> 2.1 angstrom resolution crystal structure of glycerol-3-phosphate2 dehydrogenase (gpsa) from coxiella burnetii
106	<a href="#">d2ahra2</a>	Alignment	not modelled	97.8	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
107	<a href="#">d1orra</a>	Alignment	not modelled	97.8	23	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
108	<a href="#">d1ldma1</a>	Alignment	not modelled	97.8	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
109	<a href="#">c2z1mC</a>	Alignment	not modelled	97.8	16	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> gdp-d-mannose dehydratase; <b>PDBTitle:</b> crystal structure of gdp-d-mannose dehydratase from aquifex aeolicus2 vf5
110	<a href="#">c3ojlA</a>	Alignment	not modelled	97.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cap5o; <b>PDBTitle:</b> native structure of the udp-n-acetyl-mannosamine dehydrogenase cap5o2 from staphylococcus aureus
111	<a href="#">d1l7da1</a>	Alignment	not modelled	97.8	7	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
112	<a href="#">d1ks9a2</a>	Alignment	not modelled	97.8	14	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
113	<a href="#">c3orgA</a>	Alignment	not modelled	97.8	15	<b>PDB header:</b> ligase,biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> n5-carboxyaminoimidazole ribonucleotide synthetase; <b>PDBTitle:</b> crystal structure of n5-carboxyaminoimidazole synthetase from2 staphylococcus aureus complexed with adp
114	<a href="#">c2hunB</a>	Alignment	not modelled	97.8	23	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 336aa long hypothetical dtdp-glucose 4,6-dehydratase; <b>PDBTitle:</b> crystal structure of hypothetical protein ph0414 from pyrococcus2 horikoshii ot3
115	<a href="#">d1leha1</a>	Alignment	not modelled	97.8	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
116	<a href="#">c2v6bB</a>	Alignment	not modelled	97.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> l-lactate dehydrogenase; <b>PDBTitle:</b> crystal structure of lactate dehydrogenase from deinococcus2 radiodurans (apo form)
117	<a href="#">c3gvpB</a>	Alignment	not modelled	97.7	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> adenosylhomocysteinase 3; <b>PDBTitle:</b> human sahh-like domain of human adenosylhomocysteinase 3
118	<a href="#">c3i5mA</a>	Alignment	not modelled	97.7	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative leucoanthocyanidin reductase 1; <b>PDBTitle:</b> structure of the apo form of leucoanthocyanidin reductase from vitis2 vinifera
119	<a href="#">c3d64A</a>	Alignment	not modelled	97.7	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
120	<a href="#">c2q3eH</a>	Alignment	not modelled	97.7	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> udp-glucose 6-dehydrogenase; <b>PDBTitle:</b> structure of human udp-glucose dehydrogenase complexed with nadh and2 udp-glucose