





















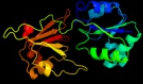
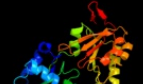




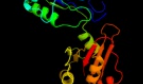




Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1pjtB_</a>	 Alignment		100.0	90	<b>PDB header:</b> transferase/oxidoreductase/lyase <b>Chain:</b> B: <b>PDB Molecule:</b> siroheme synthase; <b>PDBTitle:</b> the structure of the ser128ala point-mutant variant of cysg,2 the multifunctional3 methyltransferase/dehydrogenase/ferrochelatase for4 siroheme synthesis
2	<a href="#">dls4da_</a>	 Alignment		100.0	44	<b>Fold:</b> Tetrapyrrole methylase <b>Superfamily:</b> Tetrapyrrole methylase <b>Family:</b> Tetrapyrrole methylase
3	<a href="#">dlpjqaz</a>	 Alignment		100.0	91	<b>Fold:</b> Tetrapyrrole methylase <b>Superfamily:</b> Tetrapyrrole methylase <b>Family:</b> Tetrapyrrole methylase
4	<a href="#">c2yboA_</a>	 Alignment		100.0	55	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> the x-ray structure of the sam-dependent uroporphyrinogen2 iii methyltransferase nire from pseudomonas aeruginosa in3 complex with sah
5	<a href="#">c1kyqC_</a>	 Alignment		100.0	21	<b>PDB header:</b> oxidoreductase, lyase <b>Chain:</b> C: <b>PDB Molecule:</b> siroheme biosynthesis protein met8; <b>PDBTitle:</b> met8p: a bifunctional nad-dependent dehydrogenase and2 ferrochelatase involved in siroheme synthesis.
6	<a href="#">d1cbfa_</a>	 Alignment		100.0	30	<b>Fold:</b> Tetrapyrrole methylase <b>Superfamily:</b> Tetrapyrrole methylase <b>Family:</b> Tetrapyrrole methylase
7	<a href="#">c1cbfA_</a>	 Alignment		100.0	30	<b>PDB header:</b> methyltransferase <b>Chain:</b> A: <b>PDB Molecule:</b> cobalt-precorrin-4 transmethyase; <b>PDBTitle:</b> the x-ray structure of a cobalamin biosynthetic enzyme, cobalt2 precorrin-4 methyltransferase, cbif
8	<a href="#">c3dfzB_</a>	 Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> precorrin-2 dehydrogenase; <b>PDBTitle:</b> sirc, precorrin-2 dehydrogenase
9	<a href="#">dlve2a1</a>	 Alignment		100.0	42	<b>Fold:</b> Tetrapyrrole methylase <b>Superfamily:</b> Tetrapyrrole methylase <b>Family:</b> Tetrapyrrole methylase
10	<a href="#">c3ndcB_</a>	 Alignment		100.0	32	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> precorrin-4 c(11)-methyltransferase; <b>PDBTitle:</b> crystal structure of precorrin-4 c11-methyltransferase from2 rhodobacter capsulatus
11	<a href="#">c3kwpA_</a>	 Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> predicted methyltransferase; <b>PDBTitle:</b> crystal structure of putative methyltransferase from lactobacillus2 brevis

12	<a href="#">d1va0a1</a>	Alignment		100.0	39	<b>Fold:</b> Tetrapyrrole methylase <b>Superfamily:</b> Tetrapyrrole methylase <b>Family:</b> Tetrapyrrole methylase
13	<a href="#">c2zvbA_</a>	Alignment		100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> precorrin-3 c17-methyltransferase; <b>PDBTitle:</b> crystal structure of tt0207 from thermus thermophilus hb8
14	<a href="#">d1wdea_</a>	Alignment		100.0	18	<b>Fold:</b> Tetrapyrrole methylase <b>Superfamily:</b> Tetrapyrrole methylase <b>Family:</b> Tetrapyrrole methylase
15	<a href="#">c3nutC_</a>	Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> precorrin-3 methylase; <b>PDBTitle:</b> crystal structure of the methyltransferase cobj
16	<a href="#">c2e0kA_</a>	Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> precorrin-2 c20-methyltransferase; <b>PDBTitle:</b> crystal structure of cbil, a methyltransferase involved in anaerobic2 vitamin b12 biosynthesis
17	<a href="#">d1wyza1</a>	Alignment		100.0	14	<b>Fold:</b> Tetrapyrrole methylase <b>Superfamily:</b> Tetrapyrrole methylase <b>Family:</b> Tetrapyrrole methylase
18	<a href="#">c3i4tA_</a>	Alignment		100.0	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> diphthine synthase; <b>PDBTitle:</b> crystal structure of putative diphthine synthase from2 entamoeba histolytica
19	<a href="#">d2deka1</a>	Alignment		100.0	18	<b>Fold:</b> Tetrapyrrole methylase <b>Superfamily:</b> Tetrapyrrole methylase <b>Family:</b> Tetrapyrrole methylase
20	<a href="#">d1vhva_</a>	Alignment		100.0	18	<b>Fold:</b> Tetrapyrrole methylase <b>Superfamily:</b> Tetrapyrrole methylase <b>Family:</b> Tetrapyrrole methylase
21	<a href="#">c2qbuA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> precorrin-2 methyltransferase; <b>PDBTitle:</b> crystal structure of methanothermobacter thermautotrophicus cbil
22	<a href="#">c2npnA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cobalamin synthesis related protein; <b>PDBTitle:</b> crystal structure of putative cobalamin synthesis related protein2 (cobf) from corynebacterium diphtheriae
23	<a href="#">c3nd1B_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> precorrin-6a synthase/cobf protein; <b>PDBTitle:</b> crystal structure of precorrin-6a synthase from rhodobacter capsulatus
24	<a href="#">c2bb3B_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cobalamin biosynthesis precorrin-6y methylase (cbie); <b>PDBTitle:</b> crystal structure of cobalamin biosynthesis precorrin-6y methylase2 (cbie) from archaeoglobus fulgidus
25	<a href="#">d2bb3a1</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Tetrapyrrole methylase <b>Superfamily:</b> Tetrapyrrole methylase <b>Family:</b> Tetrapyrrole methylase
26	<a href="#">d1kyqa1</a>	Alignment	not modelled	100.0	21	<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
27	<a href="#">d1pjqa1</a>	Alignment	not modelled	100.0	90	<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
28	<a href="#">c3hh1D_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> tetrapyrrole methylase family protein; <b>PDBTitle:</b> the structure of a tetrapyrrole methylase family protein

						domain from2 chlorobium tepidum t1s
29	<a href="#">d1pjqaz</a>	Alignment	not modelled	99.8	87	<b>Fold:</b> Siroheme synthase middle domains-like <b>Superfamily:</b> Siroheme synthase middle domains-like <b>Family:</b> Siroheme synthase middle domains-like
30	<a href="#">d1kyqa2</a>	Alignment	not modelled	99.5	20	<b>Fold:</b> Siroheme synthase middle domains-like <b>Superfamily:</b> Siroheme synthase middle domains-like <b>Family:</b> Siroheme synthase middle domains-like
31	<a href="#">c3fq6A_</a>	Alignment	not modelled	99.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> the crystal structure of a methyltransferase domain from bacteroides2 thetaiotaomicron vpi
32	<a href="#">c3d4oA_</a>	Alignment	not modelled	98.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dipicolinate synthase subunit a; <b>PDBTitle:</b> crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from bacillus halodurans at 2.10 a resolution
33	<a href="#">c2rirA_</a>	Alignment	not modelled	98.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dipicolinate synthase, a chain; <b>PDBTitle:</b> crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
34	<a href="#">d2jfga1</a>	Alignment	not modelled	98.1	16	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
35	<a href="#">d1lssa_</a>	Alignment	not modelled	97.8	19	<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
36	<a href="#">d1e5qa1</a>	Alignment	not modelled	97.7	18	<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
37	<a href="#">c2g1uA_</a>	Alignment	not modelled	97.6	22	<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
38	<a href="#">d1li4a1</a>	Alignment	not modelled	97.6	18	<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
39	<a href="#">c3gvpB_</a>	Alignment	not modelled	97.6	18	<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
40	<a href="#">c1gpiA_</a>	Alignment	not modelled	97.6	19	<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
41	<a href="#">c1y8qA_</a>	Alignment	not modelled	97.5	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-like 1 activating enzyme e1a; <b>PDBTitle:</b> sumo e1 activating enzyme sae1-sae2-mg-atp complex
42	<a href="#">c1d4fD_</a>	Alignment	not modelled	97.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> s-adenosylhomocysteine hydrolase; <b>PDBTitle:</b> crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
43	<a href="#">c3fwzA_</a>	Alignment	not modelled	97.5	17	<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
44	<a href="#">d1p3da1</a>	Alignment	not modelled	97.5	17	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
45	<a href="#">c3llvA_</a>	Alignment	not modelled	97.5	20	<b>PDB header:</b> nad(p) binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> exopolyphosphatase-related protein; <b>PDBTitle:</b> the crystal structure of the nad(p)-binding domain of an2 exopolyphosphatase-related protein from archaeoglobus fulgidus to3 1.7a
46	<a href="#">c3dhyC_</a>	Alignment	not modelled	97.5	22	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structures of mycobacterium tuberculosis s-adenosyl-l-2 homocysteine hydrolase in ternary complex with substrate and3 inhibitors
47	<a href="#">d1jw9b_</a>	Alignment	not modelled	97.5	29	<b>Fold:</b> Activating enzymes of the ubiquitin-like proteins <b>Superfamily:</b> Activating enzymes of the ubiquitin-like proteins <b>Family:</b> Molybdenum cofactor biosynthesis protein MoeB
48	<a href="#">c3l4bG_</a>	Alignment	not modelled	97.4	17	<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
49	<a href="#">c3n58D_</a>	Alignment	not modelled	97.4	21	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structure of s-adenosyl-l-homocysteine hydrolase from brucella2 melitensis in ternary complex with nad and adenosine, orthorhombic3 form
50	<a href="#">c3gucB_</a>	Alignment	not modelled	97.4	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ubiquitin-like modifier-activating enzyme 5; <b>PDBTitle:</b> human ubiquitin-activating enzyme 5 in complex with amppnp
51	<a href="#">c3d64A_</a>	Alignment	not modelled	97.4	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
52	<a href="#">c3eywA_</a>	Alignment	not modelled	97.4	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
53	<a href="#">d1gpja2</a>	Alignment	not modelled	97.4	20	<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
54	<a href="#">c1zfnA</a>	Alignment	not modelled	97.4	29 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenyllyltransferase thif; <b>PDBTitle:</b> structural analysis of escherichia coli thif
55	<a href="#">c1v8bA</a>	Alignment	not modelled	97.3	18 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structure of a hydrolase
56	<a href="#">c3oneA</a>	Alignment	not modelled	97.3	20 <b>PDB header:</b> hydrolase/hydrolase substrate <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structure of lupinus luteus s-adenosyl-l-homocysteine2 hydrolase in complex with adenine
57	<a href="#">d1v8ba1</a>	Alignment	not modelled	97.3	17 <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
58	<a href="#">c3ic5A</a>	Alignment	not modelled	97.2	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.
59	<a href="#">d1j6ua1</a>	Alignment	not modelled	97.2	15 <b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
60	<a href="#">c2f00A</a>	Alignment	not modelled	97.1	22 <b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate--l-alanine ligase; <b>PDBTitle:</b> escherichia coli murc
61	<a href="#">c2axqA</a>	Alignment	not modelled	97.1	15 <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
62	<a href="#">d2hmva1</a>	Alignment	not modelled	97.1	14 <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
63	<a href="#">c1e5lA</a>	Alignment	not modelled	97.1	17 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine reductase; <b>PDBTitle:</b> apo saccharopine reductase from magnaporthe grisea
64	<a href="#">d1f0ya2</a>	Alignment	not modelled	97.1	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
65	<a href="#">d1gdha1</a>	Alignment	not modelled	97.1	12 <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
66	<a href="#">d1np3a2</a>	Alignment	not modelled	97.0	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
67	<a href="#">c3gznb</a>	Alignment	not modelled	97.0	12 <b>PDB header:</b> protein binding/ligase <b>Chain:</b> B: <b>PDB Molecule:</b> nedd8-activating enzyme e1 catalytic subunit; <b>PDBTitle:</b> structure of nedd8-activating enzyme in complex with nedd82 and mln4924
68	<a href="#">c3c85A</a>	Alignment	not modelled	97.0	16 <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
69	<a href="#">d1ygya1</a>	Alignment	not modelled	97.0	15 <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
70	<a href="#">c3uagA</a>	Alignment	not modelled	97.0	16 <b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (udp-n-acetylmuramoyl-l-alanine:d-alanine:d- <b>PDBTitle:</b> udp-n-acetylmuramoyl-l-alanine:d-glutamate ligase
71	<a href="#">c1y8qD</a>	Alignment	not modelled	97.0	16 <b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> ubiquitin-like 2 activating enzyme e1b; <b>PDBTitle:</b> sumo e1 activating enzyme sae1-sae2-mg-atp complex
72	<a href="#">c3hn7A</a>	Alignment	not modelled	97.0	15 <b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate-l-alanine ligase; <b>PDBTitle:</b> crystal structure of a murein peptide ligase mpl (psyc_0032) from2 psychrobacter arcticus 273-4 at 1.65 a resolution
73	<a href="#">c1wwkA</a>	Alignment	not modelled	96.9	15 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of phosphoglycerate dehydrogenase from pyrococcus2 horikoshii ot3
74	<a href="#">c3pgjB</a>	Alignment	not modelled	96.9	19 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> shikimate dehydrogenase; <b>PDBTitle:</b> 2.49 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae o1 biovar eltor str. n169613 in complex with shikimate
75	<a href="#">c3kydB</a>	Alignment	not modelled	96.9	15 <b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> sumo-activating enzyme subunit 2; <b>PDBTitle:</b> human sumo e1~sumo1-amp tetrahedral intermediate mimic
76	<a href="#">c2eezG</a>	Alignment	not modelled	96.9	17 <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
77	<a href="#">c2nvuB</a>	Alignment	not modelled	96.9	12 <b>PDB header:</b> protein turnover, ligase <b>Chain:</b> B: <b>PDB Molecule:</b> maltose binding protein/nedd8-activating enzyme <b>PDBTitle:</b> structure of appbp1-uba3~nedd8-nedd8-mgatp-ubc12(c111a), a2 trapped ubiquitin-like protein activation complex
78	<a href="#">d1id1a</a>	Alignment	not modelled	96.9	22 <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

79	<a href="#">d2naca1</a>	Alignment	not modelled	96.9	13	<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
80	<a href="#">c2hk8B_</a>	Alignment	not modelled	96.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> shikimate dehydrogenase; <b>PDBTitle:</b> crystal structure of shikimate dehydrogenase from aquifex2 aeolicus at 2.35 angstrom resolution
81	<a href="#">c1np3B_</a>	Alignment	not modelled	96.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ketol-acid reductoisomerase; <b>PDBTitle:</b> crystal structure of class i acetohydroxy acid isomeroreductase from2 pseudomonas aeruginosa
82	<a href="#">c1gdhA_</a>	Alignment	not modelled	96.8	12	<b>PDB header:</b> oxidoreductase(choh (d)-nad(p)+ (a)) <b>Chain:</b> A: <b>PDB Molecule:</b> d-glycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of a nad-dependent d-glycerate2 dehydrogenase at 2.4 angstroms resolution
83	<a href="#">c3h9gA_</a>	Alignment	not modelled	96.8	12	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> mccb protein; <b>PDBTitle:</b> crystal structure of e. coli mccb + mcca-n7isoasn
84	<a href="#">c2eggA_</a>	Alignment	not modelled	96.8	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> shikimate 5-dehydrogenase; <b>PDBTitle:</b> crystal structure of shikimate 5-dehydrogenase (aroe) from2 geobacillus kaustophilus
85	<a href="#">dlj4aa1</a>	Alignment	not modelled	96.7	15	<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
86	<a href="#">c2g76A_</a>	Alignment	not modelled	96.7	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of human 3-phosphoglycerate dehydrogenase
87	<a href="#">dl17da1</a>	Alignment	not modelled	96.7	11	<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
88	<a href="#">c2g5cD_</a>	Alignment	not modelled	96.7	13	<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
89	<a href="#">dlpjca1</a>	Alignment	not modelled	96.6	17	<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
90	<a href="#">c1nytC_</a>	Alignment	not modelled	96.6	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> shikimate 5-dehydrogenase; <b>PDBTitle:</b> shikimate dehydrogenase aroe complexed with nadp+
91	<a href="#">d2fy8a1</a>	Alignment	not modelled	96.6	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
92	<a href="#">dlmx3a1</a>	Alignment	not modelled	96.6	14	<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
93	<a href="#">c3pwzA_</a>	Alignment	not modelled	96.6	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> shikimate dehydrogenase 3; <b>PDBTitle:</b> crystal structure of an ael1 enzyme from pseudomonas putida
94	<a href="#">c3vh3A_</a>	Alignment	not modelled	96.6	18	<b>PDB header:</b> metal binding protein/protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-like modifier-activating enzyme atg7; <b>PDBTitle:</b> crystal structure of atg7ctd-atg8 complex
95	<a href="#">c1j4aA_</a>	Alignment	not modelled	96.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-lactate dehydrogenase; <b>PDBTitle:</b> insights into domain closure, substrate specificity and2 catalysis of d-lactate dehydrogenase from lactobacillus3 bulgaricus
96	<a href="#">c2f1kD_</a>	Alignment	not modelled	96.5	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> prephenate dehydrogenase; <b>PDBTitle:</b> crystal structure of synechocystis aroenate dehydrogenase
97	<a href="#">c2dbqA_</a>	Alignment	not modelled	96.5	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxylate reductase; <b>PDBTitle:</b> crystal structure of glyoxylate reductase (ph0597) from pyrococcus2 horikoshii ot3, complexed with nadp (i41)
98	<a href="#">dlnya1</a>	Alignment	not modelled	96.5	19	<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
99	<a href="#">d2f1ka2</a>	Alignment	not modelled	96.5	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
100	<a href="#">c3g0oA_</a>	Alignment	not modelled	96.5	20	<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
101	<a href="#">c3evtA_</a>	Alignment	not modelled	96.5	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of phosphoglycerate dehydrogenase from2 lactobacillus plantarum
102	<a href="#">dlvovb1</a>	Alignment	not modelled	96.5	11	<b>Fold:</b> Activating enzymes of the ubiquitin-like proteins <b>Superfamily:</b> Activating enzymes of the ubiquitin-like proteins <b>Family:</b> Ubiquitin activating enzymes (UBA)
103	<a href="#">c3d1lB_</a>	Alignment	not modelled	96.4	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
104	<a href="#">c3vh1A_</a>	Alignment	not modelled	96.4	16	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-like modifier-activating enzyme atg7; <b>PDBTitle:</b> crystal structure of saccharomyces cerevisiae atg7 (1-595)



105	<a href="#">c3b1fA_</a>	Alignment	not modelled	96.4	10	<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
106	<a href="#">c3cmmA_</a>	Alignment	not modelled	96.4	14	<b>PDB header:</b> ligase/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-activating enzyme e1 1; <b>PDBTitle:</b> crystal structure of the uba1-ubiquitin complex
107	<a href="#">c3hwrA_</a>	Alignment	not modelled	96.4	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydropantoate 2-reductase; <b>PDBTitle:</b> crystal structure of pane/apba family ketopantoate reductase2 (yp_299159.1) from ralstonia eutropha jmp134 at 2.15 a resolution
108	<a href="#">c3o8qB_</a>	Alignment	not modelled	96.4	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> shikimate 5-dehydrogenase i alpha; <b>PDBTitle:</b> 1.45 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae
109	<a href="#">c2pv7B_</a>	Alignment	not modelled	96.4	14	<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
110	<a href="#">c3cumA_</a>	Alignment	not modelled	96.3	19	<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
111	<a href="#">d1nvta1</a>	Alignment	not modelled	96.3	18	<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
112	<a href="#">c3oj0A_</a>	Alignment	not modelled	96.3	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna reductase; <b>PDBTitle:</b> crystal structure of glutamyl-trna reductase from thermoplasma2 volcanium (nucleotide binding domain)
113	<a href="#">c3n7uD_</a>	Alignment	not modelled	96.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> formate dehydrogenase; <b>PDBTitle:</b> nad-dependent formate dehydrogenase from higher-plant arabidopsis2 thaliana in complex with nad and azide
114	<a href="#">c1l7eC_</a>	Alignment	not modelled	96.3	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nicotinamide nucleotide transhydrogenase, <b>PDBTitle:</b> crystal structure of r. rubrum transhydrogenase domain i2 with bound nadh
115	<a href="#">d1leha1</a>	Alignment	not modelled	96.3	20	<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="#">d1txga2</a>	Alignment	not modelled	96.3	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
117	<a href="#">c3kboB_</a>	Alignment	not modelled	96.2	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxylate/hydroxypyruvate reductase a; <b>PDBTitle:</b> 2.14 angstrom crystal structure of putative oxidoreductase (ycdw) from2 salmonella typhimurium in complex with nadp
118	<a href="#">c3bazA_</a>	Alignment	not modelled	96.2	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxyphenylpyruvate reductase; <b>PDBTitle:</b> structure of hydroxyphenylpyruvate reductase from coleus blumei in2 complex with nadp+
119	<a href="#">d2gz1a1</a>	Alignment	not modelled	96.2	11	<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
120	<a href="#">c2nloA_</a>	Alignment	not modelled	96.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> shikimate dehydrogenase; <b>PDBTitle:</b> crystal structure of the quinate dehydrogenase from corynebacterium2 glutamicum