

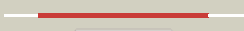





















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1q7ba_</a>	 Alignment		100.0	100	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
2	<a href="#">d1hdca_</a>	 Alignment		100.0	37	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
3	<a href="#">c3emkA_</a>	 Alignment		100.0	52	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose/ribitol dehydrogenase; <b>PDBTitle:</b> 2.5a crystal structure of glucose/ribitol dehydrogenase2 from brucella melitensis
4	<a href="#">d1k2wa_</a>	 Alignment		100.0	33	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
5	<a href="#">c3lf2B_</a>	 Alignment		100.0	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short chain oxidoreductase q9hya2; <b>PDBTitle:</b> nadph bound structure of the short chain oxidoreductase q9hya2 from2 pseudomonas aeruginosa pao1 containing an atypical catalytic center
6	<a href="#">c3rihB_</a>	 Alignment		100.0	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short chain dehydrogenase or reductase; <b>PDBTitle:</b> crystal structure of a putative short chain dehydrogenase or reductase2 from mycobacterium abscessus
7	<a href="#">c3ak4C_</a>	 Alignment		100.0	34	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nadh-dependent quinuclidinone reductase; <b>PDBTitle:</b> crystal structure of nadh-dependent quinuclidinone reductase from2 agrobacterium tumefaciens
8	<a href="#">c2pd6D_</a>	 Alignment		100.0	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> estradiol 17-beta-dehydrogenase 8; <b>PDBTitle:</b> structure of human hydroxysteroid dehydrogenase type 8, hsd17b8
9	<a href="#">c3cxtA_</a>	 Alignment		100.0	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dehydrogenase with different specificities; <b>PDBTitle:</b> quaternary complex structure of gluconate 5-dehydrogenase from2 streptococcus suis type 2
10	<a href="#">d1fmca_</a>	 Alignment		100.0	29	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
11	<a href="#">c2p68A_</a>	 Alignment		100.0	50	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] reductase; <b>PDBTitle:</b> crystal structure of aq_1716 from aquifex aeolicus vf5

12	<a href="#">d2ae2a_</a>	Alignment		100.0	31	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
13	<a href="#">d1ae1a_</a>	Alignment		100.0	31	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
14	<a href="#">c3svtA_</a>	Alignment		100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> short-chain type dehydrogenase/reductase; <b>PDBTitle:</b> structure of a short-chain type dehydrogenase/reductase from2 mycobacterium ulcerans
15	<a href="#">d1w6ua_</a>	Alignment		100.0	26	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
16	<a href="#">d1xhla_</a>	Alignment		100.0	24	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
17	<a href="#">c3pk0B_</a>	Alignment		100.0	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase sdr; <b>PDBTitle:</b> crystal structure of short-chain dehydrogenase/reductase sdr from2 mycobacterium smegmatis
18	<a href="#">c2c07A_</a>	Alignment		100.0	47	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-(acyl-carrier protein) reductase; <b>PDBTitle:</b> oxoacyl-acp reductase of plasmodium falciparum
19	<a href="#">d2c07a1</a>	Alignment		100.0	47	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
20	<a href="#">c3gvcB_</a>	Alignment		100.0	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable short-chain type <b>PDBTitle:</b> crystal structure of probable short-chain dehydrogenase-2 reductase from mycobacterium tuberculosis
21	<a href="#">c2uvdE_</a>	Alignment	not modelled	100.0	56	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> 3-oxoacyl-(acyl-carrier-protein) reductase; <b>PDBTitle:</b> the crystal structure of a 3-oxoacyl-(acyl carrier protein)2 reductase from bacillus anthracis (ba3989)
22	<a href="#">d1iy8a_</a>	Alignment	not modelled	100.0	30	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
23	<a href="#">c3toxG_</a>	Alignment	not modelled	100.0	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> short chain dehydrogenase; <b>PDBTitle:</b> crystal structure of a short chain dehydrogenase in complex with2 nad(p) from sinorhizobium meliloti 1021
24	<a href="#">c2zatC_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> dehydrogenase/reductase sdr family member 4; <b>PDBTitle:</b> crystal structure of a mammalian reductase
25	<a href="#">d1nffa_</a>	Alignment	not modelled	100.0	35	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
26	<a href="#">d1pr9a_</a>	Alignment	not modelled	100.0	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
27	<a href="#">c3nugA_</a>	Alignment	not modelled	100.0	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-(acyl-carrier protein) reductase; <b>PDBTitle:</b> crystal structure of wild type tetrameric pyridoxal 4-dehydrogenase2 from mesorhizobium loti
28	<a href="#">c3uf0A_</a>	Alignment	not modelled	100.0	35	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase sdr;

28	<a href="#">c3ur6A</a>	Alignment	not modelled	100.0	33	<b>PDBTitle:</b> crystal structure of a putative nad(p) dependent gluconate 5-2 dehydrogenase from beutenbergia cavernae(efi target efi-502044) with3 bound nadp (low occupancy)
29	<a href="#">c3gk3D</a>	Alignment	not modelled	100.0	44	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> acetoacetyl-coa reductase; <b>PDBTitle:</b> crystal structure of acetoacetyl-coa reductase from2 burkholderia pseudomallei 1710b
30	<a href="#">d1yxma1</a>	Alignment	not modelled	100.0	31	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
31	<a href="#">d1geea</a>	Alignment	not modelled	100.0	33	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
32	<a href="#">d1ydea1</a>	Alignment	not modelled	100.0	29	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
33	<a href="#">c3gr6A</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-[acyl-carrier-protein] reductase [nadh]; <b>PDBTitle:</b> crystal structure of the staphylococcus aureus enoyl-acyl2 carrier protein reductase (fabI) in complex with nadp and3 triclosan
34	<a href="#">c2cfcB</a>	Alignment	not modelled	100.0	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-(r)-hydroxypropyl-com dehydrogenase; <b>PDBTitle:</b> structural basis for stereo selectivity in the (r)- and2 (s)-hydroxypropylethane thiosulfonate dehydrogenases
35	<a href="#">d1h5qa</a>	Alignment	not modelled	100.0	28	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
36	<a href="#">c3k31B</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-(acyl-carrier-protein) reductase; <b>PDBTitle:</b> crystal structure of eonyl-(acyl-carrier-protein) reductase from2 anaplasma phagocytophilum in complex with nad at 1.9a resolution
37	<a href="#">d1ulsa</a>	Alignment	not modelled	100.0	39	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
38	<a href="#">d1zema1</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
39	<a href="#">d1bdba</a>	Alignment	not modelled	100.0	27	<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="#">c3ftpD</a>	Alignment	not modelled	100.0	60	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier protein] reductase; <b>PDBTitle:</b> crystal structure of 3-ketoacyl-(acyl-carrier-protein)2 reductase from burkholderia pseudomallei at 2.05 a3 resolution
41	<a href="#">d1xkqa</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
42	<a href="#">c3ai3A</a>	Alignment	not modelled	100.0	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh-sorbose reductase; <b>PDBTitle:</b> the crystal structure of l-sorbose reductase from gluconobacter2 frateurii complexed with nadph and l-sorbose
43	<a href="#">c2z1nA</a>	Alignment	not modelled	100.0	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dehydrogenase; <b>PDBTitle:</b> crystal structure of ape0912 from aeropyrum pernix k1
44	<a href="#">d2bgka1</a>	Alignment	not modelled	100.0	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
45	<a href="#">c2q2qG</a>	Alignment	not modelled	100.0	34	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> beta-d-hydroxybutyrate dehydrogenase; <b>PDBTitle:</b> structure of d-3-hydroxybutyrate dehydrogenase from pseudomonas putida
46	<a href="#">d2a4ka1</a>	Alignment	not modelled	100.0	32	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
47	<a href="#">c3imfA</a>	Alignment	not modelled	100.0	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> short chain dehydrogenase; <b>PDBTitle:</b> 1.99 angstrom resolution crystal structure of a short chain2 dehydrogenase from bacillus anthracis str. 'ames ancestor'
48	<a href="#">d1g0oa</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
49	<a href="#">c1w4zA</a>	Alignment	not modelled	100.0	40	<b>PDB header:</b> antibiotic biosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> ketoacyl reductase; <b>PDBTitle:</b> structure of actinorhodin polyketide (actiii) reductase
50	<a href="#">c2wdzD</a>	Alignment	not modelled	100.0	35	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase; <b>PDBTitle:</b> crystal structure of the short chain dehydrogenase2 galactitol-dehydrogenase (gatdh) of rhodobacter3 sphaeroides in complex with nad+ and 1,2-pentandiol
51	<a href="#">d1hxha</a>	Alignment	not modelled	100.0	30	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
52	<a href="#">c3f9iB</a>	Alignment	not modelled	100.0	41	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] reductase; <b>PDBTitle:</b> crystal structure of 3-ketoacyl-(acyl-carrier-protein) reductase2 rickettsia prowazekii
53	<a href="#">d2rhca1</a>	Alignment	not modelled	100.0	30	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains

						<b>Family:</b> Tyrosine-dependent oxidoreductases
54	<a href="#">c2b4qB_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> rhannolipids biosynthesis 3-oxoacyl-[acyl- <b>PDBTitle:</b> pseudomonas aeruginosa rhlg/nadp active-site complex
55	<a href="#">c2p91A_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-[acyl-carrier-protein] reductase [nadh]; <b>PDBTitle:</b> crystal structure of enoyl-[acyl-carrier-protein] reductase (nadh)2 from aquifex aeolicus vf5
56	<a href="#">c3v2gA_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] reductase; <b>PDBTitle:</b> crystal structure of a dehydrogenase/reductase from sinorhizobium2 meliloti 1021
57	<a href="#">c3oidA_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-[acyl-carrier-protein] reductase [nadph]; <b>PDBTitle:</b> crystal structure of enoyl-acp reductases iii (fabl) from b. subtilis2 (complex with nadp and tcl)
58	<a href="#">c3iccA_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative 3-oxoacyl-(acyl carrier protein) reductase; <b>PDBTitle:</b> crystal structure of a putative 3-oxoacyl-(acyl carrier protein)2 reductase from bacillus anthracis at 1.87 a resolution
59	<a href="#">c3ijrF_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> oxidoreductase, short chain dehydrogenase/reductase family; <b>PDBTitle:</b> 2.05 angstrom resolution crystal structure of a short chain2 dehydrogenase from bacillus anthracis str. 'ames ancestor' in complex3 with nad+
60	<a href="#">d2pd4a1</a>	Alignment	not modelled	100.0	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
61	<a href="#">c3grkE_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> enoyl-(acyl-carrier-protein) reductase (nadh); <b>PDBTitle:</b> crystal structure of short chain dehydrogenase reductase2 sdr glucose-ribitol dehydrogenase from brucella melitensis
62	<a href="#">c3itdA_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 17beta-hydroxysteroid dehydrogenase; <b>PDBTitle:</b> crystal structure of an inactive 17beta-hydroxysteroid dehydrogenase2 (y167f mutated form) from fungus cochliobolus lunatus
63	<a href="#">d2d1ya1</a>	Alignment	not modelled	100.0	36	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
64	<a href="#">d2ew8a1</a>	Alignment	not modelled	100.0	37	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
65	<a href="#">c3ezlA_</a>	Alignment	not modelled	100.0	44	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acetoacetyl-coa reductase; <b>PDBTitle:</b> crystal structure of acetylacetyl-coa reductase from2 burkholderia pseudomallei 1710b
66	<a href="#">c3lylB_</a>	Alignment	not modelled	100.0	59	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-oxoacyl-(acyl-carrier-protein) reductase; <b>PDBTitle:</b> structure of 3-oxoacyl-acylcarrier protein reductase, fabg2 from francisella tularensis
67	<a href="#">c3osuA_</a>	Alignment	not modelled	100.0	54	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] reductase; <b>PDBTitle:</b> crystal structure of the 3-oxoacyl-acyl carrier protein reductase,2 fabg, from staphylococcus aureus
68	<a href="#">d1o5ia_</a>	Alignment	not modelled	100.0	35	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
69	<a href="#">c3sjuA_</a>	Alignment	not modelled	100.0	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> keto reductase; <b>PDBTitle:</b> hedamycin polyketide ketoreductase bound to nadph
70	<a href="#">c3gdfA_</a>	Alignment	not modelled	100.0	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable nadp-dependent mannitol dehydrogenase; <b>PDBTitle:</b> crystal structure of the nadp-dependent mannitol dehydrogenase from2 cladospirum herbarum.
71	<a href="#">d1edoa_</a>	Alignment	not modelled	100.0	50	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
72	<a href="#">c3rkuC_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> oxidoreductase ymr226c; <b>PDBTitle:</b> substrate fingerprint and the structure of nadp+ dependent serine2 dehydrogenase from saccharomyces cerevisiae complexed with nadp+
73	<a href="#">d1ja9a_</a>	Alignment	not modelled	100.0	29	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
74	<a href="#">d1cyda_</a>	Alignment	not modelled	100.0	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
75	<a href="#">d1zk4a1</a>	Alignment	not modelled	100.0	30	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
76	<a href="#">c3o38D_</a>	Alignment	not modelled	100.0	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> short chain dehydrogenase; <b>PDBTitle:</b> crystal structure of a short chain dehydrogenase from

						mycobacterium2 smegmatis
77	<a href="#">c3uxyC_</a>	Alignment	not modelled	100.0	34	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase sdr; <b>PDBTitle:</b> the crystal structure of short chain dehydrogenase from rhodobacter2 sphaeroides
78	<a href="#">c3ppiA_</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxyacyl-coa dehydrogenase type-2; <b>PDBTitle:</b> crystal structure of 3-hydroxyacyl-coa dehydrogenase type-2 from2 mycobacterium avium
79	<a href="#">c3r3sD_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> structure of the ygha oxidoreductase from salmonella enterica
80	<a href="#">c3afnC_</a>	Alignment	not modelled	100.0	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> carbonyl reductase; <b>PDBTitle:</b> crystal structure of aldose reductase a1-r complexed with nadp
81	<a href="#">c3ek2D_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> enoyl-(acyl-carrier-protein) reductase (nahh); <b>PDBTitle:</b> crystal structure of enoyl-(acyl carrier protein) reductase2 from burkholderia pseudomallei 1719b
82	<a href="#">dlqsga_</a>	Alignment	not modelled	100.0	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
83	<a href="#">dlulua_</a>	Alignment	not modelled	100.0	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
84	<a href="#">dlvl8a_</a>	Alignment	not modelled	100.0	31	<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="#">c3n74A_</a>	Alignment	not modelled	100.0	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-ketoacyl-(acyl-carrier-protein) reductase; <b>PDBTitle:</b> crystal structure of 3-ketoacyl-(acyl-carrier-protein) reductase from2 brucella melitensis
86	<a href="#">dlgega_</a>	Alignment	not modelled	100.0	32	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
87	<a href="#">dle6wa_</a>	Alignment	not modelled	100.0	30	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
88	<a href="#">c3t7cC_</a>	Alignment	not modelled	100.0	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> carveol dehydrogenase; <b>PDBTitle:</b> crystal structure of carveol dehydrogenase from mycobacterium avium2 bound to nad
89	<a href="#">c3bmrA_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pteridine reductase; <b>PDBTitle:</b> structure of pteridine reductase 1 (ptr1) from trypanosoma2 brucei in ternary complex with cofactor (nadp+) and3 inhibitor (compound ax6)
90	<a href="#">c2qioA_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-(acyl-carrier-protein) reductase; <b>PDBTitle:</b> x-ray structure of enoyl-acyl carrier protein reductase from bacillus2 anthracis with triclosan
91	<a href="#">dlx1ta1</a>	Alignment	not modelled	100.0	35	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
92	<a href="#">dlspxa_</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
93	<a href="#">c2jyD_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> enoyl-[acyl-carrier-protein] reductase; <b>PDBTitle:</b> crystal structure of francisella tularensis enoyl reductase2 (ffabi) with bound nad
94	<a href="#">c3ctmH_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> carbonyl reductase; <b>PDBTitle:</b> crystal structure of a carbonyl reductase from candida2 parapsilosis with anti-prelog stereo-specificity
95	<a href="#">c3r1iB_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short-chain type dehydrogenase/reductase; <b>PDBTitle:</b> crystal structure of a short-chain type dehydrogenase/reductase from2 mycobacterium marinum
96	<a href="#">c3pgxB_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> carveol dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative carveol dehydrogenase from2 mycobacterium paratuberculosis bound to nicotinamide adenine3 dinucleotide
97	<a href="#">c2ph3B_</a>	Alignment	not modelled	100.0	47	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-oxoacyl-[acyl carrier protein] reductase; <b>PDBTitle:</b> crystal structure of 3-oxoacyl-[acyl carrier protein] reductase2 tha0415 from thermus thermophilus
98	<a href="#">c3uveC_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> carveol dehydrogenase ((+)-trans-carveol dehydrogenase); <b>PDBTitle:</b> crystal structure of carveol dehydrogenase ((+)-trans-carveol2 dehydrogenase) from mycobacterium avium
99	<a href="#">c2dteB_</a>	Alignment	not modelled	100.0	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glucose 1-dehydrogenase related protein; <b>PDBTitle:</b> structure of thermoplasma acidophilum aldohexose dehydrogenase (aldt)2 in complex with nadh
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier protein]



100	<a href="#">c3i4fD_</a>	Alignment	not modelled	100.0	33	reductase; <b>PDBTitle:</b> structure of putative 3-oxoacyl-reductase from bacillus thuringiensis
101	<a href="#">c3oecA_</a>	Alignment	not modelled	100.0	37	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> carveol dehydrogenase (mytha.01326.c, a0r518 homolog); <b>PDBTitle:</b> crystal structure of carveol dehydrogenase from mycobacterium2 thermoresistibile
102	<a href="#">c3v8bC_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative dehydrogenase, possibly 3-oxoacyl-[acyl-carrier <b>PDBTitle:</b> crystal structure of a 3-ketoacyl-acp reductase from sinorhizobium2 meliloti 1021
103	<a href="#">c3llsB_</a>	Alignment	not modelled	100.0	40	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-ketoacyl-(acyl-carrier-protein) reductase; <b>PDBTitle:</b> crystal structure of 3-ketoacyl-(acyl-carrier-protein) reductase from2 mycobacterium tuberculosis
104	<a href="#">d2ag5a1</a>	Alignment	not modelled	100.0	30	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
105	<a href="#">c2et6A_</a>	Alignment	not modelled	100.0	35	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> (3r)-hydroxyacyl-coa dehydrogenase; <b>PDBTitle:</b> (3r)-hydroxyacyl-coa dehydrogenase domain of candida tropicalis2 peroxisomal multifunctional enzyme type 2
106	<a href="#">c3v2hB_</a>	Alignment	not modelled	100.0	35	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> d-beta-hydroxybutyrate dehydrogenase; <b>PDBTitle:</b> the crystal structure of d-beta-hydroxybutyrate dehydrogenase from2 sinorhizobium meliloti
107	<a href="#">d1p33a_</a>	Alignment	not modelled	100.0	30	<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="#">c2qhxB_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> pteridine reductase 1; <b>PDBTitle:</b> structure of pteridine reductase from leishmania major2 complexed with a ligand
109	<a href="#">c3diiB_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase sdr; <b>PDBTitle:</b> crystal structure of a carbohydrate specific scor enzyme2 from clostridium thermocellum, ligand-free form
110	<a href="#">c2fwmX_</a>	Alignment	not modelled	100.0	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> X: <b>PDB Molecule:</b> 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase; <b>PDBTitle:</b> crystal structure of e. coli enta, a 2,3-dihydrodihydroxy benzoate2 dehydrogenase
111	<a href="#">d2gdza1</a>	Alignment	not modelled	100.0	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
112	<a href="#">c3un1D_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> probable oxidoreductase; <b>PDBTitle:</b> crystal structure of an oxidoreductase from sinorhizobium meliloti2 1021
113	<a href="#">d1uzma1</a>	Alignment	not modelled	100.0	42	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
114	<a href="#">d1mxha_</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
115	<a href="#">c2nm0B_</a>	Alignment	not modelled	100.0	43	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable 3-oxacyl-(acyl-carrier-protein) reductase; <b>PDBTitle:</b> crystal structure of sco1815: a beta-ketoacyl-acyl carrier protein2 reductase from streptomyces coelicolor a3(2)
116	<a href="#">c3e03C_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> short chain dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative dehydrogenase from2 xanthomonas campestris
117	<a href="#">c2hq1A_</a>	Alignment	not modelled	100.0	34	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose/ribitol dehydrogenase; <b>PDBTitle:</b> crystal structure of orf 1438 a putative glucose/ribitol2 dehydrogenase from clostridium thermocellum
118	<a href="#">c3s55F_</a>	Alignment	not modelled	100.0	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> putative short-chain dehydrogenase/reductase; <b>PDBTitle:</b> crystal structure of a putative short-chain dehydrogenase/reductase2 from mycobacterium abscessus bound to nad
119	<a href="#">c3t4xA_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, short chain dehydrogenase/reductase family; <b>PDBTitle:</b> short chain dehydrogenase/reductase family oxidoreductase from2 bacillus anthracis str. ames ancestor
120	<a href="#">d1uaya_</a>	Alignment	not modelled	100.0	30	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases