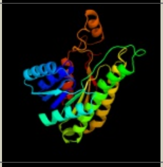
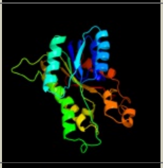
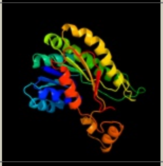
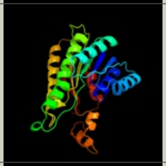
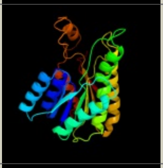
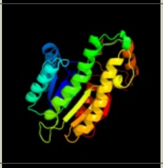
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P52037
Date	Thu Jan 5 12:04:56 GMT 2012
Unique Job ID	7837d2689ebf7dc4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3toxG_	Alignment		100.0	36	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**short chain dehydrogenase; **PDBTitle:** crystal structure of a short chain dehydrogenase in complex with2 nad(p) from sinorhizobium meliloti 1021
2	c3afnC_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**carbonyl reductase; **PDBTitle:** crystal structure of aldose reductase a1-r complexed with nadp
3	d1geea_	Alignment		100.0	30	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
4	d1xhla_	Alignment		100.0	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
5	c3iccA_	Alignment		100.0	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative 3-oxoacyl-(acyl carrier protein) reductase; **PDBTitle:** crystal structure of a putative 3-oxoacyl-(acyl carrier protein)2 reductase from bacillus anthracis at 1.87 a resolution
6	d1ja9a_	Alignment		100.0	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
7	c2cfcB_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**2-(r)-hydroxypropyl-com dehydrogenase; **PDBTitle:** structural basis for stereo selectivity in the (r)- and2 (s)-hydroxypropylethane thiosulfonate dehydrogenases
8	c3ijrF_	Alignment		100.0	34	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**oxidoreductase, short chain dehydrogenase/reductase family; **PDBTitle:** 2.05 angstrom resolution crystal structure of a short chain2 dehydrogenase from bacillus anthracis str. 'ames ancestor' in complex3 with nad+
9	c3svtA_	Alignment		100.0	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short-chain type dehydrogenase/reductase; **PDBTitle:** structure of a short-chain type dehydrogenase/reductase from2 mycobacterium ulcerans
10	c3rihB_	Alignment		100.0	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**short chain dehydrogenase or reductase; **PDBTitle:** crystal structure of a putative short chain dehydrogenase or reductase2 from mycobacterium abscessus
11	d1g0oa_	Alignment		100.0	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases

12	d1w6ua_	Alignment		100.0	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
13	d1fmca_	Alignment		100.0	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
14	d1iy8a_	Alignment		100.0	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
15	d2rhca1	Alignment		100.0	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
16	c3bmrA_	Alignment		100.0	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pteridine reductase; **PDBTitle:** structure of pteridine reductase 1 (ptr1) from trypanosoma2 brucei in ternary complex with cofactor (nadp+) and3 inhibitor (compound ax6)
17	c3sjuA_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**keto reductase; **PDBTitle:** hedamycin polyketide ketoreductase bound to nadph
18	c3itdA_	Alignment		100.0	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**17beta-hydroxysteroid dehydrogenase; **PDBTitle:** crystal structure of an inactive 17beta-hydroxysteroid dehydrogenase2 (y167f mutated form) from fungus cochliobolus lunatus
19	d2ae2a_	Alignment		100.0	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
20	c1w4zA_	Alignment		100.0	28	**PDB header:**antibiotic biosynthesis **Chain:** A: **PDB Molecule:**ketoacyl reductase; **PDBTitle:** structure of actinorhodin polyketide (actiii) reductase
21	c3ezlA_	Alignment	not modelled	100.0	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**acetoacetyl-coa reductase; **PDBTitle:** crystal structure of acetyacetyl-coa reductase from2 burkholderia pseudomallei 1710b
22	c2uvdE_	Alignment	not modelled	100.0	29	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**3-oxoacyl-(acyl-carrier-protein) reductase; **PDBTitle:** the crystal structure of a 3-oxoacyl-(acyl carrier protein)2 reductase from bacillus anthracis (ba3989)
23	d1yxma1	Alignment	not modelled	100.0	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
24	c2zatC_	Alignment	not modelled	100.0	27	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**dehydrogenase/reductase sdr family member 4; **PDBTitle:** crystal structure of a mammalian reductase
25	c3pk0B_	Alignment	not modelled	100.0	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**short-chain dehydrogenase/reductase sdr; **PDBTitle:** crystal structure of short-chain dehydrogenase/reductase sdr from2 mycobacterium smegmatis
26	c2qhxB_	Alignment	not modelled	100.0	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**pteridine reductase 1; **PDBTitle:** structure of pteridine reductase from leishmania major2 complexed with a ligand
27	c3lf2B_	Alignment	not modelled	100.0	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**short chain oxidoreductase q9hya2; **PDBTitle:** nadph bound structure of the short chain oxidoreductase q9hya2 from2 pseudomonas aeruginosa pao1 containing an atypical catalytic center
						Fold:NAD(P)-binding Rossmann-fold domains

28	d1xkqa_	Alignment	not modelled	100.0	23	**Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
29	d1edoa_	Alignment	not modelled	100.0	31	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
30	d1k2wa_	Alignment	not modelled	100.0	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
31	c3gk3D_	Alignment	not modelled	100.0	25	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**acetoacetyl-coa reductase; **PDBTitle:** crystal structure of acetoacetyl-coa reductase from2 burkholderia pseudomallei 1710b
32	d1zema1	Alignment	not modelled	100.0	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
33	c3v2gA_	Alignment	not modelled	100.0	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] reductase; **PDBTitle:** crystal structure of a dehydrogenase/reductase from sinorhizobium2 meliloti 1021
34	c3i4fD_	Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**3-oxoacyl-[acyl-carrier protein] reductase; **PDBTitle:** structure of putative 3-oxoacyl-reductase from bacillus thuringiensis
35	c3osuA_	Alignment	not modelled	100.0	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] reductase; **PDBTitle:** crystal structure of the 3-oxoacyl-acyl carrier protein reductase,2 fabg, from staphylococcus aureus
36	d1gega_	Alignment	not modelled	100.0	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
37	c3nugA_	Alignment	not modelled	100.0	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-oxoacyl-(acyl-carrier protein) reductase; **PDBTitle:** crystal structure of wild type tetrameric pyridoxal 4-dehydrogenase2 from mesorhizobium loti
38	d1ae1a_	Alignment	not modelled	100.0	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
39	c3oidA_	Alignment	not modelled	100.0	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-[acyl-carrier-protein] reductase [nadph]; **PDBTitle:** crystal structure of enoyl-acp reductases iii (fabl) from b. subtilis2 (complex with nadp and tcl)
40	d2bgka1	Alignment	not modelled	100.0	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
41	c3t7cC_	Alignment	not modelled	100.0	24	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**carveol dehydrogenase; **PDBTitle:** crystal structure of carveol dehydrogenase from mycobacterium avium2 bound to nad
42	c3cxtA_	Alignment	not modelled	100.0	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehydrogenase with different specificities; **PDBTitle:** quaternary complex structure of gluconate 5-dehydrogenase from2 streptococcus suis type 2
43	d2pd4a1	Alignment	not modelled	100.0	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
44	d1h5qa_	Alignment	not modelled	100.0	31	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
45	d1mxha_	Alignment	not modelled	100.0	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
46	c3gr6A_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-[acyl-carrier-protein] reductase [nadh]; **PDBTitle:** crystal structure of the staphylococcus aureus enoyl-acyl2 carrier protein reductase (fabi) in complex with nadp and3 triclosan
47	c3o38D_	Alignment	not modelled	100.0	24	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**short chain dehydrogenase; **PDBTitle:** crystal structure of a short chain dehydrogenase from mycobacterium2 smegmatis
48	c3r3sD_	Alignment	not modelled	100.0	37	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase; **PDBTitle:** structure of the ygha oxidoreductase from salmonella enterica
49	c2p68A_	Alignment	not modelled	100.0	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] reductase; **PDBTitle:** crystal structure of aq_1716 from aquifex aeolicus vf5
50	c3ai3A_	Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph-sorbose reductase; **PDBTitle:** the crystal structure of l-sorbose reductase from gluconobacter2 frateurii complexed with nadph and l-sorbose
51	c2pd6D_	Alignment	not modelled	100.0	29	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**estradiol 17-beta-dehydrogenase 8; **PDBTitle:** structure of human hydroxysteroid dehydrogenase type 8, hsd17b8
52	d1bdba_	Alignment	not modelled	100.0	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases

53	c3v8bC_	Alignment	not modelled	100.0	33	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative dehydrogenase, possibly 3-oxoacyl-[acyl-carrier **PDBTitle:** crystal structure of a 3-ketoacyl-acp reductase from sinorhizobium2 meliloti 1021
54	d1pr9a_	Alignment	not modelled	100.0	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
55	c3grkE_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**enoyl-(acyl-carrier-protein) reductase (nadh); **PDBTitle:** crystal structure of short chain dehydrogenase reductase2 sdr glucose-ribitol dehydrogenase from brucella melitensis
56	c3uf0A_	Alignment	not modelled	100.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short-chain dehydrogenase/reductase sdr; **PDBTitle:** crystal structure of a putative nad(p) dependent gluconate 5-2 dehydrogenase from beutenbergia cavernae(efi target efi-502044) with3 bound nadp (low occupancy)
57	d1x1ta1	Alignment	not modelled	100.0	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
58	d1q7ba_	Alignment	not modelled	100.0	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
59	c3k31B_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**enoyl-(acyl-carrier-protein) reductase; **PDBTitle:** crystal structure of eonyl-(acyl-carrier-protein) reductase from2 anaplasma phagocytophilum in complex with nad at 1.9a resolution
60	d1qsga_	Alignment	not modelled	100.0	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
61	c3ak4C_	Alignment	not modelled	100.0	28	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh-dependent quinuclidinone reductase; **PDBTitle:** crystal structure of nadh-dependent quinuclidinone reductase from2 agrobacterium tumefaciens
62	c2ph3B_	Alignment	not modelled	100.0	30	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-oxoacyl-[acyl carrier protein] reductase; **PDBTitle:** crystal structure of 3-oxoacyl-[acyl carrier protein] reductase2 ttha0415 from thermus thermophilus
63	c3imfA_	Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short chain dehydrogenase; **PDBTitle:** 1.99 angstrom resolution crystal structure of a short chain2 dehydrogenase from bacillus anthracis str. 'ames ancestor'
64	c2q2qG_	Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**beta-d-hydroxybutyrate dehydrogenase; **PDBTitle:** structure of d-3-hydroxybutyrate dehydrogenase from pseudomonas putida
65	c3v2hB_	Alignment	not modelled	100.0	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**d-beta-hydroxybutyrate dehydrogenase; **PDBTitle:** the crystal structure of d-beta-hydroxybutyrate dehydrogenase from2 sinorhizobium meliloti
66	d1hdca_	Alignment	not modelled	100.0	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
67	c2p91A_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-[acyl-carrier-protein] reductase [nadh]; **PDBTitle:** crystal structure of enoyl-[acyl-carrier-protein] reductase (nadh)2 from aquifex aeolicus vf5
68	d2c07a1	Alignment	not modelled	100.0	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
69	c2c07A_	Alignment	not modelled	100.0	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-oxoacyl-(acyl-carrier protein) reductase; **PDBTitle:** oxoacyl-acp reductase of plasmodium falciparum
70	c3ftpD_	Alignment	not modelled	100.0	31	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**3-oxoacyl-[acyl-carrier protein] reductase; **PDBTitle:** crystal structure of 3-ketoacyl-(acyl-carrier-protein)2 reductase from burkholderia pseudomallei at 2.05 a3 resolution
71	d1nffa_	Alignment	not modelled	100.0	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
72	c3gdfA_	Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable nadp-dependent mannitol dehydrogenase; **PDBTitle:** crystal structure of the nadp-dependent mannitol dehydrogenase from2 cladosporium herbarum.
73	d1o5ia_	Alignment	not modelled	100.0	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
74	c2b4qB_	Alignment	not modelled	100.0	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**rhamnolipids biosynthesis 3-oxoacyl-[acyl- **PDBTitle:** pseudomonas aeruginosa rhlg/nadp active-site complex
75	c2jjyD_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**enoyl-[acyl-carrier-protein] reductase; **PDBTitle:** crystal structure of francisella tularensis enoyl reductase2 (ftfabi) with bound nad
76	d1ydea1	Alignment	not modelled	100.0	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains

						Family: Tyrosine-dependent oxidoreductases
77	d1p33a_	Alignment	not modelled	100.0	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
78	c3uveC_	Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**carveol dehydrogenase ((+)-trans-carveol dehydrogenase); **PDBTitle:** crystal structure of carveol dehydrogenase ((+)-trans-carveol2 dehydrogenase) from mycobacterium avium
79	c2qioA_	Alignment	not modelled	100.0	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**enoyl-(acyl-carrier-protein) reductase; **PDBTitle:** x-ray structure of enoyl-acyl carrier protein reductase from bacillus2 anthracis with triclosan
80	c2z1nA_	Alignment	not modelled	100.0	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure of ape0912 from aeropyrum pernix k1
81	c3pgxB_	Alignment	not modelled	100.0	29	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**carveol dehydrogenase; **PDBTitle:** crystal structure of a putative carveol dehydrogenase from2 mycobacterium paratuberculosis bound to nicotinamide adenine3 dinucleotide
82	c3emkA_	Alignment	not modelled	100.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glucose/ribitol dehydrogenase; **PDBTitle:** 2.5a crystal structure of glucose/ribitol dehydrogenase2 from brucella melitensis
83	c3ppiA_	Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-hydroxyacyl-coa dehydrogenase type-2; **PDBTitle:** crystal structure of 3-hydroxyacyl-coa dehydrogenase type-2 from2 mycobacterium avium
84	c3ek2D_	Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**enoyl-(acyl-carrier-protein) reductase (nadh); **PDBTitle:** crystal structure of eonyl-(acyl carrier protein) reductase2 from burkholderia pseudomallei 1719b
85	d1zk4a1	Alignment	not modelled	100.0	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
86	d1vl8a_	Alignment	not modelled	100.0	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
87	d1ulua_	Alignment	not modelled	100.0	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
88	c3rkuC_	Alignment	not modelled	100.0	24	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**oxidoreductase ymr226c; **PDBTitle:** substrate fingerprint and the structure of nadp+ dependent serine2 dehydrogenase from saccharomyces cerevisiae complexed with nadp+
89	c3lylB_	Alignment	not modelled	100.0	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-oxoacyl-(acyl-carrier-protein) reductase; **PDBTitle:** structure of 3-oxoacyl-acylcarrier protein reductase, fabg2 from francisella tularensis
90	c3gvcB_	Alignment	not modelled	100.0	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable short-chain type **PDBTitle:** crystal structure of probable short-chain dehydrogenase-2 reductase from mycobacterium tuberculosis
91	d2ew8a1	Alignment	not modelled	100.0	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
92	d1ulsa_	Alignment	not modelled	100.0	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
93	d1xg5a_	Alignment	not modelled	100.0	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
94	c3sx2F_	Alignment	not modelled	100.0	25	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**putative 3-ketoacyl-(acyl-carrier-protein) reductase; **PDBTitle:** crystal structure of a putative 3-ketoacyl-(acyl-carrier-protein)2 reductase from mycobacterium paratuberculosis in complex with nad
95	c3r1iB_	Alignment	not modelled	100.0	31	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**short-chain type dehydrogenase/reductase; **PDBTitle:** crystal structure of a short-chain type dehydrogenase/reductase from2 mycobacterium marinum
96	c3uxyC_	Alignment	not modelled	100.0	28	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**short-chain dehydrogenase/reductase sdr; **PDBTitle:** the crystal structure of short chain dehydrogenase from rhodobacter2 sphaeroides
97	d2d1ya1	Alignment	not modelled	100.0	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
98	d1hxha_	Alignment	not modelled	100.0	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
99	c3oecA_	Alignment	not modelled	100.0	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**carveol dehydrogenase (mytha.01326.c, a0r518 homolog); **PDBTitle:** crystal structure of carveol dehydrogenase from mycobacterium2 thermoresistibile
						Fold:NAD(P)-binding Rossmann-fold domains

100	d1spxa_	Alignment	not modelled	100.0	24	**Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
101	c2wdzD_	Alignment	not modelled	100.0	27	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**short-chain dehydrogenase/reductase; **PDBTitle:** crystal structure of the short chain dehydrogenase2 galactitol-dehydrogenase (gatdh) of rhodobacter3 sphaeroides in complex with nad+ and 1,2-pentandiol
102	c3n74A_	Alignment	not modelled	100.0	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-ketoacyl-(acyl-carrier-protein) reductase; **PDBTitle:** crystal structure of 3-ketoacyl-(acyl-carrier-protein) reductase from2 brucella melitensis
103	d2a4ka1	Alignment	not modelled	100.0	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
104	d1cyda_	Alignment	not modelled	100.0	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
105	d1e6wa_	Alignment	not modelled	100.0	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
106	c3ctmH_	Alignment	not modelled	100.0	25	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**carbonyl reductase; **PDBTitle:** crystal structure of a carbonyl reductase from candida2 parapsilosis with anti-prelog stereo-specificity
107	c3f9iB_	Alignment	not modelled	100.0	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] reductase; **PDBTitle:** crystal structure of 3-ketoacyl-(acyl-carrier-protein) reductase2 rickettsia prowazekii
108	c3llsB_	Alignment	not modelled	100.0	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-ketoacyl-(acyl-carrier-protein) reductase; **PDBTitle:** crystal structure of 3-ketoacyl-(acyl-carrier-protein) reductase from2 mycobacterium tuberculosis
109	d1uh5a_	Alignment	not modelled	100.0	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
110	c3tl3A_	Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short-chain type dehydrogenase/reductase; **PDBTitle:** structure of a short-chain type dehydrogenase/reductase from2 mycobacterium ulcerans
111	d2h7ma1	Alignment	not modelled	100.0	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
112	c2ekqB_	Alignment	not modelled	100.0	32	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**2-deoxy-d-gluconate 3-dehydrogenase; **PDBTitle:** structure of tt0495 protein from thermus thermophilus
113	c3sc4A_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short chain dehydrogenase (a0qtm2 homolog); **PDBTitle:** crystal structure of a short chain dehydrogenase (a0qtm2 homolog)2 mycobacterium thermoresistibile
114	c2hq1A_	Alignment	not modelled	100.0	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glucose/ribitol dehydrogenase; **PDBTitle:** crystal structure of orf 1438 a putative glucose/ribitol2 dehydrogenase from clostridium thermocellum
115	d1uaya_	Alignment	not modelled	100.0	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
116	c3a28H_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**l-2.3-butanediol dehydrogenase; **PDBTitle:** crystal structure of l-2,3-butanediol dehydrogenase
117	d2ag5a1	Alignment	not modelled	100.0	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
118	c2nm0B_	Alignment	not modelled	100.0	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable 3-oxacyl-(acyl-carrier-protein) reductase; **PDBTitle:** crystal structure of sco1815: a beta-ketoacyl-acyl carrier protein2 reductase from streptomyces coelicolor a3(2)
119	c3diiB_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**short-chain dehydrogenase/reductase sdr; **PDBTitle:** crystal structure of a carbohydrate specific scor enzyme2 from clostridium thermocellum, ligand-free form
120	c2dteB_	Alignment	not modelled	100.0	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glucose 1-dehydrogenase related protein; **PDBTitle:** structure of thermoplasma acidophilum aldohexose dehydrogenase (aldt)2 in complex with nadh