Phyre^2

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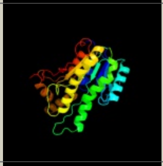
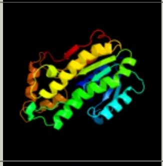
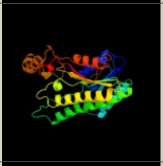
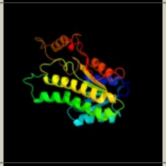
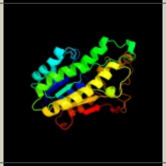
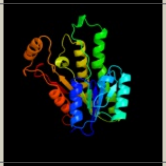
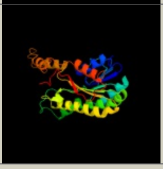
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3lf2B_	Alignment		100.0	30	**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
2	d1k2wa_	Alignment		100.0	30	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
3	c3cxtA_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehydrogenase with different specificities; **PDBTitle:** quaternary complex structure of gluconate 5-dehydrogenase from2 streptococcus suis type 2
4	c3rihB_	Alignment		100.0	32	**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
5	c3ak4C_	Alignment		100.0	31	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh-dependent quinuclidinone reductase; **PDBTitle:** crystal structure of nadh-dependent quinuclidinone reductase from2 agrobacterium tumefaciens
6	d1xhla_	Alignment		100.0	34	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
7	d2ae2a_	Alignment		100.0	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
8	d1hdca_	Alignment		100.0	32	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
9	c3k31B_	Alignment		100.0	23	**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
10	d1iy8a_	Alignment		100.0	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
11	c3itdA_	Alignment		100.0	23	**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

12	c3ai3A_	Alignment		100.0	28	**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
13	c3svtA_	Alignment		100.0	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short-chain type dehydrogenase/reductase; **PDBTitle:** structure of a short-chain type dehydrogenase/reductase from2 mycobacterium ulcerans
14	d1geea_	Alignment		100.0	30	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
15	d1g0oa_	Alignment		100.0	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
16	c3r3sD_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase; **PDBTitle:** structure of the ygha oxidoreductase from salmonella enterica
17	c3grkE_	Alignment		100.0	26	**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
18	d1w6ua_	Alignment		100.0	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
19	c2q2qG_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**beta-d-hydroxybutyrate dehydrogenase; **PDBTitle:** structure of d-3-hydroxybutyrate dehydrogenase from pseudomonas putida
20	d1ydea1	Alignment		100.0	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
21	d1fmca_	Alignment	not modelled	100.0	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
22	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
23	c3gk3D_	Alignment	not modelled	100.0	29	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**acetoacetyl-coa reductase; **PDBTitle:** crystal structure of acetoacetyl-coa reductase from2 burkholderia pseudomallei 1710b
24	c3uxyC_	Alignment	not modelled	100.0	34	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**short-chain dehydrogenase/reductase sdr; **PDBTitle:** the crystal structure of short chain dehydrogenase from rhodobacter2 sphaeroides
25	d1q7ba_	Alignment	not modelled	100.0	34	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
26	c3ijrF_	Alignment	not modelled	100.0	25	**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+
27	c2dteB_	Alignment	not modelled	100.0	32	**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
						Fold:NAD(P)-binding Rossmann-fold domains

28	d1ae1a_	Alignment	not modelled	100.0	30	**Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
29	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
30	c3iccA_	Alignment	not modelled	100.0	22	**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
31	d1yxma1	Alignment	not modelled	100.0	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
32	c3emkA_	Alignment	not modelled	100.0	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glucose/ribitol dehydrogenase; **PDBTitle:** 2.5a crystal structure of glucose/ribitol dehydrogenase2 from brucella melitensis
33	c2c07A_	Alignment	not modelled	100.0	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-oxoacyl-(acyl-carrier protein) reductase; **PDBTitle:** oxoacyl-acp reductase of plasmodium falciparum
34	d2c07a1	Alignment	not modelled	100.0	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
35	d1xkqa_	Alignment	not modelled	100.0	30	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
36	c3pk0B_	Alignment	not modelled	100.0	30	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**short-chain dehydrogenase/reductase sdr; **PDBTitle:** crystal structure of short-chain dehydrogenase/reductase sdr from2 mycobacterium smegmatis
37	c2p68A_	Alignment	not modelled	100.0	34	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] reductase; **PDBTitle:** crystal structure of aq_1716 from aquifex aeolicus vf5
38	d2pd4a1	Alignment	not modelled	100.0	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
39	d1qsga_	Alignment	not modelled	100.0	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
40	c2cfcB_	Alignment	not modelled	100.0	32	**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
41	d2rhca1	Alignment	not modelled	100.0	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
42	d1nffa_	Alignment	not modelled	100.0	32	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
43	c3toxG_	Alignment	not modelled	100.0	30	**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
44	c2uvdE_	Alignment	not modelled	100.0	31	**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)
45	c1w4zA_	Alignment	not modelled	100.0	26	**PDB header:**antibiotic biosynthesis **Chain:** A: **PDB Molecule:**ketoacyl reductase; **PDBTitle:** structure of actinorhodin polyketide (actiii) reductase
46	c3gr6A_	Alignment	not modelled	100.0	18	**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	c3gvcB_	Alignment	not modelled	100.0	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable short-chain type **PDBTitle:** crystal structure of probable short-chain dehydrogenase-2 reductase from mycobacterium tuberculosis
48	d1ulua_	Alignment	not modelled	100.0	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
49	d1ulsa_	Alignment	not modelled	100.0	36	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
50	d1pr9a_	Alignment	not modelled	100.0	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
51	d1ja9a_	Alignment	not modelled	100.0	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
52	c2zatC_	Alignment	not modelled	100.0	26	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**dehydrogenase/reductase sdr family member 4; **PDBTitle:** crystal structure of a mammalian reductase
53	c3uveC_	Alignment	not modelled	100.0	24	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**carveol dehydrogenase ((+)-trans-carveol dehydrogenase);

						PDBTitle: crystal structure of carveol dehydrogenase ((+)-trans-carveol2 dehydrogenase) from mycobacterium avium
54	c3uf0A_	Alignment	not modelled	100.0	35	**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)
55	c3ftpD_	Alignment	not modelled	100.0	32	**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
56	c3oidA_	Alignment	not modelled	100.0	26	**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)
57	c3gdfA_	Alignment	not modelled	100.0	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable nadp-dependent mannitol dehydrogenase; **PDBTitle:** crystal structure of the nadp-dependent mannitol dehydrogenase from2 cladosporium herbarum.
58	d2ew8a1	Alignment	not modelled	100.0	30	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
59	c2fwmX_	Alignment	not modelled	100.0	100	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase; **PDBTitle:** crystal structure of e. coli enta, a 2,3-dihydrodihydroxy benzoate2 dehydrogenase
60	c3pgxB_	Alignment	not modelled	100.0	27	**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
61	d1h5qa_	Alignment	not modelled	100.0	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
62	c3imfA_	Alignment	not modelled	100.0	26	**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'
63	c3ezlA_	Alignment	not modelled	100.0	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**acetoacetyl-coa reductase; **PDBTitle:** crystal structure of acetyacetyl-coa reductase from2 burkholderia pseudomallei 1710b
64	c2z1nA_	Alignment	not modelled	100.0	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure of ape0912 from aeropyrum pernix k1
65	c3ek2D_	Alignment	not modelled	100.0	24	**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
66	c3nugA_	Alignment	not modelled	100.0	27	**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
67	c3sjuA_	Alignment	not modelled	100.0	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**keto reductase; **PDBTitle:** hedamycin polyketide ketoreductase bound to nadph
68	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
69	d2d1ya1	Alignment	not modelled	100.0	35	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
70	c2qioA_	Alignment	not modelled	100.0	21	**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
71	d1gega_	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	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
73	c3v2gA_	Alignment	not modelled	100.0	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] reductase; **PDBTitle:** crystal structure of a dehydrogenase/reductase from sinorhizobium2 meliloti 1021
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	23	**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	d2bgka1	Alignment	not modelled	100.0	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
77	c3o38D_	Alignment	not modelled	100.0	33	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**short chain dehydrogenase;

77	c3o38D_	Alignment	not modelled	100.0	33	**PDBTitle:** crystal structure of a short chain dehydrogenase from mycobacterium2 smegmatis
78	c3oecA_	Alignment	not modelled	100.0	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**carveol dehydrogenase (mytha.01326.c, a0r518 homolog); **PDBTitle:** crystal structure of carveol dehydrogenase from mycobacterium2 thermoresistibile
79	c2pd6D_	Alignment	not modelled	100.0	28	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**estradiol 17-beta-dehydrogenase 8; **PDBTitle:** structure of human hydroxysteroid dehydrogenase type 8, hsd17b8
80	c3afnC_	Alignment	not modelled	100.0	28	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**carbonyl reductase; **PDBTitle:** crystal structure of aldose reductase a1-r complexed with nadp
81	c3lylB_	Alignment	not modelled	100.0	31	**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
82	c2p91A_	Alignment	not modelled	100.0	23	**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
83	c3bmrA_	Alignment	not modelled	100.0	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pteridine reductase; **PDBTitle:** crystal structure of pteridine reductase 1 (ptr1) from trypanosoma2 brucei in ternary complex with cofactor (nadp+) and3 inhibitor (compound ax6)
84	c3llsB_	Alignment	not modelled	100.0	29	**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
85	d1x1ta1	Alignment	not modelled	100.0	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
86	d1zk4a1	Alignment	not modelled	100.0	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
87	d1vl8a_	Alignment	not modelled	100.0	30	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
88	d2a4ka1	Alignment	not modelled	100.0	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
89	c3ppiA_	Alignment	not modelled	100.0	20	**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
90	d1hxha_	Alignment	not modelled	100.0	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
91	c3r1iB_	Alignment	not modelled	100.0	36	**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
92	d1edoa_	Alignment	not modelled	100.0	33	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
93	c3un1D_	Alignment	not modelled	100.0	27	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**probable oxidoreductase; **PDBTitle:** crystal structure of an oxidoreductase from sinorhizobium meliloti2 1021
94	c3ctmH_	Alignment	not modelled	100.0	26	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**carbonyl reductase; **PDBTitle:** crystal structure of a carbonyl reductase from candida2 parapsilosis with anti-prelog stereo-specificity
95	c3osuA_	Alignment	not modelled	100.0	35	**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
96	c2wdzD_	Alignment	not modelled	100.0	32	**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
97	d1cyda_	Alignment	not modelled	100.0	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
98	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
99	c3rkuC_	Alignment	not modelled	100.0	27	**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+
100	c2et6A_	Alignment	not modelled	100.0	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**(3r)-hydroxyacyl-coa dehydrogenase; **PDBTitle:** (3r)-hydroxyacyl-coa dehydrogenase domain of candida tropicalis2 peroxisomal multifunctional enzyme type 2
						PDB header:oxidoreductase

101	c3n74A_	Alignment	not modelled	100.0	30	**Chain:** A: **PDB Molecule:**3-ketoacyl-(acyl-carrier-protein) reductase; **PDBTitle:** crystal structure of 3-ketoacyl-(acyl-carrier-protein) reductase from2 brucella melitensis
102	c2nm0B_	Alignment	not modelled	100.0	35	**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)
103	c3sx2F_	Alignment	not modelled	100.0	23	**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
104	d1uaya_	Alignment	not modelled	100.0	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
105	c2ph3B_	Alignment	not modelled	100.0	31	**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
106	c3pxxE_	Alignment	not modelled	100.0	26	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**carveol dehydrogenase; **PDBTitle:** crystal structure of carveol dehydrogenase from mycobacterium avium2 bound to nicotinamide adenine dinucleotide
107	d2ag5a1	Alignment	not modelled	100.0	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
108	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
109	c3sc4A_	Alignment	not modelled	100.0	19	**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
110	c3i4fD_	Alignment	not modelled	100.0	24	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**3-oxoacyl-[acyl-carrier protein] reductase; **PDBTitle:** structure of putative 3-oxoacyl-reductase from bacillus thuringiensis
111	c3e03C_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**short chain dehydrogenase; **PDBTitle:** crystal structure of a putative dehydrogenase from2 xanthomonas campestris
112	c3f9iB_	Alignment	not modelled	100.0	24	**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
113	d1spxa_	Alignment	not modelled	100.0	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
114	c3v2hB_	Alignment	not modelled	100.0	30	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**d-beta-hydroxybutyrate dehydrogenase; **PDBTitle:** the crystal structure of d-beta-hydroxybutyrate dehydrogenase from2 sinorhizobium meliloti
115	c3s55F_	Alignment	not modelled	100.0	26	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**putative short-chain dehydrogenase/reductase; **PDBTitle:** crystal structure of a putative short-chain dehydrogenase/reductase2 from mycobacterium abscessus bound to nad
116	c2ntnB_	Alignment	not modelled	100.0	31	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] reductase; **PDBTitle:** crystal structure of maba-c60v/g139a/s144l
117	c2qhxB_	Alignment	not modelled	100.0	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**pteridine reductase 1; **PDBTitle:** structure of pteridine reductase from leishmania major2 complexed with a ligand
118	d1uzma1	Alignment	not modelled	100.0	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
119	d1p33a_	Alignment	not modelled	100.0	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
120	d1gz6a_	Alignment	not modelled	100.0	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases