
























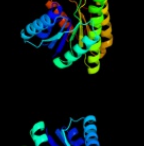
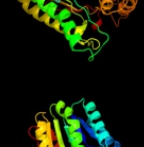
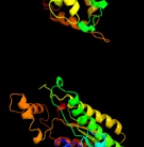


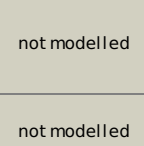


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3sjua_	 Alignment		100.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: keto reductase; PDBTitle: hedamycin polyketide ketoreductase bound to nadph
2	d2rhca1	 Alignment		100.0	29	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
3	c3lf2B_	 Alignment		100.0	21	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
4	dliy8a_	 Alignment		100.0	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
5	c1w4za_	 Alignment		100.0	24	PDB header: antibiotic biosynthesis Chain: A: PDB Molecule: ketoacyl reductase; PDBTitle: structure of actinorhodin polyketide (actiii) reductase
6	d1gega_	 Alignment		100.0	31	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
7	d1k2wa_	 Alignment		100.0	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
8	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
9	c3svtA_	 Alignment		100.0	26	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	c2cfcB_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-(r)-hydroxypropyl-com dehydrogenase; PDBTitle: structural basis for stereo selectivity in the (r)- and 2 (s)-hydroxypropylethane thiosulfonate dehydrogenases
11	c3rihB_	 Alignment		100.0	23	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

12	dlyxma1	Alignment		100.0	24 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
13	dlgeea_	Alignment		100.0	26 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
14	dlzema1	Alignment		100.0	25 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
15	dlw6ua_	Alignment		100.0	20 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
16	dlxhla_	Alignment		100.0	14 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
17	d2ae2a_	Alignment		100.0	19 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
18	dlh5qa_	Alignment		100.0	24 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
19	dlg0oa_	Alignment		100.0	24 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
20	c3cxtA_	Alignment		100.0	24 PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase with different specificities; PDBTitle: quaternary complex structure of gluconate 5-dehydrogenase from2 streptococcus suis type 2
21	c3pk0B_	Alignment	not modelled	100.0	23 PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: crystal structure of short-chain dehydrogenase/reductase sdr from2 mycobacterium smegmatis
22	dlae1a_	Alignment	not modelled	100.0	22 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
23	c3toxG_	Alignment	not modelled	100.0	22 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
24	c3itdA_	Alignment	not modelled	100.0	25 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
25	dlfmca_	Alignment	not modelled	100.0	28 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
26	c3ai3A_	Alignment	not modelled	100.0	21 PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-sorbose reductase; PDBTitle: the crystal structure of l-sorbose reductase from gluconobacter2 frateurii complexed with nadph and l-sorbose
27	c2zatC_	Alignment	not modelled	100.0	22 PDB header: oxidoreductase Chain: C: PDB Molecule: dehydrogenase/reductase sdr family member 4; PDBTitle: crystal structure of a mammalian reductase
28	dlxkqa_	Alignment	not modelled	100.0	20 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases

29	dlja9a_	Alignment	not modelled	100.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
30	d2bgka1	Alignment	not modelled	100.0	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
31	c3nugA_	Alignment	not modelled	100.0	31	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
32	c3gk3D_	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: D: PDB Molecule: acetoacetyl-coa reductase; PDBTitle: crystal structure of acetoacetyl-coa reductase from2 burkholderia pseudomallei 1710b
33	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
34	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
35	c3imfA_	Alignment	not modelled	100.0	24	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'
36	c3gvcB_	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: B: PDB Molecule: probable short-chain type PDBTitle: crystal structure of probable short-chain dehydrogenase-2 reductase from mycobacterium tuberculosis
37	c3pgxB_	Alignment	not modelled	100.0	26	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
38	c2q2qG_	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: G: PDB Molecule: beta-d-hydroxybutyrate dehydrogenase; PDBTitle: structure of d-3-hydroxybutyrate dehydrogenase from pseudomonas putida
39	d1q7ba_	Alignment	not modelled	100.0	29	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
40	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
41	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
42	c3iccA_	Alignment	not modelled	100.0	24	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
43	c3gr6A_	Alignment	not modelled	100.0	15	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
44	d1pr9a_	Alignment	not modelled	100.0	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
45	c3ijrF_	Alignment	not modelled	100.0	20	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+
46	c3o38D_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: D: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase from mycobacterium2 smegmatis
47	c2pd6D_	Alignment	not modelled	100.0	31	PDB header: oxidoreductase Chain: D: PDB Molecule: estradiol 17-beta-dehydrogenase 8; PDBTitle: structure of human hydroxysteroid dehydrogenase type 8, hsd17b8
48	c3k31B_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: enoyl-(acyl-carrier-protein) reductase; PDBTitle: crystal structure of enoyl-(acyl-carrier-protein) reductase from2 anaplasma phagocytophilum in complex with nad at 1.9a resolution
49	c3ezlA_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: acetoacetyl-coa reductase; PDBTitle: crystal structure of acetyacetyl-coa reductase from2 burkholderia pseudomallei 1710b
50	d1ydea1	Alignment	not modelled	100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
51	d1zk4a1	Alignment	not modelled	100.0	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
52	d2pd4a1	Alignment	not modelled	100.0	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
						PDB header: oxidoreductase

53	c2p68A	Alignment	not modelled	100.0	33	Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: crystal structure of aq_1716 from aquifex aeolicus vf5
54	c3rkuC	Alignment	not modelled	100.0	16	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+
55	c3r3sD	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase; PDBTitle: structure of the ygha oxidoreductase from salmonella enterica
56	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)
57	dlx1ta1	Alignment	not modelled	100.0	31	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
58	c3oidA	Alignment	not modelled	100.0	23	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)
59	c3uf0A	Alignment	not modelled	100.0	24	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)
60	c3bmrA	Alignment	not modelled	100.0	22	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)
61	c3ftpD	Alignment	not modelled	100.0	29	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
62	dlledoa	Alignment	not modelled	100.0	31	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
63	c3grkE	Alignment	not modelled	100.0	16	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
64	c2z1nA	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase; PDBTitle: crystal structure of ape0912 from aeropyrum pernix k1
65	c2qioA	Alignment	not modelled	100.0	18	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
66	c3uveC	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: C: PDB Molecule: carveol dehydrogenase ((+)-trans-carveol dehydrogenase); PDBTitle: crystal structure of carveol dehydrogenase ((+)-trans-carveol2 dehydrogenase) from mycobacterium avium
67	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
68	c3v8bC	Alignment	not modelled	100.0	22	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
69	c2p91A	Alignment	not modelled	100.0	16	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
70	c2wdzD	Alignment	not modelled	100.0	22	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
71	c3ek2D	Alignment	not modelled	100.0	17	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
72	dlvl8a	Alignment	not modelled	100.0	30	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
73	dlqsga	Alignment	not modelled	100.0	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
74	c3oecA	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: carveol dehydrogenase (mytha.01326.c, a0r518 homolog); PDBTitle: crystal structure of carveol dehydrogenase from mycobacterium2 thermoresistibile
						PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein]

75	c3osuA_	Alignment	not modelled	100.0	33	reductase; PDBTitle: crystal structure of the 3-oxoacyl-acyl carrier protein reductase,2 fabg, from staphylococcus aureus 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 PDB header: oxidoreductase Chain: D: PDB Molecule: 3-oxoacyl-[acyl-carrier protein] reductase; PDBTitle: structure of putative 3-oxoacyl-reductase from bacillus thuringiensis
76	c2ph3B_	Alignment	not modelled	100.0	30	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: crystal structure of a dehydrogenase/reductase from sinorhizobium2 meliloti 1021
77	c3i4fD_	Alignment	not modelled	100.0	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
78	d1hxha_	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
79	c3v2gA_	Alignment	not modelled	100.0	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
80	d1nffa_	Alignment	not modelled	100.0	35	PDB header: oxidoreductase Chain: C: PDB Molecule: carboxyl reductase; PDBTitle: crystal structure of aldose reductase a1-r complexed with nadp
81	d1mxha_	Alignment	not modelled	100.0	22	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	c3lylB_	Alignment	not modelled	100.0	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
83	d1o5ia_	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: B: PDB Molecule: rhamnolipids biosynthesis 3-oxoacyl-[acyl- PDBTitle: pseudomonas aeruginosa rhlg/nadp active-site complex
84	c2b4qB_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: C: PDB Molecule: carboxyl reductase; PDBTitle: crystal structure of aldose reductase a1-r complexed with nadp
85	c3afnC_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: pteridine reductase 1; PDBTitle: structure of pteridine reductase from leishmania major2 complexed with a ligand
86	c2qhxB_	Alignment	not modelled	100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
87	d1bdba_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: C: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: the crystal structure of short chain dehydrogenase from rhodobacter2 sphaeroides
88	c3uxyC_	Alignment	not modelled	100.0	27	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
89	c3r1iB_	Alignment	not modelled	100.0	30	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
90	d1ulsa_	Alignment	not modelled	100.0	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
91	d1ulua_	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
92	c3v2hB_	Alignment	not modelled	100.0	32	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
93	c3n74A_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: H: PDB Molecule: l-2,3-butanediol dehydrogenase; PDBTitle: crystal structure of l-2,3-butanediol dehydrogenase
94	c3a28H_	Alignment	not modelled	100.0	29	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
95	d2ew8a1	Alignment	not modelled	100.0	30	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
96	c3ppiA_	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: probable nadp-dependent mannitol dehydrogenase; PDBTitle: crystal structure of the nadp-dependent mannitol dehydrogenase from2 cladosporium herbarum.
97	c3gdfA_	Alignment	not modelled	100.0	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
98	d1p33a_	Alignment	not modelled	100.0	27	Fold: NAD(P)-binding Rossmann-fold domains

99	d2d1ya1	Alignment	not modelled	100.0	29	Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
100	c2dteB	Alignment	not modelled	100.0	24	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
101	c2jjyD	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: D: PDB Molecule: enoyl-[acyl-carrier-protein] reductase; PDBTitle: crystal structure of francisella tularensis enoyl reductase2 (ffabi) with bound nad
102	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
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	d2ag5a1	Alignment	not modelled	100.0	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
105	d2h7ma1	Alignment	not modelled	100.0	9	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
106	d1uh5a	Alignment	not modelled	100.0	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
107	c2ekqB	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-deoxy-d-gluconate 3-dehydrogenase; PDBTitle: structure of tt0495 protein from thermus thermophilus
108	c3ctmH	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: H: PDB Molecule: carbonyl reductase; PDBTitle: crystal structure of a carbonyl reductase from candida2 parapsilosis with anti-prelog stereo-specificity
109	c2et6A	Alignment	not modelled	100.0	26	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
110	d1e6wa	Alignment	not modelled	100.0	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
111	c2nm0B	Alignment	not modelled	100.0	28	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)
112	d2a4ka1	Alignment	not modelled	100.0	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
113	c3pxxE	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: E: PDB Molecule: carveol dehydrogenase; PDBTitle: crystal structure of carveol dehydrogenase from mycobacterium avium2 bound to nicotinamide adenine dinucleotide
114	d2gdza1	Alignment	not modelled	100.0	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
115	d1spxa	Alignment	not modelled	100.0	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
116	d1xg5a	Alignment	not modelled	100.0	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
117	c3t4xA	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase family; PDBTitle: short chain dehydrogenase/reductase family oxidoreductase from2 bacillus anthracis str. ames ancestor
118	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
119	c3diiB	Alignment	not modelled	100.0	27	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	d1uaya	Alignment	not modelled	100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases