

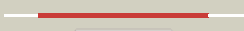

























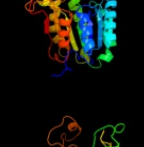
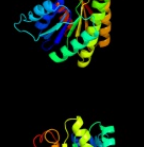
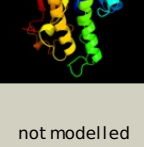


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dliy8a_	 Alignment		100.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
2	c3lf2B_	 Alignment		100.0	22	PDB header: oxidoreductase 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
3	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
4	dlw6ua_	 Alignment		100.0	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
5	d1xhla_	 Alignment		100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
6	dlyxma1	 Alignment		100.0	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
7	d2ae2a_	 Alignment		100.0	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
8	dlae1a_	 Alignment		100.0	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
9	c3o38D_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: D: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase from mycobacterium2 smegmatis
10	d2bgka1	 Alignment		100.0	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
11	d1xkqa_	 Alignment		100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases

12	dlgeea_	Alignment		100.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
13	dlnfba_	Alignment		100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
14	c2zatC_	Alignment		100.0	26	PDB header: oxidoreductase Chain: C: PDB Molecule: dehydrogenase/reductase sdr family member 4; PDBTitle: crystal structure of a mammalian reductase
15	c3rihB_	Alignment		100.0	26	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
16	c3cxtA_	Alignment		100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase with different specificities; PDBTitle: quaternary complex structure of gluconate 5-dehydrogenase from2 streptococcus suis type 2
17	c3nugA_	Alignment		100.0	22	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
18	dlfmca_	Alignment		100.0	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
19	dlzema1	Alignment		100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
20	c2cfcB_	Alignment		100.0	22	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
21	c3k31B_	Alignment	not modelled	100.0	16	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
22	dlhdca_	Alignment	not modelled	100.0	25	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	24	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	c3r3sD_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase; PDBTitle: structure of the ygha oxidoreductase from salmonella enterica
25	c3ijrF_	Alignment	not modelled	100.0	19	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+
26	c3gvcB_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: probable short-chain type PDBTitle: crystal structure of probable short-chain dehydrogenase-2 reductase from mycobacterium tuberculosis
27	dlpr9a_	Alignment	not modelled	100.0	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
						Fold: NAD(P)-binding Rossmann-fold domains

28	dlg0oa_	Alignment	not modelled	100.0	20	Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
29	c3t7cC_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: C: PDB Molecule: carveol dehydrogenase; PDBTitle: crystal structure of carveol dehydrogenase from mycobacterium avium2 bound to nad
30	c3imfA_	Alignment	not modelled	100.0	20	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'
31	c2jijD_	Alignment	not modelled	100.0	12	PDB header: oxidoreductase Chain: D: PDB Molecule: enoyl-[acyl-carrier-protein] reductase; PDBTitle: crystal structure of francisella tularensis enoyl reductase2 (ftfab1) with bound nad
32	dlzk4a1	Alignment	not modelled	100.0	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
33	c1w4zA_	Alignment	not modelled	100.0	22	PDB header: antibiotic biosynthesis Chain: A: PDB Molecule: ketoacyl reductase; PDBTitle: structure of actinorhodin polyketide (actiii) reductase
34	c3itdA_	Alignment	not modelled	100.0	16	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
35	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
36	d2rhca1	Alignment	not modelled	100.0	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
37	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
38	c3pk0B_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: crystal structure of short-chain dehydrogenase/reductase sdr from2 mycobacterium smegmatis
39	c2z1nA_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase; PDBTitle: crystal structure of ape0912 from aeropyrum pernix k1
40	dlk2wa_	Alignment	not modelled	100.0	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
41	c3ak4C_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh-dependent quinuclidinone reductase; PDBTitle: crystal structure of nadh-dependent quinuclidinone reductase from2 agrobacterium tumefaciens
42	d2c07a1	Alignment	not modelled	100.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
43	c2c07A_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-(acyl-carrier protein) reductase; PDBTitle: oxoacyl-acyl reductase of plasmodium falciparum
44	c2pd6D_	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: D: PDB Molecule: estradiol 17-beta-dehydrogenase 8; PDBTitle: structure of human hydroxysteroid dehydrogenase type 8, hsd17b8
45	dlx1ta1	Alignment	not modelled	100.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
46	dlq7ba_	Alignment	not modelled	100.0	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
47	c3uveC_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: C: PDB Molecule: carveol dehydrogenase ((+)-trans-carveol dehydrogenase); PDBTitle: crystal structure of carveol dehydrogenase ((+)-trans-carveol2 dehydrogenase) from mycobacterium avium
48	c3emkA_	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: glucose/ribitol dehydrogenase; PDBTitle: 2.5a crystal structure of glucose/ribitol dehydrogenase2 from brucella melitensis
49	c3ek2D_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: D: PDB Molecule: enoyl-(acyl-carrier-protein) reductase (nadh); PDBTitle: crystal structure of enoyl-(acyl carrier protein) reductase2 from burkholderia pseudomallei 1719b
50	dlhxha_	Alignment	not modelled	100.0	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
51	d2pd4a1	Alignment	not modelled	100.0	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
52	c3rkuC_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: C: PDB Molecule: oxi doreductase ymr226c; PDBTitle: substrate fingerprint and the structure of nadp+ dependent serine2 dehydrogenase from saccharomyces cerevisiae complexed with nadp+

53	c3grkE_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: E: PDB Molecule: enoyl-(acyl-carrier-protein) reductase (nahh); PDBTitle: crystal structure of short chain dehydrogenase reductase2 sdr glucose-ribitol dehydrogenase from brucella melitensis
54	d1ydea1	Alignment	not modelled	100.0	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
55	c2p91A_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nahh]; PDBTitle: crystal structure of enoyl-[acyl-carrier-protein] reductase (nahh)2 from aquifex aeolicus vf5
56	d2ew8a1	Alignment	not modelled	100.0	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
57	d1lulua_	Alignment	not modelled	100.0	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
58	d1bdba_	Alignment	not modelled	100.0	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
59	c3uf0A_	Alignment	not modelled	100.0	30	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	c3ftpD_	Alignment	not modelled	100.0	26	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
61	c3gr6A_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nahh]; PDBTitle: crystal structure of the staphylococcus aureus enoyl-acyl2 carrier protein reductase (fabI) in complex with nadp and3 triclosan
62	c3sjuA_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: keto reductase; PDBTitle: hedamycin polyketide ketoreductase bound to nadph
63	c3oecA_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: carveol dehydrogenase (mytha.01326.c, a0r518 homolog); PDBTitle: crystal structure of carveol dehydrogenase from mycobacterium2 thermoresistibile
64	d1ja9a_	Alignment	not modelled	100.0	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
65	c3i1jB_	Alignment	not modelled	100.0	48	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, short chain PDBTitle: structure of a putative short chain dehydrogenase from2 pseudomonas syringae
66	c3pgxB_	Alignment	not modelled	100.0	25	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
67	d2d1ya1	Alignment	not modelled	100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
68	c3v2gA_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: crystal structure of a dehydrogenase/reductase from sinorhizobium2 meliloti 1021
69	c3r1iB_	Alignment	not modelled	100.0	21	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
70	d1gega_	Alignment	not modelled	100.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
71	d1ulsa_	Alignment	not modelled	100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
72	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
73	c2uvdE_	Alignment	not modelled	100.0	25	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)
74	d1h5qa_	Alignment	not modelled	100.0	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
75	c3gk3D_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: D: PDB Molecule: acetoacetyl-coa reductase; PDBTitle: crystal structure of acetoacetyl-coa reductase from2 burkholderia pseudomallei 1710b
						PDB header: oxidoreductase

76	c2p68A	Alignment	not modelled	100.0	26	Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: crystal structure of aq_1716 from aquifex aeolicus vf5
77	d1qsga	Alignment	not modelled	100.0	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
78	c3bmrA	Alignment	not modelled	100.0	15	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)
79	d1spxa	Alignment	not modelled	100.0	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
80	d1o5ia	Alignment	not modelled	100.0	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
81	d1xg5a	Alignment	not modelled	100.0	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
82	c3n74A	Alignment	not modelled	100.0	19	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
83	c3f5sA	Alignment	not modelled	100.0	99	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase; PDBTitle: crystal structure of putative short chain dehydrogenase from shigella2 flexneri 2a str. 301
84	c2qioA	Alignment	not modelled	100.0	17	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
85	c3lylB	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
86	c3afnC	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: C: PDB Molecule: carbonyl reductase; PDBTitle: crystal structure of aldose reductase a1-r complexed with nadp
87	d1vl8a	Alignment	not modelled	100.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
88	c2b4qB	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: B: PDB Molecule: rhannolipids biosynthesis 3-oxoacyl-[acyl- PDBTitle: pseudomonas aeruginosa rhlg/nadp active-site complex
89	c3i4fD	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-oxoacyl-[acyl-carrier protein] reductase; PDBTitle: structure of putative 3-oxoacyl-reductase from bacillus thuringiensis
90	c3gdfA	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: probable nadp-dependent mannitol dehydrogenase; PDBTitle: crystal structure of the nadp-dependent mannitol dehydrogenase from2 cladosprium herbarum.
91	d2a4ka1	Alignment	not modelled	100.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
92	c3v2hB	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: B: PDB Molecule: d-beta-hydroxybutyrate dehydrogenase; PDBTitle: the crystal structure of d-beta-hydroxybutyrate dehydrogenase from2 sinorhizobium meliloti
93	c3ppiA	Alignment	not modelled	100.0	17	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
94	c3uxyC	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: C: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: the crystal structure of short chain dehydrogenase from rhodobacter2 sphaeroides
95	c3sx2F	Alignment	not modelled	100.0	22	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
96	d1e6wa	Alignment	not modelled	100.0	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
97	c2ph3B	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-oxoacyl-[acyl carrier protein] reductase; PDBTitle: crystal structure of 3-oxoacyl-[acyl carrier protein] reductase2 tha0415 from thermus thermophilus
98	d1cyda	Alignment	not modelled	100.0	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
99	c3diiB	Alignment	not modelled	100.0	21	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 PDB header: oxidoreductase Chain: B: PDB Molecule: pteridine reductase 1; PDBTitle: structure of pteridine reductase from leishmania major2 complexed with a ligand
100	c2qhxB_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nadh]; PDBTitle: crystal structure of enoyl-acp reductases iii (fabl) from b. subtilis2 (complex with nadp and tcl)
101	c3oidA_	Alignment	not modelled	100.0	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
102	d1mxha_	Alignment	not modelled	100.0	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
103	d1p33a_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: acetoacetyl-coa reductase; PDBTitle: crystal structure of acetylacetyl-coa reductase from2 burkholderia pseudomallei 1710b
104	c3ezlA_	Alignment	not modelled	100.0	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
105	d1ledoa_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: D: PDB Molecule: short-chain dehydrogenase/reductase; PDBTitle: crystal structure of the short chain dehydrogenase2 galactitol-dehydrogenase (gathd) of rhodobacter3 sphaeroides in complex with nad+ and 1,2-pentandiol
106	c2wdzD_	Alignment	not modelled	100.0	20	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
107	c3sc4A_	Alignment	not modelled	100.0	12	PDB header: oxidoreductase Chain: B: PDB Molecule: glucose 1-dehydrogenase related protein; PDBTitle: structure of thermoplasma acidophilum aldohexose dehydrogenase (aldt2) in complex with nadh
108	c2dteB_	Alignment	not modelled	100.0	23	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
109	c3t4xA_	Alignment	not modelled	100.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
110	d2h7ma1	Alignment	not modelled	100.0	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
111	d2ag5a1	Alignment	not modelled	100.0	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
112	d2gdza1	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: C: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a putative dehydrogenase from2 xanthomonas campestris
113	c3e03C_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: H: PDB Molecule: carbonyl reductase; PDBTitle: crystal structure of a carbonyl reductase from candida2 parapsilosis with anti-prelog stereo-specificity
114	c3ctmH_	Alignment	not modelled	100.0	17	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)
115	c2nm0B_	Alignment	not modelled	100.0	25	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
116	c3f9iB_	Alignment	not modelled	100.0	20	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
117	c3osuA_	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
118	c3llsB_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-acyl carrier protein reductase; PDBTitle: crystal structure of short-chain dehydrogenase from2 oenococcus oeni psu-1
119	c3ksuA_	Alignment	not modelled	100.0	18	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
120	c2fwmX_	Alignment	not modelled	100.0	24	