







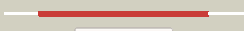
























#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dlgeea_	 Alignment		100.0	32	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
2	c3rihB_	 Alignment		100.0	37	PDB header: oxidoreductase Chain: B: PDB Molecule: short chain dehydrogenase or reductase; PDBTitle: crystal structure of a putative short chain dehydrogenase or reductase2 from mycobacterium abscessus
3	c3toxG_	 Alignment		100.0	33	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
4	dliy8a_	 Alignment		100.0	31	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
5	c3pk0B_	 Alignment		100.0	37	PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: crystal structure of short-chain dehydrogenase/reductase sdr from2 mycobacterium smegmatis
6	d1xhla_	 Alignment		100.0	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
7	c3itdA_	 Alignment		100.0	28	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
8	d2ae2a_	 Alignment		100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
9	d2pd4a1	 Alignment		100.0	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
10	c3lf2B_	 Alignment		100.0	29	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
11	d1g0oa_	 Alignment		100.0	29	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases

12	d1yxma1	Alignment		100.0	29	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
13	d2rhca1	Alignment		100.0	30	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
14	d1k2wa_	Alignment		100.0	31	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
15	c3k31B_	Alignment		100.0	25	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
16	c3grkE_	Alignment		100.0	27	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
17	c3t7cC_	Alignment		100.0	31	PDB header: oxidoreductase Chain: C: PDB Molecule: carveol dehydrogenase; PDBTitle: crystal structure of carveol dehydrogenase from mycobacterium avium2 bound to nad
18	d1ja9a_	Alignment		100.0	31	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
19	c1w4zA_	Alignment		100.0	31	PDB header: antibiotic biosynthesis Chain: A: PDB Molecule: ketoacyl reductase; PDBTitle: structure of actinorhodin polyketide (actiii) reductase
20	d1zema1	Alignment		100.0	30	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
21	c3cxtA_	Alignment	not modelled	100.0	34	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase with different specificities; PDBTitle: quaternary complex structure of gluconate 5-dehydrogenase from2 streptococcus suis type 2
22	d1qsga_	Alignment	not modelled	100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
23	c3ak4C_	Alignment	not modelled	100.0	32	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh-dependent quinuclidinone reductase; PDBTitle: crystal structure of nadh-dependent quinuclidinone reductase from2 agrobacterium tumefaciens
24	c3svtA_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: short-chain type dehydrogenase/reductase; PDBTitle: structure of a short-chain type dehydrogenase/reductase from2 mycobacterium ulcerans
25	d2bgka1	Alignment	not modelled	100.0	31	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
26	c2zatC_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: C: PDB Molecule: dehydrogenase/reductase sdr family member 4; PDBTitle: crystal structure of a mammalian reductase
27	d1w6ua_	Alignment	not modelled	100.0	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
28	c2a2aG_	Alignment	not modelled	100.0	36	PDB header: oxidoreductase Chain: G: PDB Molecule: beta-d-hydroxybutyrate dehydrogenase;

28	c2q2q9_	Alignment	not modelled	100.0	30	PDBTitle: structure of d-3-hydroxybutyrate dehydrogenase from pseudomonas putida PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase; PDBTitle: structure of the ygha oxidoreductase from salmonella enterica
29	c3r3sD_	Alignment	not modelled	100.0	26	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
30	c2p91A_	Alignment	not modelled	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
31	c3iccA_	Alignment	not modelled	100.0	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
32	d1ulua_	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'
33	c3imfA_	Alignment	not modelled	100.0	33	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
34	d1xkqa_	Alignment	not modelled	100.0	32	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
35	d1gega_	Alignment	not modelled	100.0	34	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
36	d1fmca_	Alignment	not modelled	100.0	33	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
37	d1hdca_	Alignment	not modelled	100.0	33	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
38	c3ek2D_	Alignment	not modelled	100.0	26	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
39	c3sjuA_	Alignment	not modelled	100.0	33	PDB header: oxidoreductase Chain: A: PDB Molecule: keto reductase; PDBTitle: hedamycin polyketide ketoreductase bound to nadph
40	c2qioA_	Alignment	not modelled	100.0	27	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
41	d1ae1a_	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	c3ai3A_	Alignment	not modelled	100.0	31	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
43	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
44	d2c07a1	Alignment	not modelled	100.0	35	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
45	c2c07A_	Alignment	not modelled	100.0	35	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-(acyl-carrier protein) reductase; PDBTitle: oxoacyl-acp reductase of plasmodium falciparum
46	c2uvdE_	Alignment	not modelled	100.0	39	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)
47	c3ijrF_	Alignment	not modelled	100.0	27	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+
48	c3afnC_	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: C: PDB Molecule: carbonyl reductase; PDBTitle: crystal structure of aldose reductase a1-r complexed with nadp
49	c3nugA_	Alignment	not modelled	100.0	32	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
50	c3pgxB_	Alignment	not modelled	100.0	35	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
51	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)
						PDB header: oxidoreductase Chain: A: PDB Molecule: carveol dehydrogenase (mytha.01326.c,

52	c3oecA	Alignment	not modelled	100.0	35	a0r518 homolog); PDBTitle: crystal structure of carveol dehydrogenase from mycobacterium2 thermoresistibile
53	c2dteB	Alignment	not modelled	100.0	36	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
54	c3o38D	Alignment	not modelled	100.0	36	PDB header: oxidoreductase Chain: D: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase from mycobacterium2 smegmatis
55	c2b4qB	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: B: PDB Molecule: rhamnolipids biosynthesis 3-oxoacyl-[acyl- PDBTitle: pseudomonas aeruginosa rhlg/nadp active-site complex
56	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
57	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
58	c3uveC	Alignment	not modelled	100.0	35	PDB header: oxidoreductase Chain: C: PDB Molecule: carveol dehydrogenase ((+)-trans-carveol dehydrogenase); PDBTitle: crystal structure of carveol dehydrogenase ((+)-trans-carveol2 dehydrogenase) from mycobacterium avium
59	c3gvcB	Alignment	not modelled	100.0	37	PDB header: oxidoreductase Chain: B: PDB Molecule: probable short-chain type PDBTitle: crystal structure of probable short-chain dehydrogenase-2 reductase from mycobacterium tuberculosis
60	c2cfcB	Alignment	not modelled	100.0	37	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
61	c2pd6D	Alignment	not modelled	100.0	32	PDB header: oxidoreductase Chain: D: PDB Molecule: estradiol 17-beta-dehydrogenase 8; PDBTitle: structure of human hydroxysteroid dehydrogenase type 8, hsd17b8
62	d1q7ba	Alignment	not modelled	100.0	36	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
63	c3gk3D	Alignment	not modelled	100.0	34	PDB header: oxidoreductase Chain: D: PDB Molecule: acetoacetyl-coa reductase; PDBTitle: crystal structure of acetoacetyl-coa reductase from2 burkholderia pseudomallei 1710b
64	c2p68A	Alignment	not modelled	100.0	37	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: crystal structure of aq_1716 from aquifex aeolicus vf5
65	c3emkA	Alignment	not modelled	100.0	37	PDB header: oxidoreductase Chain: A: PDB Molecule: glucose/ribitol dehydrogenase; PDBTitle: 2.5a crystal structure of glucose/ribitol dehydrogenase2 from brucella melitensis
66	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
67	c3ezlA	Alignment	not modelled	100.0	37	PDB header: oxidoreductase Chain: A: PDB Molecule: acetoacetyl-coa reductase; PDBTitle: crystal structure of acetyacetyl-coa reductase from2 burkholderia pseudomallei 1710b
68	d1pr9a	Alignment	not modelled	100.0	30	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
69	c3ftpD	Alignment	not modelled	100.0	36	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
70	c3oidA	Alignment	not modelled	100.0	27	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)
71	c2jyyD	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 (ffabi) with bound nad
72	c3ppiA	Alignment	not modelled	100.0	27	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
73	d1nffa	Alignment	not modelled	100.0	38	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
74	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
75	c3gr6A	Alignment	not modelled	100.0	23	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 (fabl) in complex with nadp and3 triclosan

76	c3rkuC	Alignment	not modelled	100.0	22	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+
77	dlhxa	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	d2ew8a1	Alignment	not modelled	100.0	38	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
79	c3bmrA	Alignment	not modelled	100.0	24	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)
80	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
81	dlulsa	Alignment	not modelled	100.0	38	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
82	c3lylB	Alignment	not modelled	100.0	33	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
83	dlledoa	Alignment	not modelled	100.0	33	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
84	dlvl8a	Alignment	not modelled	100.0	34	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
85	c2z1nA	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase; PDBTitle: crystal structure of ape0912 from aeropyrum pernix k1
86	c3uxyC	Alignment	not modelled	100.0	32	PDB header: oxidoreductase Chain: C: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: the crystal structure of short chain dehydrogenase from rhodobacter2 sphaeroides
87	d2ag5a1	Alignment	not modelled	100.0	38	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
88	c3gdfA	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: probable nadp-dependent mannitol dehydrogenase; PDBTitle: crystal structure of the nadp-dependent mannitol dehydrogenase from2 cladospirum herbarum.
89	c3i4fD	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-oxoacyl-[acyl-carrier protein] reductase; PDBTitle: structure of putative 3-oxoacyl-reductase from bacillus thuringiensis
90	c3ctmH	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: H: PDB Molecule: carbonyl reductase; PDBTitle: crystal structure of a carbonyl reductase from candida2 parapsilosis with anti-prelog stereo-specificity
91	c3osuA	Alignment	not modelled	100.0	36	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
92	dlx1ta1	Alignment	not modelled	100.0	38	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
93	dl05ia	Alignment	not modelled	100.0	30	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
94	c3pxxE	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: E: PDB Molecule: carveol dehydrogenase; PDBTitle: crystal structure of carveol dehydrogenase from mycobacterium avium2 bound to nicotinamide adenine dinucleotide
95	c3sx2F	Alignment	not modelled	100.0	30	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	dlbdba	Alignment	not modelled	100.0	22	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	36	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	c3sc4A	Alignment	not modelled	100.0	30	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
99	c2wdzD	Alignment	not modelled	100.0	29	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
100	dlspxa_	Alignment	not modelled	100.0	31	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
101	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
102	c3llsB_	Alignment	not modelled	100.0	33	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
103	d1cyda_	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	d1e6wa_	Alignment	not modelled	100.0	33	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
105	c2et6A_	Alignment	not modelled	100.0	34	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
106	c3un1D_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: D: PDB Molecule: probable oxidoreductase; PDBTitle: crystal structure of an oxidoreductase from sinorhizobium meliloti2 1021
107	c3v2hB_	Alignment	not modelled	100.0	37	PDB header: oxidoreductase Chain: B: PDB Molecule: d-beta-hydroxybutyrate dehydrogenase; PDBTitle: the crystal structure of d-beta-hydroxybutyrate dehydrogenase from2 sinorhizobium meliloti
108	d1mxha_	Alignment	not modelled	100.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
109	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
110	c2qhxB_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: B: PDB Molecule: pteridine reductase 1; PDBTitle: structure of pteridine reductase from leishmania major2 complexed with a ligand
111	c3e03C_	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: C: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a putative dehydrogenase from2 xanthomonas campestris
112	d1p33a_	Alignment	not modelled	100.0	29	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
113	c3f9iB_	Alignment	not modelled	100.0	34	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
114	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
115	d2gdza1	Alignment	not modelled	100.0	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
116	c3qljB_	Alignment	not modelled	100.0	32	PDB header: oxidoreductase Chain: B: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase from mycobacterium2 avium
117	d1uh5a_	Alignment	not modelled	100.0	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
118	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
119	d1uaya_	Alignment	not modelled	100.0	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
120	c2o2sA_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: enoyl-acyl carrier reductase; PDBTitle: the structure of t. gondii enoyl acyl carrier protein reductase in2 complex with nad and triclosan