





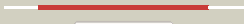


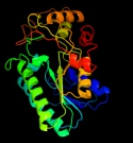





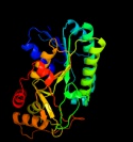





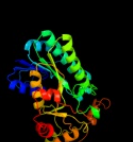


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1z45A_	 Alignment		100.0	18	PDB header: isomerase Chain: A: PDB Molecule: gal10 bifunctional protein; PDBTitle: crystal structure of the gal10 fusion protein galactose2 mutarotase/udp-galactose 4-epimerase from saccharomyces3 cerevisiae complexed with nad, udp-glucose, and galactose
2	c1z7eC_	 Alignment		100.0	14	PDB header: hydrolase Chain: C: PDB Molecule: protein arna; PDBTitle: crystal structure of full length arna
3	c3oh8A_	 Alignment		100.0	31	PDB header: isomerase Chain: A: PDB Molecule: nucleoside-diphosphate sugar epimerase (sula family); PDBTitle: crystal structure of the nucleoside-diphosphate sugar epimerase from2 corynebacterium glutamicum. northeast structural genomics consortium3 target cgr91
4	d1i24a_	 Alignment		100.0	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
5	d2b69a1	 Alignment		100.0	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
6	c2b69A_	 Alignment		100.0	18	PDB header: lyase Chain: A: PDB Molecule: udp-glucuronate decarboxylase 1; PDBTitle: crystal structure of human udp-glucuronic acid decarboxylase
7	c3m2pD_	 Alignment		100.0	16	PDB header: isomerase Chain: D: PDB Molecule: udp-n-acetylglucosamine 4-epimerase; PDBTitle: the crystal structure of udp-n-acetylglucosamine 4-epimerase2 from bacillus cereus
8	d1oc2a_	 Alignment		100.0	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
9	c3iusB_	 Alignment		100.0	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized conserved protein; PDBTitle: the structure of a functionally unknown conserved protein2 from silicibacter pomeroyi dss
10	c2p5uC_	 Alignment		100.0	19	PDB header: isomerase Chain: C: PDB Molecule: udp-glucose 4-epimerase; PDBTitle: crystal structure of thermus thermophilus hb8 udp-glucose 4-2 epimerase complex with nad
11	c2pk3B_	 Alignment		100.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: gdp-6-deoxy-d-lyxo-4-hexulose reductase; PDBTitle: crystal structure of a gdp-4-keto-6-deoxy-d-mannose reductase

12	c2z1mC_	Alignment		100.0	11	PDB header: lyase Chain: C: PDB Molecule: gdp-d-mannose dehydratase; PDBTitle: crystal structure of gdp-d-mannose dehydratase from aquifex aeolicus2 vf5
13	d1r6da_	Alignment		100.0	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
14	d1vl0a_	Alignment		100.0	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
15	c2hrzA_	Alignment		100.0	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: nucleoside-diphosphate-sugar epimerase; PDBTitle: the crystal structure of the nucleoside-diphosphate-sugar epimerase2 from agrobacterium tumefaciens
16	c2c20D_	Alignment		100.0	15	PDB header: isomerase Chain: D: PDB Molecule: udp-glucose 4-epimerase; PDBTitle: crystal structure of udp-glucose 4-epimerase
17	c1n7gB_	Alignment		100.0	13	PDB header: lyase Chain: B: PDB Molecule: gdp-d-mannose-4,6-dehydratase; PDBTitle: crystal structure of the gdp-mannose 4,6-dehydratase2 ternary complex with nadph and gdp-rhamnose.
18	c3sc6F_	Alignment		100.0	13	PDB header: oxidoreductase Chain: F: PDB Molecule: ddtp-4-dehydrorhamnose reductase; PDBTitle: 2.65 angstrom resolution crystal structure of dtdp-4-dehydrorhamnose2 reductase (rfbd) from bacillus anthracis str. ames in complex with3 nadp
19	c3icpA_	Alignment		100.0	18	PDB header: isomerase Chain: A: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: crystal structure of udp-galactose 4-epimerase
20	d2c5aa1	Alignment		100.0	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
21	c2x4gA_	Alignment	not modelled	100.0	18	PDB header: isomerase Chain: A: PDB Molecule: nucleoside-diphosphate-sugar epimerase; PDBTitle: crystal structure of pa4631, a nucleoside-diphosphate-sugar2 epimerase from pseudomonas aeruginosa
22	d1db3a_	Alignment	not modelled	100.0	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
23	c2hunB_	Alignment	not modelled	100.0	15	PDB header: lyase Chain: B: PDB Molecule: 336aa long hypothetical dtdp-glucose 4,6-dehydratase; PDBTitle: crystal structure of hypothetical protein ph0414 from pyrococcus2 horikoshii ot3
24	d1rpna_	Alignment	not modelled	100.0	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
25	c3gpiA_	Alignment	not modelled	100.0	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: structure of putative nad-dependent epimerase/dehydratase2 from methylobacillus flagellatus
26	c2v6gA_	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: progesterone 5-beta-reductase; PDBTitle: structure of progesterone 5beta-reductase from digitalis2 lanata in complex with nadp
27	d1kewa_	Alignment	not modelled	100.0	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
28	d1n7ha_	Alignment	not modelled	100.0	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases

29	d1t2aa	Alignment	not modelled	100.0	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
30	c3enkB	Alignment	not modelled	100.0	18	PDB header: isomerase Chain: B: PDB Molecule: udp-glucose 4-epimerase; PDBTitle: 1.9a crystal structure of udp-glucose 4-epimerase from2 burkholderia pseudomallei
31	c2iodD	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydroflavonol 4-reductase; PDBTitle: binding of two substrate analogue molecules to2 dihydroflavonol-4-reductase alters the functional geometry3 of the catalytic site
32	d1gy8a	Alignment	not modelled	100.0	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
33	c1t2aC	Alignment	not modelled	100.0	15	PDB header: structural genomics,lyase Chain: C: PDB Molecule: gdp-mannose 4,6 dehydratase; PDBTitle: crystal structure of human gdp-d-mannose 4,6-dehydratase
34	c2p4hX	Alignment	not modelled	100.0	19	PDB header: plant protein Chain: X: PDB Molecule: vestitone reductase; PDBTitle: crystal structure of vestitone reductase from alfalfa2 (medicago sativa l.)
35	c2yy7B	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: B: PDB Molecule: l-threonine dehydrogenase; PDBTitle: crystal structure of thermolabile l-threonine dehydrogenase from2 flavobacterium frigidimaris kuc-1
36	d1y1pa1	Alignment	not modelled	100.0	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
37	d1n2sa	Alignment	not modelled	100.0	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
38	d1e6ua	Alignment	not modelled	100.0	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
39	c2pz1B	Alignment	not modelled	100.0	14	PDB header: sugar binding protein Chain: B: PDB Molecule: putative nucleotide sugar epimerase/ dehydratase; PDBTitle: crystal structure of the bordetella bronchiseptica enzyme2 wbmj in complex with nad and udp
40	c3eheB	Alignment	not modelled	100.0	20	PDB header: isomerase Chain: B: PDB Molecule: udp-glucose 4-epimerase (gale-1); PDBTitle: crystal structure of udp-glucose 4 epimerase (gale-1) from2 archaeoglobus fulgidus
41	c2rh8A	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: anthocyanidin reductase; PDBTitle: structure of apo anthocyanidin reductase from vitis vinifera
42	c2q1wC	Alignment	not modelled	100.0	14	PDB header: sugar binding protein Chain: C: PDB Molecule: putative nucleotide sugar epimerase/ dehydratase; PDBTitle: crystal structure of the bordetella bronchiseptica enzyme wbmh in2 complex with nad+
43	d1rkxa	Alignment	not modelled	100.0	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
44	c3a1nB	Alignment	not modelled	100.0	12	PDB header: oxidoreductase Chain: B: PDB Molecule: ndp-sugar epimerase; PDBTitle: crystal structure of l-threonine dehydrogenase from2 hyperthermophilic archaeon thermoplasma volcanium
45	d1bxka	Alignment	not modelled	100.0	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
46	d1udca	Alignment	not modelled	100.0	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
47	d1ek6a	Alignment	not modelled	100.0	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
48	d1z45a2	Alignment	not modelled	100.0	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
49	c3lu1C	Alignment	not modelled	100.0	13	PDB header: isomerase Chain: C: PDB Molecule: wbgu; PDBTitle: crystal structure analysis of wbgu: a udp-galnac 4-epimerase
50	c2ggsB	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: 273aa long hypothetical dtdp-4-dehydrorhamnose PDBTitle: crystal structure of hypothetical dtdp-4-dehydrorhamnose2 reductase from sulfolobus tokodaii
51	d2bli1	Alignment	not modelled	100.0	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
52	d1eq2a	Alignment	not modelled	100.0	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
53	c2x86K	Alignment	not modelled	100.0	16	PDB header: isomerase Chain: K: PDB Molecule: adp-l-glycero-d-manno-heptose-6-epimerase; PDBTitle: agme bound to adp-b-mannose
54	d1wvga1	Alignment	not modelled	100.0	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains

					Family: Tyrosine-dependent oxidoreductases
55	d1sb8a_	Alignment	not modelled	100.0	15 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
56	d1orra_	Alignment	not modelled	100.0	13 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
57	c2zklA_	Alignment	not modelled	100.0	17 PDB header: isomerase Chain: A: PDB Molecule: capsular polysaccharide synthesis enzyme cap5f; PDBTitle: crystal structure of capsular polysaccharide assembling protein capf2 from staphylococcus aureus
58	c2ydyA_	Alignment	not modelled	100.0	13 PDB header: oxidoreductase Chain: A: PDB Molecule: methionine adenosyltransferase 2 subunit beta; PDBTitle: crystal structure of human s-adenosylmethionine synthetase2 2, beta subunit in orthorhombic crystal form
59	c2q1uA_	Alignment	not modelled	100.0	16 PDB header: sugar binding protein Chain: A: PDB Molecule: putative nucleotide sugar epimerase/dehydratase; PDBTitle: crystal structure of the bordetella bronchiseptica enzyme wbmf in2 complex with nad+ and udp
60	c2gn9B_	Alignment	not modelled	100.0	18 PDB header: lyase Chain: B: PDB Molecule: udp-glcna6 c6 dehydratase; PDBTitle: crystal structure of udp-glcna6 inverting 4,6-dehydratase in complex2 with nadp and udp-glc
61	c3slgB_	Alignment	not modelled	100.0	13 PDB header: transferase Chain: B: PDB Molecule: pbgp3 protein; PDBTitle: crystal structure of pbgp3 protein from burkholderia pseudomallei
62	c3c1oA_	Alignment	not modelled	100.0	18 PDB header: oxidoreductase Chain: A: PDB Molecule: eugenol synthase; PDBTitle: the multiple phenylpropene synthases in both clarkia2 breweri and petunia hybrida represent two distinct lineages
63	c2qx7A_	Alignment	not modelled	99.9	19 PDB header: plant protein Chain: A: PDB Molecule: eugenol synthase 1; PDBTitle: structure of eugenol synthase from ocimum basilicum
64	d1qyda_	Alignment	not modelled	99.9	15 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
65	c3i5mA_	Alignment	not modelled	99.9	14 PDB header: oxidoreductase Chain: A: PDB Molecule: putative leucoanthocyanidin reductase 1; PDBTitle: structure of the apo form of leucoanthocyanidin reductase from vitis2 vinifera
66	c3e48B_	Alignment	not modelled	99.9	17 PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative nucleoside-diphosphate-sugar epimerase; PDBTitle: crystal structure of a nucleoside-diphosphate-sugar epimerase2 (sav0421) from staphylococcus aureus, northeast structural genomics3 consortium target zr319
67	c2vrcD_	Alignment	not modelled	99.9	16 PDB header: oxidoreductase Chain: D: PDB Molecule: triphenylmethane reductase; PDBTitle: crystal structure of the citrobacter sp. triphenylmethane2 reductase complexed with nadp(h)
68	d1qyca_	Alignment	not modelled	99.9	15 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
69	d1xgka_	Alignment	not modelled	99.9	17 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
70	c2gasA_	Alignment	not modelled	99.9	16 PDB header: oxidoreductase Chain: A: PDB Molecule: isoflavone reductase; PDBTitle: crystal structure of isoflavone reductase
71	c3ay3C_	Alignment	not modelled	99.9	17 PDB header: oxidoreductase Chain: C: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: crystal structure of glucuronic acid dehydrogenase from2 chromohalobacter salexigens
72	c2exxB_	Alignment	not modelled	99.9	15 PDB header: unknown function Chain: B: PDB Molecule: hscarg protein; PDBTitle: crystal structure of hscarg from homo sapiens in complex with nadp
73	c3rfxB_	Alignment	not modelled	99.9	20 PDB header: oxidoreductase Chain: B: PDB Molecule: uronate dehydrogenase; PDBTitle: crystal structure of uronate dehydrogenase from agrobacterium2 tumefaciens, y136a mutant complexed with nad
74	c2zcuA_	Alignment	not modelled	99.9	18 PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized oxidoreductase ytfg; PDBTitle: crystal structure of a new type of nadph-dependent quinone2 oxidoreductase (qor2) from escherichia coli
75	c3nzoB_	Alignment	not modelled	99.9	13 PDB header: lyase Chain: B: PDB Molecule: udp-n-acetylglucosamine 4,6-dehydratase; PDBTitle: udp-n-acetylglucosamine 4,6-dehydratase from vibrio fischeri.
76	c3e8xA_	Alignment	not modelled	99.9	12 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative nad-dependent epimerase/dehydratase; PDBTitle: putative nad-dependent epimerase/dehydratase from bacillus halodurans.
77	c3h2sA_	Alignment	not modelled	99.9	15 PDB header: oxidoreductase Chain: A: PDB Molecule: putative nadh-flavin reductase; PDBTitle: crystal structure of the q03b84 protein from lactobacillus2 casei. northeast structural genomics consortium target3 lcr19.
78	c3dhna_	Alignment	not modelled	99.9	12 PDB header: isomerase, lyase Chain: A: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: crystal structure of the putative epimerase q89z24_bactn2 from bacteroides thetaiotaomicron. northeast

					structural3 genomics consortium target btr310.
79	d2q46a1	Alignment	not modelled	99.9	16 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
80	d2a35a1	Alignment	not modelled	99.8	11 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
81	c3dqpA	Alignment	not modelled	99.8	12 PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase ylbe; PDBTitle: crystal structure of the oxidoreductase ylbe from2 lactococcus lactis, northeast structural genomics3 consortium target kr121.
82	c3ew7A	Alignment	not modelled	99.8	23 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lmo0794 protein; PDBTitle: crystal structure of the lmo0794 protein from listeria2 monocytogenes. northeast structural genomics consortium3 target lmr162.
83	d1hdoa	Alignment	not modelled	99.8	16 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
84	d2bkaa1	Alignment	not modelled	99.8	14 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
85	c3qvoA	Alignment	not modelled	99.8	16 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: nmra family protein; PDBTitle: structure of a rosmann-fold nad(p)-binding family protein from2 shigella flexneri.
86	c3r6dA	Alignment	not modelled	99.6	12 PDB header: lyase, isomerase Chain: A: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: crystal structure of nad-dependent epimerase/dehydratase from2 veillonella parvula dsm 2008 with cz-methylated lysine
87	d2fmua1	Alignment	not modelled	99.6	16 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
88	c2jahB	Alignment	not modelled	99.3	11 PDB header: oxidoreductase Chain: B: PDB Molecule: clavulanic acid dehydrogenase; PDBTitle: biochemical and structural analysis of the clavulanic acid2 dehydrogenase (cad) from streptomyces clavuligerus
89	c3p19A	Alignment	not modelled	99.2	14 PDB header: oxidoreductase Chain: A: PDB Molecule: putative blue fluorescent protein; PDBTitle: improved nadph-dependent blue fluorescent protein
90	c3l77A	Alignment	not modelled	99.2	15 PDB header: oxidoreductase Chain: A: PDB Molecule: short-chain alcohol dehydrogenase; PDBTitle: x-ray structure alcohol dehydrogenase from archaeon thermococcus2 sibiricus complexed with 5-hydroxy-nadp
91	d2gdza1	Alignment	not modelled	99.2	12 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
92	d1o0ea	Alignment	not modelled	99.2	13 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
93	c2yutA	Alignment	not modelled	99.2	16 PDB header: oxidoreductase Chain: A: PDB Molecule: putative short-chain oxidoreductase; PDBTitle: crystal structure of putative short-chain oxidoreductase tthb094 from2 thermus thermophilus hb8
94	c3d7lG	Alignment	not modelled	99.2	12 PDB header: structural genomics, unknown function Chain: G: PDB Molecule: lin1944 protein; PDBTitle: the crystal structure of the protein lin1944 from listeria innocua .
95	d1hyea1	Alignment	not modelled	99.1	16 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
96	c3orfC	Alignment	not modelled	99.1	10 PDB header: oxidoreductase Chain: C: PDB Molecule: dihydropteridine reductase; PDBTitle: crystal structure of dihydropteridine reductase from dictyostelium2 discoideum
97	d1jtvA	Alignment	not modelled	99.1	14 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
98	d1sbya1	Alignment	not modelled	99.1	11 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
99	c3lylB	Alignment	not modelled	99.1	10 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
100	c2dteB	Alignment	not modelled	99.1	8 PDB header: oxidoreductase Chain: B: PDB Molecule: glucose 1-dehydrogenase related protein; PDBTitle: structure of thermoplasma acidophilum aldohexose dehydrogenase (aldt2) in complex with nadh
101	c3l6eA	Alignment	not modelled	99.1	14 PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, short-chain dehydrogenase/reductase family; PDBTitle: crystal structure of putative short chain dehydrogenase/reductase2 family oxidoreductase from aeromonas hydrophila subsp. hydrophila3 atcc 7966
102	c3i4fD	Alignment	not modelled	99.1	11 PDB header: oxidoreductase Chain: D: PDB Molecule: 3-oxoacyl-[acyl-carrier protein] reductase; PDBTitle: structure of putative 3-oxoacyl-reductase from bacillus thuringiensis
					Fold: NAD(P)-binding Rossmann-fold domains

103	d1dhra_	Alignment	not modelled	99.0	9	Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
104	c2nm0B_	Alignment	not modelled	99.0	9	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)
105	c3un1D_	Alignment	not modelled	99.0	16	PDB header: oxidoreductase Chain: D: PDB Molecule: probable oxidoreductase; PDBTitle: crystal structure of an oxidoreductase from sinorhizobium meliloti2 1021
106	c3ppiA_	Alignment	not modelled	99.0	14	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
107	d1uzma1	Alignment	not modelled	99.0	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
108	c3f9iB_	Alignment	not modelled	99.0	12	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
109	d1ulsa_	Alignment	not modelled	99.0	9	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
110	d2d1ya1	Alignment	not modelled	99.0	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
111	d1o5ia_	Alignment	not modelled	99.0	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
112	d1mlda1	Alignment	not modelled	99.0	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
113	d2a4ka1	Alignment	not modelled	99.0	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
114	c3tfoD_	Alignment	not modelled	99.0	17	PDB header: oxidoreductase Chain: D: PDB Molecule: putative 3-oxoacyl-(acyl-carrier-protein) reductase; PDBTitle: crystal structure of a putative 3-oxoacyl-(acyl-carrier-protein)2 reductase from sinorhizobium meliloti
115	c3cxtA_	Alignment	not modelled	99.0	10	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase with different specificities; PDBTitle: quaternary complex structure of gluconate 5-dehydrogenase from2 streptococcus suis type 2
116	c3uxyC_	Alignment	not modelled	99.0	13	PDB header: oxidoreductase Chain: C: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: the crystal structure of short chain dehydrogenase from rhodobacter2 sphaeroides
117	c2nwqA_	Alignment	not modelled	99.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: probable short-chain dehydrogenase; PDBTitle: short chain dehydrogenase from pseudomonas aeruginosa
118	c3ai3A_	Alignment	not modelled	98.9	16	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
119	c2p68A_	Alignment	not modelled	98.9	11	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: crystal structure of aq_1716 from aquifex aeolicus vf5
120	c3m1aF_	Alignment	not modelled	98.9	11	PDB header: oxidoreductase Chain: F: PDB Molecule: putative dehydrogenase; PDBTitle: the crystal structure of a short-chain dehydrogenase from2 streptomyces avermitilis to 2a