
































#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2a35a1	 Alignment		100.0	45	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
2	d2bkaa1	 Alignment		100.0	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
3	c1z7eC	 Alignment		100.0	15	PDB header: hydrolase Chain: C: PDB Molecule: protein arna; PDBTitle: crystal structure of full length arna
4	c3oh8A	 Alignment		100.0	14	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
5	c1z45A	 Alignment		99.9	19	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
6	d2fmua1	 Alignment		99.9	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
7	c2qx7A	 Alignment		99.9	16	PDB header: plant protein Chain: A: PDB Molecule: eugenol synthase 1; PDBTitle: structure of eugenol synthase from ocimum basilicum
8	c2zklA	 Alignment		99.9	18	PDB header: isomerase Chain: A: PDB Molecule: capsular polysaccharide synthesis enzyme cap5f; PDBTitle: crystal structure of capsular polysaccharide assembling protein capf2 from staphylococcus aureus
9	d1i24a	 Alignment		99.9	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
10	c2gn9B	 Alignment		99.9	15	PDB header: lyase Chain: B: PDB Molecule: udp-glcnac c6 dehydratase; PDBTitle: crystal structure of udp-glcnac inverting 4,6-dehydratase in complex2 with nadp and udp-glc
11	c3c1oA	 Alignment		99.9	14	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

12	c2v6gA_	Alignment		99.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: progesterone 5-beta-reductase; PDBTitle: structure of progesterone 5beta-reductase from digitalis2 lanata in complex with nadp
13	d1hdoa_	Alignment		99.9	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
14	c3dhnA_	Alignment		99.9	18	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.
15	c3e8xA_	Alignment		99.9	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative nad-dependent epimerase/dehydratase; PDBTitle: putative nad-dependent epimerase/dehydratase from bacillus halodurans.
16	d2q46a1	Alignment		99.9	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
17	d1qyda_	Alignment		99.9	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
18	d1oc2a_	Alignment		99.9	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
19	d1y1pa1	Alignment		99.9	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
20	c3rfxB_	Alignment		99.9	14	PDB header: oxidoreductase Chain: B: PDB Molecule: uronate dehydrogenase; PDBTitle: crystal structure of uronate dehydrogenase from agrobacterium2 tumefaciens, y136a mutant complexed with nad
21	c3dqpA_	Alignment	not modelled	99.9	18	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.
22	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
23	c3ay3C_	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: C: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: crystal structure of glucuronic acid dehydrogeanse from2 chromohalobacter salexigens
24	c3i5mA_	Alignment	not modelled	99.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: putative leucoanthocyanidin reductase 1; PDBTitle: structure of the apo form of leucoanthocyanidin reductase from vitis2 vinifera
25	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.
26	c3ew7A_	Alignment	not modelled	99.9	20	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.
27	c2iodD_	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydroflavonol 4-reductase; PDBTitle: binding of two substrate analogue molecules to2

						dihydroflavonol-4-reductase alters the functional geometry ³ of the catalytic site
28	c3qvoA	Alignment	not modelled	99.9	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: nmra family protein; PDBTitle: structure of a rossmann-fold nad(p)-binding family protein from <i>Shigella flexneri</i> .
29	c3h2sA	Alignment	not modelled	99.9	10	PDB header: oxidoreductase Chain: A: PDB Molecule: putative nadh-flavin reductase; PDBTitle: crystal structure of the q03b84 protein from <i>Lactobacillus casei</i> . northeast structural genomics consortium target3 lcr19.
30	c2p4hX	Alignment	not modelled	99.9	13	PDB header: plant protein Chain: X: PDB Molecule: vestitone reductase; PDBTitle: crystal structure of vestitone reductase from alfalfa2 (<i>Medicago sativa</i> L.)
31	d1xgka	Alignment	not modelled	99.9	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
32	c2b69A	Alignment	not modelled	99.9	16	PDB header: lyase Chain: A: PDB Molecule: udp-glucuronate decarboxylase 1; PDBTitle: crystal structure of human udp-glucuronic acid decarboxylase
33	d2b69a1	Alignment	not modelled	99.9	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
34	d1qyca	Alignment	not modelled	99.8	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
35	c2gasA	Alignment	not modelled	99.8	19	PDB header: oxidoreductase Chain: A: PDB Molecule: isoflavone reductase; PDBTitle: crystal structure of isoflavone reductase
36	c2vrcD	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: D: PDB Molecule: triphenylmethane reductase; PDBTitle: crystal structure of the citrobacter sp. triphenylmethane2 reductase complexed with nadp(h)
37	c2hunB	Alignment	not modelled	99.8	13	PDB header: lyase Chain: B: PDB Molecule: 336aa long hypothetical dtdp-glucose 4,6-dehydratase; PDBTitle: crystal structure of hypothetical protein ph0414 from <i>Pyrococcus horikoshii</i> ot3
38	c3iusB	Alignment	not modelled	99.8	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized conserved protein; PDBTitle: the structure of a functionally unknown conserved protein2 from <i>Silicibacter pomeroyi</i> dss
39	d1n2sa	Alignment	not modelled	99.8	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
40	c3sc6F	Alignment	not modelled	99.8	19	PDB header: oxidoreductase Chain: F: PDB Molecule: dtdp-4-dehydrorhamnose reductase; PDBTitle: 2.65 angstrom resolution crystal structure of dtdp-4-dehydrorhamnose2 reductase (rfbd) from <i>Bacillus anthracis</i> str. ames in complex with3 nadp
41	c2exxB	Alignment	not modelled	99.8	18	PDB header: unknown function Chain: B: PDB Molecule: hscarg protein; PDBTitle: crystal structure of hscarg from <i>Homo sapiens</i> in complex with nadp
42	d1vl0a	Alignment	not modelled	99.8	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
43	c2rh8A	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: anthocyanidin reductase; PDBTitle: structure of apo anthocyanidin reductase from <i>Vitis vinifera</i>
44	c3m2pD	Alignment	not modelled	99.8	17	PDB header: isomerase Chain: D: PDB Molecule: udp-n-acetylglucosamine 4-epimerase; PDBTitle: the crystal structure of udp-n-acetylglucosamine 4-epimerase2 from <i>Bacillus cereus</i>
45	c3gpiA	Alignment	not modelled	99.8	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: structure of putative nad-dependent epimerase/dehydratase2 from <i>Methylobacillus flagellatus</i>
46	c2x4gA	Alignment	not modelled	99.8	18	PDB header: isomerase Chain: A: PDB Molecule: nucleoside-diphosphate-sugar epimerase; PDBTitle: crystal structure of pa4631, a nucleoside-diphosphate-sugar2 epimerase from <i>Pseudomonas aeruginosa</i>
47	c2ggsB	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: B: PDB Molecule: 273aa long hypothetical dtdp-4-dehydrorhamnose PDBTitle: crystal structure of hypothetical dtdp-4-dehydrorhamnose2 reductase from <i>Sulfolobus tokodaii</i>
48	c2q1wC	Alignment	not modelled	99.8	11	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+
49	d1e6ua	Alignment	not modelled	99.8	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
50	c2yy7B	Alignment	not modelled	99.8	14	PDB header: oxidoreductase Chain: B: PDB Molecule: l-threonine dehydrogenase; PDBTitle: crystal structure of thermolabile l-threonine dehydrogenase from <i>Flavobacterium frigidimarum</i> kuc-1
51	d1r6da	Alignment	not modelled	99.8	17	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

52	d2c5aa1	Alignment	not modelled	99.8	18	Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
53	d1db3a	Alignment	not modelled	99.8	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
54	d1bxka	Alignment	not modelled	99.8	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
55	c3enkB	Alignment	not modelled	99.8	15	PDB header: isomerase Chain: B: PDB Molecule: udp-glucose 4-epimerase; PDBTitle: 1.9a crystal structure of udp-glucose 4-epimerase from2 burkholderia pseudomallei
56	c2z1mC	Alignment	not modelled	99.8	13	PDB header: lyase Chain: C: PDB Molecule: gdp-d-mannose dehydratase; PDBTitle: crystal structure of gdp-d-mannose dehydratase from aquifex aeolicus2 vf5
57	c2pzlB	Alignment	not modelled	99.8	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
58	c1n7gB	Alignment	not modelled	99.8	14	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.
59	c3eheB	Alignment	not modelled	99.8	17	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
60	c2ydyA	Alignment	not modelled	99.8	18	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
61	c2hrzA	Alignment	not modelled	99.8	13	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
62	d1z45a2	Alignment	not modelled	99.8	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
63	c2pk3B	Alignment	not modelled	99.8	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
64	d1eq2a	Alignment	not modelled	99.8	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
65	d1kewa	Alignment	not modelled	99.8	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
66	d1rkxa	Alignment	not modelled	99.8	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
67	d1ek6a	Alignment	not modelled	99.8	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
68	d1wvga1	Alignment	not modelled	99.8	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
69	c3icpA	Alignment	not modelled	99.8	13	PDB header: isomerase Chain: A: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: crystal structure of udp-galactose 4-epimerase
70	d1n7ha	Alignment	not modelled	99.8	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
71	d1gy8a	Alignment	not modelled	99.8	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
72	c2c20D	Alignment	not modelled	99.7	16	PDB header: isomerase Chain: D: PDB Molecule: udp-glucose 4-epimerase; PDBTitle: crystal structure of udp-glucose 4-epimerase
73	c3a1nB	Alignment	not modelled	99.7	10	PDB header: oxidoreductase Chain: B: PDB Molecule: ndp-sugar epimerase; PDBTitle: crystal structure of l-threonine dehydrogenase from2 hyperthermophilic archaeon thermoplasma volcanium
74	d1rpna	Alignment	not modelled	99.7	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
75	d1t2aa	Alignment	not modelled	99.7	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
76	c1t2aC	Alignment	not modelled	99.7	14	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
77	c2p5uC	Alignment	not modelled	99.7	16	PDB header: isomerase Chain: C: PDB Molecule: udp-glucose 4-epimerase; PDBTitle: crystal structure of thermophilus hb8 udp-glucose 4-2 epimerase complex with nad
						Fold: NAD(P)-binding Rossmann-fold domains

78	dlorra_	Alignment	not modelled	99.7	11	Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
79	c3lu1C_	Alignment	not modelled	99.7	15	PDB header: isomerase Chain: C: PDB Molecule: wbgu; PDBTitle: crystal structure analysis of wbgu: a udp-galnac 4-epimerase
80	c2zcuA_	Alignment	not modelled	99.7	17	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
81	d1sb8a_	Alignment	not modelled	99.7	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
82	d2blla1	Alignment	not modelled	99.7	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
83	c3r6dA_	Alignment	not modelled	99.7	14	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
84	c2q1uA_	Alignment	not modelled	99.7	17	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
85	dludca_	Alignment	not modelled	99.7	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
86	c2x86K_	Alignment	not modelled	99.7	13	PDB header: isomerase Chain: K: PDB Molecule: adp-l-glycero-d-manno-heptose-6-epimerase; PDBTitle: agme bound to adp-b-mannose
87	c3slgB_	Alignment	not modelled	99.7	14	PDB header: transferase Chain: B: PDB Molecule: pbgp3 protein; PDBTitle: crystal structure of pbgp3 protein from burkholderia pseudomallei
88	d1mlda1	Alignment	not modelled	99.4	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
89	d1hyea1	Alignment	not modelled	99.3	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
90	c2jahB_	Alignment	not modelled	99.3	16	PDB header: oxidoreductase Chain: B: PDB Molecule: clavulanic acid dehydrogenase; PDBTitle: biochemical and structural analysis of the clavulanic acid2 dehydrogenase (cad) from streptomyces clavuligerus
91	c3p19A_	Alignment	not modelled	99.3	13	PDB header: oxidoreductase Chain: A: PDB Molecule: putative blue fluorescent protein; PDBTitle: improved nadph-dependent blue fluorescent protein
92	c3un1D_	Alignment	not modelled	99.1	15	PDB header: oxidoreductase Chain: D: PDB Molecule: probable oxidoreductase; PDBTitle: crystal structure of an oxidoreductase from sinorhizobium meliloti2 1021
93	c3l77A_	Alignment	not modelled	99.1	16	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
94	d1o5ia_	Alignment	not modelled	99.0	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
95	d1sbya1	Alignment	not modelled	99.0	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
96	d1jtva_	Alignment	not modelled	99.0	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
97	c2dteB_	Alignment	not modelled	99.0	11	PDB header: oxidoreductase Chain: B: PDB Molecule: glucose 1-dehydrogenase related protein; PDBTitle: structure of thermoplasma acidophilum aldohexose dehydrogenase (aldt2) in complex with nadh
98	d1uzma1	Alignment	not modelled	99.0	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
99	d1o0ea_	Alignment	not modelled	99.0	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
100	c2nm0B_	Alignment	not modelled	98.9	16	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)
101	c2hlpB_	Alignment	not modelled	98.9	11	PDB header: oxidoreductase Chain: B: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of the e267r mutant of a halophilic2 malate dehydrogenase in the apo form
102	c2p68A_	Alignment	not modelled	98.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: crystal structure of aq_1716 from aquifex aeolicus vf5
103	c3f9iB_	Alignment	not modelled	98.9	16	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
104	c3l6eA_	Alignment	not modelled	98.9	17	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
105	c2cfcB_	Alignment	not modelled	98.9	14	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
106	d1uaya_	Alignment	not modelled	98.9	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
107	c3d7lG_	Alignment	not modelled	98.9	15	PDB header: structural genomics, unknown function Chain: G: PDB Molecule: lin1944 protein; PDBTitle: the crystal structure of the protein lin1944 from listeria innocua .
108	c3i4fD_	Alignment	not modelled	98.9	16	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-oxoacyl-[acyl-carrier protein] reductase; PDBTitle: structure of putative 3-oxoacyl-reductase from bacillus thuringiensis
109	c3lylB_	Alignment	not modelled	98.9	12	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-oxoacyl-(acyl-carrier-protein) reductase; PDBTitle: structure of 3-oxoacyl-acyl carrier protein reductase, fabg2 from francisella tularensis
110	c2yutA_	Alignment	not modelled	98.9	22	PDB header: oxidoreductase Chain: A: PDB Molecule: putative short-chain oxidoreductase; PDBTitle: crystal structure of putative short-chain oxidoreductase tthb094 from2 thermus thermophilus hb8
111	c3cxtA_	Alignment	not modelled	98.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase with different specificities; PDBTitle: quaternary complex structure of gluconate 5-dehydrogenase from2 streptococcus suis type 2
112	d1ulsa_	Alignment	not modelled	98.8	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
113	c1fdvA_	Alignment	not modelled	98.8	18	PDB header: dehydrogenase Chain: A: PDB Molecule: 17-beta-hydroxysteroid dehydrogenase; PDBTitle: human 17-beta-hydroxysteroid-dehydrogenase type 1 mutant2 h221l complexed with nad+
114	c3uxyC_	Alignment	not modelled	98.8	18	PDB header: oxidoreductase Chain: C: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: the crystal structure of short chain dehydrogenase from rhodobacter2 sphaeroides
115	d2cmda1	Alignment	not modelled	98.8	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
116	d2gdza1	Alignment	not modelled	98.8	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
117	c3toxG_	Alignment	not modelled	98.8	13	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
118	c2nwqA_	Alignment	not modelled	98.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: probable short-chain dehydrogenase; PDBTitle: short chain dehydrogenase from pseudomonas aeruginosa
119	c3ijrF_	Alignment	not modelled	98.8	14	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+
120	d1geea_	Alignment	not modelled	98.8	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases