



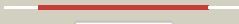









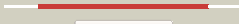


















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">dle6ua_</a>	 Alignment		100.0	99	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
2	<a href="#">c1z45A_</a>	 Alignment		100.0	20	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> gal10 bifunctional protein; <b>PDBTitle:</b> crystal structure of the gal10 fusion protein galactose2 mutarotase/udp-galactose 4-epimerase from saccharomyces3 cerevisiae complexed with nad, udp-glucose, and galactose
3	<a href="#">c1z7eC_</a>	 Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> protein arna; <b>PDBTitle:</b> crystal structure of full length arna
4	<a href="#">d1i24a_</a>	 Alignment		100.0	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
5	<a href="#">c3enkB_</a>	 Alignment		100.0	20	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-glucose 4-epimerase; <b>PDBTitle:</b> 1.9a crystal structure of udp-glucose 4-epimerase from2 burkholderia pseudomallei
6	<a href="#">d1ek6a_</a>	 Alignment		100.0	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
7	<a href="#">d1orra_</a>	 Alignment		100.0	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
8	<a href="#">d2c5aa1</a>	 Alignment		100.0	24	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
9	<a href="#">c2b69A_</a>	 Alignment		100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-glucuronate decarboxylase 1; <b>PDBTitle:</b> crystal structure of human udp-glucuronic acid decarboxylase
10	<a href="#">d2b69a1</a>	 Alignment		100.0	22	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
11	<a href="#">d1gy8a_</a>	 Alignment		100.0	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases

12	<a href="#">c2hunB</a>	Alignment		100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 336aa long hypothetical dtdp-glucose 4,6-dehydratase; <b>PDBTitle:</b> crystal structure of hypothetical protein ph0414 from pyrococcus2 horikoshii ot3
13	<a href="#">c1n7gB</a>	Alignment		100.0	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> gdp-d-mannose-4,6-dehydratase; <b>PDBTitle:</b> crystal structure of the gdp-mannose 4,6-dehydratase2 ternary complex with nadph and gdp-rhamnose.
14	<a href="#">c2c20D</a>	Alignment		100.0	18	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> udp-glucose 4-epimerase; <b>PDBTitle:</b> crystal structure of udp-glucose 4-epimerase
15	<a href="#">d1db3a</a>	Alignment		100.0	20	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
16	<a href="#">d1wvga1</a>	Alignment		100.0	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
17	<a href="#">d1n7ha</a>	Alignment		100.0	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
18	<a href="#">c3lu1C</a>	Alignment		100.0	22	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> wbgu; <b>PDBTitle:</b> crystal structure analysis of wbgu: a udp-galnac 4-epimerase
19	<a href="#">d1oc2a</a>	Alignment		100.0	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
20	<a href="#">d1z45a2</a>	Alignment		100.0	20	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
21	<a href="#">c2z1mC</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> gdp-d-mannose dehydratase; <b>PDBTitle:</b> crystal structure of gdp-d-mannose dehydratase from aquifex aeolicus2 vf5
22	<a href="#">d1kewa</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
23	<a href="#">d1rkxa</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
24	<a href="#">d1bxka</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
25	<a href="#">c2pk3B</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> gdp-6-deoxy-d-lyxo-4-hexulose reductase; <b>PDBTitle:</b> crystal structure of a gdp-4-keto-6-deoxy-d-mannose reductase
26	<a href="#">c2p5uC</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> udp-glucose 4-epimerase; <b>PDBTitle:</b> crystal structure of thermus thermophilus hb8 udp-glucose 4-2 epimerase complex with nad
27	<a href="#">d1rpna</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
28	<a href="#">c2q1uA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative nucleotide sugar epimerase/dehydratase; <b>PDBTitle:</b> crystal structure of the bordetella bronchiseptica enzyme wbmf in2 complex with nad+ and udp
						<b>Fold:</b> NAD(P)-binding Rossmann-fold domains

29	<a href="#">dludca_</a>	Alignment	not modelled	100.0	20	<b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
30	<a href="#">d2bl1a1</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
31	<a href="#">d1t2aa_</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
32	<a href="#">d1r6da_</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
33	<a href="#">c1t2aC_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> structural genomics, lyase <b>Chain:</b> C: <b>PDB Molecule:</b> gdp-mannose 4,6 dehydratase; <b>PDBTitle:</b> crystal structure of human gdp-d-mannose 4,6-dehydratase
34	<a href="#">c2yy7B_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> l-threonine dehydrogenase; <b>PDBTitle:</b> crystal structure of thermolabile l-threonine dehydrogenase from2 flavobacterium frigidimaris kuc-1
35	<a href="#">d1sb8a_</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
36	<a href="#">c2hrzA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoside-diphosphate-sugar epimerase; <b>PDBTitle:</b> the crystal structure of the nucleoside-diphosphate-sugar epimerase2 from agrobacterium tumefaciens
37	<a href="#">c3slgB_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pbgp3 protein; <b>PDBTitle:</b> crystal structure of pbgp3 protein from burkholderia pseudomallei
38	<a href="#">c3a1nB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ndp-sugar epimerase; <b>PDBTitle:</b> crystal structure of l-threonine dehydrogenase from2 hyperthermophilic archaeon thermoplasma volcanium
39	<a href="#">c2p4hX_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> plant protein <b>Chain:</b> X: <b>PDB Molecule:</b> vestitone reductase; <b>PDBTitle:</b> crystal structure of vestitone reductase from alfalfa2 (medicago sativa l.)
40	<a href="#">c3eheB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-glucose 4-epimerase (gale-1); <b>PDBTitle:</b> crystal structure of udp-glucose 4 epimerase (gale-1) from2 archaeoglobus fulgidus
41	<a href="#">c2iodD_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> dihydroflavonol 4-reductase; <b>PDBTitle:</b> binding of two substrate analogue molecules to2 dihydroflavonol-4-reductase alters the functional geometry3 of the catalytic site
42	<a href="#">c2pzlB_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative nucleotide sugar epimerase/dehydratase; <b>PDBTitle:</b> crystal structure of the bordetella bronchiseptica enzyme2 wbmj in complex with nad and udp
43	<a href="#">c2q1wC_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> sugar binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> putative nucleotide sugar epimerase/dehydratase; <b>PDBTitle:</b> crystal structure of the bordetella bronchiseptica enzyme wbmh in2 complex with nad+
44	<a href="#">c2x4gA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoside-diphosphate-sugar epimerase; <b>PDBTitle:</b> crystal structure of pa4631, a nucleoside-diphosphate-sugar2 epimerase from pseudomonas aeruginosa
45	<a href="#">c2rh8A_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> anthocyanidin reductase; <b>PDBTitle:</b> structure of apo anthocyanidin reductase from vitis vinifera
46	<a href="#">c2v6gA_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> progesterone 5-beta-reductase; <b>PDBTitle:</b> structure of progesterone 5beta-reductase from digitalis2 lanata in complex with nadp
47	<a href="#">c3sc6F_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> ddtp-4-dehydrorhamnose reductase; <b>PDBTitle:</b> 2.65 angstrom resolution crystal structure of dtdp-4-dehydrorhamnose2 reductase (rfbd) from bacillus anthracis str. ames in complex with3 nadp
48	<a href="#">c2ydyA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> methionine adenosyltransferase 2 subunit beta; <b>PDBTitle:</b> crystal structure of human s-adenosylmethionine synthetase2 2, beta subunit in orthorhombic crystal form
49	<a href="#">d1vl0a_</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
50	<a href="#">c3m2pD_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> udp-n-acetylglucosamine 4-epimerase; <b>PDBTitle:</b> the crystal structure of udp-n-acetylglucosamine 4-epimerase2 from bacillus cereus
51	<a href="#">c3icpA_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent epimerase/dehydratase; <b>PDBTitle:</b> crystal structure of udp-galactose 4-epimerase
52	<a href="#">d1ylpa1</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
53	<a href="#">d1n2sa_</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases

54	<a href="#">c2x86K</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> isomerase <b>Chain:</b> K: <b>PDB Molecule:</b> adp-l-glycero-d-manno-heptose-6-epimerase; <b>PDBTitle:</b> agme bound to adp-b-mannose
55	<a href="#">c3oh8A</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoside-diphosphate sugar epimerase (sula family); <b>PDBTitle:</b> crystal structure of the nucleoside-diphosphate sugar epimerase from2 corynebacterium glutamicum. northeast structural genomics consortium3 target cgr91
56	<a href="#">c3gpiA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent epimerase/dehydratase; <b>PDBTitle:</b> structure of putative nad-dependent epimerase/dehydratase2 from methylobacillus flagellatus
57	<a href="#">dlq2a</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
58	<a href="#">c2ggsB</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 273aa long hypothetical dtdp-4-dehydrorhamnose <b>PDBTitle:</b> crystal structure of hypothetical dtdp-4-dehydrorhamnose2 reductase from sulfolobus tokodaii
59	<a href="#">c3iusB</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized conserved protein; <b>PDBTitle:</b> the structure of a functionally unknown conserved protein2 from silicibacter pomeroyi dss
60	<a href="#">c2gn9B</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-glcna6 c6 dehydratase; <b>PDBTitle:</b> crystal structure of udp-glcna6 inverting 4,6-dehydratase in complex2 with nadp and udp-glc
61	<a href="#">c2zklA</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> capsular polysaccharide synthesis enzyme cap5f; <b>PDBTitle:</b> crystal structure of capsular polysaccharide assembling protein capf2 from staphylococcus aureus
62	<a href="#">c3e48B</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative nucleoside-diphosphate-sugar epimerase; <b>PDBTitle:</b> crystal structure of a nucleoside-diphosphate-sugar epimerase2 (sav0421) from staphylococcus aureus, northeast structural genomics3 consortium target zr319
63	<a href="#">c2qx7A</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> eugenol synthase 1; <b>PDBTitle:</b> structure of eugenol synthase from ocimum basilicum
64	<a href="#">dlqyca</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
65	<a href="#">c3nzoB</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-n-acetylglucosamine 4,6-dehydratase; <b>PDBTitle:</b> udp-n-acetylglucosamine 4,6-dehydratase from vibrio fischeri.
66	<a href="#">c2exxB</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hscarg protein; <b>PDBTitle:</b> crystal structure of hscarg from homo sapiens in complex with nadp
67	<a href="#">c3c1oA</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> eugenol synthase; <b>PDBTitle:</b> the multiple phenylpropene synthases in both clarkia2 breweri and petunia hybrida represent two distinct lineages
68	<a href="#">dlxgka</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
69	<a href="#">dlqyda</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
70	<a href="#">c2gasA</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> isoflavone reductase; <b>PDBTitle:</b> crystal structure of isoflavone reductase
71	<a href="#">c3ay3C</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nad-dependent epimerase/dehydratase; <b>PDBTitle:</b> crystal structure of glucuronic acid dehydrogenase from2 chromohalobacter salexigens
72	<a href="#">c3i5mA</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative leucoanthocyanidin reductase 1; <b>PDBTitle:</b> structure of the apo form of leucoanthocyanidin reductase from vitis2 vinifera
73	<a href="#">c3rfxB</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> uronate dehydrogenase; <b>PDBTitle:</b> crystal structure of uronate dehydrogenase from agrobacterium2 tumefaciens, y136a mutant complexed with nad
74	<a href="#">c2zcuA</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized oxidoreductase ytfq; <b>PDBTitle:</b> crystal structure of a new type of nadph-dependent quinone2 oxidoreductase (qor2) from escherichia coli
75	<a href="#">c2vrcD</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> triphenylmethane reductase; <b>PDBTitle:</b> crystal structure of the citrobacter sp. triphenylmethane2 reductase complexed with nadp(h)
76	<a href="#">dlhdoa</a>	Alignment	not modelled	99.8	20	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
77	<a href="#">c3e8xA</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative nad-dependent epimerase/dehydratase; <b>PDBTitle:</b> putative nad-dependent epimerase/dehydratase from bacillus halodurans.
						<b>Fold:</b> NAD(P)-binding Rossmann-fold domains

78	<a href="#">d2q46a1</a>	Alignment	not modelled	99.8	17	<b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
79	<a href="#">c3dhnA</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> isomerase, lyase <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent epimerase/dehydratase; <b>PDBTitle:</b> crystal structure of the putative epimerase q89z24_bactn2 from bacteroides thetaiotaomicron. northeast structural3 genomics consortium target btr310.
80	<a href="#">c3h2sA</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative nadh-flavin reductase; <b>PDBTitle:</b> crystal structure of the q03b84 protein from lactobacillus2 casei. northeast structural genomics consortium target3 lcr19.
81	<a href="#">c3dqpA</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase ylb;e; <b>PDBTitle:</b> crystal structure of the oxidoreductase ylb from2 lactococcus lactis, northeast structural genomics3 consortium target kr121.
82	<a href="#">d2bkaa1</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
83	<a href="#">c3qvoA</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> nmra family protein; <b>PDBTitle:</b> structure of a rossmann-fold nad(p)-binding family protein from2 shigella flexneri.
84	<a href="#">d2a35a1</a>	Alignment	not modelled	99.6	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
85	<a href="#">d2fmua1</a>	Alignment	not modelled	99.6	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
86	<a href="#">c3ew7A</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lmo0794 protein; <b>PDBTitle:</b> crystal structure of the lmo0794 protein from listeria2 monocytogenes. northeast structural genomics consortium3 target lmr162.
87	<a href="#">c2jahB</a>	Alignment	not modelled	99.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> clavulanic acid dehydrogenase; <b>PDBTitle:</b> biochemical and structural analysis of the clavulanic acid2 dehydrogenase (cad) from streptomyces clavuligerus
88	<a href="#">d1mlda1</a>	Alignment	not modelled	99.3	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
89	<a href="#">c3r6dA</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> lyase, isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent epimerase/dehydratase; <b>PDBTitle:</b> crystal structure of nad-dependent epimerase/dehydratase from2 veillonella parvula dsm 2008 with cz-methylated lysine
90	<a href="#">d1hyea1</a>	Alignment	not modelled	99.2	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
91	<a href="#">d1looea</a>	Alignment	not modelled	99.1	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
92	<a href="#">c2dteB</a>	Alignment	not modelled	99.1	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glucose 1-dehydrogenase related protein; <b>PDBTitle:</b> structure of thermoplasma acidophilum aldohexose dehydrogenase (aldt2) in complex with nadh
93	<a href="#">c3lylB</a>	Alignment	not modelled	99.1	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-oxoacyl-(acyl-carrier-protein) reductase; <b>PDBTitle:</b> structure of 3-oxoacyl-acylcarrier protein reductase, fabg2 from francisella tularensis
94	<a href="#">c3un1D</a>	Alignment	not modelled	99.1	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> probable oxidoreductase; <b>PDBTitle:</b> crystal structure of an oxidoreductase from sinorhizobium meliloti2 1021
95	<a href="#">c2yutA</a>	Alignment	not modelled	99.1	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative short-chain oxidoreductase; <b>PDBTitle:</b> crystal structure of putative short-chain oxidoreductase tthb094 from2 thermus thermophilus hb8
96	<a href="#">c3p19A</a>	Alignment	not modelled	99.1	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative blue fluorescent protein; <b>PDBTitle:</b> improved nadph-dependent blue fluorescent protein
97	<a href="#">c2qioA</a>	Alignment	not modelled	99.1	9	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-(acyl-carrier-protein) reductase; <b>PDBTitle:</b> x-ray structure of enoyl-acyl carrier protein reductase from bacillus2 anthracis with triclosan
98	<a href="#">c3toxG</a>	Alignment	not modelled	99.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> short chain dehydrogenase; <b>PDBTitle:</b> crystal structure of a short chain dehydrogenase in complex with2 nad(p) from sinorhizobium meliloti 1021
99	<a href="#">d1qsga</a>	Alignment	not modelled	99.0	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
100	<a href="#">c3ioyB</a>	Alignment	not modelled	99.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase sdr; <b>PDBTitle:</b> structure of putative short-chain dehydrogenase (saro_0793)2 from novosphingobium aromaticivorans
101	<a href="#">c2p68A</a>	Alignment	not modelled	99.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] reductase; <b>PDBTitle:</b> crystal structure of aq_1716 from aquifex aeolicus vf5
102	<a href="#">d2gdza1</a>	Alignment	not modelled	99.0	12	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases



103	<a href="#">c2q2qG_</a>	Alignment	not modelled	99.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> beta-d-hydroxybutyrate dehydrogenase; <b>PDBTitle:</b> structure of d-3-hydroxybutyrate dehydrogenase from pseudomonas putida
104	<a href="#">c3ctmH_</a>	Alignment	not modelled	99.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> carbonyl reductase; <b>PDBTitle:</b> crystal structure of a carbonyl reductase from candida2 parapsilosis with anti-prelog stereo-specificity
105	<a href="#">c2nm0B_</a>	Alignment	not modelled	99.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable 3-oxacyl-(acyl-carrier-protein) reductase; <b>PDBTitle:</b> crystal structure of sco1815: a beta-ketoacyl-acyl carrier protein2 reductase from streptomyces coelicolor a3(2)
106	<a href="#">d1sbya1</a>	Alignment	not modelled	99.0	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
107	<a href="#">c3rkrC_</a>	Alignment	not modelled	99.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> short chain oxidoreductase; <b>PDBTitle:</b> crystal structure of a metagenomic short-chain oxidoreductase (sdr) in2 complex with nadp
108	<a href="#">d2ae2a_</a>	Alignment	not modelled	99.0	14	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
109	<a href="#">d1geea_</a>	Alignment	not modelled	99.0	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
110	<a href="#">d2pd4a1</a>	Alignment	not modelled	99.0	9	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
111	<a href="#">c3l77A_</a>	Alignment	not modelled	99.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> short-chain alcohol dehydrogenase; <b>PDBTitle:</b> x-ray structure alcohol dehydrogenase from archaeon thermococcus2 sibiricus complexed with 5-hydroxy-nadp
112	<a href="#">c3t7cC_</a>	Alignment	not modelled	99.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> carveol dehydrogenase; <b>PDBTitle:</b> crystal structure of carveol dehydrogenase from mycobacterium avium2 bound to nad
113	<a href="#">c3iccA_</a>	Alignment	not modelled	99.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative 3-oxoacyl-(acyl carrier protein) reductase; <b>PDBTitle:</b> crystal structure of a putative 3-oxoacyl-(acyl carrier protein)2 reductase from bacillus anthracis at 1.87 a resolution
114	<a href="#">c3l6eA_</a>	Alignment	not modelled	99.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, short-chain dehydrogenase/reductase family; <b>PDBTitle:</b> crystal structure of putative short chain dehydrogenase/reductase2 family oxidoreductase from aeromonas hydrophila subsp. hydrophila3 atcc 7966
115	<a href="#">d1zk4a1</a>	Alignment	not modelled	99.0	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
116	<a href="#">d2ew8a1</a>	Alignment	not modelled	99.0	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
117	<a href="#">c2hlpB_</a>	Alignment	not modelled	99.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> crystal structure of the e267r mutant of a halophilic2 malate dehydrogenase in the apo form
118	<a href="#">c3pgxB_</a>	Alignment	not modelled	99.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> carveol dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative carveol dehydrogenase from2 mycobacterium paratuberculosis bound to nicotinamide adenine3 dinucleotide
119	<a href="#">c2cfcB_</a>	Alignment	not modelled	99.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-(r)-hydroxypropyl-com dehydrogenase; <b>PDBTitle:</b> structural basis for stereo selectivity in the (r)- and2 (s)-hydroxypropylethane thiosulfonate dehydrogenases
120	<a href="#">c3gr6A_</a>	Alignment	not modelled	99.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-[acyl-carrier-protein] reductase [nadh]; <b>PDBTitle:</b> crystal structure of the staphylococcus aureus enoyl-acyl2 carrier protein reductase (fabI) in complex with nadp and3 triclosan