



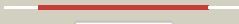

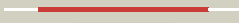


























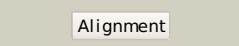
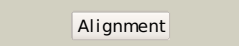
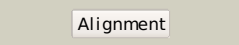



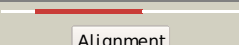


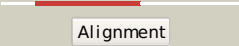


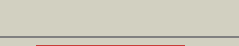
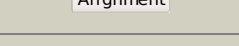



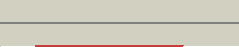
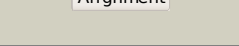
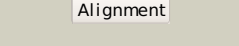
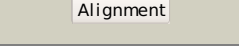
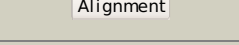


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1n2sa_</a>	 Alignment		100.0	85	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
2	<a href="#">c1z7eC_</a>	 Alignment		100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> protein arna; <b>PDBTitle:</b> crystal structure of full length arna
3	<a href="#">c1z45A_</a>	 Alignment		100.0	19	<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
4	<a href="#">d1vl0a_</a>	 Alignment		100.0	35	<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="#">c3sc6F_</a>	 Alignment		100.0	37	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> dtdp-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
6	<a href="#">d1i24a_</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
7	<a href="#">c2pzlB_</a>	 Alignment		100.0	17	<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
8	<a href="#">c2pk3B_</a>	 Alignment		100.0	12	<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
9	<a href="#">d1db3a_</a>	 Alignment		100.0	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
10	<a href="#">c2q1wC_</a>	 Alignment		100.0	17	<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+
11	<a href="#">c2vdyA_</a>	 Alignment		100.0	23	<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

12	<a href="#">dlkewa_</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
13	<a href="#">c2z1mC_</a>	Alignment		100.0	16	<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
14	<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
15	<a href="#">c3icpA_</a>	Alignment		100.0	16	<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
16	<a href="#">d1t2aa_</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
17	<a href="#">c2x4gA_</a>	Alignment		100.0	12	<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
18	<a href="#">c2yy7B_</a>	Alignment		100.0	15	<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
19	<a href="#">c2p5uC_</a>	Alignment		100.0	20	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> udp-glucose 4-epimerase; <b>PDBTitle:</b> crystal structure of thermophilus hb8 udp-glucose 4-2 epimerase complex with nad
20	<a href="#">d2blla1</a>	Alignment		100.0	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
21	<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
22	<a href="#">d2c5aa1</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
23	<a href="#">d1r6da_</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
24	<a href="#">c2ggsB_</a>	Alignment	not modelled	100.0	29	<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
25	<a href="#">c1n7gB_</a>	Alignment	not modelled	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.
26	<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
27	<a href="#">d1n7ha_</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
28	<a href="#">d1gy8a_</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

29	<a href="#">d2b69a1</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
30	<a href="#">c2b69A_</a>	Alignment	not modelled	100.0	16	<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
31	<a href="#">c2hunB_</a>	Alignment	not modelled	100.0	19	<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
32	<a href="#">c3eheB_</a>	Alignment	not modelled	100.0	17	<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
33	<a href="#">dludca_</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
34	<a href="#">dlwvga1</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
35	<a href="#">c3enkB_</a>	Alignment	not modelled	100.0	16	<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
36	<a href="#">c3m2pD_</a>	Alignment	not modelled	100.0	16	<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
37	<a href="#">c3lu1C_</a>	Alignment	not modelled	100.0	15	<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
38	<a href="#">dle6ua_</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
39	<a href="#">c2hrzA_</a>	Alignment	not modelled	100.0	17	<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
40	<a href="#">c2c20D_</a>	Alignment	not modelled	100.0	19	<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
41	<a href="#">dlek6a_</a>	Alignment	not modelled	100.0	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
42	<a href="#">dlbxka_</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
43	<a href="#">dlrkxa_</a>	Alignment	not modelled	100.0	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
44	<a href="#">dl5b8a_</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
45	<a href="#">dlorra_</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
46	<a href="#">c3a1nB_</a>	Alignment	not modelled	100.0	15	<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
47	<a href="#">c3gpiA_</a>	Alignment	not modelled	100.0	19	<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
48	<a href="#">dlz45a2</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
49	<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
50	<a href="#">c2q1uA_</a>	Alignment	not modelled	100.0	14	<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 wbmfi n2 complex with nad+ and udp
51	<a href="#">c3oh8A_</a>	Alignment	not modelled	100.0	16	<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
52	<a href="#">c2iodD_</a>	Alignment	not modelled	100.0	13	<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
53	<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
						<b>PDB header:</b> isomerase

54	<a href="#">c2x86K</a>	Alignment	not modelled	100.0	16	<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="#">d1y1pa1</a>	Alignment	not modelled	100.0	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
56	<a href="#">c3iusB</a>	Alignment	not modelled	100.0	18	<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
57	<a href="#">c2p4hX</a>	Alignment	not modelled	100.0	12	<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.)
58	<a href="#">d1eq2a</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
59	<a href="#">c2rh8A</a>	Alignment	not modelled	100.0	11	<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
60	<a href="#">c2zklA</a>	Alignment	not modelled	100.0	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
61	<a href="#">d1qyda</a>	Alignment	not modelled	100.0	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
62	<a href="#">c3c1oA</a>	Alignment	not modelled	100.0	12	<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
63	<a href="#">c2qx7A</a>	Alignment	not modelled	100.0	14	<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="#">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
65	<a href="#">d1qyca</a>	Alignment	not modelled	99.9	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
66	<a href="#">c2gn9B</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-glcnaC6 dehydratase; <b>PDBTitle:</b> crystal structure of udp-glcnaC6 inverting 4,6-dehydratase in complex2 with nadp and udp-glc
67	<a href="#">d1xgka</a>	Alignment	not modelled	99.9	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
68	<a href="#">c2vrcD</a>	Alignment	not modelled	99.9	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)
69	<a href="#">c3i5mA</a>	Alignment	not modelled	99.9	13	<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
70	<a href="#">c2zcuA</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized oxidoreductase ytfG; <b>PDBTitle:</b> crystal structure of a new type of nadph-dependent quinone2 oxidoreductase (qor2) from escherichia coli
71	<a href="#">c2gasA</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> isoflavone reductase; <b>PDBTitle:</b> crystal structure of isoflavone reductase
72	<a href="#">c2exxB</a>	Alignment	not modelled	99.9	15	<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
73	<a href="#">c3nzoB</a>	Alignment	not modelled	99.9	14	<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.
74	<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
75	<a href="#">d2q46a1</a>	Alignment	not modelled	99.9	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
76	<a href="#">c3ay3C</a>	Alignment	not modelled	99.9	15	<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
77	<a href="#">c3e8xA</a>	Alignment	not modelled	99.8	15	<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.
78	<a href="#">c3dhna</a>	Alignment	not modelled	99.8	14	<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.

79	<a href="#">c3dqpA</a>	 Alignment	not modelled	99.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase ylbe; <b>PDBTitle:</b> crystal structure of the oxidoreductase ylbe from2 lactococcus lactis, northeast structural genomics3 consortium target kr121.
80	<a href="#">c3h2sA</a>	 Alignment	not modelled	99.8	9	<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="#">d1hdoa</a>	 Alignment	not modelled	99.8	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
82	<a href="#">c3qvoA</a>	 Alignment	not modelled	99.7	14	<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.
83	<a href="#">d2a35a1</a>	 Alignment	not modelled	99.7	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
84	<a href="#">d2bkaa1</a>	 Alignment	not modelled	99.7	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
85	<a href="#">c3r6dA</a>	 Alignment	not modelled	99.7	17	<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
86	<a href="#">c3ew7A</a>	 Alignment	not modelled	99.7	15	<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="#">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
88	<a href="#">d1hyea1</a>	 Alignment	not modelled	99.2	19	<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="#">d1mlda1</a>	 Alignment	not modelled	99.2	16	<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
90	<a href="#">c3d7lG</a>	 Alignment	not modelled	99.1	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> G: <b>PDB Molecule:</b> lin1944 protein; <b>PDBTitle:</b> the crystal structure of the protein lin1944 from listeria innocua .
91	<a href="#">c2jahB</a>	 Alignment	not modelled	99.0	16	<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
92	<a href="#">c3l6eA</a>	 Alignment	not modelled	98.9	13	<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
93	<a href="#">d1ooea</a>	 Alignment	not modelled	98.9	10	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
94	<a href="#">c3grkE</a>	 Alignment	not modelled	98.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> enoyl-(acyl-carrier-protein) reductase (nadh); <b>PDBTitle:</b> crystal structure of short chain dehydrogenase reductase2 sdr glucose-ribitol dehydrogenase from brucella melitensis
95	<a href="#">c3ppiA</a>	 Alignment	not modelled	98.9	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxyacyl-coa dehydrogenase type-2; <b>PDBTitle:</b> crystal structure of 3-hydroxyacyl-coa dehydrogenase type-2 from2 mycobacterium avium
96	<a href="#">c2yutA</a>	 Alignment	not modelled	98.8	16	<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
97	<a href="#">c3i4fD</a>	 Alignment	not modelled	98.8	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier protein] reductase; <b>PDBTitle:</b> structure of putative 3-oxoacyl-reductase from bacillus thuringiensis
98	<a href="#">c2hlpB</a>	 Alignment	not modelled	98.8	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
99	<a href="#">d2gdza1</a>	 Alignment	not modelled	98.8	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
100	<a href="#">d1ulua</a>	 Alignment	not modelled	98.8	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
101	<a href="#">c3lylB</a>	 Alignment	not modelled	98.8	14	<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
102	<a href="#">c3toxG</a>	 Alignment	not modelled	98.7	11	<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
103	<a href="#">c3p19A_</a>	Alignment	not modelled	98.7	9	<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
104	<a href="#">c3l77A_</a>	Alignment	not modelled	98.7	19	<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 archaean thermococcus2 sibiricus complexed with 5-hydroxy-nadp
105	<a href="#">c3un1D_</a>	Alignment	not modelled	98.7	16	<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
106	<a href="#">c3ioyB_</a>	Alignment	not modelled	98.7	17	<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
107	<a href="#">c3k31B_</a>	Alignment	not modelled	98.7	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-(acyl-carrier-protein) reductase; <b>PDBTitle:</b> crystal structure of eonyl-(acyl-carrier-protein) reductase from2 anaplasma phagocytophilum in complex with nad at 1.9a resolution
108	<a href="#">d2pd4a1</a>	Alignment	not modelled	98.7	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="#">d1uaya_</a>	Alignment	not modelled	98.7	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="#">d2cmda1</a>	Alignment	not modelled	98.7	14	<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
111	<a href="#">c3ctmH_</a>	Alignment	not modelled	98.6	13	<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
112	<a href="#">c2z5lA_</a>	Alignment	not modelled	98.6	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tylactone synthase starter module and modules 1 <b>PDBTitle:</b> the first ketoreductase of the tylosin pks
113	<a href="#">d1luaa1</a>	Alignment	not modelled	98.6	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
114	<a href="#">c3gdfA_</a>	Alignment	not modelled	98.6	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable nadp-dependent mannitol dehydrogenase; <b>PDBTitle:</b> crystal structure of the nadp-dependent mannitol dehydrogenase from2 cladospirum herbarum.
115	<a href="#">c3tfoD_</a>	Alignment	not modelled	98.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <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 sinorhizobium meliloti
116	<a href="#">c2p68A_</a>	Alignment	not modelled	98.6	10	<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
117	<a href="#">c2qioA_</a>	Alignment	not modelled	98.6	14	<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
118	<a href="#">c3afnC_</a>	Alignment	not modelled	98.6	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> carbonyl reductase; <b>PDBTitle:</b> crystal structure of aldose reductase a1-r complexed with nadp
119	<a href="#">d1fjha_</a>	Alignment	not modelled	98.6	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
120	<a href="#">c2dteB_</a>	Alignment	not modelled	98.6	12	<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 (aldt)2 in complex with nadh