


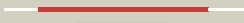














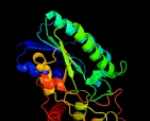




# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD3266c\_(rmlD)\_3646892\_3647806  
 Date Thu Aug 8 16:20:47 BST 2019  
 Unique Job ID 7f79a0c3af798079

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1z45A_</a>	 Alignment		100.0	18	<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 saccharomyces cerevisiae3 complexed with nad, udp-glucose, and galactose
2	<a href="#">c1z7eC_</a>	 Alignment		100.0	17	<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="#">c3sc6F_</a>	 Alignment		100.0	36	<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
4	<a href="#">d1vl0a_</a>	 Alignment		100.0	37	<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="#">c4wpgA_</a>	 Alignment		100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dtdp-4-dehydrorhamnose reductase; <b>PDBTitle:</b> group a streptococcus gaca is an essential dtdp-4-dehydrorhamnose2 reductase (rmlD)
6	<a href="#">c5u9cC_</a>	 Alignment		100.0	25	<b>PDB header:</b> hydrolase,oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> dtdp-4-dehydrorhamnose reductase; <b>PDBTitle:</b> 1.9 angstrom resolution crystal structure of dtdp-4-dehydrorhamnose2 reductase from yersinia enterocolitica
7	<a href="#">d1n2sa_</a>	 Alignment		100.0	31	<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="#">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
9	<a href="#">d2b69a1</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
10	<a href="#">c2b69A_</a>	 Alignment		100.0	19	<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
11	<a href="#">d1oc2a_</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

12	<a href="#">c2ydyA_</a>	Alignment		100.0	26	<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 synthetase 2, beta2 subunit in orthorhombic crystal form
13	<a href="#">d1r6da_</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
14	<a href="#">c2pzlB_</a>	Alignment		100.0	18	<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 enzyme wbmj in2 complex with nad and udp
15	<a href="#">c6aaqD_</a>	Alignment		100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> gdp-l-fucose synthetase; <b>PDBTitle:</b> crystal structure of a gdp-l-fucose synthetase from naegleria fowleri
16	<a href="#">c2hunB_</a>	Alignment		100.0	16	<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
17	<a href="#">d1db3a_</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="#">d1e6ua_</a>	Alignment		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
19	<a href="#">c4b8wB_</a>	Alignment		100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> gdp-l-fucose synthase; <b>PDBTitle:</b> crystal structure of human gdp-l-fucose synthase with bound nadp and2 gdp, tetragonal crystal form
20	<a href="#">c6dntA_</a>	Alignment		100.0	11	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent epimerase/dehydratase; <b>PDBTitle:</b> udp-n-acetylglucosamine 4-epimerase from methanobrevibacter2 ruminantium m1 in complex with udp-n-acetylmuramic acid
21	<a href="#">c2pk3B_</a>	Alignment	not modelled	100.0	16	<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
22	<a href="#">c4lisA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-glucose 4-epimerase; <b>PDBTitle:</b> crystal structure of udp-galactose-4-epimerase from aspergillus2 nidulans
23	<a href="#">c6bwlA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> pal; <b>PDBTitle:</b> x-ray structure of pal from bacillus thuringiensis
24	<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.
25	<a href="#">d2c5aa1</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
26	<a href="#">c2x4gA_</a>	Alignment	not modelled	100.0	19	<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-sugar epimerase2 from pseudomonas aeruginosa
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="#">c4r1sB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cinnamoyl coa reductase; <b>PDBTitle:</b> crystal structure of petunia hybrida cinnamoyl-coa reductase
29	<a href="#">c2z1mC_</a>	Alignment	not modelled	100.0	15	<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
30	<a href="#">c2hrzA_</a>	Alignment	not modelled	100.0	15	<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
31	<a href="#">c6nbrC_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> kavalactone reductase 1; <b>PDBTitle:</b> crystal structure of piper methysticum kavalactone reductase 1 in2 complex with nadp
32	<a href="#">c4egbC_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> dtdp-glucose 4,6-dehydratase; <b>PDBTitle:</b> 3.0 angstrom resolution crystal structure of dtdp-glucose 4,6-2 dehydratase (rfbb) from bacillus anthracis str. ames in complex with3 nad
33	<a href="#">c4b4oA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> epimerase family protein sdr39u1; <b>PDBTitle:</b> crystal structure of human epimerase family protein sdr39u1 (isoform2)2 with nadph
34	<a href="#">c4pvcB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadph-dependent methylglyoxal reductase gre2; <b>PDBTitle:</b> crystal structure of yeast methylglyoxal/ isovaleraldehyde reductase2 gre2
35	<a href="#">c4ej0D_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> adp-l-glycero-d-manno-heptose-6-epimerase; <b>PDBTitle:</b> crystal structure of adp-l-glycero-d-manno-heptose-6-epimerase from2 burkholderia thailandensis
36	<a href="#">c3m2pD_</a>	Alignment	not modelled	100.0	12	<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="#">c3enkB_</a>	Alignment	not modelled	100.0	17	<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 from burkholderia2 pseudomallei
38	<a href="#">c3eheB_</a>	Alignment	not modelled	100.0	19	<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
39	<a href="#">c5gmoA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein induced by osmotic stress; <b>PDBTitle:</b> x-ray structure of carbonyl reductase sscr
40	<a href="#">c5j9aB_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> l-threonine 3-dehydrogenase; <b>PDBTitle:</b> l-threonine dehydrogenase from trypanosoma brucei.
41	<a href="#">d1rpna_</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
42	<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
43	<a href="#">d1ek6a_</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
44	<a href="#">c5zedA_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein adh; <b>PDBTitle:</b> crystal structure of kluyveromyces polyspora adh (kpadh) mutant2 (e214v/t215s)
45	<a href="#">c6d2vA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> terb oxidoreductase; <b>PDBTitle:</b> apo structure of terb, an nadp dependent oxidoreductase in the2 terfestatin biosynthesis pathway
46	<a href="#">c4twrA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> nad binding site:nad-dependent epimerase/dehydratase:udp- <b>PDBTitle:</b> structure of udp-glucose 4-epimerase from brucella abortus
47	<a href="#">d1kewa_</a>	Alignment	not modelled	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
48	<a href="#">c2p5uC_</a>	Alignment	not modelled	100.0	19	<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-epimerase2 complex with nad
49	<a href="#">c2v6gA_</a>	Alignment	not modelled	100.0	14	<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="#">c5df1A_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> iridoid synthase; <b>PDBTitle:</b> iridoid synthase from catharanthus roseus - ternary complex with nadp+2 and geranic acid
51	<a href="#">c2iodD_</a>	Alignment	not modelled	100.0	11	<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
52	<a href="#">c2q1wC_</a>	Alignment	not modelled	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+
53	<a href="#">c4qqrB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 3,5-epimerase/4-reductase; <b>PDBTitle:</b> structural insight into nucleotide rhamnose

						synthase/epimerase-2 reductase from arabidopsis thaliana
54	<a href="#">c4zrmB_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-glucose 4-epimerase; <b>PDBTitle:</b> crystal structure of udp-glucose 4-epimerase (tm0509) from2 hyperthermophilic eubacterium thermotoga maritima
55	<a href="#">c2yy7B_</a>	Alignment	not modelled	100.0	13	<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
56	<a href="#">c4idgB_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase; <b>PDBTitle:</b> crystal structure of a short-chain dehydrogenase/reductase superfamily2 protein from agrobacterium tumefaciens (target efi-506441) with bound3 nad, monoclinic form 2
57	<a href="#">d1sb8a_</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
58	<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.)
59	<a href="#">c5uzhA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nafoa.00085.b; <b>PDBTitle:</b> crystal structure of a gdp-mannose dehydratase from naegleria fowleri
60	<a href="#">d1t2aa_</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
61	<a href="#">c5b6kA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein cgkr1; <b>PDBTitle:</b> crystal strucutre of ketoreductase 1 from candida glabrata
62	<a href="#">c1t2aC_</a>	Alignment	not modelled	100.0	16	<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
63	<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
64	<a href="#">c2c20D_</a>	Alignment	not modelled	100.0	15	<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
65	<a href="#">c3icpA_</a>	Alignment	not modelled	100.0	15	<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
66	<a href="#">c6el3A_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxo-delta(4,5)-steroid 5-beta-reductase; <b>PDBTitle:</b> structure of progesterone 5beta-reductase from arabidopsis thaliana in2 complex with nadp
67	<a href="#">c3lu1C_</a>	Alignment	not modelled	100.0	13	<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
68	<a href="#">d1wvga1</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
69	<a href="#">d1z45a2</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
70	<a href="#">c4lw8B_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative epimerase; <b>PDBTitle:</b> crystal structure of a putative epimerase from burkholderia2 cenocepacia j2315
71	<a href="#">c3wj7B_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of gox2253
72	<a href="#">d2blla1</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
73	<a href="#">d1rkxa_</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
74	<a href="#">c2q1uA_</a>	Alignment	not modelled	100.0	17	<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
75	<a href="#">c2rh8A_</a>	Alignment	not modelled	100.0	12	<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
76	<a href="#">c2ggsB_</a>	Alignment	not modelled	100.0	30	<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
77	<a href="#">d1bxka_</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
78	<a href="#">c3vpsB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> nad-dependent epimerase/dehydratase; <b>PDBTitle:</b> structure of a novel nad dependent-ndp-hexosamine 5,6-dehydratase,2 tuna, involved in tunicamycin biosynthesis
79	<a href="#">c3iucB_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized conserved protein;

79	<a href="#">c3usb_</a>	Alignment	not modelled	100.0	17	<b>PDBTitle:</b> the structure of a functionally unknown conserved protein2 from silicibacter pomeroyi dss <b>PDB header:</b> oxidoreductase
80	<a href="#">c3qukA_</a>	Alignment	not modelled	100.0	13	<b>Chain:</b> A: <b>PDB Molecule:</b> dihydroflavonol-4-reductase; <b>PDBTitle:</b> crystal structure of cinnamyl-alcohol dehydrogenase 2 mutant k169a
81	<a href="#">d1udca_</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
82	<a href="#">d1gy8a_</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
83	<a href="#">c3gpiA_</a>	Alignment	not modelled	100.0	17	<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/dehydratase from2 methylobacillus flagellatus
84	<a href="#">c3a1nB_</a>	Alignment	not modelled	100.0	14	<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 from hyperthermophilic2 archaeon thermoplasma volcanium
85	<a href="#">c3wmxC_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nad dependent epimerase/dehydratase; <b>PDBTitle:</b> gale-like l-threonine dehydrogenase from cupriavidus necator (holo2 form)
86	<a href="#">c4f6cA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aUSA reductase domain protein; <b>PDBTitle:</b> crystal structure of aureusimine biosynthetic cluster reductase domain
87	<a href="#">c4w4tA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mXaa; <b>PDBTitle:</b> the crystal structure of the terminal r domain from the myxalamid pks-2 nrps biosynthetic pathway
88	<a href="#">c2x86K_</a>	Alignment	not modelled	100.0	13	<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
89	<a href="#">c3slgB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pbpgp3 protein; <b>PDBTitle:</b> crystal structure of pbpgp3 protein from burkholderia pseudomallei
90	<a href="#">c3slgF_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> pbpgp3 protein; <b>PDBTitle:</b> crystal structure of pbpgp3 protein from burkholderia pseudomallei
91	<a href="#">d1orra_</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
92	<a href="#">c3pvzD_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> udp-n-acetylglucosamine 4,6-dehydratase; <b>PDBTitle:</b> udp-n-acetylglucosamine 4,6-dehydratase from vibrio fischeri
93	<a href="#">c3w1vA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> capsular polysaccharide synthesis enzyme cap8e; <b>PDBTitle:</b> crystal structure of capsular polysaccharide synthesizing enzyme cape2 from staphylococcus aureus in complex with inhibitor
94	<a href="#">c5y1dB_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nad dependent epimerase/dehydratase family; <b>PDBTitle:</b> monomeric l-threonine 3-dehydrogenase from metagenome database (apo2 form)
95	<a href="#">c5bjUA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> wlal protein; <b>PDBTitle:</b> x-ray structure of the pglf dehydratase from campylobacter jejuni in2 complex with udp and nad(h)
96	<a href="#">c4j2oD_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> udp-n-acetylglucosamine 4,6-dehydratase/5-epimerase; <b>PDBTitle:</b> crystal structure of nadp-bound wbjb from a. baumannii community2 strain d1279779
97	<a href="#">c4lk3A_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-glucuronic acid decarboxylase 1; <b>PDBTitle:</b> crystal structure of human udp-xylose synthase r236a substitution
98	<a href="#">d1eq2a_</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
99	<a href="#">c5lnkd_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> <b>PDBTitle:</b> entire ovine respiratory complex i
100	<a href="#">c5u4qB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> lipid-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dtdp-glucose 4,6-dehydratase; <b>PDBTitle:</b> 1.5 angstrom resolution crystal structure of nad-dependent epimerase2 from klebsiella pneumoniae in complex with nad.
101	<a href="#">c3sxpD_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> adp-l-glycero-d-mannoheptose-6-epimerase; <b>PDBTitle:</b> crystal structure of helicobacter pylori adp-l-glycero-d-manno-2 heptose-6-epimerase (rfad, hp0859)
102	<a href="#">c4yraD_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> l-threonine 3-dehydrogenase, mitochondrial; <b>PDBTitle:</b> mouse tdh in the apo form
103	<a href="#">c5z76D_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> artificial l-threonine 3-dehydrogenase; <b>PDBTitle:</b> artificial l-threonine 3-dehydrogenase designed by full consensus2 design
						<b>PDB header:</b> isomerase



104	<a href="#">c2zkA_</a>	Alignment	not modelled	100.0	15	<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
105	<a href="#">c2qx7A_</a>	Alignment	not modelled	100.0	13	<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
106	<a href="#">c6gcsE_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> nuem subunit; <b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica
107	<a href="#">c6bwcA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> polysaccharide biosynthesis protein capd; <b>PDBTitle:</b> x-ray structure of pen from bacillus thuringiensis
108	<a href="#">c5msuC_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> carboxylic acid reductase; <b>PDBTitle:</b> structure of the r domain of carboxylic acid reductase (car) from2 mycobacterium marinum in complex with nadp, p21 form
109	<a href="#">c2gn9B_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-glcnaC 6 dehydratase; <b>PDBTitle:</b> crystal structure of udp-glcnaC inverting 4,6-dehydratase in complex2 with nadp and udp-glc
110	<a href="#">c3c1oA_</a>	Alignment	not modelled	100.0	11	<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
111	<a href="#">c3wmwB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nad dependent epimerase/dehydratase; <b>PDBTitle:</b> gale-like l-threonine dehydrogenase from cupriavidus necator (apo2 form)
112	<a href="#">d1qyca_</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
113	<a href="#">d1qyda_</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
114	<a href="#">c2gasA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> isoflavone reductase; <b>PDBTitle:</b> crystal structure of isoflavone reductase
115	<a href="#">c4dqvA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> probable peptide synthetase nrp (peptide synthase); <b>PDBTitle:</b> crystal structure of reductase (r) domain of non-ribosomal peptide2 synthetase from mycobacterium tuberculosis
116	<a href="#">c3i5mA_</a>	Alignment	not modelled	100.0	15	<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
117	<a href="#">c5i3zA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> polyketide ketoreductase simc7; <b>PDBTitle:</b> polyketide ketoreductase simc7 - binary complex with nadp+
118	<a href="#">c3e48B_</a>	Alignment	not modelled	100.0	15	<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
119	<a href="#">d1xgka_</a>	Alignment	not modelled	99.9	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
120	<a href="#">c2vrcD_</a>	Alignment	not modelled	99.9	14	<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)