




















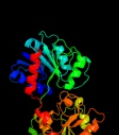











#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2iw1a1</a>	 Alignment		100.0	100	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Glycosyl transferases group 1
2	<a href="#">c3c4vB</a>	 Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> predicted glycosyltransferases; <b>PDBTitle:</b> structure of the retaining glycosyltransferase msha:the2 first step in mycothiol biosynthesis. organism:3 corynebacterium glutamicum : complex with udp and 1l-ins-1-4 p.
3	<a href="#">c2r60A</a>	 Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyl transferase, group 1; <b>PDBTitle:</b> structure of apo sucrose phosphate synthase (sps) of2 halothermothrix oronii
4	<a href="#">d2bisa1</a>	 Alignment		100.0	20	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Glycosyl transferases group 1
5	<a href="#">c3s29C</a>	 Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> sucrose synthase 1; <b>PDBTitle:</b> the crystal structure of sucrose synthase-1 from arabidopsis thaliana2 and its functional implications.
6	<a href="#">c2jjmH</a>	 Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> glycosyl transferase, group 1 family protein; <b>PDBTitle:</b> crystal structure of a family gt4 glycosyltransferase from2 bacillus anthracis orf ba1558.
7	<a href="#">c2gejA</a>	 Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatidylinositol mannosyltransferase (pima); <b>PDBTitle:</b> crystal structure of phosphatidylinositol mannosyltransferase (pima)2 from mycobacterium smegmatis in complex with gdp-man
8	<a href="#">c3okaA</a>	 Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> gdp-mannose-dependent alpha-(1-6)-phosphatidylinositol <b>PDBTitle:</b> crystal structure of corynebacterium glutamicum pimb' in complex with2 gdp-man (triclinic crystal form)
9	<a href="#">c2qzsA</a>	 Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycogen synthase; <b>PDBTitle:</b> crystal structure of wild-type e.coli gs in complex with adp2 and glucose(wtgsb)
10	<a href="#">d1rzua</a>	 Alignment		100.0	15	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Glycosyl transferases group 1
11	<a href="#">c3oy2A</a>	 Alignment		100.0	14	<b>PDB header:</b> viral protein,transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyltransferase b736l; <b>PDBTitle:</b> crystal structure of a putative glycosyltransferase from paramecium2 bursaria chlorella virus ny2a

12	<a href="#">c2x6rA_</a>	Alignment		100.0	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> trehalose-synthase tret; <b>PDBTitle:</b> crystal structure of trehalose synthase tret from p.2 horikoshi produced by soaking in trehalose
13	<a href="#">c2xmpB_</a>	Alignment		100.0	16	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> trehalose-synthase tret; <b>PDBTitle:</b> crystal structure of trehalose synthase tret mutant e326a2 from p.horishiki in complex with udp
14	<a href="#">c1uquB_</a>	Alignment		100.0	15	<b>PDB header:</b> synthase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha, alpha-trehalose-phosphate synthase; <b>PDBTitle:</b> trehalose-6-phosphate from e. coli bound with udp-glucose.
15	<a href="#">d1uqta_</a>	Alignment		100.0	13	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Trehalose-6-phosphate synthase, OtsA
16	<a href="#">c2x0dA_</a>	Alignment		100.0	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> wsaf; <b>PDBTitle:</b> apo structure of wsaf
17	<a href="#">c3nb0A_</a>	Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycogen [starch] synthase isoform 2; <b>PDBTitle:</b> glucose-6-phosphate activated form of yeast glycogen synthase
18	<a href="#">c2iv3B_</a>	Alignment		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyltransferase; <b>PDBTitle:</b> crystal structure of avigt4, a glycosyltransferase involved2 in avilamycin a biosynthesis
19	<a href="#">c3o3cD_</a>	Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> glycogen [starch] synthase isoform 2; <b>PDBTitle:</b> glycogen synthase basal state udp complex
20	<a href="#">d1f6da_</a>	Alignment		100.0	13	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDP-N-acetylglucosamine 2-epimerase
21	<a href="#">c3dzcA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine 2-epimerase; <b>PDBTitle:</b> 2.35 angstrom resolution structure of webc (vc0917), a udp-n-2 acetylglucosamine 2-epimerase from vibrio cholerae.
22	<a href="#">c3ot5D_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> udp-n-acetylglucosamine 2-epimerase; <b>PDBTitle:</b> 2.2 angstrom resolution crystal structure of putative udp-n-2 acetylglucosamine 2-epimerase from listeria monocytogenes
23	<a href="#">d1v4va_</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDP-N-acetylglucosamine 2-epimerase
24	<a href="#">c3rhzb_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> nucleotide sugar synthetase-like protein; <b>PDBTitle:</b> structure and functional analysis of a new subfamily of2 glycosyltransferases required for glycosylation of serine-rich3 streptococcal adhesions
25	<a href="#">c2xcuC_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> 3-deoxy-d-manno-2-octulosonic acid transferase; <b>PDBTitle:</b> membrane-embedded monofunctional glycosyltransferase waaa of aquifex2 aeolicus, comlex with cmp
26	<a href="#">c2q6vA_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucuronosyltransferase gumk; <b>PDBTitle:</b> crystal structure of gumk in complex with udp
27	<a href="#">d1o6ca_</a>	Alignment	not modelled	99.9	12	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDP-N-acetylglucosamine 2-epimerase
28	<a href="#">d1f0ka_</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Peptidoglycan biosynthesis glycosyltransferase MurG

29	<a href="#">c3ia7A_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> calg4; <b>PDBTitle:</b> crystal structure of calg4, the calicheamicin glycosyltransferase
30	<a href="#">c3iaaB_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> calg2; <b>PDBTitle:</b> crystal structure of calg2, calicheamicin glycosyltransferase, tdp2 bound form
31	<a href="#">c3othB_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> B: <b>PDB Molecule:</b> calg1; <b>PDBTitle:</b> crystal structure of calg1, calicheamicin glycosyltransferase, tdp2 and calicheamicin alpha3i bound form
32	<a href="#">c2p6pB_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyl transferase; <b>PDBTitle:</b> x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2
33	<a href="#">c2iyaB_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> oleandomycin glycosyltransferase; <b>PDBTitle:</b> the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
34	<a href="#">c2iyfA_</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> oleandomycin glycosyltransferase; <b>PDBTitle:</b> the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
35	<a href="#">c2vsnB_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> xcogt; <b>PDBTitle:</b> structure and topological arrangement of an o-glcnac2 transferase homolog: insight into molecular control of3 intracellular glycosylation
36	<a href="#">d2f9fa1</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Glycosyl transferases group 1
37	<a href="#">d2bfwa1</a>	Alignment	not modelled	99.8	23	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Glycosyl transferases group 1
38	<a href="#">c3qhpB_</a>	Alignment	not modelled	99.8	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> type 1 capsular polysaccharide biosynthesis protein j <b>PDBTitle:</b> crystal structure of the catalytic domain of cholesterol-alpha-2 glucosyltransferase from helicobacter pylori
39	<a href="#">c3d0qB_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein calg3; <b>PDBTitle:</b> crystal structure of calg3 from micromonospora echinospora determined2 in space group i222
40	<a href="#">d1iira_</a>	Alignment	not modelled	99.7	13	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Gtf glycosyltransferase
41	<a href="#">c3pe3D_</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> udp-n-acetylglucosamine--peptide n- <b>PDBTitle:</b> structure of human o-glcnac transferase and its complex with a peptide2 substrate
42	<a href="#">d1pn3a_</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Gtf glycosyltransferase
43	<a href="#">d1rrva_</a>	Alignment	not modelled	99.6	13	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Gtf glycosyltransferase
44	<a href="#">d2acva1</a>	Alignment	not modelled	99.5	12	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDPGT-like
45	<a href="#">c3hbjA_</a>	Alignment	not modelled	99.3	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> flavonoid 3-o-glucosyltransferase; <b>PDBTitle:</b> structure of ugt78g1 complexed with udp
46	<a href="#">d2pq6a1</a>	Alignment	not modelled	99.3	11	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDPGT-like
47	<a href="#">d2c1xa1</a>	Alignment	not modelled	99.0	13	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDPGT-like
48	<a href="#">c3l7mC_</a>	Alignment	not modelled	98.9	11	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> teichoic acid biosynthesis protein f; <b>PDBTitle:</b> structure of the wall teichoic acid polymerase tagf, h548a
49	<a href="#">d2vcha1</a>	Alignment	not modelled	98.7	11	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDPGT-like
50	<a href="#">c3hbmA_</a>	Alignment	not modelled	98.6	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-sugar hydrolase; <b>PDBTitle:</b> crystal structure of pseg from campylobacter jejuni
51	<a href="#">c3q3hA_</a>	Alignment	not modelled	98.4	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hmw1c-like glycosyltransferase; <b>PDBTitle:</b> crystal structure of the actinobacillus pleuropneumoniae hmw1c2 glycosyltransferase in complex with udp-glc
52	<a href="#">c2c4mA_</a>	Alignment	not modelled	97.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycogen phosphorylase; <b>PDBTitle:</b> starch phosphorylase: structural studies explain oxyanion-2 dependent kinetic stability and regulatory control.
53	<a href="#">c3ddsB_</a>	Alignment	not modelled	97.6	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycogen phosphorylase, liver form; <b>PDBTitle:</b> crystal structure of glycogen phosphorylase complexed with an2 anthranilimide based inhibitor gsk261
54	<a href="#">c2h1fB_</a>	Alignment	not modelled	97.6	9	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> lipopolysaccharide heptosyltransferase-1; <b>PDBTitle:</b> e. coli heptosyltransferase waac with adp

55	<a href="#">c2o6lA</a>	<div><div></div><div>Alignment</div></div>	not modelled	97.6	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-glucuronosyltransferase 2b7; <b>PDBTitle:</b> crystal structure of the udp-glucuronic acid binding domain2 of the human drug metabolizing udp-glucuronosyltransferase3 2b7
56	<a href="#">d2atia1</a>	<div><div></div><div>Alignment</div></div>	not modelled	97.5	16	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Oligosaccharide phosphorylase
57	<a href="#">d1ygpA</a>	<div><div></div><div>Alignment</div></div>	not modelled	97.5	12	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Oligosaccharide phosphorylase
58	<a href="#">d1l5wa</a>	<div><div></div><div>Alignment</div></div>	not modelled	97.4	16	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Oligosaccharide phosphorylase
59	<a href="#">d2gj4a1</a>	<div><div></div><div>Alignment</div></div>	not modelled	97.3	16	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Oligosaccharide phosphorylase
60	<a href="#">d1pswa</a>	<div><div></div><div>Alignment</div></div>	not modelled	97.0	8	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> ADP-heptose LPS heptosyltransferase II
61	<a href="#">c3tovB</a>	<div><div></div><div>Alignment</div></div>	not modelled	96.1	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyl transferase family 9; <b>PDBTitle:</b> the crystal structure of the glycosyl transferase family 9 from2 veillonella parvula dsm 2008
62	<a href="#">c2jzcA</a>	<div><div></div><div>Alignment</div></div>	not modelled	95.4	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine transferase subunit <b>PDBTitle:</b> nmr solution structure of alg13: the sugar donor subunit of2 a yeast n-acetylglucosamine transferase. northeast3 structural genomics consortium target yg1
63	<a href="#">d1s3ia2</a>	<div><div></div><div>Alignment</div></div>	not modelled	93.8	13	<b>Fold:</b> Formyltransferase <b>Superfamily:</b> Formyltransferase <b>Family:</b> Formyltransferase
64	<a href="#">d1jaya</a>	<div><div></div><div>Alignment</div></div>	not modelled	93.5	33	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
65	<a href="#">c1gshA</a>	<div><div></div><div>Alignment</div></div>	not modelled	92.9	5	<b>PDB header:</b> glutathione biosynthesis ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione biosynthetic ligase; <b>PDBTitle:</b> structure of escherichia coli glutathione synthetase at ph 7.5
66	<a href="#">d1ydga</a>	<div><div></div><div>Alignment</div></div>	not modelled	92.9	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> WrbA-like
67	<a href="#">c2pk3B</a>	<div><div></div><div>Alignment</div></div>	not modelled	92.8	13	<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
68	<a href="#">c1y6gB</a>	<div><div></div><div>Alignment</div></div>	not modelled	92.7	14	<b>PDB header:</b> transferase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> dna alpha-glucosyltransferase; <b>PDBTitle:</b> alpha-glucosyltransferase in complex with udp and a 13_mer2 dna containing a hmu base at 2.8 a resolution
69	<a href="#">d1gsaa1</a>	<div><div></div><div>Alignment</div></div>	not modelled	92.5	5	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> Prokaryotic glutathione synthetase, N-terminal domain
70	<a href="#">d2bw0a2</a>	<div><div></div><div>Alignment</div></div>	not modelled	92.4	13	<b>Fold:</b> Formyltransferase <b>Superfamily:</b> Formyltransferase <b>Family:</b> Formyltransferase
71	<a href="#">d1udca</a>	<div><div></div><div>Alignment</div></div>	not modelled	92.3	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
72	<a href="#">d1vl0a</a>	<div><div></div><div>Alignment</div></div>	not modelled	92.0	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
73	<a href="#">c2ixdB</a>	<div><div></div><div>Alignment</div></div>	not modelled	91.8	8	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lmbe-related protein; <b>PDBTitle:</b> crystal structure of the putative deacetylase bc1534 from2 bacilus cereus
74	<a href="#">d1kewa</a>	<div><div></div><div>Alignment</div></div>	not modelled	91.5	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
75	<a href="#">d2d1pa1</a>	<div><div></div><div>Alignment</div></div>	not modelled	91.4	19	<b>Fold:</b> DsrEFH-like <b>Superfamily:</b> DsrEFH-like <b>Family:</b> DsrEF-like
76	<a href="#">c2ggsB</a>	<div><div></div><div>Alignment</div></div>	not modelled	91.3	15	<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="#">c3m2pD</a>	<div><div></div><div>Alignment</div></div>	not modelled	91.3	17	<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
78	<a href="#">d2hy5a1</a>	<div><div></div><div>Alignment</div></div>	not modelled	91.2	19	<b>Fold:</b> DsrEFH-like <b>Superfamily:</b> DsrEFH-like <b>Family:</b> DsrEF-like
79	<a href="#">c1s3iA</a>	<div><div></div><div>Alignment</div></div>	not modelled	91.2	14	<b>PDB header:</b> hydrolase, oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 10-formyltetrahydrofolate dehydrogenase; <b>PDBTitle:</b> crystal structure of the n terminal hydrolase domain of 10-2 formyltetrahydrofolate dehydrogenase
						<b>Fold:</b> LmbE-like

80	<a href="#">dluana_</a>	Alignment	not modelled	90.8	8	<b>Superfamily:</b> LmbE-like <b>Family:</b> LmbE-like
81	<a href="#">c3icpA_</a>	Alignment	not modelled	90.4	18	<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
82	<a href="#">d1fjha_</a>	Alignment	not modelled	90.3	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
83	<a href="#">c2ofpB_</a>	Alignment	not modelled	90.1	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ketopantoate reductase; <b>PDBTitle:</b> crystal structure of escherichia coli ketopantoate2 reductase in a ternary complex with nadp+ and pantoate
84	<a href="#">c2x4gA_</a>	Alignment	not modelled	90.1	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-sugar2 epimerase from pseudomonas aeruginosa
85	<a href="#">c2p5uC_</a>	Alignment	not modelled	89.8	22	<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
86	<a href="#">d1n2sa_</a>	Alignment	not modelled	89.8	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
87	<a href="#">c2pzlB_</a>	Alignment	not modelled	89.7	19	<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
88	<a href="#">d1txga2</a>	Alignment	not modelled	89.5	24	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
89	<a href="#">d2f1ka2</a>	Alignment	not modelled	89.4	22	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
90	<a href="#">d1fmta2</a>	Alignment	not modelled	89.3	12	<b>Fold:</b> Formyltransferase <b>Superfamily:</b> Formyltransferase <b>Family:</b> Formyltransferase
91	<a href="#">d2c5aa1</a>	Alignment	not modelled	89.1	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="#">c3l4bG_</a>	Alignment	not modelled	88.7	22	<b>PDB header:</b> transport protein <b>Chain:</b> G: <b>PDB Molecule:</b> trka k+ channel protien tm1088b; <b>PDBTitle:</b> crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
93	<a href="#">c3sc6F_</a>	Alignment	not modelled	88.1	10	<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 ddtp-4-dehydrorhamnose2 reductase (rfd) from bacillus anthracis str. ames in complex with3 nadp
94	<a href="#">d1ks9a2</a>	Alignment	not modelled	87.9	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
95	<a href="#">c1ks9A_</a>	Alignment	not modelled	87.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydropantoate 2-reductase; <b>PDBTitle:</b> ketopantoate reductase from escherichia coli
96	<a href="#">c3oh8A_</a>	Alignment	not modelled	87.2	17	<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
97	<a href="#">d1mv8a2</a>	Alignment	not modelled	86.8	38	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
98	<a href="#">c2f1kD_</a>	Alignment	not modelled	86.7	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> prephenate dehydrogenase; <b>PDBTitle:</b> crystal structure of synechocystis arogenate dehydrogenase
99	<a href="#">d2blna2</a>	Alignment	not modelled	86.3	14	<b>Fold:</b> Formyltransferase <b>Superfamily:</b> Formyltransferase <b>Family:</b> Formyltransferase
100	<a href="#">c2q1wC_</a>	Alignment	not modelled	86.0	24	<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+
101	<a href="#">d1bxka_</a>	Alignment	not modelled	86.0	11	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
102	<a href="#">c1yrwA_</a>	Alignment	not modelled	85.7	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein arna; <b>PDBTitle:</b> crystal structure of e.coli arna transformylase domain
103	<a href="#">c3tqgA_</a>	Alignment	not modelled	84.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna formyltransferase; <b>PDBTitle:</b> structure of the methionyl-trna formyltransferase (fmt) from coxiella2 burnetii
104	<a href="#">c1n7gB_</a>	Alignment	not modelled	84.8	11	<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.



105	<a href="#">c3dojA_</a>	Alignment	not modelled	84.6	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dehydrogenase-like protein; <b>PDBTitle:</b> structure of glyoxylate reductase 1 from arabidopsis2 (atglyr1)
106	<a href="#">c1z7eC_</a>	Alignment	not modelled	84.5	11	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> protein arna; <b>PDBTitle:</b> crystal structure of full length arna
107	<a href="#">c3g17H_</a>	Alignment	not modelled	84.5	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> H: <b>PDB Molecule:</b> similar to 2-dehydropantoate 2-reductase; <b>PDBTitle:</b> structure of putative 2-dehydropantoate 2-reductase from2 staphylococcus aureus
108	<a href="#">c3kigB_</a>	Alignment	not modelled	84.3	13	<b>PDB header:</b> hydrolase, metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> co dehydrogenase/acetyl-coa synthase complex, accessory <b>PDBTitle:</b> adp-bound state of cooc1
109	<a href="#">c1z45A_</a>	Alignment	not modelled	84.2	12	<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
110	<a href="#">c3l77A_</a>	Alignment	not modelled	84.1	26	<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
111	<a href="#">c3g0oA_</a>	Alignment	not modelled	84.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxyisobutyrate dehydrogenase; <b>PDBTitle:</b> crystal structure of 3-hydroxyisobutyrate dehydrogenase2 (ygbj) from salmonella typhimurium
112	<a href="#">d1pgja2</a>	Alignment	not modelled	83.8	28	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
113	<a href="#">d2afhe1</a>	Alignment	not modelled	83.8	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
114	<a href="#">c1bxgA_</a>	Alignment	not modelled	83.3	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol-3-phosphate dehydrogenase [nad(p)+]; <b>PDBTitle:</b> structure of glycerol-3-phosphate dehydrogenase from archaeoglobus2 fulgidus
115	<a href="#">c2gf2B_</a>	Alignment	not modelled	83.2	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-hydroxyisobutyrate dehydrogenase; <b>PDBTitle:</b> crystal structure of human hydroxyisobutyrate dehydrogenase
116	<a href="#">c1fmtA_</a>	Alignment	not modelled	83.1	13	<b>PDB header:</b> formyltransferase <b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna fmet formyltransferase; <b>PDBTitle:</b> methionyl-trnafmet formyltransferase from escherichia coli
117	<a href="#">d1e7wa_</a>	Alignment	not modelled	82.8	26	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
118	<a href="#">c2qhxB_</a>	Alignment	not modelled	82.7	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> pteridine reductase 1; <b>PDBTitle:</b> structure of pteridine reductase from leishmania major2 complexed with a ligand
119	<a href="#">c2hunB_</a>	Alignment	not modelled	82.5	14	<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
120	<a href="#">d2bli1a1</a>	Alignment	not modelled	82.4	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