
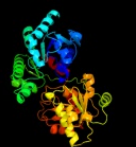





















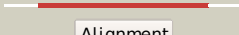





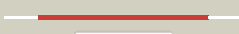






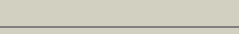
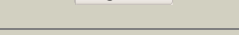
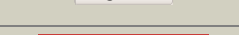
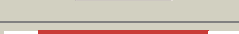




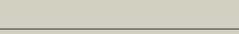
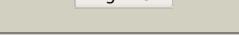
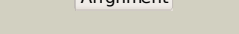
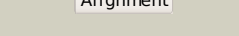


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3c4vB_</a>	 Alignment		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> predicted glycosyltransferases; <b>PDBTitle:</b> structure of the retaining glycosyltransferase msha:the2 first step in mycothiol biosynthesis. organism:3 corynebacterium glutamicum : complex with udp and 1l-ins-1-4 p.
2	<a href="#">c2r60A_</a>	 Alignment		100.0	15	<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 orenii
3	<a href="#">c3s29C_</a>	 Alignment		100.0	12	<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.
4	<a href="#">d2bisa1</a>	 Alignment		100.0	16	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Glycosyl transferases group 1
5	<a href="#">c3okaA_</a>	 Alignment		100.0	16	<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)
6	<a href="#">c2qzsA_</a>	 Alignment		100.0	14	<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)
7	<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
8	<a href="#">c2jimH_</a>	 Alignment		100.0	15	<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.
9	<a href="#">c2gejA_</a>	 Alignment		100.0	13	<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
10	<a href="#">d2iw1a1</a>	 Alignment		100.0	16	<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	13	<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="#">c2xmpB_</a>	Alignment		100.0	11	<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
13	<a href="#">c2x6rA_</a>	Alignment		100.0	11	<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
14	<a href="#">c2iv3B_</a>	Alignment		100.0	12	<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
15	<a href="#">c1uquB_</a>	Alignment		100.0	14	<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.
16	<a href="#">c3o3cD_</a>	Alignment		100.0	16	<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
17	<a href="#">c3nb0A_</a>	Alignment		100.0	15	<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="#">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
19	<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
20	<a href="#">c2q6vA_</a>	Alignment		99.9	13	<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
21	<a href="#">c3rhzb_</a>	Alignment	not modelled	99.9	16	<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
22	<a href="#">c3ot5D_</a>	Alignment	not modelled	99.9	8	<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="#">c3dzcA_</a>	Alignment	not modelled	99.9	10	<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.
24	<a href="#">d1f6da_</a>	Alignment	not modelled	99.9	10	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDP-N-acetylglucosamine 2-epimerase
25	<a href="#">d1f0ka_</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Peptidoglycan biosynthesis glycosyltransferase MurG
26	<a href="#">d1v4va_</a>	Alignment	not modelled	99.9	11	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDP-N-acetylglucosamine 2-epimerase
27	<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
28	<a href="#">c3ia7A_</a>	Alignment	not modelled	99.8	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> calg4; <b>PDBTitle:</b> crystal structure of calg4, the calicheamicin glycosyltransferase

29	<a href="#">c2xcuC</a>	 Alignment	not modelled	99.8	11	<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, complex with cmp
30	<a href="#">c2iyaB</a>	 Alignment	not modelled	99.8	8	<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
31	<a href="#">c3othB</a>	 Alignment	not modelled	99.8	12	<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	99.8	13	<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="#">dl06ca</a>	 Alignment	not modelled	99.8	10	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDP-N-acetylglucosamine 2-epimerase
34	<a href="#">c2iyfA</a>	 Alignment	not modelled	99.8	11	<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="#">dl1ira</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
36	<a href="#">c2vsnB</a>	 Alignment	not modelled	99.6	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> xcogt; <b>PDBTitle:</b> structure and topological arrangement of an o-glcna2 transferase homolog: insight into molecular control of3 intracellular glycosylation
37	<a href="#">d2f9fa1</a>	 Alignment	not modelled	99.6	13	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Glycosyl transferases group 1
38	<a href="#">c3d0qB</a>	 Alignment	not modelled	99.6	10	<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
39	<a href="#">dlpn3a</a>	 Alignment	not modelled	99.6	11	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Gtf glycosyltransferase
40	<a href="#">dlrrva</a>	 Alignment	not modelled	99.5	11	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Gtf glycosyltransferase
41	<a href="#">d2bfwa1</a>	 Alignment	not modelled	99.5	10	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Glycosyl transferases group 1
42	<a href="#">c3qhpB</a>	 Alignment	not modelled	99.4	15	<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
43	<a href="#">c3pe3D</a>	 Alignment	not modelled	99.2	8	<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-glcna2 transferase and its complex with a peptide2 substrate
44	<a href="#">d2acva1</a>	 Alignment	not modelled	99.1	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	99.1	11	<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="#">d2vcha1</a>	 Alignment	not modelled	98.9	10	<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	98.7	13	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDPGT-like
48	<a href="#">d2pq6a1</a>	 Alignment	not modelled	98.5	8	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDPGT-like
49	<a href="#">c3hbmA</a>	 Alignment	not modelled	97.8	11	<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
50	<a href="#">c2o6lA</a>	 Alignment	not modelled	96.6	13	<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
51	<a href="#">c3l7mC</a>	 Alignment	not modelled	96.3	12	<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
52	<a href="#">c2h1fB</a>	 Alignment	not modelled	95.4	10	<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
53	<a href="#">c3q3hA</a>	 Alignment	not modelled	95.1	8	<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
54	<a href="#">dl1ydgA</a>	 Alignment	not modelled	94.1	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins

					<b>Family:</b> WrbA-like
55	<a href="#">c3icpA_</a>	Alignment	not modelled	94.1	26 <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
56	<a href="#">dludca_</a>	Alignment	not modelled	93.9	23 <b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
57	<a href="#">d2d1pa1</a>	Alignment	not modelled	93.9	22 <b>Fold:</b> DsrEFH-like <b>Superfamily:</b> DsrEFH-like <b>Family:</b> DsrEF-like
58	<a href="#">c2p5uC_</a>	Alignment	not modelled	93.8	30 <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
59	<a href="#">c3m2pD_</a>	Alignment	not modelled	93.6	13 <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
60	<a href="#">c2pk3B_</a>	Alignment	not modelled	93.4	20 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> gdp-6-deoxy-d-lyxo-4-hexulose reductase; <b>PDBTitle:</b> crystal structure of a gdp-4-keto-6-deoxy-d-mannose reductase
61	<a href="#">c2x4gA_</a>	Alignment	not modelled	93.4	22 <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
62	<a href="#">c2pzlB_</a>	Alignment	not modelled	93.4	26 <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
63	<a href="#">d2hy5a1</a>	Alignment	not modelled	93.3	22 <b>Fold:</b> DsrEFH-like <b>Superfamily:</b> DsrEFH-like <b>Family:</b> DsrEF-like
64	<a href="#">d2c5aa1</a>	Alignment	not modelled	93.1	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
65	<a href="#">c2ggsB_</a>	Alignment	not modelled	92.6	17 <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
66	<a href="#">dljaya_</a>	Alignment	not modelled	92.5	29 <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
67	<a href="#">dlpswa_</a>	Alignment	not modelled	92.5	11 <b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> ADP-heptose LPS heptosyltransferase II
68	<a href="#">c2q1wC_</a>	Alignment	not modelled	92.4	20 <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+
69	<a href="#">c3l4bG_</a>	Alignment	not modelled	92.3	18 <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
70	<a href="#">c3oh8A_</a>	Alignment	not modelled	92.2	13 <b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoside-diphosphate sugar epimerase (sula family); <b>PDBTitle:</b> crystal structure of the nucleoside-diphosphate sugar epimerase from2 corynebacterium glutamicum. northeast structural genomics consortium3 target cgr91
71	<a href="#">c3lcmB_</a>	Alignment	not modelled	92.2	16 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of smu.1420 from streptococcus mutans ua159
72	<a href="#">d1vl0a_</a>	Alignment	not modelled	91.8	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
73	<a href="#">c2ofpB_</a>	Alignment	not modelled	91.5	38 <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
74	<a href="#">d1kewa_</a>	Alignment	not modelled	91.3	24 <b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
75	<a href="#">c2hunB_</a>	Alignment	not modelled	90.5	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
76	<a href="#">c2v4oB_</a>	Alignment	not modelled	90.5	13 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> multifunctional protein sur e; <b>PDBTitle:</b> crystal structure of salmonella typhimurium sure at 2.752 angstrom resolution in monoclinic form
77	<a href="#">d1ks9a2</a>	Alignment	not modelled	90.3	40 <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
78	<a href="#">d1txga2</a>	Alignment	not modelled	90.3	26 <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
79	<a href="#">d2f1ka2</a>	Alignment	not modelled	90.2	31	<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
80	<a href="#">c1gshA</a>	Alignment	not modelled	90.0	10	<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
81	<a href="#">d2bli1a1</a>	Alignment	not modelled	89.7	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
82	<a href="#">d1n2sa</a>	Alignment	not modelled	89.7	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
83	<a href="#">c1ks9A</a>	Alignment	not modelled	89.7	40	<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
84	<a href="#">c3tovB</a>	Alignment	not modelled	89.6	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
85	<a href="#">d1bxka</a>	Alignment	not modelled	89.2	24	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
86	<a href="#">d1j9ja</a>	Alignment	not modelled	89.0	18	<b>Fold:</b> SurE-like <b>Superfamily:</b> SurE-like <b>Family:</b> SurE-like
87	<a href="#">d1r6da</a>	Alignment	not modelled	88.6	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="#">c3ibgF</a>	Alignment	not modelled	88.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> atpase, subunit of the get complex; <b>PDBTitle:</b> crystal structure of aspergillus fumigatus get3 with bound2 adp
89	<a href="#">d1mv8a2</a>	Alignment	not modelled	88.0	31	<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="#">c2wooc</a>	Alignment	not modelled	87.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> atpase get3; <b>PDBTitle:</b> nucleotide-free form of s. pombe get3
91	<a href="#">c3ew7A</a>	Alignment	not modelled	87.8	29	<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.
92	<a href="#">c3dhnA</a>	Alignment	not modelled	87.6	24	<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.
93	<a href="#">c2f1kD</a>	Alignment	not modelled	87.6	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> prephenate dehydrogenase; <b>PDBTitle:</b> crystal structure of synechocystis aroenate dehydrogenase
94	<a href="#">c3sc6F</a>	Alignment	not modelled	87.1	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 dtdp-4-dehydrorhamnose2 reductase (rfbd) from bacillus anthracis str. ames in complex with3 nadp
95	<a href="#">d1lssa</a>	Alignment	not modelled	87.1	27	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Potassium channel NAD-binding domain
96	<a href="#">c3g17H</a>	Alignment	not modelled	86.9	15	<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
97	<a href="#">d1fjha</a>	Alignment	not modelled	86.6	25	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
98	<a href="#">c3dojA</a>	Alignment	not modelled	86.3	27	<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)
99	<a href="#">d1oc2a</a>	Alignment	not modelled	86.3	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
100	<a href="#">c2e6gl</a>	Alignment	not modelled	85.7	26	<b>PDB header:</b> hydrolase <b>Chain:</b> I: <b>PDB Molecule:</b> 5'-nucleotidase sure; <b>PDBTitle:</b> crystal structure of the stationary phase survival protein sure from2 thermus thermophilus hb8 in complex with phosphate
101	<a href="#">c2gf2B</a>	Alignment	not modelled	85.5	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
102	<a href="#">c3kjgB</a>	Alignment	not modelled	85.1	15	<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
103	<a href="#">c1bxgA</a>	Alignment	not modelled	85.0	26	<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



104	<a href="#">dlgsaa1</a>	Alignment	not modelled	84.8	10	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> Prokaryotic glutathione synthetase, N-terminal domain
105	<a href="#">c1hyqA</a>	Alignment	not modelled	84.7	20	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell division inhibitor (mind-1); <b>PDBTitle:</b> mind bacterial cell division regulator from a. fulgidus
106	<a href="#">d1hyqa</a>	Alignment	not modelled	84.7	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
107	<a href="#">c3ghyA</a>	Alignment	not modelled	84.7	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ketopantoate reductase protein; <b>PDBTitle:</b> crystal structure of a putative ketopantoate reductase from ralstonia2 solanacearum molk2
108	<a href="#">c2z04A</a>	Alignment	not modelled	84.5	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase atpase <b>PDBTitle:</b> crystal structure of phosphoribosylaminoimidazole2 carboxylase atpase subunit from aquifex aeolicus
109	<a href="#">d1qrda</a>	Alignment	not modelled	84.3	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
110	<a href="#">c3e8xA</a>	Alignment	not modelled	84.2	24	<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.
111	<a href="#">c3h2sA</a>	Alignment	not modelled	84.1	32	<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.
112	<a href="#">d2afhe1</a>	Alignment	not modelled	83.3	27	<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
113	<a href="#">c3etjB</a>	Alignment	not modelled	83.3	14	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase atpase <b>PDBTitle:</b> crystal structure e. coli purk in complex with mg, adp, and2 pi
114	<a href="#">d1ygpa</a>	Alignment	not modelled	83.3	13	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Oligosaccharide phosphorylase
115	<a href="#">c3rfxB</a>	Alignment	not modelled	83.2	32	<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
116	<a href="#">d1gy8a</a>	Alignment	not modelled	83.2	23	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
117	<a href="#">c1vkzA</a>	Alignment	not modelled	83.1	24	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylamine--glycine ligase; <b>PDBTitle:</b> crystal structure of phosphoribosylamine--glycine ligase (tm1250) from2 thermotoga maritima at 2.30 a resolution
118	<a href="#">c3g0oA</a>	Alignment	not modelled	83.1	12	<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
119	<a href="#">d1rta</a>	Alignment	not modelled	83.0	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> NADPH-dependent FMN reductase
120	<a href="#">d1pgja2</a>	Alignment	not modelled	82.7	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