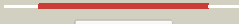



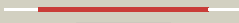




























#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2wawA_</a>	 Alignment		100.0	20	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> moba relate protein; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis rv0371c2 homolog from mycobacterium sp. strain jc1
2	<a href="#">d1e5ka_</a>	 Alignment		100.0	17	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Molybdenum cofactor biosynthesis protein MobA
3	<a href="#">c2we9A_</a>	 Alignment		100.0	20	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> moba-related protein; <b>PDBTitle:</b> crystal structure of rv0371c from mycobacterium2 tuberculosis h37rv
4	<a href="#">c2e8bA_</a>	 Alignment		100.0	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable molybdopterin-guanine dinucleotide biosynthesis <b>PDBTitle:</b> crystal structure of the putative protein (aq1419) from aquifex2 aeolicus vf5
5	<a href="#">c3ngwA_</a>	 Alignment		100.0	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin-guanine dinucleotide biosynthesis protein a <b>PDBTitle:</b> crystal structure of molybdopterin-guanine dinucleotide biosynthesis2 protein a from archaeoglobus fulgidus, northeast structural genomics3 consortium target gr189
6	<a href="#">d1w55a1</a>	 Alignment		100.0	14	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
7	<a href="#">d1i52a_</a>	 Alignment		100.0	19	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
8	<a href="#">c2xwlB_</a>	 Alignment		100.0	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; <b>PDBTitle:</b> crystal structure of ispd from mycobacterium smegmatis in complex2 with ctp and mg
9	<a href="#">d1vpaa_</a>	 Alignment		100.0	14	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
10	<a href="#">c1w57A_</a>	 Alignment		100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ispd/ispf bifunctional enzyme; <b>PDBTitle:</b> structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
11	<a href="#">d2oi6a2</a>	 Alignment		100.0	13	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> UDP-glucose pyrophosphorylase

12	<a href="#">c3d5nB_</a>	Alignment		100.0	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> q97w15_sulso; <b>PDBTitle:</b> crystal structure of the q97w15_sulso protein from2 sulfolobus solfataricus. nesg target ssr125.
13	<a href="#">dlw77a1</a>	Alignment		100.0	14	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidyltransferase
14	<a href="#">c3rsbB_</a>	Alignment		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> adenosylcobinamide-phosphate guanylyltransferase; <b>PDBTitle:</b> structure of the archaeal gtp:adocbi-p guanylyltransferase (coby) from2 methanocaldococcus jannaschii
15	<a href="#">c3f1cB_</a>	Alignment		99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative 2-c-methyl-d-erythritol 4- phosphate <b>PDBTitle:</b> crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase from listeria monocytogenes
16	<a href="#">d1eyra_</a>	Alignment		99.9	16	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidyltransferase
17	<a href="#">c3oamD_</a>	Alignment		99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 3-deoxy-manno-octulosonate cytidyltransferase; <b>PDBTitle:</b> crystal structure of cytidyltransferase from vibrio cholerae
18	<a href="#">dlqwja_</a>	Alignment		99.9	15	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidyltransferase
19	<a href="#">dlh7ea_</a>	Alignment		99.9	16	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidyltransferase
20	<a href="#">dlvica_</a>	Alignment		99.9	16	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidyltransferase
21	<a href="#">c2px7A_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 4-phosphate <b>PDBTitle:</b> crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase from thermus thermophilus hb8
22	<a href="#">c3polA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-deoxy-manno-octulosonate cytidyltransferase; <b>PDBTitle:</b> 2.3 angstrom crystal structure of 3-deoxy-manno- octulosonate2 cytidyltransferase (kdsb) from acinetobacter baumannii.
23	<a href="#">dlg97a2</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> UDP-glucose pyrophosphorylase
24	<a href="#">d2dpwa1</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> TTHA0179-like
25	<a href="#">c3hl3A_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-1-phosphate thymidyltransferase; <b>PDBTitle:</b> 2.76 angstrom crystal structure of a putative glucose-1- phosphate2 thymidyltransferase from bacillus anthracis in complex with a3 sucrose.
26	<a href="#">c2y6pC_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> 3-deoxy-manno-octulosonate cytidyltransferase; <b>PDBTitle:</b> evidence for a two-metal-ion-mechanism in the2 kdo- cytidyltransferase kdsb
27	<a href="#">dljyka_</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidyltransferase

28	<a href="#">c1jylC_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> ctp:phosphocholine cytidylyltransferase; <b>PDBTitle:</b> catalytic mechanism of ctp:phosphocholine2 cytidylyltransferase from streptococcus pneumoniae (licc)
29	<a href="#">dliina_</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidyltransferase
30	<a href="#">c2e3dB_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> utp--glucose-1-phosphate uridylyltransferase; <b>PDBTitle:</b> crystal structure of e. coli glucose-1-phosphate2 uridylyltransferase
31	<a href="#">c2ux8G_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> glucose-1-phosphate uridylyltransferase; <b>PDBTitle:</b> crystal structure of sphingomonas elodea atcc 31461 glucose-2 1-phosphate uridylyltransferase in complex with glucose-3 1-phosphate.
32	<a href="#">c3jukA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-glucose pyrophosphorylase (galu); <b>PDBTitle:</b> the crystal structure of udp-glucose pyrophosphorylase complexed with2 udp-glucose
33	<a href="#">c3okrA_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; <b>PDBTitle:</b> structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
34	<a href="#">d1h5ra_</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidyltransferase
35	<a href="#">d1fxoa_</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidyltransferase
36	<a href="#">c3tqdA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-deoxy-manno-octulosonate cytidyltransferase; <b>PDBTitle:</b> structure of the 3-deoxy-d-manno-octulosonate cytidyltransferase2 (kdsb) from coxiella burnetii
37	<a href="#">d1vgwa_</a>	Alignment	not modelled	99.9	12	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
38	<a href="#">c3pnnA_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> conserved domain protein; <b>PDBTitle:</b> the crystal structure of a glycosyltransferase from porphyromonas2 gingivalis w83
39	<a href="#">c2pa4B_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> utp-glucose-1-phosphate uridylyltransferase; <b>PDBTitle:</b> crystal structure of udp-glucose pyrophosphorylase from corynebacteria2 glutamicum in complex with magnesium and udp-glucose
40	<a href="#">d1mc3a_</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidyltransferase
41	<a href="#">c3okrC_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; <b>PDBTitle:</b> structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
42	<a href="#">d1tzfa_</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
43	<a href="#">c2vshB_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 4-phosphate <b>PDBTitle:</b> synthesis of cdp-activated ribitol for teichoic acid2 precursors in streptococcus pneumoniae
44	<a href="#">d1lvwa_</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidyltransferase
45	<a href="#">c2v0hA_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein glmu; <b>PDBTitle:</b> characterization of substrate binding and catalysis of the2 potential antibacterial target n-acetylglucosamine-1-3 phosphate uridylyltransferase (glmu)
46	<a href="#">d1vh1a_</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
47	<a href="#">c2oi6A_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein glmu; <b>PDBTitle:</b> e. coli glmu- complex with udp-glcnac, coa and glcn-1-po4
48	<a href="#">c1hm8A_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine-1-phosphate uridylyltransferase; <b>PDBTitle:</b> crystal structure of s.pneumoniae n-acetylglucosamine-1-phosphate2 uridylyltransferase, glmu, bound to acetyl coenzyme a
49	<a href="#">c3d98A_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein glmu; <b>PDBTitle:</b> crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
50	<a href="#">c3brkX_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> glucose-1-phosphate adenyltransferase; <b>PDBTitle:</b> crystal structure of adp-glucose pyrophosphorylase from2 agrobacterium tumefaciens
51	<a href="#">c1fwyA_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine pyrophosphorylase;

						<b>PDBTitle:</b> crystal structure of n-acetylglucosamine 1-phosphate2 uridylyltransferase bound to udp-glcna
52	<a href="#">d2cu2a2</a>	Alignment	not modelled	99.8	13	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> mannose-1-phosphate guanylyl transferase
53	<a href="#">c2qkxA</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein glmu; <b>PDBTitle:</b> n-acetyl glucosamine 1-phosphate uridylyltransferase from mycobacterium2 tuberculosis complex with n-acetyl glucosamine 1-phosphate
54	<a href="#">d1yp2a2</a>	Alignment	not modelled	99.8	16	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidyltransferase
55	<a href="#">c1yp3C</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> glucose-1-phosphate adenyltransferase small <b>PDBTitle:</b> crystal structure of potato tuber adp-glucose2 pyrophosphorylase in complex with atp
56	<a href="#">c2gggA</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 401aa long hypothetical glucose-1-phosphate <b>PDBTitle:</b> complex of hypothetical glucose-1-phosphate thymidyltransferase from2 sulfobolus tokodaii
57	<a href="#">c2cu2A</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative mannose-1-phosphate guanylyl transferase; <b>PDBTitle:</b> crystal structure of mannose-1-phosphate geranyltransferase from2 thermus thermophilus hb8
58	<a href="#">c2xmhB</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ctp-inositol-1-phosphate cytidyltransferase; <b>PDBTitle:</b> the x-ray structure of ctp:inositol-1-phosphate2 cytidyltransferase from archaeoglobus fulgidus
59	<a href="#">c2x5sB</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> mannose-1-phosphate guanylyltransferase; <b>PDBTitle:</b> crystal structure of t. maritima gdp-mannose2 pyrophosphorylase in apo state.
60	<a href="#">c2qh5B</a>	Alignment	not modelled	99.3	12	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> mannose-6-phosphate isomerase; <b>PDBTitle:</b> crystal structure of mannose-6-phosphate isomerase from helicobacter2 pylori
61	<a href="#">d1vh3a</a>	Alignment	not modelled	99.3	11	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidyltransferase
62	<a href="#">c3cgxA</a>	Alignment	not modelled	98.8	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative nucleotide-diphospho-sugar transferase; <b>PDBTitle:</b> crystal structure of putative nucleotide-diphospho-sugar transferase2 (yp_389115.1) from desulfovibrio desulfuricans g20 at 1.90 a3 resolution
63	<a href="#">d2i5ea1</a>	Alignment	not modelled	98.8	13	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> MM2497-like
64	<a href="#">c3oc9A</a>	Alignment	not modelled	98.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine pyrophosphorylase; <b>PDBTitle:</b> crystal structure of putative udp-n-acetylglucosamine2 pyrophosphorylase from entamoeba histolytica
65	<a href="#">d1vm8a</a>	Alignment	not modelled	98.6	16	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> UDP-glucose pyrophosphorylase
66	<a href="#">d1jv1a</a>	Alignment	not modelled	98.5	16	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> UDP-glucose pyrophosphorylase
67	<a href="#">d2icya2</a>	Alignment	not modelled	98.5	13	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> UDP-glucose pyrophosphorylase
68	<a href="#">c2q4jB</a>	Alignment	not modelled	98.5	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> probable utp-glucose-1-phosphate uridylyltransferase 2; <b>PDBTitle:</b> ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at3g03250, a putative udp-glucose3 pyrophosphorylase
69	<a href="#">c3gueB</a>	Alignment	not modelled	98.4	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> utp-glucose-1-phosphate uridylyltransferase 2; <b>PDBTitle:</b> crystal structure of udp-glucose phosphorylase from trypanosoma2 brucei, (tb10.389.0330)
70	<a href="#">c2yqsA</a>	Alignment	not modelled	98.4	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine pyrophosphorylase; <b>PDBTitle:</b> crystal structure of uridine-diphospho-n-acetylglucosamine2 pyrophosphorylase from candida albicans, in the product-binding form
71	<a href="#">c2i5kB</a>	Alignment	not modelled	98.2	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> utp--glucose-1-phosphate uridylyltransferase; <b>PDBTitle:</b> crystal structure of ugp1p
72	<a href="#">c2oefA</a>	Alignment	not modelled	98.2	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> utp-glucose-1-phosphate uridylyltransferase 2, <b>PDBTitle:</b> open and closed structures of the udp-glucose2 pyrophosphorylase from leishmania major
73	<a href="#">c3ogzA</a>	Alignment	not modelled	98.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-sugar pyrophosphorylase; <b>PDBTitle:</b> protein structure of usp from l. major in apo-form

74	<a href="#">d1omza_</a>	Alignment	not modelled	96.1	13	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Exostosin
75	<a href="#">c1omxB_</a>	Alignment	not modelled	94.7	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-1,4-n-acetylhexosaminyltransferase extl2; <b>PDBTitle:</b> crystal structure of mouse alpha-1,4-n-2 acetylhexosaminyltransferase (extl2)
76	<a href="#">c2ffuA_</a>	Alignment	not modelled	93.7	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polypeptide n-acetylgalactosaminyltransferase 2; <b>PDBTitle:</b> crystal structure of human ppgalnact-2 complexed with udp2 and ea2
77	<a href="#">c3ckvA_</a>	Alignment	not modelled	91.2	9	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of a mycobacterial protein
78	<a href="#">c1xhbA_</a>	Alignment	not modelled	90.0	7	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polypeptide n-acetylgalactosaminyltransferase 1; <b>PDBTitle:</b> the crystal structure of udp-galnac: polypeptide alpha-n-2 acetylgalactosaminyltransferase-t1
79	<a href="#">c3f1yC_</a>	Alignment	not modelled	87.6	9	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> mannosyl-3-phosphoglycerate synthase; <b>PDBTitle:</b> mannosyl-3-phosphoglycerate synthase from rubrobacter xylanophilus
80	<a href="#">d1xhba2</a>	Alignment	not modelled	86.6	8	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Polypeptide N-acetylgalactosaminyltransferase 1, N-terminal domain
81	<a href="#">c2z86D_</a>	Alignment	not modelled	85.0	14	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> chondroitin synthase; <b>PDBTitle:</b> crystal structure of chondroitin polymerase from2 escherichia coli strain k4 (k4cp) complexed with udp-glucua3 and udp
82	<a href="#">c2d7iA_</a>	Alignment	not modelled	71.4	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polypeptide n-acetylgalactosaminyltransferase 10; <b>PDBTitle:</b> crsytal structure of pp-galnac-t10 with udp, galnac and mn2+
83	<a href="#">d1o6za1</a>	Alignment	not modelled	39.1	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
84	<a href="#">d2bo4a1</a>	Alignment	not modelled	38.1	16	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> MG5-like
85	<a href="#">c3bcvA_</a>	Alignment	not modelled	32.5	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative glycosyltransferase protein; <b>PDBTitle:</b> crystal structure of a putative glycosyltransferase from bacteroides2 fragilis
86	<a href="#">c8ldhA_</a>	Alignment	not modelled	32.0	21	<b>PDB header:</b> oxidoreductase(choh(d)-nad(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> m4 apo-lactate dehydrogenase; <b>PDBTitle:</b> refined crystal structure of dogfish m4 apo-lactate2 dehydrogenase
87	<a href="#">d1qg8a_</a>	Alignment	not modelled	31.7	18	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Spore coat polysaccharide biosynthesis protein SpsA
88	<a href="#">c1hygA_</a>	Alignment	not modelled	30.1	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate/malate dehydrogenase; <b>PDBTitle:</b> crystal structure of mj0490 gene product, the family of2 lactate/malate dehydrogenase
89	<a href="#">c1a5zA_</a>	Alignment	not modelled	27.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase; <b>PDBTitle:</b> lactate dehydrogenase from thermotoga maritima (tml dh)
90	<a href="#">c1llcA_</a>	Alignment	not modelled	17.1	13	<b>PDB header:</b> oxidoreductase(choh(d)-nad(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase; <b>PDBTitle:</b> structure determination of the allosteric l-lactate dehydrogenase from2 lactobacillus casei at 3.0 angstroms resolution
91	<a href="#">c2fnzA_</a>	Alignment	not modelled	15.8	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> lactate dehydrogenase; <b>PDBTitle:</b> crystal structure of the lactate dehydrogenase from cryptosporidium2 parvum complexed with cofactor (b-nicotinamide adenine dinucleotide)3 and inhibitor (oxamic acid)
92	<a href="#">c2qgiA_</a>	Alignment	not modelled	15.4	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> atp synthase subunits region orf 6; <b>PDBTitle:</b> the udp complex structure of the sixth gene product of the f1-atpase2 operon of rhodobacter blasticus
93	<a href="#">d1mlda1</a>	Alignment	not modelled	14.6	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
94	<a href="#">d1b8pa1</a>	Alignment	not modelled	12.9	14	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
95	<a href="#">c1ez4B_</a>	Alignment	not modelled	12.4	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> lactate dehydrogenase; <b>PDBTitle:</b> crystal structure of non-allosteric l-lactate dehydrogenase2 from lactobacillus pentosus at 2.3 angstrom resolution
96	<a href="#">c2zkrh_</a>	Alignment	not modelled	11.9	16	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> H: <b>PDB Molecule:</b> rna expansion segment es12; <b>PDBTitle:</b> structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
97	<a href="#">c3d0oA_</a>	Alignment	not modelled	11.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase 1; <b>PDBTitle:</b> crystal structure of lactate dehydrogenase from2 staphylococcus aureus

98	<a href="#">dlhyea1</a>	<div>Alignment</div>	not modelled	11.6	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
99	<a href="#">dla5za1</a>	<div>Alignment</div>	not modelled	10.1	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like