







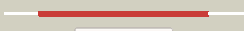
















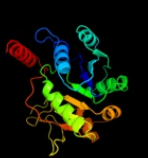
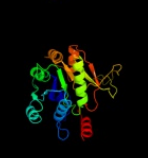

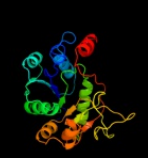




#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dli52a_	 Alignment		100.0	100	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: Cytidylyltransferase
2	c2xwlB_	 Alignment		100.0	36	PDB header: transferase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: crystal structure of ispd from mycobacterium smegmatis in complex2 with ctp and mg
3	dlvpaa_	 Alignment		100.0	28	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: Cytidylyltransferase
4	c1w57A_	 Alignment		100.0	27	PDB header: transferase Chain: A: PDB Molecule: ispd/ispf bifunctional enzyme; PDBTitle: structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
5	dlw55a1	 Alignment		100.0	25	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: Cytidylyltransferase
6	c3f1cB_	 Alignment		100.0	22	PDB header: transferase Chain: B: PDB Molecule: putative 2-c-methyl-d-erythritol 4-phosphate PDBTitle: crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase from listeria monocytogenes
7	c2px7A_	 Alignment		100.0	32	PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate PDBTitle: crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase from thermus thermophilus hb8
8	d2oi6a2	 Alignment		100.0	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: UDP-glucose pyrophosphorylase
9	c3okrA_	 Alignment		100.0	31	PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
10	dlvgwa_	 Alignment		100.0	45	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: Cytidylyltransferase
11	dlw77a1	 Alignment		100.0	30	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: Cytidylyltransferase

12	dlg97a2	Alignment		100.0	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
13	c3oamD	Alignment		100.0	10	PDB header: transferase Chain: D: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: crystal structure of cytidyltransferase from vibrio cholerae
14	c2vshB	Alignment		100.0	24	PDB header: transferase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate PDBTitle: synthesis of cdp-activated ribitol for teichoic acid2 precursors in streptococcus pneumoniae
15	dlh7ea	Alignment		100.0	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
16	c3okrC	Alignment		100.0	32	PDB header: transferase Chain: C: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
17	dlqwja	Alignment		100.0	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
18	c3polA	Alignment		100.0	13	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: 2.3 angstrom crystal structure of 3-deoxy-manno-octulosonate2 cytidyltransferase (kdsb) from acinetobacter baumannii.
19	dlvica	Alignment		100.0	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
20	c2wawA	Alignment		100.0	21	PDB header: unknown function Chain: A: PDB Molecule: moba relate protein; PDBTitle: crystal structure of mycobacterium tuberculosis rv0371c2 homolog from mycobacterium sp. strain jc1
21	dlh5ra	Alignment	not modelled	100.0	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
22	dleyra	Alignment	not modelled	100.0	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
23	c3pnnA	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: conserved domain protein; PDBTitle: the crystal structure of a glycosyltransferase from porphyromonas2 gingivalis w83
24	c3hl3A	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: glucose-1-phosphate thymidyltransferase; PDBTitle: 2.76 angstrom crystal structure of a putative glucose-1-phosphate2 thymidyltransferase from bacillus anthracis in complex with a3 sucrose.
25	dliina	Alignment	not modelled	100.0	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
26	dlfxoa	Alignment	not modelled	100.0	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
27	dlvwva	Alignment	not modelled	100.0	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
28	dljyka	Alignment	not modelled	100.0	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase

29	c1jylC_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: C: PDB Molecule: ctp:phosphocholine cytidyltransferase; PDBTitle: catalytic mechanism of ctp:phosphocholine2 cytidyltransferase from streptococcus pneumoniae (licc)
30	c1hm8A_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine-1-phosphate uridyltransferase; PDBTitle: crystal structure of s.pneumoniae n-acetylglucosamine- 1-phosphate2 uridyltransferase, glmu, bound to acetyl coenzyme a
31	c2we9A_	Alignment	not modelled	100.0	17	PDB header: unknown function Chain: A: PDB Molecule: moba-related protein; PDBTitle: crystal structure of rv0371c from mycobacterium2 tuberculosis h37rv
32	d1mc3a_	Alignment	not modelled	100.0	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
33	c2pa4B_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: B: PDB Molecule: utp-glucose-1-phosphate uridyltransferase; PDBTitle: crystal structure of udp-glucose pyrophosphorylase from corynebacteria2 glutamicum in complex with magnesium and udp- glucose
34	c3tqdA_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: structure of the 3-deoxy-d-manno-octulosonate cytidyltransferase2 (kdsb) from coxiella burnetii
35	c2y6pC_	Alignment	not modelled	99.9	12	PDB header: transferase Chain: C: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: evidence for a two-metal-ion-mechanism in the2 kdo- cytidyltransferase kdsb
36	d1e5ka_	Alignment	not modelled	99.9	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: Molybdenum cofactor biosynthesis protein MobA
37	c2e3dB_	Alignment	not modelled	99.9	21	PDB header: transferase Chain: B: PDB Molecule: utp--glucose-1-phosphate uridyltransferase; PDBTitle: crystal structure of e. coli glucose-1-phosphate2 uridyltransferase
38	c3ngwA_	Alignment	not modelled	99.9	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis protein a PDBTitle: crystal structure of molybdopterin-guanine dinucleotide biosynthesis2 protein a from archaeoglobus fulgidus, northeast structural genomics3 consortium target gr189
39	d1tzfa_	Alignment	not modelled	99.9	14	Fold: Nucleotide-di-phospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: Cytidyltransferase
40	c3jukA_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: udp-glucose pyrophosphorylase (galu); PDBTitle: the crystal structure of udp-glucose pyrophosphorylase complexed with2 udp-glucose
41	c2v0hA_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: characterization of substrate binding and catalysis of the2 potential antibacterial target n-acetylglucosamine-1-3 phosphate uridyltransferase (glmu)
42	d2dpwa1	Alignment	not modelled	99.9	17	Fold: Nucleotide-di-phospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: TTHA0179-like
43	c2oi6A_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: e. coli glmu- complex with udp-glcnac, coa and glcn-1- po4
44	c3d98A_	Alignment	not modelled	99.9	21	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
45	c3rsbB_	Alignment	not modelled	99.9	13	PDB header: transferase Chain: B: PDB Molecule: adenosylcobinamide-phosphate guanylyltransferase; PDBTitle: structure of the archaeal gtp:adocbi-p guanylyltransferase (coby) from2 methanocaldococcus jannaschii
46	c2ux8G_	Alignment	not modelled	99.9	13	PDB header: transferase Chain: G: PDB Molecule: glucose-1-phosphate uridyltransferase; PDBTitle: crystal structure of sphingomonas elodea atcc 31461 glucose-2 1-phosphate uridyltransferase in complex with glucose-3 1-phosphate.
47	c2qkxA_	Alignment	not modelled	99.9	21	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: n-acetyl glucosamine 1-phosphate uridyltransferase from mycobacterium2 tuberculosis complex with n-acetyl glucosamine 1-phosphate
48	c1fwyA_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: crystal structure of n-acetylglucosamine 1-phosphate2 uridyltransferase bound to udp-glcnac
49	d2cu2a2	Alignment	not modelled	99.9	23	Fold: Nucleotide-di-phospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: mannose-1-phosphate guanylyl transferase
50	d1vh1a_	Alignment	not modelled	99.9	14	Fold: Nucleotide-di-phospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: Cytidyltransferase
51	c1yp3C_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: C: PDB Molecule: glucose-1-phosphate adenyltransferase small PDBTitle: crystal structure of potato tuber adp-glucose2

					pyrophosphorylase in complex with atp
52	d1yp2a2	Alignment	not modelled	99.9	15 Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
53	c2cu2A	Alignment	not modelled	99.9	21 PDB header: transferase Chain: A: PDB Molecule: putative mannose-1-phosphate guanylyl transferase; PDBTitle: crystal structure of mannose-1-phosphate geranyltransferase from2 thermus thermophilus hb8
54	c2x5sB	Alignment	not modelled	99.9	17 PDB header: transferase Chain: B: PDB Molecule: mannose-1-phosphate guanylyltransferase; PDBTitle: crystal structure of t. maritima gdp-mannose2 pyrophosphorylase in apo state.
55	c3brkX	Alignment	not modelled	99.9	16 PDB header: transferase Chain: X: PDB Molecule: glucose-1-phosphate adenyltransferase; PDBTitle: crystal structure of adp-glucose pyrophosphorylase from2 agrobacterium tumefaciens
56	c2e8bA	Alignment	not modelled	99.8	16 PDB header: biosynthetic protein Chain: A: PDB Molecule: probable molybdopterin-guanine dinucleotide biosynthesis PDBTitle: crystal structure of the putative protein (aq1419) from aquifex2 aeolicus vf5
57	c2ggqA	Alignment	not modelled	99.8	15 PDB header: transferase Chain: A: PDB Molecule: 401aa long hypothetical glucose-1-phosphate PDBTitle: complex of hypothetical glucose-1-phosphate thymidyltransferase from2 sulfolobus tokodaii
58	c3d5nB	Alignment	not modelled	99.7	18 PDB header: structural genomics, unknown function Chain: B: PDB Molecule: q97w15_sulso; PDBTitle: crystal structure of the q97w15_sulso protein from2 sulfolobus solfataricus. nesg target ssr125.
59	c2xmhB	Alignment	not modelled	99.7	12 PDB header: transferase Chain: B: PDB Molecule: ctp-inositol-1-phosphate cytidyltransferase; PDBTitle: the x-ray structure of ctp:inositol-1-phosphate2 cytidyltransferase from archaeoglobus fulgidus
60	c2qh5B	Alignment	not modelled	99.7	11 PDB header: isomerase Chain: B: PDB Molecule: mannose-6-phosphate isomerase; PDBTitle: crystal structure of mannose-6-phosphate isomerase from helicobacter2 pylori
61	d1vh3a	Alignment	not modelled	99.6	10 Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: Cytidyltransferase
62	c3cgxA	Alignment	not modelled	98.6	9 PDB header: transferase Chain: A: PDB Molecule: putative nucleotide-diphospho-sugar transferase; PDBTitle: crystal structure of putative nucleotide-diphospho-sugar transferase2 (yp_389115.1) from desulfovibrio desulfuricans g20 at 1.90 a3 resolution
63	d1vm8a	Alignment	not modelled	98.6	12 Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: UDP-glucose pyrophosphorylase
64	c3oc9A	Alignment	not modelled	98.6	27 PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: crystal structure of putative udp-n-acetylglucosamine2 pyrophosphorylase from entamoeba histolytica
65	d2icya2	Alignment	not modelled	98.5	20 Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: UDP-glucose pyrophosphorylase
66	d2i5ea1	Alignment	not modelled	98.5	16 Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: MM2497-like
67	c2q4jB	Alignment	not modelled	98.5	20 PDB header: transferase Chain: B: PDB Molecule: probable utp-glucose-1-phosphate uridylyltransferase 2; PDBTitle: ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at3g03250, a putative udp-glucose3 pyrophosphorylase
68	c2yqsA	Alignment	not modelled	98.4	16 PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: crystal structure of uridine-diphospho-n-acetylglucosamine2 pyrophosphorylase from candida albicans, in the product-binding form
69	d1jv1a	Alignment	not modelled	98.4	24 Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: UDP-glucose pyrophosphorylase
70	c2oefA	Alignment	not modelled	98.4	15 PDB header: transferase Chain: A: PDB Molecule: utp-glucose-1-phosphate uridylyltransferase 2, PDBTitle: open and closed structures of the udp-glucose2 pyrophosphorylase from leishmania major
71	c3gueB	Alignment	not modelled	98.4	24 PDB header: transferase Chain: B: PDB Molecule: utp-glucose-1-phosphate uridylyltransferase 2; PDBTitle: crystal structure of udp-glucose phosphorylase from trypanosoma2 brucei, (tb10.389.0330)
72	c2i5kB	Alignment	not modelled	98.3	22 PDB header: transferase Chain: B: PDB Molecule: utp--glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of ugp1p
73	c3ogzA	Alignment	not modelled	98.1	24 PDB header: transferase Chain: A: PDB Molecule: udp-sugar pyrophosphorylase; PDBTitle: protein structure of usp from l. major in apo-form
					Fold: Nucleotide-diphospho-sugar transferases

74	d1omza_	Alignment	not modelled	95.0	12	Superfamily: Nucleotide-diphospho-sugar transferases Family: Exostosin
75	c1omxB_	Alignment	not modelled	93.0	12	PDB header: transferase Chain: B: PDB Molecule: alpha-1,4-n-acetylhexosaminyltransferase ext12; PDBTitle: crystal structure of mouse alpha-1,4-n-2 acetylhexosaminyltransferase (ext12)
76	c2ffuA_	Alignment	not modelled	92.1	19	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 2; PDBTitle: crystal structure of human ppgalnact-2 complexed with udp2 and ea2
77	c1xhbA_	Alignment	not modelled	89.1	16	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 1; PDBTitle: the crystal structure of udp-galnac: polypeptide alpha-n-2 acetylgalactosaminyltransferase-t1
78	d1xhba2	Alignment	not modelled	89.0	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Polypeptide N-acetylgalactosaminyltransferase 1, N-terminal domain
79	c2d7iA_	Alignment	not modelled	83.2	15	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 10; PDBTitle: crsytal structure of pp-galnac-t10 with udp, galnac and mn2+
80	c3ckvA_	Alignment	not modelled	82.6	14	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a mycobacterial protein
81	c2z86D_	Alignment	not modelled	82.1	15	PDB header: transferase Chain: D: PDB Molecule: chondroitin synthase; PDBTitle: crystal structure of chondroitin polymerase from2 escherichia coli strain k4 (k4cp) complexed with udp-glucua3 and udp
82	c3flyC_	Alignment	not modelled	81.9	15	PDB header: transferase Chain: C: PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: mannosyl-3-phosphoglycerate synthase from rubrobacter xylanophilus
83	c3kcqA_	Alignment	not modelled	81.1	16	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of phosphoribosylglycinamide formyltransferase from2 anaplasma phagocytophilum
84	c3bcvA_	Alignment	not modelled	73.6	17	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase protein; PDBTitle: crystal structure of a putative glycosyltransferase from bacteroides2 fragilis
85	d2bo4a1	Alignment	not modelled	47.3	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: MGS-like
86	d1j2jb_	Alignment	not modelled	41.4	25	Fold: Spectrin repeat-like Superfamily: GAT-like domain Family: GAT domain
87	d1q1oa_	Alignment	not modelled	34.8	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
88	d1nh9a_	Alignment	not modelled	28.8	24	Fold: IF3-like Superfamily: AlbA-like Family: DNA-binding protein AlbA
89	c2dclB_	Alignment	not modelled	25.4	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical upf0166 protein ph1503; PDBTitle: structure of ph1503 protein from pyrococcus horikoshii ot3
90	c3s40C_	Alignment	not modelled	25.0	17	PDB header: transferase Chain: C: PDB Molecule: diacylglycerol kinase; PDBTitle: the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. Sterne
91	d1wj6a_	Alignment	not modelled	24.1	3	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
92	d1o51a_	Alignment	not modelled	22.8	10	Fold: Ferredoxin-like Superfamily: GlnB-like Family: DUF190/COG1993
93	d1pqsa_	Alignment	not modelled	19.2	15	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
94	d2bona1	Alignment	not modelled	18.6	14	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
95	d1ijwc_	Alignment	not modelled	16.2	5	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
96	d1o6za1	Alignment	not modelled	16.2	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
97	c2bonB_	Alignment	not modelled	16.0	15	PDB header: transferase Chain: B: PDB Molecule: lipid kinase; PDBTitle: structure of an escherichia coli lipid kinase (yegs)
98	d2jgra1	Alignment	not modelled	15.7	14	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
99	d1hcra_	Alignment	not modelled	13.7	5	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like

