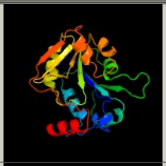
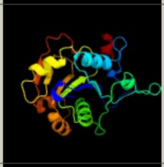
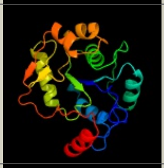
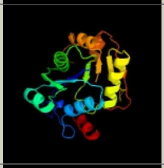
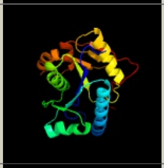
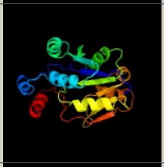
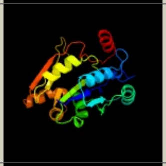
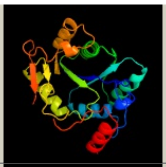
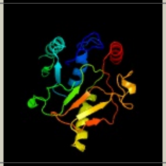
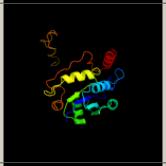
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0371c_(-)_448041_448634
Date	Tue Jul 23 14:50:44 BST 2019
Unique Job ID	acc7b9107fceccc0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2wawA_	Alignment		100.0	62	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**moba relate protein; **PDBTitle:** crystal structure of mycobacterium tuberculosis rv0371c2 homolog from mycobacterium sp. strain jc1
2	c2we9A_	Alignment		100.0	98	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**moba-related protein; **PDBTitle:** crystal structure of rv0371c from mycobacterium2 tuberculosis h37rv
3	d1e5ka_	Alignment		100.0	19	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Molybdenum cofactor biosynthesis protein MobA
4	c3ngwA_	Alignment		100.0	17	**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
5	d1i52a_	Alignment		100.0	17	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
6	d1w55a1	Alignment		100.0	13	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
7	c2xwlB_	Alignment		100.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; **PDBTitle:** crystal structure of ispd from mycobacterium smegmatis in complex with2 ctp and mg
8	c2e8bA_	Alignment		100.0	20	**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
9	c4kt7A_	Alignment		100.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; **PDBTitle:** the crystal structure of 4-diphosphocytidyl-2c-methyl-d-2 erythritolsynthase from anaerococcus prevotii dsm 20548
10	d2oi6a2	Alignment		100.0	17	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
11	d1vpaa_	Alignment		100.0	14	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase

12	c6oewB_	Alignment		100.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cytidylyltransferase; **PDBTitle:** structure of a cytidylyltransferase from leptospira borgpetersenii2 serovar hardjo-bovis (strain jb197)
13	c3rsbB_	Alignment		100.0	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**adenosylcobinamide-phosphate guanylyltransferase; **PDBTitle:** structure of the archaeal gtp:adocbi-p guanylyltransferase (coby) from2 methanocaldococcus jannaschii
14	c5ddtA_	Alignment		99.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; **PDBTitle:** crystal structure of ispd from bacillus subtilis at 1.80 angstroms2 resolution, crystal form i
15	d1qwja_	Alignment		99.9	14	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
16	d1eyra_	Alignment		99.9	14	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
17	c3oamD_	Alignment		99.9	22	**PDB header:**transferase **Chain:** D: **PDB Molecule:**3-deoxy-manno-octulosonate cytidylyltransferase; **PDBTitle:** crystal structure of cytidylyltransferase from vibrio cholerae
18	c4xwiA_	Alignment		99.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-deoxy-manno-octulosonate cytidylyltransferase; **PDBTitle:** x-ray crystal structure of cmp-kdo synthase from pseudomonas2 aeruginosa
19	c4mndA_	Alignment		99.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ctp l-myo-inositol-1-phosphate cytidylyltransferase/cdp-l- **PDBTitle:** crystal structure of archaeoglobus fulgidus ipct-dipps bifunctional2 membrane protein
20	c3polA_	Alignment		99.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-deoxy-manno-octulosonate cytidylyltransferase; **PDBTitle:** 2.3 angstrom crystal structure of 3-deoxy-manno-octulosonate2 cytidylyltransferase (kdsb) from acinetobacter baumannii.
21	d1w77a1	Alignment	not modelled	99.9	14	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
22	d1vica_	Alignment	not modelled	99.9	18	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
23	c1w57A_	Alignment	not modelled	99.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ispd/ispf bifunctional enzyme; **PDBTitle:** structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
24	c3d5nB_	Alignment	not modelled	99.9	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**q97w15_sulso; **PDBTitle:** crystal structure of the q97w15_sulso protein from sulfolobus2 solfataricus. nesg target ssr125.
25	c4jd0A_	Alignment	not modelled	99.9	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nucleotidyl transferase; **PDBTitle:** structure of the inositol-1-phosphate ctp transferase from t.2 maritima.
26	c5xhwA_	Alignment	not modelled	99.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative 6-deoxy-d-mannoheptose pathway protein; **PDBTitle:** crystal structure of hddc from yersinia pseudotuberculosis
27	c4mybA_	Alignment	not modelled	99.9	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; **PDBTitle:** crystal structure of francisella tularensis 2-c-methyl-d-erythritol 4-2 phosphate cytidylyltransferase (ispd)
28	d1g97a2	Alignment	not modelled	99.9	17	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase

29	d2dpwa1	Alignment	not modelled	99.9	19	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**TTHA0179-like
30	c3f1cB_	Alignment	not modelled	99.9	16	**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 cytidylyltransferase from listeria monocytogenes
31	d1h7ea_	Alignment	not modelled	99.9	16	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylyltransferase
32	d1jyka_	Alignment	not modelled	99.9	16	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylyltransferase
33	c3d8vA_	Alignment	not modelled	99.9	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** crystal structure of glmu from mycobacterium tuberculosis2 in complex with uridine-diphosphate-n-acetylglucosamine
34	c3pnnA_	Alignment	not modelled	99.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** the crystal structure of a glycosyltransferase from porphyromonas2 gingivalis w83
35	c1jylC_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**ctp:phosphocholine cytidylytransferase; **PDBTitle:** catalytic mechanism of ctp:phosphocholine2 cytidylytransferase from streptococcus pneumoniae (licc)
36	c4ys8B_	Alignment	not modelled	99.9	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; **PDBTitle:** crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidylyltransferase (ispd) from burkholderia thailandensis
37	d1vgwa_	Alignment	not modelled	99.9	14	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylyltransferase
38	d1iina_	Alignment	not modelled	99.9	19	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
39	c4y7uA_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nucleotidyl transferase; **PDBTitle:** structural analysis of muru
40	c2pa4B_	Alignment	not modelled	99.9	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**utp-glucose-1-phosphate uridylyltransferase; **PDBTitle:** crystal structure of udp-glucose pyrophosphorylase from corynebacteria2 glutamicum in complex with magnesium and udp-glucose
41	c3hl3A_	Alignment	not modelled	99.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucose-1-phosphate thymidylyltransferase; **PDBTitle:** 2.76 angstrom crystal structure of a putative glucose-1-phosphate2 thymidylyltransferase from bacillus anthracis in complex with a3 sucrose.
42	c3foqA_	Alignment	not modelled	99.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** crystal structure of n-acetylglucosamine-1-phosphate2 uridyltransferase (glmu) from mycobacterium tuberculosis in3 a cubic space group.
43	c3tqdA_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-deoxy-manno-octulosonate cytidylyltransferase; **PDBTitle:** structure of the 3-deoxy-d-manno-octulosonate cytidylyltransferase2 (kdsb) from coxiella burnetii
44	c2px7A_	Alignment	not modelled	99.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; **PDBTitle:** crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidylyltransferase from thermus thermophilus hb8
45	c2e3dB_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**utp--glucose-1-phosphate uridylyltransferase; **PDBTitle:** crystal structure of e. coli glucose-1-phosphate2 uridylyltransferase
46	d1h5ra_	Alignment	not modelled	99.9	18	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
47	c2y6pC_	Alignment	not modelled	99.9	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**3-deoxy-manno-octulosonate cytidylyltransferase; **PDBTitle:** evidence for a two-metal-ion-mechanism in the kdo-2 cytidylyltransferase kdsb
48	c5i1fA_	Alignment	not modelled	99.9	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**utp--glucose-1-phosphate uridylyltransferase; **PDBTitle:** crystal structure of utp-glucose-1-phosphate uridylyltransferase from2 burkholderia vietnamiensis in complex with uridine-5'-diphosphate-3 glucose
49	d1fxoa_	Alignment	not modelled	99.9	20	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
50	c4evwB_	Alignment	not modelled	99.9	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nucleoside-diphosphate-sugar pyrophosphorylase; **PDBTitle:** crystal structure of the nucleoside-diphosphate-sugar2 pyrophosphorylase from vibrio cholerae rc9. northeast structural3 genomics consortium (nesg) target vcr193.
51	c3jukA	Alignment	not modelled	99.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-glucose pyrophosphorylase (galu);

51	c3jukA_	Alignment	not modelled	99.9	15	**PDBTitle:** the crystal structure of udp-glucose pyrophosphorylase complexed with2 udp-glucose
52	d1tzfa_	Alignment	not modelled	99.9	13	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
53	c2ux8G_	Alignment	not modelled	99.9	22	**PDB header:**transferase **Chain:** G: **PDB Molecule:**glucose-1-phosphate uridylyltransferase; **PDBTitle:** crystal structure of sphingomonas elodea atcc 31461 glucose-2 1-phosphate uridylyltransferase in complex with glucose-3 1-phosphate.
54	d1mc3a_	Alignment	not modelled	99.9	21	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
55	d1lvwa_	Alignment	not modelled	99.9	23	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
56	c6b5kA_	Alignment	not modelled	99.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucose-1-phosphate thymidylyltransferase; **PDBTitle:** mycobacterium tuberculosis rmla in complex with mg/dttp
57	c2v0hA_	Alignment	not modelled	99.9	25	**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)
58	c3okrA_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; **PDBTitle:** structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
59	c2qkxA_	Alignment	not modelled	99.9	24	**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
60	d1vh1a_	Alignment	not modelled	99.9	17	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
61	c3d98A_	Alignment	not modelled	99.8	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
62	c2oi6A_	Alignment	not modelled	99.8	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** e. coli glmu- complex with udp-glcnac, coa and glcn-1-po4
63	c1fwyA_	Alignment	not modelled	99.8	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine pyrophosphorylase; **PDBTitle:** crystal structure of n-acetylglucosamine 1-phosphate2 uridyltransferase bound to udp-glcnac
64	c1hm8A_	Alignment	not modelled	99.8	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
65	c2vshB_	Alignment	not modelled	99.8	16	**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
66	d2cu2a2	Alignment	not modelled	99.8	20	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**mannose-1-phosphate guanylyl transferase
67	c5vmkB_	Alignment	not modelled	99.8	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** crystal structure of a bifunctional glmu udp-n-acetylglucosamine2 diphosphorylase/glucosamine-1- phosphate n-acetyltransferase from3 acinetobacter baumannii
68	c3okrC_	Alignment	not modelled	99.8	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; **PDBTitle:** structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
69	c4jisB_	Alignment	not modelled	99.8	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribitol-5-phosphate cytidylyltransferase; **PDBTitle:** crystal structure of ribitol 5-phosphate cytidylyltransferase (tari)2 from bacillus subtilis
70	c1yp3C_	Alignment	not modelled	99.8	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glucose-1-phosphate adenylyltransferase small **PDBTitle:** crystal structure of potato tuber adp-glucose2 pyrophosphorylase in complex with atp
71	d1yp2a2	Alignment	not modelled	99.8	16	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
72	c6ifdD_	Alignment	not modelled	99.8	18	**PDB header:**sugar binding protein **Chain:** D: **PDB Molecule:**cmp-n-acetylneuraminate synthetase; **PDBTitle:** crystal structure of cmp-n-acetylneuraminate synthetase from vibrio2 cholerae in complex with cdp and mg2+.
73	c3brkX_	Alignment	not modelled	99.8	15	**PDB header:**transferase **Chain:** X: **PDB Molecule:**glucose-1-phosphate adenylyltransferase; **PDBTitle:** crystal structure of adp-glucose pyrophosphorylase from agrobacterium2 tumefaciens
74	c5b04I_	Alignment	not modelled	99.8	17	**PDB header:**translation **Chain:** I: **PDB Molecule:**probable translation initiation factor eif-2b subunit **PDBTitle:** crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe

75	c6bwhB_	Alignment	not modelled	99.8	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**2-phospho-l-lactate guanylyltransferase; **PDBTitle:** crystal structure of mycoibacterium tuberculosis rv2983 in complex2 with pep
76	c6i3mG_	Alignment	not modelled	99.7	18	**PDB header:**translation **Chain:** G: **PDB Molecule:**translation initiation factor eif-2b subunit epsilon; **PDBTitle:** eif2b:eif2 complex, phosphorylated on eif2 alpha serine 52.
77	c2cu2A_	Alignment	not modelled	99.7	22	**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
78	c6jlwJ_	Alignment	not modelled	99.7	14	**PDB header:**translation **Chain:** J: **PDB Molecule:**translation initiation factor eif-2b subunit epsilon; **PDBTitle:** eif2 - eif2b complex
79	c4cvhA_	Alignment	not modelled	99.7	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**isoprenoid synthase domain-containing protein; **PDBTitle:** crystal structure of human isoprenoid synthase domain-containing2 protein
80	c5l6sF_	Alignment	not modelled	99.7	13	**PDB header:**transferase **Chain:** F: **PDB Molecule:**glucose-1-phosphate adenylyltransferase; **PDBTitle:** crystal structure of e. coli adp-glucose pyrophosphorylase (agpase) in2 complex with a positive allosteric regulator beta-fructose-1,6-3 diphosphate (fbp) - agpase*fbp
81	c2x5sB_	Alignment	not modelled	99.7	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**mannose-1-phosphate guanylyltransferase; **PDBTitle:** crystal structure of t. maritima gdp-mannose2 pyrophosphorylase in apo state.
82	c2ggqA_	Alignment	not modelled	99.7	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**401aa long hypothetical glucose-1-phosphate **PDBTitle:** complex of hypothetical glucose-1-phosphate thymidylyltransferase from2 sulfolobus tokodaii
83	c6ezoF_	Alignment	not modelled	99.6	18	**PDB header:**membrane protein **Chain:** F: **PDB Molecule:**translation initiation factor eif-2b subunit gamma; **PDBTitle:** eukaryotic initiation factor eif2b in complex with isrib
84	c2xmhB_	Alignment	not modelled	99.6	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ctp-inositol-1-phosphate cytidylyltransferase; **PDBTitle:** the x-ray structure of ctp:inositol-1-phosphate cytidylyltransferase2 from archaeoglobus fulgidus
85	c6qg2F_	Alignment	not modelled	99.6	15	**PDB header:**translation **Chain:** F: **PDB Molecule:**translation initiation factor eif-2b subunit gamma; **PDBTitle:** structure of eif2b-eif2 (phosphorylated at ser51) complex (model a)
86	c5b04F_	Alignment	not modelled	99.6	23	**PDB header:**translation **Chain:** F: **PDB Molecule:**probable translation initiation factor eif-2b subunit **PDBTitle:** crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
87	c2qh5B_	Alignment	not modelled	99.4	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**mannose-6-phosphate isomerase; **PDBTitle:** crystal structure of mannose-6-phosphate isomerase from helicobacter2 pylori
88	d1vh3a_	Alignment	not modelled	99.4	16	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylyltransferase
89	c6ezoJ_	Alignment	not modelled	99.2	14	**PDB header:**membrane protein **Chain:** J: **PDB Molecule:**human eukaryotic initiation factor eif2b epsilon subunits; **PDBTitle:** eukaryotic initiation factor eif2b in complex with isrib
90	c3cgxA_	Alignment	not modelled	98.9	17	**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
91	d2i5ea1	Alignment	not modelled	98.6	15	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**MM2497-like
92	c3oc9A_	Alignment	not modelled	98.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine pyrophosphorylase; **PDBTitle:** crystal structure of putative udp-n-acetylglucosamine2 pyrophosphorylase from entamoeba histolytica
93	c6i7tI_	Alignment	not modelled	98.5	14	**PDB header:**translation **Chain:** I: **PDB Molecule:**translation initiation factor eif-2b subunit gamma; **PDBTitle:** eif2b:eif2 complex
94	d2icya2	Alignment	not modelled	98.5	20	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
95	c2q4jB_	Alignment	not modelled	98.4	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
96	c3gueB_	Alignment	not modelled	98.4	17	**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)
						PDB header:transferase

97	c2i5kB_	Alignment	not modelled	98.4	13	**Chain:** B: **PDB Molecule:**utp--glucose-1-phosphate uridylyltransferase; **PDBTitle:** crystal structure of ugp1p
98	d1vm8a_	Alignment	not modelled	98.3	21	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
99	d1jv1a_	Alignment	not modelled	98.3	21	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
100	c3r2wB_	Alignment	not modelled	98.3	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**utp--glucose-1-phosphate uridylyltransferase; **PDBTitle:** crystal strucutre of udp-glucose pyrophosphorylase of homo sapiens
101	c4bmaB_	Alignment	not modelled	98.3	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**udp-n-acetylglucosamine pyrophosphorylase; **PDBTitle:** structural of aspergillus fumigatus udp-n-acetylglucosamine2 pyrophosphorylase
102	c2oefA_	Alignment	not modelled	98.3	17	**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
103	c2yqsA_	Alignment	not modelled	98.2	15	**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
104	c4bqhA_	Alignment	not modelled	98.2	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine pyrophosphorylase; **PDBTitle:** crystal structure of the uridine diphosphate n-2 acetylglucosamine pyrophosphorylase from trypanosoma3 brucei in complex with inhibitor
105	c3ogzA_	Alignment	not modelled	98.1	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-sugar pyrophosphorylase; **PDBTitle:** protein structure of usp from l. major in apo-form
106	c5mm1A_	Alignment	not modelled	90.3	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**dolichol monophosphate mannose synthase; **PDBTitle:** dolichyl phosphate mannose synthase in complex with gdp and dolichyl2 phosphate mannose
107	c3f1yC_	Alignment	not modelled	86.3	10	**PDB header:**transferase **Chain:** C: **PDB Molecule:**mannosyl-3-phosphoglycerate synthase; **PDBTitle:** mannosyl-3-phosphoglycerate synthase from rubrobacter xylanophilus
108	c1omxB_	Alignment	not modelled	81.0	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**alpha-1,4-n-acetylhexosaminyltransferase extl2; **PDBTitle:** crystal structure of mouse alpha-1,4-n-acetylhexosaminyltransferase2 (extl2)
109	d1omza_	Alignment	not modelled	80.1	12	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Exostosin
110	c4fixA_	Alignment	not modelled	79.1	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-galactofuranosyl transferase glft2; **PDBTitle:** crystal structure of glft2
111	c3ckvA_	Alignment	not modelled	78.1	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a mycobacterial protein
112	c2ffuA_	Alignment	not modelled	71.8	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polypeptide n-acetylgalactosaminyltransferase 2; **PDBTitle:** crystal structure of human ppgalnact-2 complexed with udp and ea2
113	c2z86D_	Alignment	not modelled	69.5	11	**PDB header:**transferase **Chain:** D: **PDB Molecule:**chondroitin synthase; **PDBTitle:** crystal structure of chondroitin polymerase from escherichia coli2 strain k4 (k4cp) complexed with udp-glcua and udp
114	c6h4mA_	Alignment	not modelled	57.2	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable ss-1,3-n-acetylglucosaminyltransferase; **PDBTitle:** tarp-udp-glcnac-3rbop
115	d1xhba2	Alignment	not modelled	48.2	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Polypeptide N-acetylgalactosaminyltransferase 1, N-terminal domain
116	c5tz8C_	Alignment	not modelled	47.0	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glycosyl transferase; **PDBTitle:** crystal structure of s. aureus tars
117	c1xhbA_	Alignment	not modelled	40.0	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polypeptide n-acetylgalactosaminyltransferase 1; **PDBTitle:** the crystal structure of udp-galnac: polypeptide alpha-n-2 acetylgalactosaminyltransferase-t1
118	c5heaA_	Alignment	not modelled	39.1	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative glycosyltransferase (galt1); **PDBTitle:** cgt structure in hexamer
119	d2bo4a1	Alignment	not modelled	38.6	16	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**MGS-like
120	c5nqaA_	Alignment	not modelled	35.4	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polypeptide n-acetylgalactosaminyltransferase 4; **PDBTitle:** crystal structure of galnac-t4 in complex with the


monoglycopeptide 3