








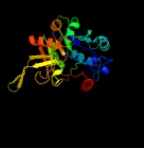
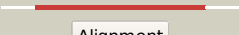






















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0993_galU_1109276_1110196
Date	Wed Jul 31 22:05:06 BST 2019
Unique Job ID	23457fcc95be319a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2pa4B_</a>	 Alignment		100.0	64	<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
2	<a href="#">c5ilfA_</a>	 Alignment		100.0	43	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> utp--glucose-1-phosphate uridylyltransferase; <b>PDBTitle:</b> crystal structure of utp-glucose-1-phosphate uridylyltransferase from2 burkholderia vietnamiensis in complex with uridine-5'-diphosphate-3 glucose
3	<a href="#">c2ux8G_</a>	 Alignment		100.0	41	<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.
4	<a href="#">c2e3dB_</a>	 Alignment		100.0	37	<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
5	<a href="#">d1iina_</a>	 Alignment		100.0	24	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidyltransferase
6	<a href="#">d1mc3a_</a>	 Alignment		100.0	24	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidyltransferase
7	<a href="#">d1h5ra_</a>	 Alignment		100.0	24	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidyltransferase
8	<a href="#">d1fxoa_</a>	 Alignment		100.0	26	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidyltransferase
9	<a href="#">d1lvwa_</a>	 Alignment		100.0	25	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidyltransferase
10	<a href="#">c3jukA_</a>	 Alignment		100.0	36	<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
11	<a href="#">c6b5kA_</a>	 Alignment		100.0	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-1-phosphate thymidyltransferase; <b>PDBTitle:</b> mycobacterium tuberculosis rmla in complex with mg/dttp

12	<a href="#">d1yp2a2</a>	Alignment		100.0	18	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidyltransferase
13	<a href="#">c1yp3C</a>	Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> glucose-1-phosphate adenylyltransferase small <b>PDBTitle:</b> crystal structure of potato tuber adp-glucose2 pyrophosphorylase in complex with atp
14	<a href="#">c3brkX</a>	Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> glucose-1-phosphate adenylyltransferase; <b>PDBTitle:</b> crystal structure of adp-glucose pyrophosphorylase from agrobacterium2 tumefaciens
15	<a href="#">c3d8vA</a>	Alignment		100.0	25	<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 tuberculosis2 in complex with uridine-diphosphate-n-acetylglucosamine
16	<a href="#">c5l6sF</a>	Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> glucose-1-phosphate adenylyltransferase; <b>PDBTitle:</b> 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
17	<a href="#">c3hl3A</a>	Alignment		100.0	23	<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.
18	<a href="#">c2cu2A</a>	Alignment		100.0	19	<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
19	<a href="#">c2x5sB</a>	Alignment		100.0	21	<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.
20	<a href="#">c3pnnA</a>	Alignment		100.0	20	<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
21	<a href="#">c6i3mG</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> translation <b>Chain:</b> G: <b>PDB Molecule:</b> translation initiation factor eif-2b subunit epsilon; <b>PDBTitle:</b> eif2b:eif2 complex, phosphorylated on eif2 alpha serine 52.
22	<a href="#">c5b04l</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> translation <b>Chain:</b> l: <b>PDB Molecule:</b> probable translation initiation factor eif-2b subunit <b>PDBTitle:</b> crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
23	<a href="#">c3d98A</a>	Alignment	not modelled	100.0	25	<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
24	<a href="#">c1hm8A</a>	Alignment	not modelled	100.0	26	<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
25	<a href="#">d2cu2a2</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> mannose-1-phosphate guanylyl transferase
26	<a href="#">c2oi6A</a>	Alignment	not modelled	100.0	25	<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-p04
27	<a href="#">c2qkxA</a>	Alignment	not modelled	100.0	25	<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 <b>PDB header:</b> transferase

28	<a href="#">c2v0hA_</a>	Alignment	not modelled	100.0	28	<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)
29	<a href="#">d1tzfa_</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
30	<a href="#">c1fwyA_</a>	Alignment	not modelled	100.0	25	<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-glcnac
31	<a href="#">c5xhwA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative 6-deoxy-d-mannoheptose pathway protein; <b>PDBTitle:</b> crystal structure of hddc from yersinia pseudotuberculosis
32	<a href="#">c4evwB_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> nucleoside-diphosphate-sugar pyrophosphorylase; <b>PDBTitle:</b> crystal structure of the nucleoside-diphosphate-sugar2 pyrophosphorylase from vibrio cholerae rc9. northeast structural3 genomics consortium (nesh) target vcr193.
33	<a href="#">d2oi6a2</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> UDP-glucose pyrophosphorylase
34	<a href="#">c6jlwJ_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> translation <b>Chain:</b> J: <b>PDB Molecule:</b> translation initiation factor eif-2b subunit epsilon; <b>PDBTitle:</b> eif2 - eif2b complex
35	<a href="#">c4jd0A_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleotidyl transferase; <b>PDBTitle:</b> structure of the inositol-1-phosphate ctp transferase from t.2 maritima.
36	<a href="#">d1g97a2</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> UDP-glucose pyrophosphorylase
37	<a href="#">c4mndA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ctp l-myo-inositol-1-phosphate cytidylyltransferase/cdp-l- <b>PDBTitle:</b> crystal structure of archaeoglobus fulgidus ipct-dipps bifunctional2 membrane protein
38	<a href="#">c4y7uA_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleotidyl transferase; <b>PDBTitle:</b> structural analysis of muru
39	<a href="#">c2ggqA_</a>	Alignment	not modelled	100.0	28	<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 thymidylyltransferase from2 sulfobolus tokodaii
40	<a href="#">c3foqA_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein glmu; <b>PDBTitle:</b> crystal structure of n-acetylglucosamine-1-phosphate2 uridylyltransferase (glmu) from mycobacterium tuberculosis in3 a cubic space group.
41	<a href="#">c5b04F_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> translation <b>Chain:</b> F: <b>PDB Molecule:</b> probable translation initiation factor eif-2b subunit <b>PDBTitle:</b> crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
42	<a href="#">c5vmkB_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein glmu; <b>PDBTitle:</b> crystal structure of a bifunctional glmu udp-n-acetylglucosamine2 diphosphorylase/glucosamine-1- phosphate n-acetyltransferase from3 acinetobacter baumannii
43	<a href="#">c6qq2F_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> translation <b>Chain:</b> F: <b>PDB Molecule:</b> translation initiation factor eif-2b subunit gamma; <b>PDBTitle:</b> structure of eif2b-eif2 (phosphorylated at ser51) complex (model a)
44	<a href="#">d1jyka_</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
45	<a href="#">c1jylC_</a>	Alignment	not modelled	100.0	19	<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)
46	<a href="#">d1vica_</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
47	<a href="#">c6ezoF_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> membrane protein <b>Chain:</b> F: <b>PDB Molecule:</b> translation initiation factor eif-2b subunit gamma; <b>PDBTitle:</b> eukaryotic initiation factor eif2b in complex with isrib
48	<a href="#">c4xwiA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-deoxy-manno-octulosonate cytidylyltransferase; <b>PDBTitle:</b> x-ray crystal structure of cmp-kdo synthase from pseudomonas2 aeruginosa
49	<a href="#">c6ezoj_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> membrane protein <b>Chain:</b> J: <b>PDB Molecule:</b> human eukaryotic initiation factor eif2b epsilon subunits; <b>PDBTitle:</b> eukaryotic initiation factor eif2b in complex with isrib
50	<a href="#">c2xmhB_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ctp-inositol-1-phosphate cytidylyltransferase; <b>PDBTitle:</b> the x-ray structure of ctp:inositol-1-phosphate cytidylyltransferase2 from archaeoglobus fulgidus
51	<a href="#">c2gh5B_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> mannose-6-phosphate isomerase;

51	<a href="#">c2qf3B</a>	Alignment	not modelled	100.0	10	<b>PDBTitle:</b> crystal structure of mannose-6-phosphate isomerase from helicobacter2 pylori <b>PDB header:</b> transferase
52	<a href="#">c3oamD</a>	Alignment	not modelled	100.0	17	<b>Chain:</b> D: <b>PDB Molecule:</b> 3-deoxy-manno-octulosonate cytidyltransferase; <b>PDBTitle:</b> crystal structure of cytidyltransferase from vibrio cholerae
53	<a href="#">c3polA</a>	Alignment	not modelled	100.0	14	<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.
54	<a href="#">c3tqdA</a>	Alignment	not modelled	100.0	16	<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
55	<a href="#">c2xw1B</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; <b>PDBTitle:</b> crystal structure of ispd from mycobacterium smegmatis in complex with2 ctp and mg
56	<a href="#">c2y6pC</a>	Alignment	not modelled	99.9	15	<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 the kdo-2 cytidyltransferase kdsb
57	<a href="#">d1i52a</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidyltransferase
58	<a href="#">d1h7ea</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
59	<a href="#">d1vpaA</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidyltransferase
60	<a href="#">d1vh1a</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidyltransferase
61	<a href="#">c5ddtA</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; <b>PDBTitle:</b> crystal structure of ispd from bacillus subtilis at 1.80 angstroms2 resolution, crystal form i
62	<a href="#">c4kt7A</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; <b>PDBTitle:</b> the crystal structure of 4-diphosphocytidyl-2c-methyl-d-2 erythritolsynthase from anaerococcus prevotii dsm 20548
63	<a href="#">c6i7tI</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> translation <b>Chain:</b> I: <b>PDB Molecule:</b> translation initiation factor eif-2b subunit gamma; <b>PDBTitle:</b> eif2b:eif2 complex
64	<a href="#">d1eyra</a>	Alignment	not modelled	99.9	11	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidyltransferase
65	<a href="#">d1w55a1</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidyltransferase
66	<a href="#">d1e5ka</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Molybdenum cofactor biosynthesis protein MobA
67	<a href="#">c4mybA</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 cytidyltransferase; <b>PDBTitle:</b> crystal structure of francisella tularensis 2-c-methyl-d-erythritol 4-2 phosphate cytidyltransferase (ispd)
68	<a href="#">d1vh3a</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidyltransferase
69	<a href="#">c2we9A</a>	Alignment	not modelled	99.9	28	<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
70	<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
71	<a href="#">d1qwja</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidyltransferase
72	<a href="#">c2wawA</a>	Alignment	not modelled	99.9	22	<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
73	<a href="#">c3f1cB</a>	Alignment	not modelled	99.9	16	<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
74	<a href="#">c4ys8B</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; <b>PDBTitle:</b> crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd) from burkholderia thailandensis <b>PDB header:</b> transferase

75	<a href="#">c2vshB_</a>	Alignment	not modelled	99.8	13	<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
76	<a href="#">d1w77a1</a>	Alignment	not modelled	99.8	16	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
77	<a href="#">c3rsbB_</a>	Alignment	not modelled	99.8	13	<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
78	<a href="#">c3okrA_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; <b>PDBTitle:</b> structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
79	<a href="#">c3ngwA_</a>	Alignment	not modelled	99.8	15	<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
80	<a href="#">c4jisB_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ribitol-5-phosphate cytidylyltransferase; <b>PDBTitle:</b> crystal structure of ribitol 5-phosphate cytidylyltransferase (tari)2 from bacillus subtilis
81	<a href="#">d1vgwa_</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
82	<a href="#">c2px7A_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; <b>PDBTitle:</b> crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidylyltransferase from thermus thermophilus hb8
83	<a href="#">c6oewB_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cytidylyltransferase; <b>PDBTitle:</b> structure of a cytidylyltransferase from leptospira borgpetersenii2 serovar hardjo-bovis (strain jb197)
84	<a href="#">c6ifdD_</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> sugar binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> cmp-n-acetylneuraminate synthetase; <b>PDBTitle:</b> crystal structure of cmp-n-acetylneuraminate synthetase from vibrio2 cholerae in complex with cdp and mg2+.
85	<a href="#">c1w57A_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ispdf/ispf bifunctional enzyme; <b>PDBTitle:</b> structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
86	<a href="#">c2e8bA_</a>	Alignment	not modelled	99.7	19	<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
87	<a href="#">c3okrC_</a>	Alignment	not modelled	99.6	20	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; <b>PDBTitle:</b> structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
88	<a href="#">c4cvhA_</a>	Alignment	not modelled	99.2	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> isoprenoid synthase domain-containing protein; <b>PDBTitle:</b> crystal structure of human isoprenoid synthase domain-containing2 protein
89	<a href="#">c3d5nB_</a>	Alignment	not modelled	99.2	20	<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 from sulfolobus2 solfataricus. nesp target ssr125.
90	<a href="#">c3oc9A_</a>	Alignment	not modelled	98.9	13	<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
91	<a href="#">d1vm8a_</a>	Alignment	not modelled	98.8	10	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> UDP-glucose pyrophosphorylase
92	<a href="#">d1jv1a_</a>	Alignment	not modelled	98.7	13	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> UDP-glucose pyrophosphorylase
93	<a href="#">c4bqhA_</a>	Alignment	not modelled	98.7	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine pyrophosphorylase; <b>PDBTitle:</b> crystal structure of the uridine diphosphate n-2 acetylglucosamine pyrophosphorylase from trypanosoma3 brucei in complex with inhibitor
94	<a href="#">d2icya2</a>	Alignment	not modelled	98.7	11	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> UDP-glucose pyrophosphorylase
95	<a href="#">c4bmaB_</a>	Alignment	not modelled	98.7	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-n-acetylglucosamine pyrophosphorylase; <b>PDBTitle:</b> structural of aspergillus fumigatus udp-n-acetylglucosamine2 pyrophosphorylase
96	<a href="#">c3gueB_</a>	Alignment	not modelled	98.7	12	<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)
97	<a href="#">c2yqsA_</a>	Alignment	not modelled	98.6	11	<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
98	<a href="#">c2oefA_</a>	Alignment	not modelled	98.4	11	<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
99	<a href="#">c2q4jB_</a>	Alignment	not modelled	98.4	10	<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
100	<a href="#">c2i5kB_</a>	Alignment	not modelled	98.4	9	<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
101	<a href="#">c3r2wB_</a>	Alignment	not modelled	98.2	13	<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 of homo sapiens
102	<a href="#">c3ogzA_</a>	Alignment	not modelled	98.2	17	<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
103	<a href="#">c6bwhB_</a>	Alignment	not modelled	97.6	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-phospho-l-lactate guanylyltransferase; <b>PDBTitle:</b> crystal structure of mycoibacterium tuberculosis rv2983 in complex2 with pep
104	<a href="#">c2ffuA_</a>	Alignment	not modelled	95.0	12	<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 udp and ea2
105	<a href="#">c2d7iA_</a>	Alignment	not modelled	91.2	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polypeptide n-acetylgalactosaminyltransferase 10; <b>PDBTitle:</b> crystal structure of pp-galnac-t10 with udp, galnac and mn2+
106	<a href="#">c1xhbA_</a>	Alignment	not modelled	87.7	15	<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
107	<a href="#">c5mm1A_</a>	Alignment	not modelled	84.6	17	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> dolichol monophosphate mannose synthase; <b>PDBTitle:</b> dolichyl phosphate mannose synthase in complex with gdp and dolichyl2 phosphate mannose
108	<a href="#">d1omza_</a>	Alignment	not modelled	81.5	13	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Exostosin
109	<a href="#">c5nqaA_</a>	Alignment	not modelled	80.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polypeptide n-acetylgalactosaminyltransferase 4; <b>PDBTitle:</b> crystal structure of galnac-t4 in complex with the monoglycopeptide 3
110	<a href="#">d2i5ea1</a>	Alignment	not modelled	79.0	16	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> MM2497-like
111	<a href="#">c6e4rB_</a>	Alignment	not modelled	77.6	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> polypeptide n-acetylgalactosaminyltransferase 9; <b>PDBTitle:</b> crystal structure of the drosophila melanogaster polypeptide n-2 acetylgalactosaminyl transferase pgant9b
112	<a href="#">c5z8bB_</a>	Alignment	not modelled	74.3	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> kfia protein; <b>PDBTitle:</b> truncated n-acetylglucosaminyl transferase kfia from e. coli k5 strain2 apo form
113	<a href="#">c6iwqE_</a>	Alignment	not modelled	70.0	12	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> n-acetylgalactosaminyltransferase 7; <b>PDBTitle:</b> crystal structure of galnac-t7 with mn2+
114	<a href="#">c1omxB_</a>	Alignment	not modelled	68.6	10	<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-acetylhexosaminyltransferase2 (extl2)
115	<a href="#">c2qgiA_</a>	Alignment	not modelled	63.2	9	<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
116	<a href="#">c3cgaA_</a>	Alignment	not modelled	59.9	17	<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
117	<a href="#">d1v7za_</a>	Alignment	not modelled	58.8	26	<b>Fold:</b> Creatininase <b>Superfamily:</b> Creatininase <b>Family:</b> Creatininase
118	<a href="#">c3no4A_</a>	Alignment	not modelled	53.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> creatinine amidohydrolase; <b>PDBTitle:</b> crystal structure of a creatinine amidohydrolase (npun_f1913) from2 nostoc punctiforme pcc 73102 at 2.00 a resolution
119	<a href="#">d1thta_</a>	Alignment	not modelled	51.0	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Thioesterases
						<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> putative creatinine amidohydrolase;

120	<a href="#">c3lubE_</a>	Alignment	not modelled	46.5	20	<b>PDBTitle:</b> crystal structure of putative creatinine amidohydrolase (yp_211512.1)2 from bacteroides fragilis nctc 9343 at 2.11 a resolution
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