Phyre^2

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Description	RVBD1516c_(-)_1707535_1708545
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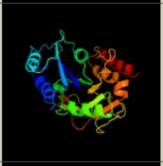
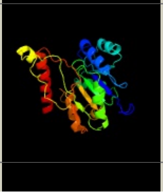
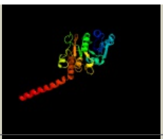
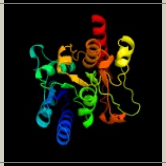
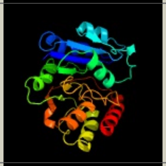
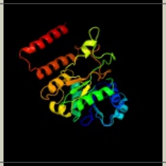
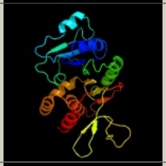
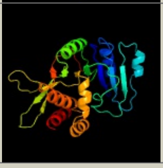
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2z86D_	Alignment		100.0	20	**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
2	d1xhba2	Alignment		100.0	15	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Polypeptide N-acetylgalactosaminyltransferase 1, N-terminal domain
3	c1xhbA_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polypeptide n-acetylgalactosaminyltransferase 1; **PDBTitle:** the crystal structure of udp-galnac: polypeptide alpha-n-2 acetylgalactosaminyltransferase-t1
4	c6h4mA_	Alignment		100.0	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable ss-1,3-n-acetylglucosaminyltransferase; **PDBTitle:** tarp-udp-glcnac-3rbop
5	c6e4rB_	Alignment		100.0	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**polypeptide n-acetylgalactosaminyltransferase 9; **PDBTitle:** crystal structure of the drosophila melanogaster polypeptide n-2 acetylgalactosaminyl transferase pgant9b
6	c2d7iA_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polypeptide n-acetylgalactosaminyltransferase 10; **PDBTitle:** crystal structure of pp-galnac-t10 with udp, galnac and mn2+
7	c5tz8C_	Alignment		100.0	21	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glycosyl transferase; **PDBTitle:** crystal structure of s. aureus tars
8	c6iwqE_	Alignment		100.0	13	**PDB header:**transferase **Chain:** E: **PDB Molecule:**n-acetylgalactosaminyltransferase 7; **PDBTitle:** crystal structure of galnac-t7 with mn2+
9	c2ffuA_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polypeptide n-acetylgalactosaminyltransferase 2; **PDBTitle:** crystal structure of human ppgalnact-2 complexed with udp and ea2
10	c5nqaA_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polypeptide n-acetylgalactosaminyltransferase 4; **PDBTitle:** crystal structure of galnac-t4 in complex with the monoglycopeptide 3
11	c4hg6A_	Alignment		100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cellulose synthase subunit a; **PDBTitle:** structure of a cellulose synthase - cellulose translocation2 intermediate

12	c5mm1A_	Alignment		100.0	15	**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
13	d1qg8a_	Alignment		100.0	20	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Spore coat polysaccharide biosynthesis protein SpsA
14	c5heaA_	Alignment		100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative glycosyltransferase (galt1); **PDBTitle:** cgt structure in hexamer
15	c3f1yC_	Alignment		100.0	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**mannosyl-3-phosphoglycerate synthase; **PDBTitle:** mannosyl-3-phosphoglycerate synthase from rubrobacter xylanophilus
16	c3ckvA_	Alignment		100.0	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a mycobacterial protein
17	c3bcvA_	Alignment		99.9	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative glycosyltransferase protein; **PDBTitle:** crystal structure of a putative glycosyltransferase from bacteroides2 fragilis
18	c4fixA_	Alignment		99.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-galactofuranosyl transferase glft2; **PDBTitle:** crystal structure of glft2
19	c1omxB_	Alignment		99.9	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**alpha-1,4-n-acetylhexosaminyltransferase extl2; **PDBTitle:** crystal structure of mouse alpha-1,4-n-acetylhexosaminyltransferase2 (extl2)
20	d1omza_	Alignment		99.9	9	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Exostosin
21	c6p61D_	Alignment	not modelled	99.9	21	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glycosyltransferase; **PDBTitle:** structure of a glycosyltransferase from leptospira borgpetersenii2 serovar hardjo-bovis (strain jb197)
22	c5ekeB_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**uncharacterized glycosyltransferase sll0501; **PDBTitle:** structure of the polyisoprenyl-phosphate glycosyltransferase gtrb2 (f215a mutant)
23	c3zf8A_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannan polymerase complexes subunit mnn9; **PDBTitle:** crystal structure of saccharomyces cerevisiae mnn9 in2 complex with gdp and mn.
24	c2qgiA_	Alignment	not modelled	99.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp synthase subunits region orf 6; **PDBTitle:** the udp complex structure of the sixth gene product of the f1-atpase2 operon of rhodobacter blasticus
25	c5ggfC_	Alignment	not modelled	99.8	16	**PDB header:**transferase, sugar binding protein **Chain:** C: **PDB Molecule:**protein o-linked-mannose beta-1,2-n- **PDBTitle:** crystal structure of human protein o-mannose beta-1,2-n-2 acetylglucosaminyltransferase form ii
26	c5z8bB_	Alignment	not modelled	99.8	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**kfia protein; **PDBTitle:** truncated n-acetylglucosaminyl transferase kfia from e. coli k5 strain2 apo form
27	d1fo8a_	Alignment	not modelled	99.3	14	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**N-acetylglucosaminyltransferase I
28	c4irqB_	Alignment	not modelled	99.1	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**beta-1,4-galactosyltransferase 7; **PDBTitle:** crystal structure of catalytic domain of human beta1,2 4galactosyltransferase 7 in closed conformation in complex with3

						manganese and udp
29	d2bo4a1	Alignment	not modelled	99.1	14	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**MGS-like
30	c6fxyA_	Alignment	not modelled	98.6	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**procollagen-lysine,2-oxoglutarate 5-dioxygenase 3; **PDBTitle:** crystal structure of full-length human lysyl hydroxylase lh3 -2 cocrystal with fe2+, mn2+, udp-gal - structure from long-wavelength3 s-sad
31	d1pzta_	Alignment	not modelled	98.6	12	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**beta 1,4 galactosyltransferase (b4GalT1)
32	c5vcmA_	Alignment	not modelled	98.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alpha-1,6-mannosyl-glycoprotein 2-beta-n- **PDBTitle:** alpha-1,6-mannosyl-glycoprotein 2-beta-n-acetylglucosaminyltransferase2 with bound udp and manganese
33	c3lw6A_	Alignment	not modelled	97.9	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**beta-4-galactosyltransferase 7; **PDBTitle:** crystal structure of drosophila beta1,4-galactosyltransferase-7
34	c4kt7A_	Alignment	not modelled	97.5	14	**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
35	c2wvmA_	Alignment	not modelled	97.3	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannosyl-3-phosphoglycerate synthase; **PDBTitle:** h309a mutant of mannosyl-3-phosphoglycerate synthase from2 thermus thermophilus hb27 in complex with3 gdp-alpha-d-mannose and mg(ii)
36	c2zu8A_	Alignment	not modelled	96.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannosyl-3-phosphoglycerate synthase; **PDBTitle:** crystal structure of mannosyl-3-phosphoglycerate synthase2 from pyrococcus horikoshii
37	d1vh3a_	Alignment	not modelled	96.7	14	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylyltransferase
38	c5vcsB_	Alignment	not modelled	96.7	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**alpha-1,6-mannosyl-glycoprotein 2-beta-n- **PDBTitle:** alpha-1,6-mannosyl-glycoprotein 2-beta-n-acetylglucosaminyltransferase2 with bound acceptor
39	c2d0jD_	Alignment	not modelled	96.3	11	**PDB header:**transferase **Chain:** D: **PDB Molecule:**galactosylgalactosylxylosylprotein 3-beta- **PDBTitle:** crystal structure of human glcat-s apo form
40	c2wawA_	Alignment	not modelled	95.8	9	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**moba relate protein; **PDBTitle:** crystal structure of mycobacterium tuberculosis rv0371c2 homolog from mycobacterium sp. strain jc1
41	c5gvvF_	Alignment	not modelled	95.7	9	**PDB header:**transferase **Chain:** F: **PDB Molecule:**glycosyl transferase family 8; **PDBTitle:** crystal structure of the glycosyltransferase glye in streptococcus2 pneumoniae tigr4
42	d3cu0a1	Alignment	not modelled	95.6	13	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**1,3-glucuronyltransferase
43	c3tztB_	Alignment	not modelled	95.6	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycosyl transferase family 8; **PDBTitle:** the structure of a protein in glycosyl transferase family 8 from2 anaerococcus prevotii.
44	c2px7A_	Alignment	not modelled	95.6	14	**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	d1v82a_	Alignment	not modelled	95.5	17	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**1,3-glucuronyltransferase
46	c6oewB_	Alignment	not modelled	95.5	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cytidylyltransferase; **PDBTitle:** structure of a cytidylyltransferase from leptospira borgpetersenii2 serovar hardjo-bovis (strain jb197)
47	d1w77a1	Alignment	not modelled	95.4	14	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylyltransferase
48	c4ys8B_	Alignment	not modelled	95.0	11	**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
49	d1mc3a_	Alignment	not modelled	94.5	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
50	c4xwiA_	Alignment	not modelled	94.5	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-deoxy-manno-octulosonate cytidylyltransferase; **PDBTitle:** x-ray crystal structure of cmp-kdo synthase from pseudomonas2 aeruginosa
51	c5ddtA_	Alignment	not modelled	93.6	10	**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
52	c2xwlB_	Alignment	not modelled	93.3	17	**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
53	d1fxoa_	Alignment	not modelled	93.1	9	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
54	c3okrA_	Alignment	not modelled	93.1	18	**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)
55	d1lvwa_	Alignment	not modelled	93.1	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
56	c3d5nB_	Alignment	not modelled	92.6	13	**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.
57	d1qwja_	Alignment	not modelled	92.6	13	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
58	d1h5ra_	Alignment	not modelled	92.6	9	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
59	c3foqA_	Alignment	not modelled	91.9	14	**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.
60	c3d8vA_	Alignment	not modelled	91.7	14	**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
61	c6b5kA_	Alignment	not modelled	91.5	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucose-1-phosphate thymidylyltransferase; **PDBTitle:** mycobacterium tuberculosis rmla in complex with mg/dttp
62	c2e8bA_	Alignment	not modelled	91.4	14	**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
63	c4cvhA_	Alignment	not modelled	91.3	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**isoprenoid synthase domain-containing protein; **PDBTitle:** crystal structure of human isoprenoid synthase domain-containing2 protein
64	c1ga8A_	Alignment	not modelled	91.1	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**galactosyl transferase lgtc; **PDBTitle:** crystal structure of galacosyltransferase lgtc in complex2 with donor and acceptor sugar analogs.
65	d1ga8a_	Alignment	not modelled	91.1	16	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Galactosyltransferase LgtC
66	c2we9A_	Alignment	not modelled	91.0	9	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**moba-related protein; **PDBTitle:** crystal structure of rv0371c from mycobacterium2 tuberculosis h37rv
67	c3oamD_	Alignment	not modelled	90.5	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**3-deoxy-manno-octulosonate cytidylyltransferase; **PDBTitle:** crystal structure of cytidylyltransferase from vibrio cholerae
68	c2gamA_	Alignment	not modelled	90.5	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**beta-1,6-n-acetylglucosaminyltransferase; **PDBTitle:** x-ray crystal structure of murine leukocyte-type core 2 b1,6-n-2 acetylglucosaminyltransferase (c2gnt-l) in complex with galb1,3galnac
69	c3f1cB_	Alignment	not modelled	90.4	10	**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
70	c3tqdA_	Alignment	not modelled	90.3	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
71	c4mybA_	Alignment	not modelled	90.1	10	**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)
72	d1i52a_	Alignment	not modelled	90.1	12	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
73	d1vpaa_	Alignment	not modelled	89.3	7	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
74	c3okrC_	Alignment	not modelled	89.3	17	**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)
75	d1e5ka_	Alignment	not modelled	89.3	14	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Molybdenum cofactor biosynthesis protein MobA

76	c3d98A_	Alignment	not modelled	89.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
77	c2vshB_	Alignment	not modelled	88.8	6	**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
78	d1vgwa_	Alignment	not modelled	88.5	12	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
79	d1h7ea_	Alignment	not modelled	88.5	12	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
80	d1vica_	Alignment	not modelled	88.3	12	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
81	d1iina_	Alignment	not modelled	88.2	8	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
82	d1w55a1	Alignment	not modelled	86.3	12	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
83	c1w57A_	Alignment	not modelled	86.2	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ispd/ispf bifunctional enzyme; **PDBTitle:** structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
84	c6bwhB_	Alignment	not modelled	85.6	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**2-phospho-l-lactate guanylyltransferase; **PDBTitle:** crystal structure of mycoibacterium tuberculosis rv2983 in complex2 with pep
85	c4jd0A_	Alignment	not modelled	84.5	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nucleotidyl transferase; **PDBTitle:** structure of the inositol-1-phosphate ctp transferase from t.2 maritima.
86	c2xmhB_	Alignment	not modelled	83.0	15	**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
87	d2oi6a2	Alignment	not modelled	81.0	9	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
88	c3rsbB_	Alignment	not modelled	80.3	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**adenosylcobinamide-phosphate guanylyltransferase; **PDBTitle:** structure of the archaeal gtp:adocbi-p guanylyltransferase (coby) from2 methanocaldococcus jannaschii
89	c2qkxA_	Alignment	not modelled	79.0	14	**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
90	c5xhwA_	Alignment	not modelled	78.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative 6-deoxy-d-mannoheptose pathway protein; **PDBTitle:** crystal structure of hddc from yersinia pseudotuberculosis
91	c4jisB_	Alignment	not modelled	78.7	6	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribitol-5-phosphate cytidylyltransferase; **PDBTitle:** crystal structure of ribitol 5-phosphate cytidylyltransferase (tari)2 from bacillus subtilis
92	c2pa4B_	Alignment	not modelled	78.2	10	**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
93	c6aokA_	Alignment	not modelled	76.7	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ceg4; **PDBTitle:** crystal structure of legionella pneumophila effector ceg4 with n-2 terminal tev protease cleavage sequence
94	c3polA_	Alignment	not modelled	76.3	12	**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.
95	c6cgjA_	Alignment	not modelled	75.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**effector protein lem4 (lpg1101); **PDBTitle:** structure of the had domain of effector protein lem4 (lpg1101) from2 legionella pneumophila
96	d1eyra_	Alignment	not modelled	75.0	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
97	d1vh1a_	Alignment	not modelled	67.4	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
98	c2y6pC_	Alignment	not modelled	66.4	11	**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
99	c3brkX_	Alignment	not modelled	64.4	12	**PDB header:**transferase **Chain:** X: **PDB Molecule:**glucose-1-phosphate adenylyltransferase; **PDBTitle:** crystal structure of adp-glucose pyrophosphorylase from agrobacterium2 tumefaciens
						PDB header:sugar binding protein

100	c6ifdD_	Alignment	not modelled	64.3	7	**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+.
101	c3brcA_	Alignment	not modelled	63.5	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein of unknown function; **PDBTitle:** crystal structure of a conserved protein of unknown function from2 methanobacterium thermoautotrophicum
102	c3pnnA_	Alignment	not modelled	63.4	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** the crystal structure of a glycosyltransferase from porphyromonas2 gingivalis w83
103	c6qg2F_	Alignment	not modelled	61.9	11	**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)
104	c3ngwA_	Alignment	not modelled	60.2	11	**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
105	c3ssmB_	Alignment	not modelled	60.0	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyltransferase; **PDBTitle:** myce methyltransferase from the mycinamycin biosynthetic pathway in2 complex with mg and sah, crystal form 1
106	c6ejeA_	Alignment	not modelled	59.7	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylosyltransferase 1; **PDBTitle:** human xylosyltransferase 1 in complex with peptide paaegsgeqdft
107	c5d5pC_	Alignment	not modelled	59.6	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**hcgb; **PDBTitle:** hcgb from methanococcus maripaludis
108	c3hl3A_	Alignment	not modelled	57.8	7	**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.
109	c3ssoE_	Alignment	not modelled	57.1	26	**PDB header:**transferase **Chain:** E: **PDB Molecule:**methyltransferase; **PDBTitle:** myce methyltransferase from the mycinamycin biosynthetic pathway in2 complex with mg and sah, crystal form 2
110	d2dpwa1	Alignment	not modelled	56.5	12	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**TTHA0179-like
111	c1jylC_	Alignment	not modelled	55.0	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**ctp:phosphocholine cytidylyltransferase; **PDBTitle:** catalytic mechanism of ctp:phosphocholine2 cytidylytransferase from streptococcus pneumoniae (licc)
112	d1g97a2	Alignment	not modelled	50.2	9	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
113	c4mndA_	Alignment	not modelled	48.8	11	**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
114	c4uegB_	Alignment	not modelled	47.4	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycogenin-2; **PDBTitle:** crystal structure of human glycogenin-2 catalytic domain
115	c5yh1A_	Alignment	not modelled	47.1	5	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**member of s1p family of ribosomal proteins; **PDBTitle:** member of s1p family of ribosomal proteins pf0399 dhh domain
116	c2x5sB_	Alignment	not modelled	45.8	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**mannose-1-phosphate guanylyltransferase; **PDBTitle:** crystal structure of t. maritima gdp-mannose2 pyrophosphorylase in apo state.
117	c4y7uA_	Alignment	not modelled	44.5	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nucleotidyl transferase; **PDBTitle:** structural analysis of muru
118	c2ux8G_	Alignment	not modelled	44.4	18	**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.
119	d1ll2a_	Alignment	not modelled	43.6	14	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Glycogenin
120	d1vkpa_	Alignment	not modelled	43.2	14	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase