























# Phyre2

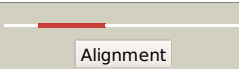
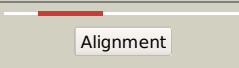
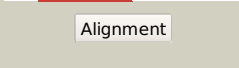
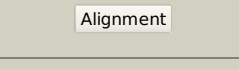
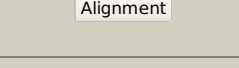
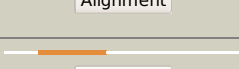
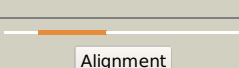
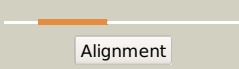
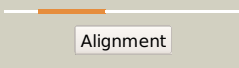
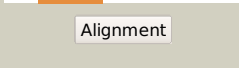
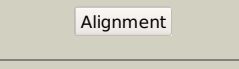
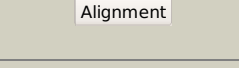
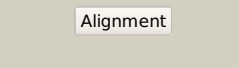
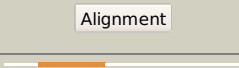
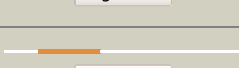

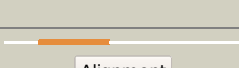
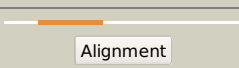
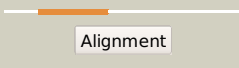
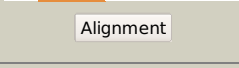
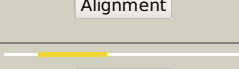

Email	mdejesus@rockefeller.edu
Description	RVBD1520_(-)_1711034_1712074
Date	Fri Aug 2 13:30:10 BST 2019
Unique Job ID	39ef3048ac96f70d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2z86D_</a>	 Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> chondroitin synthase; <b>PDBTitle:</b> crystal structure of chondroitin polymerase from escherichia coli2 strain k4 (k4cp) complexed with udp-glcua and udp
2	<a href="#">c5tz8C_</a>	 Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> glycosyl transferase; <b>PDBTitle:</b> crystal structure of s. aureus tars
3	<a href="#">d1xhba2</a>	 Alignment		100.0	14	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Polypeptide N-acetylgalactosaminyltransferase 1, N-terminal domain
4	<a href="#">c2ffuA_</a>	 Alignment		100.0	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
5	<a href="#">c6iwqE_</a>	 Alignment		100.0	13	<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+
6	<a href="#">c2d7iA_</a>	 Alignment		100.0	13	<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+
7	<a href="#">c6e4rB_</a>	 Alignment		100.0	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
8	<a href="#">c1xhbA_</a>	 Alignment		100.0	17	<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
9	<a href="#">c5nqaA_</a>	 Alignment		100.0	14	<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
10	<a href="#">c6h4mA_</a>	 Alignment		100.0	10	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> probable ss-1,3-n-acetylglucosaminyltransferase; <b>PDBTitle:</b> tarp-udp-glcnac-3rbop
11	<a href="#">d1qg8a_</a>	 Alignment		100.0	19	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Spore coat polysaccharide biosynthesis protein SpsA

12	<a href="#">c3ckvA_</a>	Alignment		100.0	16	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of a mycobacterial protein
13	<a href="#">c3flyC_</a>	Alignment		100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> mannosyl-3-phosphoglycerate synthase; <b>PDBTitle:</b> mannosyl-3-phosphoglycerate synthase from rubrobacter xylanophilus
14	<a href="#">c5heaA_</a>	Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative glycosyltransferase (galt1); <b>PDBTitle:</b> cgt structure in hexamer
15	<a href="#">c5mm1A_</a>	Alignment		100.0	16	<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
16	<a href="#">c1omxB_</a>	Alignment		100.0	7	<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)
17	<a href="#">d1omza_</a>	Alignment		100.0	8	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Exostosin
18	<a href="#">c3bcvA_</a>	Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative glycosyltransferase protein; <b>PDBTitle:</b> crystal structure of a putative glycosyltransferase from bacteroides2 fragilis
19	<a href="#">c4hg6A_</a>	Alignment		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulose synthase subunit a; <b>PDBTitle:</b> structure of a cellulose synthase - cellulose translocation2 intermediate
20	<a href="#">c6p61D_</a>	Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> glycosyltransferase; <b>PDBTitle:</b> structure of a glycosyltransferase from leptospira borgpetersenii2 serovar hardjo-bovis (strain jb197)
21	<a href="#">c4fixA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-galactofuranosyl transferase glft2; <b>PDBTitle:</b> crystal structure of glft2
22	<a href="#">c5ekeB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized glycosyltransferase sl0501; <b>PDBTitle:</b> structure of the polyisoprenyl-phosphate glycosyltransferase gtrb2 (f215a mutant)
23	<a href="#">c5z8bB_</a>	Alignment	not modelled	100.0	13	<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
24	<a href="#">c2qgiA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> atp synthase subunits region of 6; <b>PDBTitle:</b> the udp complex structure of the sixth gene product of the f1-atpase2 operon of rhodobacter blasticus
25	<a href="#">c3zf8A_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mannan polymerase complexes subunit mnn9; <b>PDBTitle:</b> crystal structure of saccharomyces cerevisiae mnn9 in2 complex with gdp and mn.
26	<a href="#">c5ggfC_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase, sugar binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> protein o-linked-mannose beta-1,2-n- <b>PDBTitle:</b> crystal structure of human protein o-mannose beta-1,2-n-2 acetylglucosaminyltransferase form ii
27	<a href="#">c4irqB_</a>	Alignment	not modelled	99.6	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-1,4-galactosyltransferase 7; <b>PDBTitle:</b> crystal structure of catalytic domain of human beta1,2 4galactosyltransferase 7 in closed conformation in complex with3 manganese and udp
						<b>Fold:</b> Nucleotide-diphospho-sugar transferases

28	<a href="#">d2bo4a1</a>	Alignment	not modelled	99.4	14	<b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> MGS-like
29	<a href="#">d1fo8a_</a>	Alignment	not modelled	99.3	14	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> N-acetylglucosaminyltransferase I
30	<a href="#">d1pzta_</a>	Alignment	not modelled	99.0	11	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> beta 1,4 galactosyltransferase (b4GalT1)
31	<a href="#">c6fxyA_</a>	Alignment	not modelled	98.9	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> procollagen-lysine,2-oxoglutarate 5-dioxygenase 3; <b>PDBTitle:</b> crystal structure of full-length human lysyl hydroxylase lh3 -2 cocrystal with fe2+, mn2+, udp-gal - structure from long-wavelength3 s-sad
32	<a href="#">c3lw6A_</a>	Alignment	not modelled	98.3	8	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-4-galactosyltransferase 7; <b>PDBTitle:</b> crystal structure of drosophila beta1,4-galactosyltransferase-7
33	<a href="#">c5vcmA_</a>	Alignment	not modelled	98.2	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-1,6-mannosyl-glycoprotein 2-beta-n- <b>PDBTitle:</b> alpha-1,6-mannosyl-glycoprotein 2-beta-n-acetylglucosaminyltransferase2 with bound udp and manganese
34	<a href="#">c2wvma_</a>	Alignment	not modelled	97.9	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mannosyl-3-phosphoglycerate synthase; <b>PDBTitle:</b> h309a mutant of mannosyl-3-phosphoglycerate synthase from2 thermus thermophilus hb27 in complex with3 gdp-alpha-d-mannose and mg(ii)
35	<a href="#">c2zu8A_</a>	Alignment	not modelled	97.5	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mannosyl-3-phosphoglycerate synthase; <b>PDBTitle:</b> crystal structure of mannosyl-3-phosphoglycerate synthase2 from pyrococcus horikoshii
36	<a href="#">d1fxoa_</a>	Alignment	not modelled	96.3	12	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidyltransferase
37	<a href="#">c2d0jD_</a>	Alignment	not modelled	96.3	12	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> galactosylgalactosylxylosylprotein 3-beta- <b>PDBTitle:</b> crystal structure of human gcat-s apo form
38	<a href="#">d1h5ra_</a>	Alignment	not modelled	95.9	13	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidyltransferase
39	<a href="#">c6b5kA_</a>	Alignment	not modelled	95.7	11	<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
40	<a href="#">d3cu0a1</a>	Alignment	not modelled	95.4	14	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> 1,3-glucuronyltransferase
41	<a href="#">c2px7A_</a>	Alignment	not modelled	95.3	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> crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase from thermus thermophilus hb8
42	<a href="#">d1vh3a_</a>	Alignment	not modelled	95.2	14	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidyltransferase
43	<a href="#">c2wawA_</a>	Alignment	not modelled	94.9	10	<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
44	<a href="#">c4kt7A_</a>	Alignment	not modelled	94.8	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
45	<a href="#">d1mc3a_</a>	Alignment	not modelled	94.4	13	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidyltransferase
46	<a href="#">c5gvvF_</a>	Alignment	not modelled	94.3	9	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> glycosyl transferase family 8; <b>PDBTitle:</b> crystal structure of the glycosyltransferase glye in streptococcus2 pneumoniae tigr4
47	<a href="#">d1v82a_</a>	Alignment	not modelled	94.3	11	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> 1,3-glucuronyltransferase
48	<a href="#">d1iina_</a>	Alignment	not modelled	94.1	13	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidyltransferase
49	<a href="#">c3d5nB_</a>	Alignment	not modelled	93.8	11	<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 sulfobolus2 solfataricus. nesc target ssr125.
50	<a href="#">c3okrA_</a>	Alignment	not modelled	93.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; <b>PDBTitle:</b> structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
51	<a href="#">c2xwIB_</a>	Alignment	not modelled	92.7	16	<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
52	<a href="#">d1lvwa_</a>	Alignment	not modelled	92.6	12	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> glucose-1-phosphate thymidyltransferase

53	<a href="#">c3f1cB</a>	 Alignment	not modelled	92.4	8	<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
54	<a href="#">d1w77a1</a>	 Alignment	not modelled	92.0	11	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidyltransferase
55	<a href="#">c3d8vA</a>	 Alignment	not modelled	91.8	12	<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
56	<a href="#">c5vcsB</a>	 Alignment	not modelled	91.7	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-1,6-mannosyl-glycoprotein 2-beta-n-acetylglucosaminyltransferase2 with bound acceptor <b>PDBTitle:</b> alpha-1,6-mannosyl-glycoprotein 2-beta-n-acetylglucosaminyltransferase2 with bound acceptor
57	<a href="#">c5ddtA</a>	 Alignment	not modelled	90.3	8	<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
58	<a href="#">c3tztB</a>	 Alignment	not modelled	89.4	8	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyl transferase family 8; <b>PDBTitle:</b> the structure of a protein in glycosyl transferase family 8 from2 anaerococcus prevotii.
59	<a href="#">c6bwhB</a>	 Alignment	not modelled	88.0	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-phospho-l-lactate guanylyltransferase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis rv2983 in complex2 with pep
60	<a href="#">c6oewB</a>	 Alignment	not modelled	86.7	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cytidyltransferase; <b>PDBTitle:</b> structure of a cytidyltransferase from leptospira borgpetersenii2 serovar hardjo-bovis (strain jb197)
61	<a href="#">c3foqA</a>	 Alignment	not modelled	86.7	14	<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.
62	<a href="#">c2vshB</a>	 Alignment	not modelled	86.3	5	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 4-phosphate <b>PDBTitle:</b> synthesis of cdp-activated ribitol for teichoic acid2 precursors in streptococcus pneumoniae
63	<a href="#">c4xwiA</a>	 Alignment	not modelled	86.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-deoxy-manno-octulosonate cytidyltransferase; <b>PDBTitle:</b> x-ray crystal structure of cmp-kdo synthase from pseudomonas2 aeruginosa
64	<a href="#">c5xhwA</a>	 Alignment	not modelled	85.1	10	<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
65	<a href="#">c4mybA</a>	 Alignment	not modelled	84.9	6	<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)
66	<a href="#">c3hl3A</a>	 Alignment	not modelled	84.6	11	<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.
67	<a href="#">d1w55a1</a>	 Alignment	not modelled	83.8	10	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidyltransferase
68	<a href="#">d1i52a</a>	 Alignment	not modelled	83.8	9	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidyltransferase
69	<a href="#">c2e8bA</a>	 Alignment	not modelled	83.7	13	<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
70	<a href="#">c4ys8B</a>	 Alignment	not modelled	82.7	13	<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
71	<a href="#">c2we9A</a>	 Alignment	not modelled	81.7	13	<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
72	<a href="#">c4jd0A</a>	 Alignment	not modelled	81.7	13	<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.
73	<a href="#">c3okrC</a>	 Alignment	not modelled	80.8	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; <b>PDBTitle:</b> structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
74	<a href="#">d1vpaa</a>	 Alignment	not modelled	80.1	10	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidyltransferase
75	<a href="#">c1ga8A</a>	Alignment	not modelled	79.5	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> galactosyl transferase lgtc; <b>PDBTitle:</b> crystal structure of galactosyltransferase lgtc in complex2 with donor and acceptor sugar analogs.
						<b>Fold:</b> Nucleotide-diphospho-sugar transferases

76	<a href="#">d1ga8a_</a>	Alignment	not modelled	79.5	10	<b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Galactosyltransferase LgtC
77	<a href="#">c1w57A_</a>	Alignment	not modelled	79.2	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ispd/ispf bifunctional enzyme; <b>PDBTitle:</b> structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
78	<a href="#">c3d98A_</a>	Alignment	not modelled	78.5	12	<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
79	<a href="#">c2gamA_</a>	Alignment	not modelled	76.1	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-1,6-n-acetylglucosaminyltransferase; <b>PDBTitle:</b> x-ray crystal structure of murine leukocyte-type core 2 b1,6-n-2 acetylglucosaminyltransferase (c2gnt-l) in complex with galb1,3galnac
80	<a href="#">c3rsbB_</a>	Alignment	not modelled	74.3	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
81	<a href="#">c2qkxA_</a>	Alignment	not modelled	74.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein glmu; <b>PDBTitle:</b> n-acetyl glucosamine 1-phosphate uridyltransferase from mycobacterium2 tuberculosis complex with n-acetyl glucosamine 1-phosphate
82	<a href="#">c3oamD_</a>	Alignment	not modelled	72.8	11	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 3-deoxy-manno-octulosonate cytidyltransferase; <b>PDBTitle:</b> crystal structure of cytidyltransferase from vibrio cholerae
83	<a href="#">d1vgwa_</a>	Alignment	not modelled	71.3	9	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidyltransferase
84	<a href="#">c2pa4B_</a>	Alignment	not modelled	69.9	9	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> utp-glucose-1-phosphate uridyltransferase; <b>PDBTitle:</b> crystal structure of udp-glucose pyrophosphorylase from corynebacteria2 glutamicum in complex with magnesium and udp-glucose
85	<a href="#">d1e5ka_</a>	Alignment	not modelled	68.8	16	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Molybdenum cofactor biosynthesis protein MobA
86	<a href="#">d1eyra_</a>	Alignment	not modelled	68.3	8	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidyltransferase
87	<a href="#">d2oi6a2</a>	Alignment	not modelled	63.8	10	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> UDP-glucose pyrophosphorylase
88	<a href="#">c3pnnA_</a>	Alignment	not modelled	63.0	9	<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
89	<a href="#">c5d5pC_</a>	Alignment	not modelled	62.8	13	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> hcgB; <b>PDBTitle:</b> hcgB from methanococcus maripaludis
90	<a href="#">c6aokA_</a>	Alignment	not modelled	62.4	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ceg4; <b>PDBTitle:</b> crystal structure of legionella pneumophila effector ceg4 with n-2 terminal tev protease cleavage sequence
91	<a href="#">c3brcA_</a>	Alignment	not modelled	61.8	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved protein of unknown function; <b>PDBTitle:</b> crystal structure of a conserved protein of unknown function from2 methanobacterium thermoautotrophicum
92	<a href="#">c4ytgA_</a>	Alignment	not modelled	61.6	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidylarginine deiminase; <b>PDBTitle:</b> crystal structure of porphyromonas gingivalis peptidylarginine2 deiminase (ppad) mutant c351a in complex with dipeptide met-arg.
93	<a href="#">d1h7ea_</a>	Alignment	not modelled	61.4	12	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidyltransferase
94	<a href="#">c1zcyA_</a>	Alignment	not modelled	54.5	5	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycogenin-1; <b>PDBTitle:</b> apo form of a mutant of glycogenin in which asp159 is replaced by ser
95	<a href="#">c4evwB_</a>	Alignment	not modelled	48.9	9	<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 (nsg) target vcr193.
96	<a href="#">c4jisB_</a>	Alignment	not modelled	48.9	7	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ribitol-5-phosphate cytidyltransferase; <b>PDBTitle:</b> crystal structure of ribitol 5-phosphate cytidyltransferase (tari)2 from bacillus subtilis
97	<a href="#">c3tqdA_</a>	Alignment	not modelled	47.6	19	<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
98	<a href="#">c2xmhB_</a>	Alignment	not modelled	45.4	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ctp-inositol-1-phosphate cytidyltransferase; <b>PDBTitle:</b> the x-ray structure of ctp:inositol-1-phosphate cytidyltransferase2 from archaeoglobus fulgidus
99	<a href="#">c3nplA_</a>	Alignment	not modelled	44.3	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-deoxy-manno-octulosonate cytidyltransferase;



99	<a href="#">c3p0tA_</a>	Alignment	not modelled	44.3	14	<b>PDBTitle:</b> 2.3 angstrom crystal structure of 3-deoxy-manno-octulosonate2 cytidyltransferase (kdsb) from acinetobacter baumannii.
100	<a href="#">c2y6pC_</a>	Alignment	not modelled	43.6	11	<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
101	<a href="#">c6qg2F_</a>	Alignment	not modelled	43.3	10	<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)
102	<a href="#">c3ngwA_</a>	Alignment	not modelled	39.8	13	<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
103	<a href="#">d1g97a2</a>	Alignment	not modelled	38.8	7	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> UDP-glucose pyrophosphorylase
104	<a href="#">c4y7uA_</a>	Alignment	not modelled	37.6	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleotidyl transferase; <b>PDBTitle:</b> structural analysis of muru
105	<a href="#">c5kojD_</a>	Alignment	not modelled	37.5	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> nitrogenase femo beta subunit protein nifk; <b>PDBTitle:</b> nitrogenase mofep protein in the ids oxidized state
106	<a href="#">c2qh5B_</a>	Alignment	not modelled	36.9	8	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> mannose-6-phosphate isomerase; <b>PDBTitle:</b> crystal structure of mannose-6-phosphate isomerase from helicobacter2 pylori
107	<a href="#">c2ux8G_</a>	Alignment	not modelled	36.0	17	<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.
108	<a href="#">d1vica_</a>	Alignment	not modelled	35.4	15	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
109	<a href="#">c2e3dB_</a>	Alignment	not modelled	35.2	12	<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
110	<a href="#">c5k2yB_</a>	Alignment	not modelled	34.6	8	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable periplasmic sugar-binding lipoprotein uspc; <b>PDBTitle:</b> crystal structure of m. tuberculosis uspc (monoclinic crystal form)
111	<a href="#">c2x5sB_</a>	Alignment	not modelled	33.7	9	<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.
112	<a href="#">c3c9hB_</a>	Alignment	not modelled	33.3	5	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter, substrate binding protein; <b>PDBTitle:</b> crystal structure of the substrate binding protein of the abc2 transporter from agrobacterium tumefaciens
113	<a href="#">d1qh8b_</a>	Alignment	not modelled	32.9	6	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
114	<a href="#">c5yh1A_</a>	Alignment	not modelled	32.5	12	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> member of s1p family of ribosomal proteins; <b>PDBTitle:</b> member of s1p family of ribosomal proteins pf0399 dhh domain
115	<a href="#">d1xkna_</a>	Alignment	not modelled	30.7	22	<b>Fold:</b> Pentain, beta/alpha-propeller <b>Superfamily:</b> Pentain <b>Family:</b> Porphyromonas-type peptidylarginine deiminase
116	<a href="#">c5xxuM_</a>	Alignment	not modelled	28.0	11	<b>PDB header:</b> ribosome <b>Chain:</b> M: <b>PDB Molecule:</b> ribosomal protein es12; <b>PDBTitle:</b> small subunit of toxoplasma gondii ribosome
117	<a href="#">c4mndA_</a>	Alignment	not modelled	26.2	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ctp l-myo-inositol-1-phosphate cytidyltransferase/cdp-l- <b>PDBTitle:</b> crystal structure of archaeoglobus fulgidus ipct-dipps bifunctional2 membrane protein
118	<a href="#">c3ssmB_</a>	Alignment	not modelled	24.0	32	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> myce methyltransferase from the mycinamycin biosynthetic pathway in2 complex with mg and sah, crystal form 1
119	<a href="#">c6cgjA_</a>	Alignment	not modelled	23.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> effector protein lem4 (lpg1101); <b>PDBTitle:</b> structure of the had domain of effector protein lem4 (lpg1101) from2 legionella pneumophila
120	<a href="#">d1m1nb_</a>	Alignment	not modelled	23.6	7	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein