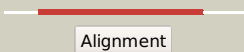

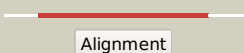

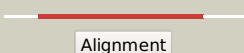

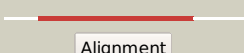





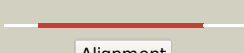

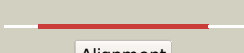


















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1525_(wbbL2)_1720023_1720808
Date	Fri Aug 2 13:30:11 BST 2019
Unique Job ID	744ed98c26153f34

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5nqaA_	 Alignment		100.0	17	PDB header: transferase Chain: A; PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 4; PDBTitle: crystal structure of galnac-t4 in complex with the monoglycopeptide 3
2	c2ffuA_	 Alignment		100.0	18	PDB header: transferase Chain: A; PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 2; PDBTitle: crystal structure of human ppgalnact-2 complexed with udp and ea2
3	c1xhbA_	 Alignment		100.0	16	PDB header: transferase Chain: A; PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 1; PDBTitle: the crystal structure of udp-galnac: polypeptide alpha-n-2 acetylgalactosaminyltransferase-t1
4	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
5	c2d7iA_	 Alignment		100.0	19	PDB header: transferase Chain: A; PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 10; PDBTitle: crystal structure of pp-galnac-t10 with udp, galnac and mn2+
6	c6iwqE_	 Alignment		100.0	15	PDB header: transferase Chain: E; PDB Molecule: n-acetylgalactosaminyltransferase 7; PDBTitle: crystal structure of galnac-t7 with mn2+
7	d1xhba2	 Alignment		100.0	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Polypeptide N-acetylgalactosaminyltransferase 1, N-terminal domain
8	c4fixA_	 Alignment		100.0	17	PDB header: transferase Chain: A; PDB Molecule: udp-galactofuranosyl transferase glft2; PDBTitle: crystal structure of glft2
9	c2z86D_	 Alignment		100.0	15	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
10	c4hg6A_	 Alignment		100.0	20	PDB header: transferase Chain: A; PDB Molecule: cellulose synthase subunit a; PDBTitle: structure of a cellulose synthase - cellulose translocation2 intermediate
11	c5tz8C_	 Alignment		100.0	9	PDB header: transferase Chain: C; PDB Molecule: glycosyl transferase; PDBTitle: crystal structure of s. aureus tars

12	c5mm1A_	Alignment		100.0	10	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	c6h4mA_	Alignment		100.0	9	PDB header: transferase Chain: A: PDB Molecule: probable ss-1,3-n-acetylglucosaminyltransferase; PDBTitle: tarp-udp-glcnac-3rbop
14	c3zf8A_	Alignment		100.0	13	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.
15	c3f1yC_	Alignment		100.0	12	PDB header: transferase Chain: C: PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: mannosyl-3-phosphoglycerate synthase from rubrobacter xylanophilus
16	c3ckvA_	Alignment		100.0	11	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a mycobacterial protein
17	c3bcvA_	Alignment		100.0	12	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase protein; PDBTitle: crystal structure of a putative glycosyltransferase from bacteroides2 fragilis
18	d1qq8a_	Alignment		100.0	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Spore coat polysaccharide biosynthesis protein SpsA
19	c5ekeB_	Alignment		100.0	13	PDB header: transferase Chain: B: PDB Molecule: uncharacterized glycosyltransferase sli0501; PDBTitle: structure of the polyisoprenyl-phosphate glycosyltransferase gtrb2 (f215a mutant)
20	c5heaA_	Alignment		100.0	11	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase (galt1); PDBTitle: cgt structure in hexamer
21	c1omxB_	Alignment	not modelled	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)
22	c6p61D_	Alignment	not modelled	99.9	19	PDB header: transferase Chain: D: PDB Molecule: glycosyltransferase; PDBTitle: structure of a glycosyltransferase from leptospira borgpetersenii2 serovar hardjo-bovis (strain jb197)
23	c2qgiA_	Alignment	not modelled	99.9	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
24	d1omza_	Alignment	not modelled	99.9	8	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Exostosin
25	c5z8bB_	Alignment	not modelled	99.9	9	PDB header: transferase Chain: B: PDB Molecule: kfia protein; PDBTitle: truncated n-acetylglucosaminyl transferase kfia from e. coli k5 strain2 apo form
26	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
27	c4irqB_	Alignment	not modelled	99.7	17	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
28	d2bo4a1	Alignment	not modelled	99.6	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: MGS-like

29	d1pzta_	Alignment	not modelled	99.5	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: beta 1,4 galactosyltransferase (b4GalT1)
30	c3lw6A_	Alignment	not modelled	99.2	16	PDB header: transferase Chain: A: PDB Molecule: beta-4-galactosyltransferase 7; PDBTitle: crystal structure of drosophila beta1,4-galactosyltransferase-7
31	d1fo8a_	Alignment	not modelled	98.7	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: N-acetylglucosaminyltransferase I
32	c6fxyA_	Alignment	not modelled	98.6	15	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
33	c5vcmA_	Alignment	not modelled	98.5	16	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
34	c2wvmA_	Alignment	not modelled	97.9	16	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)
35	c2zu8A_	Alignment	not modelled	97.7	20	PDB header: transferase Chain: A: PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: crystal structure of mannosyl-3-phosphoglycerate synthase2 from pyrococcus horikoshii
36	d1vh3a_	Alignment	not modelled	96.8	9	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
37	d3cu0a1	Alignment	not modelled	94.0	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: 1,3-glucuronyltransferase
38	c4ys8B_	Alignment	not modelled	93.4	10	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
39	c2px7A_	Alignment	not modelled	93.3	17	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
40	d1v82a_	Alignment	not modelled	92.5	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: 1,3-glucuronyltransferase
41	c4mybA_	Alignment	not modelled	92.5	7	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)
42	c2pa4B_	Alignment	not modelled	92.1	17	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
43	c4xwiA_	Alignment	not modelled	91.0	8	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate cytidylyltransferase; PDBTitle: x-ray crystal structure of cmp-kdo synthase from pseudomonas2 aeruginosa
44	c5vcsB_	Alignment	not modelled	90.9	13	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
45	c2d0jD_	Alignment	not modelled	90.8	13	PDB header: transferase Chain: D: PDB Molecule: galactosylgalactosylxylosylprotein 3-beta- PDBTitle: crystal structure of human gcat-s apo form
46	d1vica_	Alignment	not modelled	90.7	9	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
47	c2wawA_	Alignment	not modelled	88.8	11	PDB header: unknown function Chain: A: PDB Molecule: moba relate protein; PDBTitle: crystal structure of mycobacterium tuberculosis rv0371c2 homolog from mycobacterium sp. strain jc1
48	c6bwhB_	Alignment	not modelled	88.5	12	PDB header: transferase Chain: B: PDB Molecule: 2-phospho-l-lactate guanylyltransferase; PDBTitle: crystal structure of mycoibacterium tuberculosis rv2983 in complex2 with pep
49	d1vh1a_	Alignment	not modelled	88.2	10	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
50	c3okrC_	Alignment	not modelled	87.3	15	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 cytidylyltransferase (ispd)
51	c3d5nB_	Alignment	not modelled	82.6	9	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: q97w15_sulso; PDBTitle: crystal structure of the q97w15_sulso protein from sulfobolus2 solfataricus. nesg target srr125.
52	c2j0bA_	Alignment	not modelled	81.6	14	PDB header: transferase Chain: A: PDB Molecule: beta-1,3-n-acetylglucosaminyltransferase manic fringe; PDBTitle: structure of the catalytic domain of mouse manic fringe

						in2 complex with udp and manganese
53	d1mc3a_	Alignment	not modelled	79.8	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
54	c3okrA_	Alignment	not modelled	79.1	12	PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
55	c2we9A_	Alignment	not modelled	78.8	13	PDB header: unknown function Chain: A: PDB Molecule: moba-related protein; PDBTitle: crystal structure of rv0371c from mycobacterium2 tuberculosis h37rv
56	c4kt7A_	Alignment	not modelled	75.3	10	PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: the crystal structure of 4-diphosphocytidyl-2c-methyl-d-2 erythritolsynthase from anaerococcus prevotii dsm 20548
57	d2oi6a2	Alignment	not modelled	75.0	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
58	d1vpaa_	Alignment	not modelled	73.8	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
59	c3pnnA_	Alignment	not modelled	73.7	9	PDB header: transferase Chain: A: PDB Molecule: conserved domain protein; PDBTitle: the crystal structure of a glycosyltransferase from porphyromonas2 gingivalis w83
60	c3oamD_	Alignment	not modelled	73.5	11	PDB header: transferase Chain: D: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: crystal structure of cytidyltransferase from vibrio cholerae
61	c3brkX_	Alignment	not modelled	71.8	12	PDB header: transferase Chain: X: PDB Molecule: glucose-1-phosphate adenyltransferase; PDBTitle: crystal structure of adp-glucose pyrophosphorylase from agrobacterium2 tumefaciens
62	d1e5ka_	Alignment	not modelled	71.5	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Molybdenum cofactor biosynthesis protein MobA
63	d1i52a_	Alignment	not modelled	70.5	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
64	c3foqA_	Alignment	not modelled	70.1	12	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.
65	d1h5ra_	Alignment	not modelled	68.6	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
66	c3cqxA_	Alignment	not modelled	68.4	20	PDB header: transferase Chain: A: PDB Molecule: putative nucleotide-diphospho-sugar transferase; PDBTitle: crystal structure of putative nucleotide-diphospho-sugar transferase2 (yp_389115.1) from desulfovibrio desulfuricans g20 at 1.90 a3 resolution
67	c3ngwA_	Alignment	not modelled	66.6	9	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
68	c2qh5B_	Alignment	not modelled	66.3	12	PDB header: isomerase Chain: B: PDB Molecule: mannose-6-phosphate isomerase; PDBTitle: crystal structure of mannose-6-phosphate isomerase from helicobacter2 pylori
69	c3tqdA_	Alignment	not modelled	65.1	13	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: structure of the 3-deoxy-d-manno-octulosonate cytidyltransferase2 (kdsb) from coxiella burnetii
70	c2xwIB_	Alignment	not modelled	64.7	10	PDB header: transferase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: crystal structure of ispd from mycobacterium smegmatis in complex with2 ctp and mg
71	d1fxoa_	Alignment	not modelled	63.1	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
72	c3rsbB_	Alignment	not modelled	62.7	6	PDB header: transferase Chain: B: PDB Molecule: adenosylcobinamide-phosphate guanylyltransferase; PDBTitle: structure of the archaeal gtp:adocbi-p guanylyltransferase (coby) from2 methanocaldococcus jannaschii
73	c4jd0A_	Alignment	not modelled	62.0	10	PDB header: transferase Chain: A: PDB Molecule: nucleotidyl transferase; PDBTitle: structure of the inositol-1-phosphate ctp transferase from t.2 maritima.
74	c2cu2A_	Alignment	not modelled	61.6	21	PDB header: transferase Chain: A: PDB Molecule: putative mannose-1-phosphate guanylyl transferase; PDBTitle: crystal structure of mannose-1-phosphate geranyltransferase from2 thermus thermophilus hb8
75	c6b5kA_	Alignment	not modelled	61.1	15	PDB header: transferase Chain: A: PDB Molecule: glucose-1-phosphate thymidyltransferase; PDBTitle: mycobacterium tuberculosis rmla in complex with

						mg/dttp
76	d1vkpa_	Alignment	not modelled	60.9	18	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
77	d1vgwa_	Alignment	not modelled	60.3	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
78	c6cglA_	Alignment	not modelled	59.3	23	PDB header: hydrolase Chain: A: PDB Molecule: effector protein lem4 (lpg1101); PDBTitle: structure of the had domain of effector protein lem4 (lpg1101) from legionella pneumophila
79	c4urjA_	Alignment	not modelled	52.6	16	PDB header: unknown function Chain: A: PDB Molecule: protein fam83a; PDBTitle: crystal structure of human bj-tsa-9
80	d2cu2a2	Alignment	not modelled	52.4	20	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: mannose-1-phosphate guanylyl transferase
81	c5ddtA_	Alignment	not modelled	49.9	6	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
82	c2l82A_	Alignment	not modelled	49.2	15	PDB header: de novo protein Chain: A: PDB Molecule: designed protein or32; PDBTitle: solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or32
83	c2we7A_	Alignment	not modelled	48.5	14	PDB header: oxidoreductase Chain: A: PDB Molecule: xanthine dehydrogenase; PDBTitle: crystal structure of mycobacterium tuberculosis rv0376c2 homologue from mycobacterium smegmatis
84	d1w55a1	Alignment	not modelled	48.3	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
85	d2dpwa1	Alignment	not modelled	48.2	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: TTHA0179-like
86	d1w77a1	Alignment	not modelled	48.0	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
87	c4ytgA_	Alignment	not modelled	47.7	18	PDB header: hydrolase Chain: A: PDB Molecule: peptidylarginine deiminase; PDBTitle: crystal structure of porphyromonas gingivalis peptidylarginine2 deiminase (ppad) mutant c351a in complex with dipeptide met-arg.
88	c2e8bA_	Alignment	not modelled	45.2	12	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
89	d1lvwa_	Alignment	not modelled	44.3	19	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidylyltransferase
90	d1iina_	Alignment	not modelled	44.1	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidylyltransferase
91	c6oewB_	Alignment	not modelled	43.7	12	PDB header: transferase Chain: B: PDB Molecule: cytidylyltransferase; PDBTitle: structure of a cytidylyltransferase from leptospira borgpetersenii2 serovar hardjo-bovis (strain jb197)
92	d1yp2a2	Alignment	not modelled	42.9	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidylyltransferase
93	c3igfB_	Alignment	not modelled	42.4	14	PDB header: atp binding protein Chain: B: PDB Molecule: all4481 protein; PDBTitle: crystal structure of the all4481 protein from nostoc sp. pcc 7120,2 northeast structural genomics consortium target nsr300
94	c2y6pC_	Alignment	not modelled	41.1	12	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
95	c6bsvB_	Alignment	not modelled	39.8	14	PDB header: transferase Chain: B: PDB Molecule: xyloglucan 6-xylosyltransferase 1; PDBTitle: crystal structure of xyloglucan xylosyltransferase binary form
96	c1w57A_	Alignment	not modelled	38.3	15	PDB header: transferase Chain: A: PDB Molecule: ispd/ispf bifunctional enzyme; PDBTitle: structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
97	c3polA_	Alignment	not modelled	35.5	10	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.
98	c3d8vA_	Alignment	not modelled	34.4	13	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
99	c3d98A_	Alignment	not modelled	33.6	13	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
						PDB header: transferase

100	c5xhwA_	Alignment	not modelled	32.1	20	Chain: A: PDB Molecule: putative 6-deoxy-d-mannoheptose pathway protein; PDBTitle: crystal structure of hddc from yersinia pseudotuberculosis
101	c2vshB_	Alignment	not modelled	32.0	9	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
102	c6bs5B_	Alignment	not modelled	31.9	12	PDB header: unknown function Chain: B: PDB Molecule: anion transporter; PDBTitle: crystal structure of amp-pnp-bound bacterial get3-like a and b in2 mycobacterium tuberculosis
103	c1hm8A_	Alignment	not modelled	28.2	10	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine-1-phosphate uridylyltransferase; PDBTitle: crystal structure of s.pneumoniae n-acetylglucosamine-1-phosphate2 uridylyltransferase, glmu, bound to acetyl coenzyme a
104	c2xmhB_	Alignment	not modelled	24.3	17	PDB header: transferase Chain: B: PDB Molecule: ctp-inositol-1-phosphate cytidylyltransferase; PDBTitle: the x-ray structure of ctp:inositol-1-phosphate cytidylyltransferase2 from archaeoglobus fulgidus
105	d2vapa1	Alignment	not modelled	22.0	15	Fold: Tubulin nucleotide-binding domain-like Superfamily: Tubulin nucleotide-binding domain-like Family: Tubulin, GTPase domain
106	c6aokA_	Alignment	not modelled	21.6	21	PDB header: hydrolase Chain: A: PDB Molecule: ceg4; PDBTitle: crystal structure of legionella pneumophila effector ceg4 with n-2 terminal tev protease cleavage sequence
107	c6ifdD_	Alignment	not modelled	20.4	7	PDB header: sugar binding protein Chain: D: PDB Molecule: cmp-n-acetylneuraminate synthetase; PDBTitle: crystal structure of cmp-n-acetylneuraminate synthetase from vibrio2 cholerae in complex with cdp and mg2+.