Phyre²

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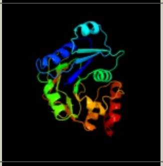
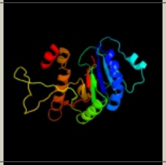
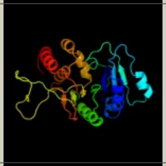
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2z86D_	Alignment		100.0	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**chondroitin synthase; **PDBTitle:** crystal structure of chondroitin polymerase from2 escherichia coli strain k4 (k4cp) complexed with udp-glcua3 and udp
2	d1xhba2	Alignment		100.0	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Polypeptide N-acetylgalactosaminyltransferase 1, N-terminal domain
3	c2ffuA_	Alignment		100.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polypeptide n-acetylgalactosaminyltransferase 2; **PDBTitle:** crystal structure of human ppgalnact-2 complexed with udp2 and ea2
4	c1xhbA_	Alignment		100.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polypeptide n-acetylgalactosaminyltransferase 1; **PDBTitle:** the crystal structure of udp-galnac: polypeptide alpha-n-2 acetylgalactosaminyltransferase-t1
5	c2d7iA_	Alignment		100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polypeptide n-acetylgalactosaminyltransferase 10; **PDBTitle:** crsytal structure of pp-galnac-t10 with udp, galnac and mn2+
6	c3bcvA_	Alignment		100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative glycosyltransferase protein; **PDBTitle:** crystal structure of a putative glycosyltransferase from bacteroides2 fragilis
7	c3f1yC_	Alignment		100.0	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**mannosyl-3-phosphoglycerate synthase; **PDBTitle:** mannosyl-3-phosphoglycerate synthase from rubrobacter xylanophilus
8	d1qg8a_	Alignment		100.0	15	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Spore coat polysaccharide biosynthesis protein SpsA
9	d1omza_	Alignment		99.9	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Exostosin
10	c1omxB_	Alignment		99.9	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**alpha-1,4-n-acetylhexosaminyltransferase extl2; **PDBTitle:** crystal structure of mouse alpha-1,4-n-2 acetylhexosaminyltransferase (extl2)
11	c3ckvA_	Alignment		99.9	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a mycobacterial protein

12	c2qgiA_	Alignment		99.8	8	**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
13	d1fo8a_	Alignment		99.1	8	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**N-acetylglucosaminyltransferase I
14	d2bo4a1	Alignment		99.0	12	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**MGS-like
15	d1pzta_	Alignment		98.8	15	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**beta 1,4 galactosyltransferase (b4GalT1)
16	c3lw6A_	Alignment		98.1	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**beta-4-galactosyltransferase 7; **PDBTitle:** crystal structure of drosophila beta1,4-galactosyltransferase-7
17	d3cu0a1	Alignment		97.1	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**1,3-glucuronyltransferase
18	c2px7A_	Alignment		96.4	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 4-phosphate **PDBTitle:** crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidylyltransferase from thermus thermophilus hb8
19	c2d0jD_	Alignment		96.3	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**galactosylgalactosylxylosylprotein 3-beta- **PDBTitle:** crystal structure of human glcat-s apo form
20	d1v82a_	Alignment		96.1	13	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**1,3-glucuronyltransferase
21	d1vh3a_	Alignment	not modelled	95.1	12	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
22	c2wvmA_	Alignment	not modelled	94.9	17	**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)
23	d1i52a_	Alignment	not modelled	93.2	12	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
24	c3oamD_	Alignment	not modelled	90.7	11	**PDB header:**transferase **Chain:** D: **PDB Molecule:**3-deoxy-manno-octulosonate cytidylyltransferase; **PDBTitle:** crystal structure of cytidylyltransferase from vibrio cholerae
25	c2wawA_	Alignment	not modelled	89.8	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**moba relate protein; **PDBTitle:** crystal structure of mycobacterium tuberculosis rv0371c2 homolog from mycobacterium sp. strain jc1
26	c2zu8A_	Alignment	not modelled	88.2	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannosyl-3-phosphoglycerate synthase; **PDBTitle:** crystal structure of mannosyl-3-phosphoglycerate synthase2 from pyrococcus horikoshii
27	c3tztB_	Alignment	not modelled	82.7	6	**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.
28	d1iina_	Alignment	not modelled	82.6	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase

29	d1lvwa_	Alignment	not modelled	78.8	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
30	d1fxoa_	Alignment	not modelled	75.6	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
31	d1h5ra_	Alignment	not modelled	74.8	12	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
32	c2xwlB_	Alignment	not modelled	74.1	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; **PDBTitle:** crystal structure of ispd from mycobacterium smegmatis in complex2 with ctp and mg
33	c2c0nA_	Alignment	not modelled	65.6	10	**PDB header:**viral protein/transferase **Chain:** A: **PDB Molecule:**a197; **PDBTitle:** crystal structure of a197 from stiv
34	c2we9A_	Alignment	not modelled	55.4	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**moba-related protein; **PDBTitle:** crystal structure of rv0371c from mycobacterium2 tuberculosis h37rv
35	c2xmhB_	Alignment	not modelled	52.2	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ctp-inositol-1-phosphate cytidylyltransferase; **PDBTitle:** the x-ray structure of ctp:inositol-1-phosphate2 cytidylyltransferase from archaeoglobus fulgidus
36	d1mc3a_	Alignment	not modelled	50.8	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
37	d2oi6a2	Alignment	not modelled	50.7	14	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
38	c1jylC_	Alignment	not modelled	50.7	12	**PDB header:**transferase **Chain:** C: **PDB Molecule:**ctp:phosphocholine cytidylyltransferase; **PDBTitle:** catalytic mechanism of ctp:phosphocholine2 cytidylytransferase from streptococcus pneumoniae (licc)
39	c3okrC_	Alignment	not modelled	50.2	11	**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)
40	d1w77a1	Alignment	not modelled	48.0	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylyltransferase
41	d1vpaa_	Alignment	not modelled	47.5	12	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylyltransferase
42	c2gamA_	Alignment	not modelled	44.7	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**beta-1,6-n-acetylglucosaminyltransferase; **PDBTitle:** x-ray crystal structure of murine leukocyte-type core 2 b1,2 6-n-acetylglucosaminyltransferase (c2gnt-l) in complex3 with galb1,3galnac
43	d1vh1a_	Alignment	not modelled	41.4	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylyltransferase
44	c3d5nB_	Alignment	not modelled	40.4	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**q97w15_sulso; **PDBTitle:** crystal structure of the q97w15_sulso protein from2 sulfolobus solfataricus. nesg target ssr125.
45	c3okrA_	Alignment	not modelled	36.4	13	**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)
46	d1vgwa_	Alignment	not modelled	36.3	8	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylyltransferase
47	c1s3mA_	Alignment	not modelled	29.6	18	**PDB header:**phosphodiesterase **Chain:** A: **PDB Molecule:**hypothetical protein mj0936; **PDBTitle:** structural and functional characterization of a novel2 archaeal phosphodiesterase
48	d1s3la_	Alignment	not modelled	29.6	18	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
49	c1w57A_	Alignment	not modelled	27.6	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ispd/ispf bifunctional enzyme; **PDBTitle:** structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
50	c3f1cB_	Alignment	not modelled	27.0	7	**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
51	d1z2wa1	Alignment	not modelled	26.1	10	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
52	d1jyka_	Alignment	not modelled	25.3	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylyltransferase
53	d1g97a2	Alignment	not modelled	23.5	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase

54	d1k3ra2	Alignment	not modelled	22.3	14	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**Hypothetical protein MTH1 (MT0001), dimerisation domain
55	c1k3rA_	Alignment	not modelled	20.4	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein mt0001; **PDBTitle:** crystal structure of the methyltransferase with a knot from2 methanobacterium thermoautotrophicum
56	d1h7ea_	Alignment	not modelled	19.4	8	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylyltransferase
57	d1zbsa2	Alignment	not modelled	19.0	33	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
58	c3rsbB_	Alignment	not modelled	17.4	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**adenosylcobinamide-phosphate guanylyltransferase; **PDBTitle:** structure of the archaeal gtp:adocbi-p guanylyltransferase (coby) from2 methanocaldococcus jannaschii
59	c3ot5D_	Alignment	not modelled	17.2	20	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**udp-n-acetylglucosamine 2-epimerase; **PDBTitle:** 2.2 angstrom resolution crystal structure of putative udp-n-2 acetylglucosamine 2-epimerase from listeria monocytogenes
60	d3b48a1	Alignment	not modelled	17.2	12	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**DhaM-like
61	c3tqdA_	Alignment	not modelled	16.1	14	**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
62	c3polA_	Alignment	not modelled	15.5	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.
63	c2lciA_	Alignment	not modelled	15.3	15	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**protein or36; **PDBTitle:** solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or36 (casd3 target)
64	d1e5ka_	Alignment	not modelled	15.2	6	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Molybdenum cofactor biosynthesis protein MobA
65	c3ssoE_	Alignment	not modelled	13.8	24	**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
66	d1vica_	Alignment	not modelled	13.5	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylyltransferase
67	c2vshB_	Alignment	not modelled	13.3	12	**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
68	c2j0bA_	Alignment	not modelled	11.2	11	**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
69	c1yt5A_	Alignment	not modelled	10.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**inorganic polyphosphate/atp-nad kinase; **PDBTitle:** crystal structure of nad kinase from thermotoga maritima
70	c1xaxA_	Alignment	not modelled	10.4	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0054 protein hi0004; **PDBTitle:** nmr structure of hi0004, a putative essential gene product2 from haemophilus influenzae
71	c1zcyA_	Alignment	not modelled	9.9	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycogenin-1; **PDBTitle:** apo form of a mutant of glycogenin in which asp159 is replaced by ser
72	c3ma0A_	Alignment	not modelled	9.8	15	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**d-xylose-binding periplasmic protein; **PDBTitle:** closed liganded crystal structure of xylose binding protein from2 escherichia coli
73	c3kf8C_	Alignment	not modelled	9.6	12	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**protein stn1; **PDBTitle:** crystal structure of c. tropicalis stn1-ten1 complex
74	c3o1hB_	Alignment	not modelled	9.6	8	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**periplasmic protein tort; **PDBTitle:** crystal structure of the tors sensor domain - tort complex in the2 presence of tmao
75	c1z0zC_	Alignment	not modelled	9.6	24	**PDB header:**transferase **Chain:** C: **PDB Molecule:**probable inorganic polyphosphate/atp-nad kinase; **PDBTitle:** crystal structure of a nad kinase from archaeoglobus2 fulgidus in complex with nad
76	d1z0sa1	Alignment	not modelled	9.6	24	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**NAD kinase-like
77	d1vkpa_	Alignment	not modelled	9.5	11	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
78	d8abpa_	Alignment	not modelled	9.5	11	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like

79	d1w55a1	Alignment	not modelled	9.4	8	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
80	d1guda_	Alignment	not modelled	9.0	13	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
81	c2e8bA_	Alignment	not modelled	8.9	10	**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
82	c1dxyA_	Alignment	not modelled	8.7	7	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-2-hydroxyisocaproate dehydrogenase; **PDBTitle:** structure of d-2-hydroxyisocaproate dehydrogenase
83	d1uasa2	Alignment	not modelled	8.3	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
84	d1jyea_	Alignment	not modelled	8.0	14	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
85	c1jyeA_	Alignment	not modelled	8.0	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**lactose operon repressor; **PDBTitle:** structure of a dimeric lac repressor with c-terminal deletion and k84l2 substitution
86	c3mk3L_	Alignment	not modelled	7.5	18	**PDB header:**transferase **Chain:** L: **PDB Molecule:**6,7-dimethyl-8-ribityllumazine synthase; **PDBTitle:** crystal structure of lumazine synthase from salmonella typhimurium lt2
87	c3agrB_	Alignment	not modelled	7.4	56	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nucleoside triphosphate hydrolase; **PDBTitle:** crystal structure of nucleoside triphosphate hydrolases from neospora2 caninum
88	d1szna2	Alignment	not modelled	7.3	7	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
89	c3ngwA_	Alignment	not modelled	7.2	7	**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
90	d2aifa1	Alignment	not modelled	7.0	8	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
91	c2lbwA_	Alignment	not modelled	6.9	7	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**h/aca ribonucleoprotein complex subunit 2; **PDBTitle:** solution structure of the s. cerevisiae h/aca rnp protein nhp2p-s82w2 mutant
92	c3ecsD_	Alignment	not modelled	6.9	7	**PDB header:**translation **Chain:** D: **PDB Molecule:**translation initiation factor eif-2b subunit **PDBTitle:** crystal structure of human eif2b alpha
93	c2e3dB_	Alignment	not modelled	6.9	7	**PDB header:**transferase **Chain:** B: **PDB Molecule:**utp--glucose-1-phosphate uridylyltransferase; **PDBTitle:** crystal structure of e. coli glucose-1-phosphate2 uridylyltransferase
94	c2qh5B_	Alignment	not modelled	6.9	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**mannose-6-phosphate isomerase; **PDBTitle:** crystal structure of mannose-6-phosphate isomerase from helicobacter2 pylori
95	d1ga8a_	Alignment	not modelled	6.8	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Galactosyltransferase LgtC
96	c1ga8A_	Alignment	not modelled	6.8	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**galactosyl transferase lgtc; **PDBTitle:** crystal structure of galacosyltransferase lgtc in complex2 with donor and acceptor sugar analogs.
97	c1t0oA_	Alignment	not modelled	6.6	3	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** the structure of alpha-galactosidase from trichoderma reesei complexed2 with beta-d-galactose
98	d1zxoa1	Alignment	not modelled	6.6	38	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
99	c1uasA_	Alignment	not modelled	6.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** crystal structure of rice alpha-galactosidase