Phyre^{2}

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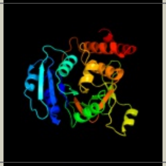
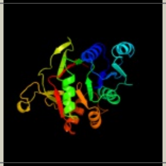
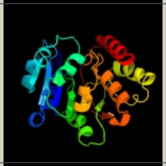
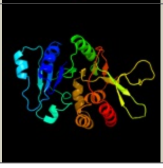
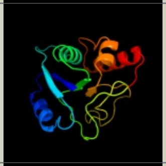
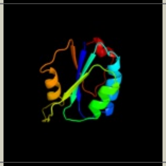
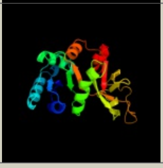
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1xhba2	Alignment		100.0	9	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Polypeptide N-acetylgalactosaminyltransferase 1, N-terminal domain
2	c2ffuA_	Alignment		100.0	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polypeptide n-acetylgalactosaminyltransferase 2; **PDBTitle:** crystal structure of human ppgalnact-2 complexed with udp2 and ea2
3	c1xhbA_	Alignment		100.0	9	**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	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+
5	c2z86D_	Alignment		100.0	15	**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
6	c3f1yC_	Alignment		100.0	11	**PDB header:**transferase **Chain:** C: **PDB Molecule:**mannosyl-3-phosphoglycerate synthase; **PDBTitle:** mannosyl-3-phosphoglycerate synthase from rubrobacter xylanophilus
7	d1qg8a_	Alignment		100.0	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Spore coat polysaccharide biosynthesis protein SpsA
8	c3bcvA_	Alignment		100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative glycosyltransferase protein; **PDBTitle:** crystal structure of a putative glycosyltransferase from bacteroides2 fragilis
9	c3ckvA_	Alignment		100.0	9	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a mycobacterial protein
10	d1omza_	Alignment		99.9	13	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Exostosin
11	c1omxB_	Alignment		99.9	12	**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)

12	c2qgiA_	Alignment		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
13	d1pzta_	Alignment		99.2	22	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**beta 1,4 galactosyltransferase (b4GalT1)
14	d2bo4a1	Alignment		99.1	9	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**MGS-like
15	d1fo8a_	Alignment		99.0	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**N-acetylglucosaminyltransferase I
16	c3lw6A_	Alignment		98.7	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**beta-4-galactosyltransferase 7; **PDBTitle:** crystal structure of drosophila beta1,4-galactosyltransferase-7
17	c2d0jD_	Alignment		96.6	10	**PDB header:**transferase **Chain:** D: **PDB Molecule:**galactosylgalactosylxylosylprotein 3-beta- **PDBTitle:** crystal structure of human glcat-s apo form
18	d1v82a_	Alignment		96.5	7	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**1,3-glucuronyltransferase
19	d3cu0a1	Alignment		96.5	9	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**1,3-glucuronyltransferase
20	d1vh3a_	Alignment		95.9	14	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
21	c2wvmA_	Alignment	not modelled	94.5	11	**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)
22	c3tqdA_	Alignment	not modelled	90.2	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
23	c2zu8A_	Alignment	not modelled	89.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannosyl-3-phosphoglycerate synthase; **PDBTitle:** crystal structure of mannosyl-3-phosphoglycerate synthase2 from pyrococcus horikoshii
24	c3polA_	Alignment	not modelled	88.2	13	**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.
25	d1vgwa_	Alignment	not modelled	86.9	12	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
26	c3tztB_	Alignment	not modelled	85.9	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.
27	d1ga8a_	Alignment	not modelled	78.5	12	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Galactosyltransferase LgtC
						PDB header:transferase

28	c1ga8A_	Alignment	not modelled	78.5	12	**Chain:** A: **PDB Molecule:**galactosyl transferase lgtc; **PDBTitle:** crystal structure of galacosyltransferase lgtc in complex2 with donor and acceptor sugar analogs.
29	d1fxoa_	Alignment	not modelled	76.4	7	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
30	c2px7A_	Alignment	not modelled	75.3	12	**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
31	d1vpaa_	Alignment	not modelled	74.3	8	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylyltransferase
32	d1h5ra_	Alignment	not modelled	71.1	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
33	d1w77a1	Alignment	not modelled	68.3	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylyltransferase
34	d1mc3a_	Alignment	not modelled	67.8	8	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
35	d1lvwa_	Alignment	not modelled	66.7	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
36	d1iina_	Alignment	not modelled	63.6	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
37	c3okrA_	Alignment	not modelled	62.3	8	**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)
38	c2vshB_	Alignment	not modelled	60.5	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
39	d1eyra_	Alignment	not modelled	58.7	9	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylyltransferase
40	d1vh1a_	Alignment	not modelled	57.0	12	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylyltransferase
41	c3okrC_	Alignment	not modelled	56.2	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)
42	d1ll2a_	Alignment	not modelled	54.9	6	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Glycogenin
43	c2gamA_	Alignment	not modelled	51.9	15	**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
44	c2wawA_	Alignment	not modelled	49.7	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**moba relate protein; **PDBTitle:** crystal structure of mycobacterium tuberculosis rv0371c2 homolog from mycobacterium sp. strain jc1
45	c1zcyA_	Alignment	not modelled	48.2	6	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycogenin-1; **PDBTitle:** apo form of a mutant of glycogenin in which asp159 is replaced by ser
46	c2pa4B_	Alignment	not modelled	44.5	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
47	c2xwlB_	Alignment	not modelled	43.3	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
48	c3f1cB_	Alignment	not modelled	41.6	14	**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
49	d1vica_	Alignment	not modelled	41.5	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylyltransferase
50	c2we9A_	Alignment	not modelled	41.2	9	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**moba-related protein; **PDBTitle:** crystal structure of rv0371c from mycobacterium2 tuberculosis h37rv
51	d1w55a1	Alignment	not modelled	38.6	13	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylyltransferase
52	c1w57A_	Alignment	not modelled	37.5	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ispd/ispf bifunctional enzyme; **PDBTitle:** structure of the bifunctional ispdf from campylobacter2 jejuni containing zn

53	c3ecsD_	Alignment	not modelled	36.5	18	**PDB header:**translation **Chain:** D: **PDB Molecule:**translation initiation factor eif-2b subunit **PDBTitle:** crystal structure of human eif2b alpha
54	d1i52a_	Alignment	not modelled	30.4	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
55	d1h7ea_	Alignment	not modelled	29.9	12	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
56	c1zctB_	Alignment	not modelled	27.4	6	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycogenin-1; **PDBTitle:** structure of glycogenin truncated at residue 270 in a2 complex with udp
57	c3a11D_	Alignment	not modelled	26.9	16	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**translation initiation factor eif-2b, delta **PDBTitle:** crystal structure of ribose-1,5-bisphosphate isomerase from2 thermococcus kodakaraensis kod1
58	c3oamD_	Alignment	not modelled	24.0	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**3-deoxy-manno-octulosonate cytidylyltransferase; **PDBTitle:** crystal structure of cytidylyltransferase from vibrio cholerae
59	c3hl3A_	Alignment	not modelled	23.1	12	**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.
60	c3ssoE_	Alignment	not modelled	21.6	10	**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
61	d1qwja_	Alignment	not modelled	19.0	9	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
62	d1vb5a_	Alignment	not modelled	16.4	7	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
63	c3rsbB_	Alignment	not modelled	16.1	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**adenosylcobinamide-phosphate guanylyltransferase; **PDBTitle:** structure of the archaeal gtp:adocbi-p guanylyltransferase (coby) from2 methanocaldococcus jannaschii
64	c3brkX_	Alignment	not modelled	15.6	16	**PDB header:**transferase **Chain:** X: **PDB Molecule:**glucose-1-phosphate adenylyltransferase; **PDBTitle:** crystal structure of adp-glucose pyrophosphorylase from2 agrobacterium tumefaciens
65	d3b48a1	Alignment	not modelled	14.7	18	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**DhaM-like
66	c2j0bA_	Alignment	not modelled	13.6	16	**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
67	c3iprC_	Alignment	not modelled	11.6	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pts system, iia component; **PDBTitle:** crystal structure of the enterococcus faecalis gluconate2 specific eiia phosphotransferase system component
68	d1j4aa2	Alignment	not modelled	11.4	9	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
69	d1zbsa2	Alignment	not modelled	11.0	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
70	c3d98A_	Alignment	not modelled	10.8	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
71	c1z9vA_	Alignment	not modelled	9.9	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein mth0776; **PDBTitle:** solution structure of mth0776 from methanobacterium2 thermoautotrophicum (strain h)
72	d1g97a2	Alignment	not modelled	9.4	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
73	c2qkxA_	Alignment	not modelled	9.4	12	**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
74	d1uasa2	Alignment	not modelled	8.2	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
75	c1uasA_	Alignment	not modelled	8.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** crystal structure of rice alpha-galactosidase
76	c2y6pC_	Alignment	not modelled	8.1	12	**PDB header:**transferase **Chain:** C: **PDB Molecule:**3-deoxy-manno-octulosonate cytidylyltransferase; **PDBTitle:** evidence for a two-metal-ion-mechanism in the2 kdo-cytidylyltransferase kdsb

77	d1yp2a2	Alignment	not modelled	8.0	12	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
78	c1t0oA_	Alignment	not modelled	7.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** the structure of alpha-galactosidase from trichoderma reesei complexed2 with beta-d-galactose
79	c3pnnA_	Alignment	not modelled	7.5	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** the crystal structure of a glycosyltransferase from porphyromonas2 gingivalis w83
80	c2f59B_	Alignment	not modelled	7.5	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**6,7-dimethyl-8-ribityllumazine synthase 1; **PDBTitle:** lumazine synthase ribh1 from brucella abortus (gene bruab1_0785,2 swiss-prot entry q57dy1) complexed with inhibitor 5-nitro-6-(d-3 ribitylamino)-2,4(1h,3h) pyrimidinedione
81	c2l82A_	Alignment	not modelled	7.5	19	**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
82	d2dlda2	Alignment	not modelled	7.5	5	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
83	c3iccA_	Alignment	not modelled	7.3	4	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative 3-oxoacyl-(acyl carrier protein) reductase; **PDBTitle:** crystal structure of a putative 3-oxoacyl-(acyl carrier protein)2 reductase from bacillus anthracis at 1.87 a resolution
84	d1szna2	Alignment	not modelled	7.2	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
85	c3jukA_	Alignment	not modelled	6.9	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-glucose pyrophosphorylase (galu); **PDBTitle:** the crystal structure of udp-glucose pyrophosphorylase complexed with2 udp-glucose
86	d2aifa1	Alignment	not modelled	6.6	7	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
87	c3d5nB_	Alignment	not modelled	6.6	16	**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.
88	d2d0ob1	Alignment	not modelled	6.3	6	**Fold:**Anticodon-binding domain-like **Superfamily:**B12-dependent dehydatase associated subunit **Family:**Dehydratase-reactivating factor beta subunit
89	d1ei7a_	Alignment	not modelled	6.3	12	**Fold:**Four-helical up-and-down bundle **Superfamily:**TMV-like viral coat proteins **Family:**TMV-like viral coat proteins
90	d1s4na_	Alignment	not modelled	6.1	6	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Glycolipid 2-alpha-mannosyltransferase
91	c2qu7B_	Alignment	not modelled	5.7	6	**PDB header:**transcription **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of a putative transcription regulator2 from staphylococcus saprophyticus subsp. saprophyticus
92	c3brcA_	Alignment	not modelled	5.6	5	**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
93	d2oi6a2	Alignment	not modelled	5.4	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
94	c3cc1B_	Alignment	not modelled	5.4	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-n-acetylgalactosaminidase; **PDBTitle:** crystal structure of a putative alpha-n-acetylgalactosaminidase2 (bh1870) from bacillus halodurans c-125 at 2.00 a resolution
95	c3qk7C_	Alignment	not modelled	5.4	3	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulators; **PDBTitle:** crystal structure of putative transcriptional regulator from yersinia2 pestis biovar microtus str. 91001
96	c1jyeA_	Alignment	not modelled	5.3	6	**PDB header:**transcription **Chain:** A: **PDB Molecule:**lactose operon repressor; **PDBTitle:** structure of a dimeric lac repressor with c-terminal deletion and k84l2 substitution
97	d1jyea_	Alignment	not modelled	5.3	6	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
98	c2e8bA_	Alignment	not modelled	5.3	13	**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
99	d1e5ka_	Alignment	not modelled	5.2	5	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Molybdenum cofactor biosynthesis protein MobA