Phyre^2

Email	l.a.kelley@imperial.ac.uk
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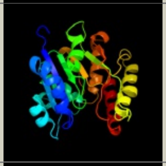
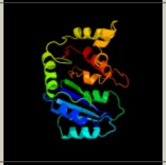
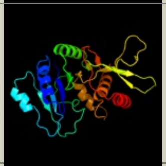
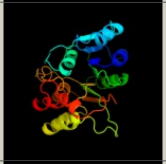
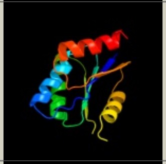
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	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
2	c2d7iA_	Alignment		100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polypeptide n-acetylgalactosaminyltransferase 10; **PDBTitle:** crsytal structure of pp-galnac-t10 with udp, galnac and mn2+
3	c2ffuA_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polypeptide n-acetylgalactosaminyltransferase 2; **PDBTitle:** crystal structure of human ppgalnact-2 complexed with udp2 and ea2
4	d1xhba2	Alignment		100.0	15	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Polypeptide N-acetylgalactosaminyltransferase 1, N-terminal domain
5	c2z86D_	Alignment		100.0	19	**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	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**mannosyl-3-phosphoglycerate synthase; **PDBTitle:** mannosyl-3-phosphoglycerate synthase from rubrobacter xylanophilus
7	c3ckvA_	Alignment		100.0	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a mycobacterial protein
8	d1qg8a_	Alignment		100.0	17	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Spore coat polysaccharide biosynthesis protein SpsA
9	c3bcvA_	Alignment		99.9	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative glycosyltransferase protein; **PDBTitle:** crystal structure of a putative glycosyltransferase from bacteroides2 fragilis
10	c1omxB_	Alignment		99.9	10	**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	d1omza_	Alignment		99.9	8	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Exostosin

12	c2qgiA_	Alignment		99.8	10	**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	d2bo4a1	Alignment		99.5	16	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**MGS-like
14	d1pzta_	Alignment		98.8	17	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**beta 1,4 galactosyltransferase (b4GalT1)
15	d1fo8a_	Alignment		98.7	14	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**N-acetylglucosaminyltransferase I
16	c3lw6A_	Alignment		98.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**beta-4-galactosyltransferase 7; **PDBTitle:** crystal structure of drosophila beta1,4-galactosyltransferase-7
17	c2wvmA_	Alignment		97.6	21	**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)
18	c2zu8A_	Alignment		97.2	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannosyl-3-phosphoglycerate synthase; **PDBTitle:** crystal structure of mannosyl-3-phosphoglycerate synthase2 from pyrococcus horikoshii
19	d1vh3a_	Alignment		96.9	15	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
20	d1h5ra_	Alignment		96.7	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
21	c2d0jD_	Alignment	not modelled	96.4	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**galactosylgalactosylxylosylprotein 3-beta- **PDBTitle:** crystal structure of human glcat-s apo form
22	d1v82a_	Alignment	not modelled	96.3	18	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**1,3-glucuronyltransferase
23	d1fxoa_	Alignment	not modelled	96.2	12	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
24	d1lvwa_	Alignment	not modelled	96.2	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
25	d1mc3a_	Alignment	not modelled	96.1	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
26	d1iina_	Alignment	not modelled	96.0	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
27	d3cu0a1	Alignment	not modelled	95.3	13	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**1,3-glucuronyltransferase
28	c2px7A_	Alignment	not modelled	95.1	17	**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
						PDB header:transferase **Chain:** A: **PDB Molecule:**glucose-1-phosphate

29	c3hl3A_	Alignment	not modelled	94.9	14	thymidylyltransferase; **PDBTitle:** 2.76 angstrom crystal structure of a putative glucose-1-phosphate2 thymidylyltransferase from bacillus anthracis in complex with a3 sucrose.
30	c2xwlB_	Alignment	not modelled	93.3	16	**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
31	c2gamA_	Alignment	not modelled	92.5	14	**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
32	c3tqdA_	Alignment	not modelled	92.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-deoxy-manno-octulosonate cytidylyltransferase; **PDBTitle:** structure of the 3-deoxy-d-manno-octulosonate cytidylyltransferase2 (kdsb) from coxiella burnetii
33	c2qh5B_	Alignment	not modelled	92.0	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**mannose-6-phosphate isomerase; **PDBTitle:** crystal structure of mannose-6-phosphate isomerase from helicobacter2 pylori
34	c2x5sB_	Alignment	not modelled	91.8	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**mannose-1-phosphate guanylyltransferase; **PDBTitle:** crystal structure of t. maritima gdp-mannose2 pyrophosphorylase in apo state.
35	c2pa4B_	Alignment	not modelled	91.4	11	**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
36	d1vh1a_	Alignment	not modelled	91.4	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
37	c3brkX_	Alignment	not modelled	90.8	12	**PDB header:**transferase **Chain:** X: **PDB Molecule:**glucose-1-phosphate adenylyltransferase; **PDBTitle:** crystal structure of adp-glucose pyrophosphorylase from2 agrobacterium tumefaciens
38	c2j0bA_	Alignment	not modelled	90.7	13	**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
39	c3tztB_	Alignment	not modelled	90.0	9	**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.
40	d1vgwa_	Alignment	not modelled	89.3	12	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
41	c1w57A_	Alignment	not modelled	88.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ispd/ispf bifunctional enzyme; **PDBTitle:** structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
42	d1w55a1	Alignment	not modelled	88.2	13	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
43	c3polA_	Alignment	not modelled	87.7	15	**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.
44	d1i52a_	Alignment	not modelled	87.6	16	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
45	c2ux8G_	Alignment	not modelled	87.1	7	**PDB header:**transferase **Chain:** G: **PDB Molecule:**glucose-1-phosphate uridylyltransferase; **PDBTitle:** crystal structure of sphingomonas elodea atcc 31461 glucose-2 1-phosphate uridylyltransferase in complex with glucose-3 1-phosphate.
46	c3d5nB_	Alignment	not modelled	86.9	15	**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.
47	c2wawA_	Alignment	not modelled	85.4	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
48	c2c0nA_	Alignment	not modelled	85.2	16	**PDB header:**viral protein/transferase **Chain:** A: **PDB Molecule:**a197; **PDBTitle:** crystal structure of a197 from stiv
49	c1hm8A_	Alignment	not modelled	84.0	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine-1-phosphate uridyltransferase; **PDBTitle:** crystal structure of s.pneumoniae n-acetylglucosamine-1-phosphate2 uridyltransferase, glmu, bound to acetyl coenzyme a
50	c2cu2A_	Alignment	not modelled	84.0	19	**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
						PDB header:transferase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 4-phosphate

51	c3okrA_	Alignment	not modelled	83.8	16	cytidylyltransferase; **PDBTitle:** structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
52	d1vica_	Alignment	not modelled	83.5	17	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
53	c3d98A_	Alignment	not modelled	83.4	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
54	d1vpaa_	Alignment	not modelled	83.2	9	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
55	c2e3dB_	Alignment	not modelled	82.0	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**utp--glucose-1-phosphate uridylyltransferase; **PDBTitle:** crystal structure of e. coli glucose-1-phosphate2 uridylyltransferase
56	c3oamD_	Alignment	not modelled	81.8	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**3-deoxy-manno-octulosonate cytidylyltransferase; **PDBTitle:** crystal structure of cytidylyltransferase from vibrio cholerae
57	c1ga8A_	Alignment	not modelled	81.4	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**galactosyl transferase lgtc; **PDBTitle:** crystal structure of galacosyltransferase lgtc in complex2 with donor and acceptor sugar analogs.
58	d1ga8a_	Alignment	not modelled	81.4	14	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Galactosyltransferase LgtC
59	d1ll2a_	Alignment	not modelled	80.5	12	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Glycogenin
60	c2qkxA_	Alignment	not modelled	80.4	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
61	d1qwja_	Alignment	not modelled	79.8	13	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
62	d1eyra_	Alignment	not modelled	78.8	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
63	d1w77a1	Alignment	not modelled	78.1	12	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
64	c1zcyA_	Alignment	not modelled	77.7	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycogenin-1; **PDBTitle:** apo form of a mutant of glycogenin in which asp159 is replaced by ser
65	d1yp2a2	Alignment	not modelled	75.3	13	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
66	c1zctB_	Alignment	not modelled	70.5	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycogenin-1; **PDBTitle:** structure of glycogenin truncated at residue 270 in a2 complex with udp
67	c3jukA_	Alignment	not modelled	68.2	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-glucose pyrophosphorylase (galu); **PDBTitle:** the crystal structure of udp-glucose pyrophosphorylase complexed with2 udp-glucose
68	c3okrC_	Alignment	not modelled	64.6	18	**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)
69	c3pnnA_	Alignment	not modelled	64.3	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** the crystal structure of a glycosyltransferase from porphyromonas2 gingivalis w83
70	c2vshB_	Alignment	not modelled	64.1	13	**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
71	d1vkpa_	Alignment	not modelled	63.4	21	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
72	c1yp3C_	Alignment	not modelled	62.5	15	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glucose-1-phosphate adenylyltransferase small **PDBTitle:** crystal structure of potato tuber adp-glucose2 pyrophosphorylase in complex with atp
73	d1g97a2	Alignment	not modelled	61.5	9	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
74	c1jylC_	Alignment	not modelled	61.3	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**ctp:phosphocholine cytidylyltransferase; **PDBTitle:** catalytic mechanism of ctp:phosphocholine2 cytidylytransferase from streptococcus pneumoniae (licc)
75	c2oi6A_	Alignment	not modelled	60.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** e. coli glmu- complex with udp-glcnac, coa and glcn-1-po4
						PDB header:transferase **Chain:** B: **PDB Molecule:**ctp-inositol-1-phosphate

76	c2xmhB_	Alignment	not modelled	58.9	11	cytidylyltransferase; **PDBTitle:** the x-ray structure of ctp:inositol-1-phosphate2 cytidylyltransferase from archaeoglobus fulgidus
77	c3f1cB_	Alignment	not modelled	58.5	11	**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
78	c2v0hA_	Alignment	not modelled	54.1	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** characterization of substrate binding and catalysis of the2 potential antibacterial target n-acetylglucosamine-1-3 phosphate uridyltransferase (glmu)
79	d2jera1	Alignment	not modelled	54.0	19	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
80	c3zq4C_	Alignment	not modelled	54.0	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ribonuclease j 1; **PDBTitle:** unusual, dual endo- and exo-nuclease activity in the degradosome2 explained by crystal structure analysis of rnase j1
81	c2e8bA_	Alignment	not modelled	53.9	21	**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	c2jerG_	Alignment	not modelled	53.2	19	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**agmatine deiminase; **PDBTitle:** agmatine deiminase of enterococcus faecalis catalyzing its2 reaction.
83	d2oi6a2	Alignment	not modelled	52.3	12	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
84	d1h7ea_	Alignment	not modelled	51.5	15	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
85	d2ewoa1	Alignment	not modelled	51.3	22	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
86	c3bk2A_	Alignment	not modelled	49.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metal dependent hydrolase; **PDBTitle:** crystal structure analysis of the rnase j/ump complex
87	d1e5ka_	Alignment	not modelled	48.1	17	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Molybdenum cofactor biosynthesis protein MobA
88	d1zbra1	Alignment	not modelled	45.1	13	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
89	d1xkna_	Alignment	not modelled	42.8	13	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
90	d2cu2a2	Alignment	not modelled	39.9	20	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**mannose-1-phosphate guanylyl transferase
91	d1jyka_	Alignment	not modelled	39.5	13	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
92	c3ngwA_	Alignment	not modelled	36.3	8	**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
93	c2we9A_	Alignment	not modelled	33.6	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**moba-related protein; **PDBTitle:** crystal structure of rv0371c from mycobacterium2 tuberculosis h37rv
94	c2uvgA_	Alignment	not modelled	33.6	13	**PDB header:**sugar-binding protein **Chain:** A: **PDB Molecule:**abc type periplasmic sugar-binding protein; **PDBTitle:** structure of a periplasmic oligogalacturonide binding2 protein from yersinia enterocolitica
95	d1tzfa_	Alignment	not modelled	30.2	9	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
96	c1fwyA_	Alignment	not modelled	27.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine pyrophosphorylase; **PDBTitle:** crystal structure of n-acetylglucosamine 1-phosphate2 uridyltransferase bound to udp-glcnac
97	c2y6pC_	Alignment	not modelled	27.5	7	**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
98	d2cmua1	Alignment	not modelled	22.7	35	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
99	c3rsbB_	Alignment	not modelled	21.5	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**adenosylcobinamide-phosphate guanylyltransferase; **PDBTitle:** structure of the archaeal gtp:adocbi-p guanylyltransferase (coby) from2 methanocaldococcus jannaschii