Phyre²

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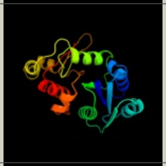
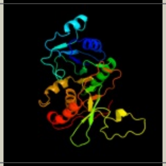
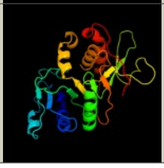
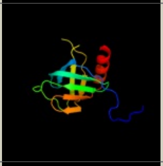
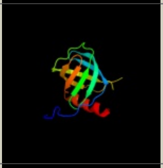
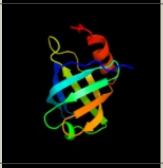
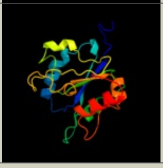
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2z86D_	Alignment		100.0	21	**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	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
3	c3f1yC_	Alignment		100.0	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**mannosyl-3-phosphoglycerate synthase; **PDBTitle:** mannosyl-3-phosphoglycerate synthase from rubrobacter xylanophilus
4	c1xhbA_	Alignment		100.0	15	**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	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polypeptide n-acetylgalactosaminyltransferase 10; **PDBTitle:** crsytal structure of pp-galnac-t10 with udp, galnac and mn2+
6	d1xhba2	Alignment		100.0	16	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Polypeptide N-acetylgalactosaminyltransferase 1, N-terminal domain
7	c3ckvA_	Alignment		99.9	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a mycobacterial protein
8	d1qg8a_	Alignment		99.9	20	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Spore coat polysaccharide biosynthesis protein SpsA
9	c3bcvA_	Alignment		99.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative glycosyltransferase protein; **PDBTitle:** crystal structure of a putative glycosyltransferase from bacteroides2 fragilis
10	c1omxB_	Alignment		99.8	13	**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		99.8	13	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Exostosin

12	c2qgiA_	Alignment		99.7	11	**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		99.2	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**MGS-like
14	c1ywuA_	Alignment		99.2	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pa4608; **PDBTitle:** solution nmr structure of pseudomonas aeruginosa protein pa4608.2 northeast structural genomics target pat7
15	d1ywua1	Alignment		99.2	13	**Fold:**Split barrel-like **Superfamily:**PilZ domain-like **Family:**PilZ domain
16	c3kygB_	Alignment		98.8	15	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein vca0042; **PDBTitle:** crystal structure of vca0042 (l135r) complexed with c-di-gmp
17	c2rdeB_	Alignment		98.8	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein vca0042; **PDBTitle:** crystal structure of vca0042 complexed with c-di-gmp
18	d2rdea1	Alignment		98.6	16	**Fold:**Split barrel-like **Superfamily:**PilZ domain-like **Family:**PilZ domain
19	d1fo8a_	Alignment		98.5	15	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**N-acetylglucosaminyltransferase I
20	d1pzta_	Alignment		98.4	21	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**beta 1,4 galactosyltransferase (b4GalT1)
21	c2gjgA_	Alignment	not modelled	98.2	13	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**hypothetical protein pp4397; **PDBTitle:** crystal structure of a pilz-containing protein (pp4397) from2 pseudomonas putida kt2440 at 2.25 a resolution
22	c3lw6A_	Alignment	not modelled	96.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**beta-4-galactosyltransferase 7; **PDBTitle:** crystal structure of drosophila beta1,4-galactosyltransferase-7
23	c3cnrA_	Alignment	not modelled	96.8	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**type iv fimbriae assembly protein; **PDBTitle:** crystal structure of pilz (xac1133) from xanthomonas2 axonopodis pv citri
24	c3ph1C_	Alignment	not modelled	96.5	17	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** the crystal structure of a pathogenic protein from the xanthomonas2 campestris reveals a new tetrameric pilz domain self-assembled via a3 unusual helical bundle
25	c2wvmA_	Alignment	not modelled	96.4	23	**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)
26	d1vh3a_	Alignment	not modelled	96.1	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
27	c2zu8A_	Alignment	not modelled	96.0	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannosyl-3-phosphoglycerate synthase; **PDBTitle:** crystal structure of mannosyl-3-phosphoglycerate synthase2 from pyrococcus horikoshii
						PDB header:transferase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 4-phosphate

28	c3okrA_	Alignment	not modelled	95.4	9	cytidylyltransferase; **PDBTitle:** structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidylyltransferase (ispd)
29	c2xwlB_	Alignment	not modelled	95.1	12	**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
30	c2wawA_	Alignment	not modelled	94.8	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
31	c1w57A_	Alignment	not modelled	94.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ispd/ispf bifunctional enzyme; **PDBTitle:** structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
32	d1i52a_	Alignment	not modelled	92.3	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
33	c2xmhB_	Alignment	not modelled	91.6	13	**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
34	c3polA_	Alignment	not modelled	91.5	8	**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.
35	c2px7A_	Alignment	not modelled	91.3	11	**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
36	d2oi6a2	Alignment	not modelled	91.3	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
37	c3d5nB_	Alignment	not modelled	91.0	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.
38	c1jylC_	Alignment	not modelled	91.0	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**ctp:phosphocholine cytidylyltransferase; **PDBTitle:** catalytic mechanism of ctp:phosphocholine2 cytidylytransferase from streptococcus pneumoniae (licc)
39	c3tqdA_	Alignment	not modelled	90.7	13	**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
40	c2we9A_	Alignment	not modelled	89.9	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**moba-related protein; **PDBTitle:** crystal structure of rv0371c from mycobacterium2 tuberculosis h37rv
41	d1w77a1	Alignment	not modelled	89.5	9	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
42	d1fxoa_	Alignment	not modelled	89.5	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
43	d1vgwa_	Alignment	not modelled	89.4	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
44	c3ngwA_	Alignment	not modelled	88.5	11	**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
45	c2d0jD_	Alignment	not modelled	88.5	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**galactosylgalactosylxylosylprotein 3-beta- **PDBTitle:** crystal structure of human glcat-s apo form
46	d1v82a_	Alignment	not modelled	87.7	19	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**1,3-glucuronyltransferase
47	d1w55a1	Alignment	not modelled	87.5	14	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
48	c3oamD_	Alignment	not modelled	87.3	10	**PDB header:**transferase **Chain:** D: **PDB Molecule:**3-deoxy-manno-octulosonate cytidylyltransferase; **PDBTitle:** crystal structure of cytidylyltransferase from vibrio cholerae
49	d1vpaa_	Alignment	not modelled	87.2	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
50	d1h5ra_	Alignment	not modelled	86.5	12	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
51	d1jyka_	Alignment	not modelled	85.8	12	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
52	c3okrC_	Alignment	not modelled	85.0	10	**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)
53	d1iina_	Alignment	not modelled	84.6	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
54	c1ga8A_	Alignment	not modelled	83.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**galactosyl transferase lgtc; **PDBTitle:** crystal structure of galacosyltransferase lgtc in complex2 with donor and acceptor sugar analogs.
55	d1ga8a_	Alignment	not modelled	83.5	16	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Galactosyltransferase LgtC
56	c3f1cB_	Alignment	not modelled	83.1	9	**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
57	c2oi6A_	Alignment	not modelled	83.0	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** e. coli glmu- complex with udp-glcnac, coa and glcn-1-po4
58	d1vica_	Alignment	not modelled	81.5	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
59	c2x5sB_	Alignment	not modelled	79.7	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**mannose-1-phosphate guanylyltransferase; **PDBTitle:** crystal structure of t. maritima gdp-mannose2 pyrophosphorylase in apo state.
60	c2vshB_	Alignment	not modelled	76.8	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
61	c2j0bA_	Alignment	not modelled	75.2	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
62	d1lvwa_	Alignment	not modelled	72.8	9	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
63	d1eyra_	Alignment	not modelled	71.7	14	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
64	c2cu2A_	Alignment	not modelled	70.6	14	**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
65	c2v0hA_	Alignment	not modelled	69.2	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)
66	c3tztB_	Alignment	not modelled	68.9	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.
67	c1hm8A_	Alignment	not modelled	68.9	7	**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
68	c3hl3A_	Alignment	not modelled	68.4	7	**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.
69	d1e5ka_	Alignment	not modelled	67.7	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Molybdenum cofactor biosynthesis protein MobA
70	c2qh5B_	Alignment	not modelled	67.5	7	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**mannose-6-phosphate isomerase; **PDBTitle:** crystal structure of mannose-6-phosphate isomerase from helicobacter2 pylori
71	d1mc3a_	Alignment	not modelled	65.9	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
72	d3cu0a1	Alignment	not modelled	64.2	16	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**1,3-glucuronyltransferase
73	c1fwyA_	Alignment	not modelled	63.1	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine pyrophosphorylase; **PDBTitle:** crystal structure of n-acetylglucosamine 1-phosphate2 uridyltransferase bound to udp-glcnac
74	c2y6pC_	Alignment	not modelled	63.1	3	**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
75	c3brkX_	Alignment	not modelled	61.0	9	**PDB header:**transferase **Chain:** X: **PDB Molecule:**glucose-1-phosphate adenylyltransferase; **PDBTitle:** crystal structure of adp-glucose pyrophosphorylase from2 agrobacterium tumefaciens

76	c2e3dB_	Alignment	not modelled	59.5	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**utp--glucose-1-phosphate uridylyltransferase; **PDBTitle:** crystal structure of e. coli glucose-1-phosphate2 uridylyltransferase
77	d1qwja_	Alignment	not modelled	58.5	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
78	c3hz7A_	Alignment	not modelled	55.8	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the sira-like protein (dsy4693) from2 desulfitobacterium hafniense, northeast structural genomics3 consortium target dhr2a
79	c2ux8G_	Alignment	not modelled	55.1	8	**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.
80	d1h7ea_	Alignment	not modelled	52.9	9	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
81	c3louB_	Alignment	not modelled	51.5	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
82	d1g97a2	Alignment	not modelled	49.5	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
83	c2bkdN_	Alignment	not modelled	47.8	14	**PDB header:**nuclear protein **Chain:** N: **PDB Molecule:**fragile x mental retardation 1 protein; **PDBTitle:** structure of the n-terminal domain of fragile x mental2 retardation protein
84	c3rsbB_	Alignment	not modelled	41.5	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**adenosylcobinamide-phosphate guanylyltransferase; **PDBTitle:** structure of the archaeal gtp:adocbi-p guanylyltransferase (coby) from2 methanocaldococcus jannaschii
85	c3n0vD_	Alignment	not modelled	40.3	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
86	d1pava_	Alignment	not modelled	38.0	12	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
87	d2ix0a3	Alignment	not modelled	35.8	29	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
88	c1zcyA_	Alignment	not modelled	35.8	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycogenin-1; **PDBTitle:** apo form of a mutant of glycogenin in which asp159 is replaced by ser
89	c2e8bA_	Alignment	not modelled	35.6	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
90	c2pa4B_	Alignment	not modelled	35.2	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
91	d1ll2a_	Alignment	not modelled	34.6	8	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Glycogenin
92	d1je3a_	Alignment	not modelled	32.9	12	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
93	c3nrbD_	Alignment	not modelled	32.8	10	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (puru,2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
94	c2vs1A_	Alignment	not modelled	32.6	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized rna methyltransferase pyrab10780; **PDBTitle:** the crystal structure of pyrococcus abyssi trna (uracil-54,2 c5)-methyltransferase in complex with s-adenosyl-l-3 homocysteine
95	d1yp2a2	Alignment	not modelled	31.9	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
96	d2cu2a2	Alignment	not modelled	31.1	16	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**mannose-1-phosphate guanylyl transferase
97	d1vh1a_	Alignment	not modelled	31.1	7	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
98	c1fftG_	Alignment	not modelled	29.3	18	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**ubiquinol oxidase; **PDBTitle:** the structure of ubiquinol oxidase from escherichia coli
99	c3d98A_	Alignment	not modelled	28.5	5	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** crystal structure of glmu from mycobacterium

						tuberculosis, ligand-free2 form
100	c2ag1A_	Alignment	not modelled	28.4	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**benzaldehyde lyase; **PDBTitle:** crystal structure of benzaldehyde lyase (bal)- semet
101	c2rreA_	Alignment	not modelled	28.0	22	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** structure and function of the n-terminal nucleolin binding domain of2 nuclear valocine containing protein like 2 (nvl2) harboring a3 nucleolar localization signal
102	c3pnnA_	Alignment	not modelled	27.5	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** the crystal structure of a glycosyltransferase from porphyromonas2 gingivalis w83
103	d1nxza1	Alignment	not modelled	27.1	11	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**YggJ N-terminal domain-like
104	d1ybha1	Alignment	not modelled	27.0	11	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
105	c1yp3C_	Alignment	not modelled	26.9	13	**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
106	c2vbgB_	Alignment	not modelled	25.4	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**branched-chain alpha-ketoacid decarboxylase; **PDBTitle:** the complex structure of the branched-chain keto acid2 decarboxylase (kdca) from lactococcus lactis with 2r-1-3 hydroxyethyl-deazathdp
107	c3o1lB_	Alignment	not modelled	25.1	7	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
108	d1jdqa_	Alignment	not modelled	24.7	17	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
109	d1pj3a2	Alignment	not modelled	23.0	22	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Malic enzyme N-domain
110	c2qkxA_	Alignment	not modelled	21.2	5	**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
111	c3zq4C_	Alignment	not modelled	21.2	26	**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
112	d1dcja_	Alignment	not modelled	20.8	16	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like