Phyre^2

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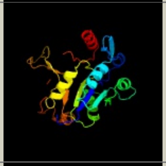
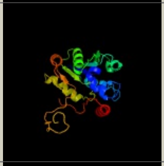
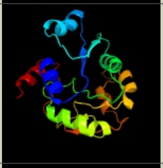
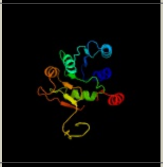
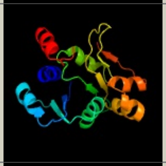
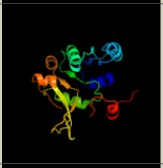
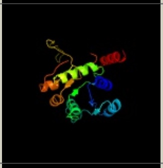
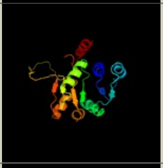
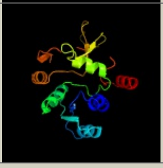
Description	RVBD0540_(-)_632375_633037
Date	Fri Jul 26 01:50:09 BST 2019
Unique Job ID	7585845243fd9e0e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3cgxA_	Alignment		100.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative nucleotide-diphospho-sugar transferase; **PDBTitle:** crystal structure of putative nucleotide-diphospho-sugar transferase2 (yp_389115.1) from desulfovibrio desulfuricans g20 at 1.90 a3 resolution
2	d2i5ea1	Alignment		100.0	13	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**MM2497-like
3	c6bwhB_	Alignment		100.0	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**2-phospho-l-lactate guanylyltransferase; **PDBTitle:** crystal structure of mycoibacterium tuberculosis rv2983 in complex2 with pep
4	c2wawA_	Alignment		98.9	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**moba relate protein; **PDBTitle:** crystal structure of mycobacterium tuberculosis rv0371c2 homolog from mycobacterium sp. strain jc1
5	c3okrA_	Alignment		98.8	14	**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)
6	d1e5ka_	Alignment		98.7	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Molybdenum cofactor biosynthesis protein MobA
7	c4kt7A_	Alignment		98.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; **PDBTitle:** the crystal structure of 4-diphosphocytidyl-2c-methyl-d-2 erythritolsynthase from anaerococcus prevotii dsm 20548
8	d1w77a1	Alignment		98.7	14	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
9	d1i52a_	Alignment		98.7	18	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
10	c2vshB_	Alignment		98.6	14	**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
11	c2xwlB_	Alignment		98.6	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; **PDBTitle:** crystal structure of ispd from mycobacterium smegmatis in complex with2 ctp and mg

12	c5ddtA_	Alignment		98.6	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; **PDBTitle:** crystal structure of ispd from bacillus subtilis at 1.80 angstroms2 resolution, crystal form i
13	c2we9A_	Alignment		98.5	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**moba-related protein; **PDBTitle:** crystal structure of rv0371c from mycobacterium2 tuberculosis h37rv
14	d1vgwa_	Alignment		98.5	17	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
15	c4jisB_	Alignment		98.5	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribitol-5-phosphate cytidylyltransferase; **PDBTitle:** crystal structure of ribitol 5-phosphate cytidylyltransferase (tari)2 from bacillus subtilis
16	c2px7A_	Alignment		98.5	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; **PDBTitle:** crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidylyltransferase from thermus thermophilus hb8
17	d1w55a1	Alignment		98.5	12	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
18	c3okrC_	Alignment		98.5	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; **PDBTitle:** crystal structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
19	c4ys8B_	Alignment		98.5	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; **PDBTitle:** crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidylyltransferase (ispd) from burkholderia thailandensis
20	c4mybA_	Alignment		98.4	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; **PDBTitle:** crystal structure of francisella tularensis 2-c-methyl-d-erythritol 4-2 phosphate cytidylyltransferase (ispd)
21	d1vpaa_	Alignment	not modelled	98.4	13	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
22	c1w57A_	Alignment	not modelled	98.4	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ispd/ispf bifunctional enzyme; **PDBTitle:** structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
23	d2oi6a2	Alignment	not modelled	98.4	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
24	c3f1cB_	Alignment	not modelled	98.4	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
25	c6oewB_	Alignment	not modelled	98.3	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cytidylyltransferase; **PDBTitle:** structure of a cytidylyltransferase from leptospira borgpetersenii2 serovar hardjo-bovis (strain jb197)
26	c3oamD_	Alignment	not modelled	98.2	20	**PDB header:**transferase **Chain:** D: **PDB Molecule:**3-deoxy-manno-octulosonate cytidylyltransferase; **PDBTitle:** crystal structure of cytidylyltransferase from vibrio cholerae
27	c3tqdA_	Alignment	not modelled	98.2	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
28	d1vica_	Alignment	not modelled	98.1	17	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase

29	c4xwiA_	Alignment	not modelled	98.1	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-deoxy-manno-octulosonate cytidylyltransferase; **PDBTitle:** x-ray crystal structure of cmp-kdo synthase from pseudomonas2 aeruginosa
30	c3polA_	Alignment	not modelled	98.1	16	**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.
31	d1eyra_	Alignment	not modelled	97.8	13	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
32	d2dpwa1	Alignment	not modelled	97.7	19	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**TTHA0179-like
33	c3d5nB_	Alignment	not modelled	97.7	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**q97w15_sulso; **PDBTitle:** crystal structure of the q97w15_sulso protein from sulfolobus2 solfataricus. nesg target ssr125.
34	d1qwja_	Alignment	not modelled	97.7	13	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
35	c3ngwA_	Alignment	not modelled	97.6	15	**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
36	c6ifdD_	Alignment	not modelled	97.6	10	**PDB header:**sugar binding protein **Chain:** D: **PDB Molecule:**cmp-n-acetylneuraminate synthetase; **PDBTitle:** crystal structure of cmp-n-acetylneuraminate synthetase from vibrio2 cholerae in complex with cdp and mg2+.
37	c4jd0A_	Alignment	not modelled	97.3	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nucleotidyl transferase; **PDBTitle:** structure of the inositol-1-phosphate ctp transferase from t.2 maritima.
38	d1vh1a_	Alignment	not modelled	97.3	18	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
39	c2e8bA_	Alignment	not modelled	97.2	14	**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
40	c3rsbB_	Alignment	not modelled	97.0	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**adenosylcobinamide-phosphate guanylyltransferase; **PDBTitle:** structure of the archaeal gtp:adocbi-p guanylyltransferase (coby) from2 methanocaldococcus jannaschii
41	d1h7ea_	Alignment	not modelled	96.9	12	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
42	c4y7uA_	Alignment	not modelled	96.6	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nucleotidyl transferase; **PDBTitle:** structural analysis of muru
43	d1vh3a_	Alignment	not modelled	96.5	13	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
44	c2y6pC_	Alignment	not modelled	96.4	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**3-deoxy-manno-octulosonate cytidylyltransferase; **PDBTitle:** evidence for a two-metal-ion-mechanism in the kdo-2 cytidylyltransferase kdsb
45	d1tzfa_	Alignment	not modelled	96.3	13	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
46	c4mndA_	Alignment	not modelled	96.1	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ctp l-myo-inositol-1-phosphate cytidylyltransferase/cdp-l- **PDBTitle:** crystal structure of archaeoglobus fulgidus ipct-dipps bifunctional2 membrane protein
47	c5xhwA_	Alignment	not modelled	95.9	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative 6-deoxy-d-mannoheptose pathway protein; **PDBTitle:** crystal structure of hddc from yersinia pseudotuberculosis
48	c2qh5B_	Alignment	not modelled	95.5	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**mannose-6-phosphate isomerase; **PDBTitle:** crystal structure of mannose-6-phosphate isomerase from helicobacter2 pylori
49	d1h5ra_	Alignment	not modelled	94.9	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
50	d1jyka_	Alignment	not modelled	93.4	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
51	c3hl3A_	Alignment	not modelled	93.0	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.
52	c1jylC_	Alignment	not modelled	92.7	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**ctp:phosphocholine cytidylyltransferase; **PDBTitle:** catalytic mechanism of ctp:phosphocholine2

						cytidylyltransferase from streptococcus pneumoniae (licc)
53	d1g97a2	Alignment	not modelled	92.4	14	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
54	c4evwB_	Alignment	not modelled	92.2	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nucleoside-diphosphate-sugar pyrophosphorylase; **PDBTitle:** crystal structure of the nucleoside-diphosphate-sugar2 pyrophosphorylase from vibrio cholerae rc9. northeast structural3 genomics consortium (nesg) target vcr193.
55	c3foqA_	Alignment	not modelled	92.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** crystal structure of n-acetylglucosamine-1-phosphate2 uridyltransferase (glmu) from mycobacterium tuberculosis in3 a cubic space group.
56	c2x5sB_	Alignment	not modelled	91.1	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**mannose-1-phosphate guanylyltransferase; **PDBTitle:** crystal structure of t. maritima gdp-mannose2 pyrophosphorylase in apo state.
57	c2oi6A_	Alignment	not modelled	90.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** e. coli glmu- complex with udp-glcnac, coa and glcn-1-po4
58	d1iina_	Alignment	not modelled	90.7	9	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
59	c4cvhA_	Alignment	not modelled	90.6	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**isoprenoid synthase domain-containing protein; **PDBTitle:** crystal structure of human isoprenoid synthase domain-containing2 protein
60	c2cu2A_	Alignment	not modelled	90.5	17	**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
61	c2v0hA_	Alignment	not modelled	90.1	12	**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)
62	c3pnnA_	Alignment	not modelled	89.3	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** the crystal structure of a glycosyltransferase from porphyromonas2 gingivalis w83
63	c3d8vA_	Alignment	not modelled	86.8	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** crystal structure of glmu from mycobacterium tuberculosis2 in complex with uridine-diphosphate-n-acetylglucosamine
64	c1fwyA_	Alignment	not modelled	86.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine pyrophosphorylase; **PDBTitle:** crystal structure of n-acetylglucosamine 1-phosphate2 uridyltransferase bound to udp-glcnac
65	d1fxoa_	Alignment	not modelled	85.7	12	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
66	c3d98A_	Alignment	not modelled	84.3	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
67	d1mc3a_	Alignment	not modelled	83.6	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
68	c6b5kA_	Alignment	not modelled	82.7	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucose-1-phosphate thymidylyltransferase; **PDBTitle:** mycobacterium tuberculosis rmla in complex with mg/dttp
69	c1yp3C_	Alignment	not modelled	70.7	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
70	c1omxB_	Alignment	not modelled	68.6	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**alpha-1,4-n-acetylhexosaminyltransferase extl2; **PDBTitle:** crystal structure of mouse alpha-1,4-n-acetylhexosaminyltransferase2 (extl2)
71	c2pa4B_	Alignment	not modelled	63.1	12	**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
72	d1yp2a2	Alignment	not modelled	63.0	15	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
73	c2qkxA_	Alignment	not modelled	60.8	20	**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	d2bo4a1	Alignment	not modelled	60.8	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**MGS-like
						PDB header:transferase

75	c1hm8A_	Alignment	not modelled	60.5	12	**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
76	c2xmhB_	Alignment	not modelled	57.9	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ctp-inositol-1-phosphate cytidylyltransferase; **PDBTitle:** the x-ray structure of ctp:inositol-1-phosphate cytidylyltransferase2 from archaeoglobus fulgidus
77	c5ekeB_	Alignment	not modelled	54.2	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**uncharacterized glycosyltransferase sll0501; **PDBTitle:** structure of the polyisoprenyl-phosphate glycosyltransferase gtrb2 (f215a mutant)
78	c6jlwJ_	Alignment	not modelled	53.7	12	**PDB header:**translation **Chain:** J: **PDB Molecule:**translation initiation factor eif-2b subunit epsilon; **PDBTitle:** eif2 - eif2b complex
79	d1omza_	Alignment	not modelled	47.6	15	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Exostosin
80	c2ggqA_	Alignment	not modelled	47.5	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**401aa long hypothetical glucose-1-phosphate **PDBTitle:** complex of hypothetical glucose-1-phosphate thymidylyltransferase from2 sulfolobus tokodaii
81	d1lvwa_	Alignment	not modelled	46.9	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
82	c3t8tA_	Alignment	not modelled	44.3	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**staphylococcus aureus cymr (oxidized form); **PDBTitle:** crystal structure of staphylococcus aureus cymr oxidized form
83	c4hf1B_	Alignment	not modelled	43.5	16	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator iscr; **PDBTitle:** crystal structure of iscr bound to its promoter
84	c2y75F_	Alignment	not modelled	42.9	16	**PDB header:**transcription **Chain:** F: **PDB Molecule:**hth-type transcriptional regulator cymr; **PDBTitle:** the structure of cymr (yrzc) the global cysteine regulator of b.2 subtilis
85	c4qysA_	Alignment	not modelled	42.7	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase beta chain 2; **PDBTitle:** trpb2 enzymes
86	d2ji7a3	Alignment	not modelled	42.4	9	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
87	c2e3dB_	Alignment	not modelled	42.2	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**utp--glucose-1-phosphate uridylyltransferase; **PDBTitle:** crystal structure of e. coli glucose-1-phosphate2 uridylyltransferase
88	c3jukA_	Alignment	not modelled	40.2	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-glucose pyrophosphorylase (galu); **PDBTitle:** the crystal structure of udp-glucose pyrophosphorylase complexed with2 udp-glucose
89	c4cicB_	Alignment	not modelled	38.5	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator, badm/rrf2 family; **PDBTitle:** t. potens iscr
90	c6i3mG_	Alignment	not modelled	37.8	13	**PDB header:**translation **Chain:** G: **PDB Molecule:**translation initiation factor eif-2b subunit epsilon; **PDBTitle:** eif2b:eif2 complex, phosphorylated on eif2 alpha serine 52.
91	d2djia3	Alignment	not modelled	35.4	9	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
92	d2cu2a2	Alignment	not modelled	35.3	16	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**mannose-1-phosphate guanylyl transferase
93	c5j43F_	Alignment	not modelled	33.4	19	**PDB header:**toxin **Chain:** F: **PDB Molecule:**trna nuclease cdia; **PDBTitle:** cdia-ct from uropathogenic escherichia coli in complex with cysk
94	d1fuia2	Alignment	not modelled	29.6	17	**Fold:**FucI/AraA N-terminal and middle domains **Superfamily:**FucI/AraA N-terminal and middle domains **Family:**L-fucose isomerase, N-terminal and second domains
95	d1ylfa1	Alignment	not modelled	29.1	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator Rrf2
96	c5vmkB_	Alignment	not modelled	28.8	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** crystal structure of a bifunctional glmu udp-n-acetylglucosamine2 diphosphorylase/glucosamine-1- phosphate n-acetyltransferase from3 acinetobacter baumannii
97	d1ybha3	Alignment	not modelled	28.8	11	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
98	c5mm1A_	Alignment	not modelled	28.6	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**dolichol monophosphate mannose synthase; **PDBTitle:** dolichyl phosphate mannose synthase in complex with gdp and dolichyl2 phosphate mannose
99	d1q6za3	Alignment	not modelled	27.1	14	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding)

						Family: Pyruvate oxidase and decarboxylase PP module
100	c3brkX_	Alignment	not modelled	26.8	10	**PDB header:**transferase **Chain:** X: **PDB Molecule:**glucose-1-phosphate adenylyltransferase; **PDBTitle:** crystal structure of adp-glucose pyrophosphorylase from agrobacterium2 tumefaciens
101	c6hsdB_	Alignment	not modelled	26.5	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**rrf2 family transcriptional regulator; **PDBTitle:** crystal structure of the oxidized form of the transcription regulator2 rsrr
102	c6iwqE_	Alignment	not modelled	26.5	9	**PDB header:**transferase **Chain:** E: **PDB Molecule:**n-acetylgalactosaminyltransferase 7; **PDBTitle:** crystal structure of galnac-t7 with mn2+
103	c5n07A_	Alignment	not modelled	26.2	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hth-type transcriptional repressor nsrr; **PDBTitle:** structure of the [4fe-4s] form of the no response regulator nsrr
104	d2ez9a3	Alignment	not modelled	25.0	8	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
105	c3dmqA_	Alignment	not modelled	24.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna polymerase-associated protein rapa; **PDBTitle:** crystal structure of rapa, a swi2/snf2 protein that recycles rna2 polymerase during transcription
106	d1t9ba3	Alignment	not modelled	24.1	11	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
107	c4xrpA_	Alignment	not modelled	23.0	32	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**pnkp1; **PDBTitle:** structure of the pnkp1/rnl/hen1 rna repair complex
108	d2cbia2	Alignment	not modelled	21.9	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**alpha-D-glucuronidase/Hyaluronidase catalytic domain
109	d1xd7a_	Alignment	not modelled	21.6	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator Rrf2
110	c1fuiB_	Alignment	not modelled	20.9	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**l-fucose isomerase; **PDBTitle:** l-fucose isomerase from escherichia coli