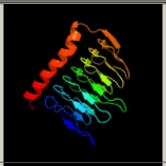
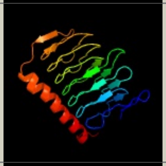
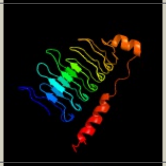
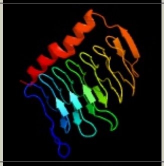
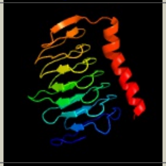
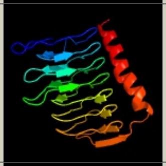
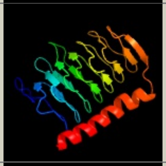
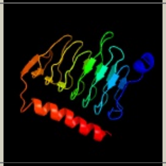
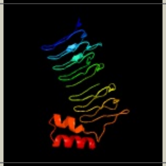
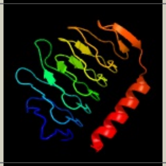
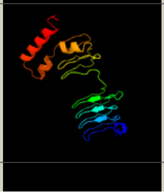
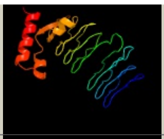
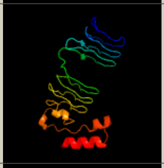
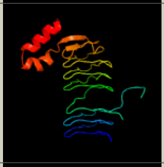
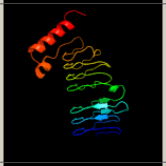
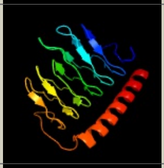
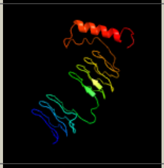
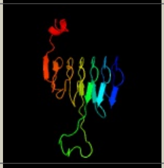
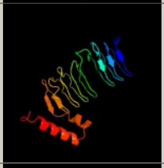
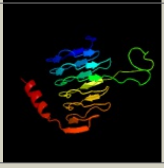
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3525c_(-)_3961979_3962503
Date	Fri Aug 9 18:20:20 BST 2019
Unique Job ID	2fd72ff72be5bb10

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1v3wa_	Alignment		100.0	39	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**gamma-carbonic anhydrase-like
2	c4n27D_	Alignment		100.0	37	**PDB header:**transferase **Chain:** D: **PDB Molecule:**bacterial transferase hexapeptide repeat; **PDBTitle:** x-ray structure of brucella abortus rica
3	c6iveA_	Alignment		100.0	48	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**ferripyochelin-binding protein; **PDBTitle:** molecular structure of a thermostable and a zinc ion binding gamma-2 class carbonic anhydrase
4	d1xhda_	Alignment		100.0	33	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**gamma-carbonic anhydrase-like
5	c3ixcA_	Alignment		100.0	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hexapeptide transferase family protein; **PDBTitle:** crystal structure of hexapeptide transferase family protein from2 anaplasma phagocytophilum
6	c3r3rA_	Alignment		100.0	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ferripyochelin binding protein; **PDBTitle:** structure of the yrda ferripyochelin binding protein from salmonella2 enterica
7	c3r1wA_	Alignment		100.0	34	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** crystal structure of a carbonic anhydrase from a crude oil degrading2 psychrophilic library
8	c4mfgA_	Alignment		100.0	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acyltransferase; **PDBTitle:** 2.0 angstrom resolution crystal structure of putative carbonic2 anhydrase from clostridium difficile.
9	c3i3aC_	Alignment		100.0	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**acyl-[acyl-carrier-protein]--udp-n- **PDBTitle:** structural basis for the sugar nucleotide and acyl chain2 selectivity of leptospira interrogans lpxa
10	c5afuV_	Alignment		100.0	19	**PDB header:**motor protein **Chain:** V: **PDB Molecule:**dynactin; **PDBTitle:** cryo-em structure of dynein tail-dynactin-bicd2n complex
11	c5jxxC_	Alignment		100.0	23	**PDB header:**transferase **Chain:** C: **PDB Molecule:**acyl-[acyl-carrier-protein]--udp-n-acetylglucosamine o- **PDBTitle:** crystal structure of udp-n-acetylglucosamine o-acyltransferase (lpxa)2 from moraxella catarrhalis rh4.

12	c5f42B_	Alignment		100.0	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acyl-[acyl-carrier-protein]--udp-n-acetylglucosamine o- **PDBTitle:** activity and crystal structure of francisella novicida udp-n-2 acetylglucosamine acyltransferase
13	c4eqyC_	Alignment		100.0	21	**PDB header:**transferase **Chain:** C: **PDB Molecule:**acyl-[acyl-carrier-protein]--udp-n-acetylglucosamine o- **PDBTitle:** crystal structure of acyl-[acyl-carrier-protein]--udp-n-2 acetylglucosamine o-acyltransferase from burkholderia thailandensis
14	c3r0sA_	Alignment		100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acyl-[acyl-carrier-protein]--udp-n-acetylglucosamine o- **PDBTitle:** udp-n-acetylglucosamine acyltransferase from campylobacter jejuni
15	c4r36A_	Alignment		99.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acyl-[acyl-carrier-protein]--udp-n- **PDBTitle:** crystal structure analysis of lpxa, a udp-n-acetylglucosamine2 acyltransferase from bacteroides fragilis 9343
16	c5afuU_	Alignment		99.9	21	**PDB header:**motor protein **Chain:** U: **PDB Molecule:**dynactin; **PDBTitle:** cryo-em structure of dynein tail-dynactin-bicd2n complex
17	c5dg3D_	Alignment		99.9	23	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acyl-[acyl-carrier-protein]--udp-n-acetylglucosamine o- **PDBTitle:** structure of pseudomonas aeruginosa lpxa in complex with udp-3-o-(r-3-2 hydroxydecanoyl)-glcnac
18	d1krra_	Alignment		99.9	19	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Galactoside acetyltransferase-like
19	d1j2za_	Alignment		99.9	18	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**UDP N-acetylglucosamine acyltransferase
20	c3vbnA_	Alignment		99.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**galactoside o-acetyltransferase; **PDBTitle:** crystal structure of the d94a mutant of antd, an n-acyltransferase2 from bacillus cereus in complex with dtdp and coenzyme a
21	d2jf2a1	Alignment	not modelled	99.9	18	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**UDP N-acetylglucosamine acyltransferase
22	c3t57A_	Alignment	not modelled	99.9	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine o-acyltransferase domain-containing **PDBTitle:** activity and crystal structure of arabidopsis udp-n-acetylglucosamine2 acyltransferase
23	c4e6tA_	Alignment	not modelled	99.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acyl-[acyl-carrier-protein]--udp-n-acetylglucosamine o- **PDBTitle:** structure of lpxa from acinetobacter baumannii at 1.8a resolution2 (p212121 form)
24	c3ectA_	Alignment	not modelled	99.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hexapeptide-repeat containing-acetyltransferase; **PDBTitle:** crystal structure of the hexapeptide-repeat containing-2 acetyltransferase vca0836 from vibrio cholerae
25	c3kwcD_	Alignment	not modelled	99.9	29	**PDB header:**lyase, protein binding, photosynthesis **Chain:** D: **PDB Molecule:**carbon dioxide concentrating mechanism protein; **PDBTitle:** oxidized, active structure of the beta-carboxysomal gamma-carbonic2 anhydrase, ccmm
26	c4mzuG_	Alignment	not modelled	99.9	21	**PDB header:**isomerase, transferase **Chain:** G: **PDB Molecule:**wxcm-like protein; **PDBTitle:** crystal structure of fdtd, a bifunctional ketoisomerase/n-2 acetyltransferase from shewanella denitrificans
27	c3cj8B_	Alignment	not modelled	99.9	33	**PDB header:**transferase **Chain:** B: **PDB Molecule:**2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n- **PDBTitle:** crystal structure of 2,3,4,5-tetrahydropyridine-2-carboxylate n-2 succinyltransferase from enterococcus faecalis v583
						PDB header:transferase

28	c6mfkA_	Alignment	not modelled	99.9	18	**Chain:** A: **PDB Molecule:**chloramphenicol acetyltransferase; **PDBTitle:** crystal structure of chloramphenicol acetyltransferase from2 elizabethkingia anophelis
29	c2iu9C_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] glucosamine **PDBTitle:** chlamydia trachomatis lpxd with 100mm udpglcnac (complex ii)
30	d1mr7a_	Alignment	not modelled	99.9	15	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Galactoside acetyltransferase-like
31	c3fttA_	Alignment	not modelled	99.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetyltransferase sacol2570; **PDBTitle:** crystal structure of the galactoside o-acetyltransferase from2 staphylococcus aureus
32	c3pmoA_	Alignment	not modelled	99.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] glucosamine n-acyltransferase; **PDBTitle:** the structure of lpxd from pseudomonas aeruginosa at 1.3 a resolution
33	c4e8lC_	Alignment	not modelled	99.9	15	**PDB header:**transferase **Chain:** C: **PDB Molecule:**virginiamycin a acetyltransferase; **PDBTitle:** crystal structure of streptogramin group a antibiotic2 acetyltransferase vata from staphylococcus aureus
34	c3jqyB_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**polysialic acid o-acetyltransferase; **PDBTitle:** crystal strucutre of the polysia specific acetyltransferase neuo
35	c3srtB_	Alignment	not modelled	99.9	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**maltose o-acetyltransferase; **PDBTitle:** the crystal structure of a maltose o-acetyltransferase from2 clostridium difficile 630
36	c2ic7A_	Alignment	not modelled	99.9	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**maltose transacetylase; **PDBTitle:** crystal structure of maltose transacetylase from geobacillus2 kaustophilus
37	c3tv0A_	Alignment	not modelled	99.9	23	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**dynactin subunit 6; **PDBTitle:** structure of dynactin p27 subunit
38	c3r8yD_	Alignment	not modelled	99.9	28	**PDB header:**transferase **Chain:** D: **PDB Molecule:**2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n- **PDBTitle:** structure of the bacillus anthracis tetrahydropicolinate2 succinyltransferase
39	d1xata_	Alignment	not modelled	99.9	15	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Galactoside acetyltransferase-like
40	c3eh0C_	Alignment	not modelled	99.9	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] glucosamine n- **PDBTitle:** crystal structure of lpxd from escherichia coli
41	d1g97a1	Alignment	not modelled	99.9	23	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**GlmU C-terminal domain-like
42	d1ocxa_	Alignment	not modelled	99.9	20	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Galactoside acetyltransferase-like
43	c3eevC_	Alignment	not modelled	99.9	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**chloramphenicol acetyltransferase; **PDBTitle:** crystal structure of chloramphenicol acetyltransferase vca0300 from2 vibrio cholerae o1 biovar eltor
44	c5ux9D_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**chloramphenicol acetyltransferase; **PDBTitle:** the crystal structure of chloramphenicol acetyltransferase from vibrio2 fischeri es114
45	c2wlgA_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polysialic acid o-acetyltransferase; **PDBTitle:** crystallographic analysis of the polysialic acid o-2 acetyltransferase oatwy
46	c3mqhD_	Alignment	not modelled	99.9	22	**PDB header:**transferase **Chain:** D: **PDB Molecule:**lipopolysaccharides biosynthesis acetyltransferase; **PDBTitle:** crystal structure of the 3-n-acetyl transferase wlbb from bordetella2 petrii in complex with coa and udp-3-amino-2-acetamido-2,3-dideoxy3 glucuronic acid
47	c4m98A_	Alignment	not modelled	99.9	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pilin glycosylation protein; **PDBTitle:** acetyltransferase domain of pglb from neisseria gonorrhoeae fa1090
48	c4e75A_	Alignment	not modelled	99.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-3-o-acylglucosamine n-acyltransferase; **PDBTitle:** structure of lpxd from acinetobacter baumannii at 2.85a resolution2 (p21 form)
49	c3d8vA_	Alignment	not modelled	99.9	19	**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
50	c4aa7A_	Alignment	not modelled	99.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** e.coli glmu in complex with an antibacterial inhibitor
51	c4ea8A_	Alignment	not modelled	99.9	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**perosamine n-acetyltransferase; **PDBTitle:** x-ray crystal structure of perb from caulobacter crescentus in complex2 with coenzyme a and gdp-n-acetylperosamine at 1 angstrom resolution
52	c3fsbB	Alignment	not modelled	99.9	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**qdtc; **PDBTitle:** crystal structure of qdtc, the dtdp-3-amino-3,6-dideoxy-d-

		Alignment	not modelled			2 glucose n-acetyl transferase from thermoanaerobacterium3 thermosaccharolyticum in complex with coa and dtdp-3-amino-4 quinovose
53	c1qreA_	Alignment	not modelled	99.9	32	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** a closer look at the active site of gamma-carbonic anhydrases: high2 resolution crystallographic studies of the carbonic anhydrase from3 methanosarcina thermophila
54	d1qrea_	Alignment	not modelled	99.9	32	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**gamma-carbonic anhydrase-like
55	c3kwdA_	Alignment	not modelled	99.9	29	**PDB header:**lyase, protein binding, photosynthesis **Chain:** A: **PDB Molecule:**carbon dioxide concentrating mechanism protein; **PDBTitle:** inactive truncation of the beta-carboxysomal gamma-carbonic anhydrase,2 ccmm, form 1
56	c3c8vA_	Alignment	not modelled	99.9	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetyltransferase; **PDBTitle:** crystal structure of putative acetyltransferase (yp_390128.1) from2 desulfovibrio desulfuricans g20 at 2.28 a resolution
57	d2oi6a1	Alignment	not modelled	99.9	14	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**GlmU C-terminal domain-like
58	d3bswa1	Alignment	not modelled	99.9	18	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**PglD-like
59	c4m9cC_	Alignment	not modelled	99.9	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**bacterial transferase hexapeptide (three repeats) family **PDBTitle:** weei from acinetobacter baumannii aye
60	c3foqA_	Alignment	not modelled	99.8	18	**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.
61	d1t3da_	Alignment	not modelled	99.8	23	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Serine acetyltransferase
62	c1hm8A_	Alignment	not modelled	99.8	18	**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
63	c1t3dB_	Alignment	not modelled	99.8	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine acetyltransferase; **PDBTitle:** crystal structure of serine acetyltransferase from e.coli at 2.2a
64	d1ssqa_	Alignment	not modelled	99.8	20	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Serine acetyltransferase
65	c4n6bB_	Alignment	not modelled	99.8	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine acetyltransferase apoenzyme; **PDBTitle:** soybean serine acetyltransferase complexed with coa
66	c3mc4A_	Alignment	not modelled	99.8	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ww/rsp5/wwp domain:bacterial transferase hexapeptide **PDBTitle:** crystal structure of ww/rsp5/wwp domain: bacterial transferase2 hexapeptide repeat: serine o-acetyltransferase from brucella3 melitensis
67	c2v0hA_	Alignment	not modelled	99.8	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)
68	c2oi6A_	Alignment	not modelled	99.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** e. coli glmu- complex with udp-glcnac, coa and glcn-1-po4
69	d3tdta_	Alignment	not modelled	99.8	21	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Tetrahydrodipicolinate-N-succinlytransferase, THDP-succinlytransferase, DapD
70	c5b04I_	Alignment	not modelled	99.8	13	**PDB header:**translation **Chain:** I: **PDB Molecule:**probable translation initiation factor eif-2b subunit **PDBTitle:** crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
71	c6cktA_	Alignment	not modelled	99.7	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n- **PDBTitle:** crystal structure of 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n-2 succinyltransferase from legionella pneumophila philadelphia 1
72	c3eg4A_	Alignment	not modelled	99.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n- **PDBTitle:** crystal structure of 2,3,4,5-tetrahydropyridine-2-2 carboxylate n-succinyltransferase from brucella melitensis3 biovar abortus 2308
73	c5vmkB_	Alignment	not modelled	99.7	12	**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
74	c3r5dA_	Alignment	not modelled	99.7	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tetrahydrodipicolinate n-succinyletransferase; **PDBTitle:** pseudomonas aeruginosa dapd (pa3666) apoprotein

75	c3q1xA_	Alignment	not modelled	99.7	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine acetyltransferase; **PDBTitle:** crystal structure of entamoeba histolytica serine acetyltransferase 12 in complex with l-serine
76	c3f1xA_	Alignment	not modelled	99.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine acetyltransferase; **PDBTitle:** three dimensional structure of the serine acetyltransferase from2 bacteroides vulgatus, northeast structural genomics consortium target3 bvr62.
77	c6jlwJ_	Alignment	not modelled	99.6	17	**PDB header:**translation **Chain:** J: **PDB Molecule:**translation initiation factor eif-2b subunit epsilon; **PDBTitle:** eif2 - eif2b complex
78	c6i3mG_	Alignment	not modelled	99.6	15	**PDB header:**translation **Chain:** G: **PDB Molecule:**translation initiation factor eif-2b subunit epsilon; **PDBTitle:** eif2b:eif2 complex, phosphorylated on eif2 alpha serine 52.
79	c5e3pA_	Alignment	not modelled	99.6	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n- **PDBTitle:** crystal strcuture of dapd from corynebacterium glutamicum
80	c6ezoJ_	Alignment	not modelled	99.6	17	**PDB header:**membrane protein **Chain:** J: **PDB Molecule:**human eukaryotic initiation factor eif2b epsilon subunits; **PDBTitle:** eukaryotic initiation factor eif2b in complex with isrib
81	c3d98A_	Alignment	not modelled	99.6	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
82	c3fsyC_	Alignment	not modelled	99.5	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**tetrahydrodipicolinate n-succinyltransferase; **PDBTitle:** structure of tetrahydrodipicolinate n-succinyltransferase2 (rv1201c;dapd) in complex with succinyl-coa from mycobacterium3 tuberculosis
83	c2qkxA_	Alignment	not modelled	99.5	22	**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
84	d2f9ca1	Alignment	not modelled	99.4	12	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**YdcK-like
85	d1yp2a1	Alignment	not modelled	99.4	16	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**GlmU C-terminal domain-like
86	c2ggqA_	Alignment	not modelled	99.4	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**401aa long hypothetical glucose-1-phosphate **PDBTitle:** complex of hypothetical glucose-1-phosphate thymidylyltransferase from2 sulfolobus tokodaii
87	c5b04F_	Alignment	not modelled	99.3	16	**PDB header:**translation **Chain:** F: **PDB Molecule:**probable translation initiation factor eif-2b subunit **PDBTitle:** crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
88	c1yp3C_	Alignment	not modelled	99.3	18	**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
89	c6ezoF_	Alignment	not modelled	99.2	20	**PDB header:**membrane protein **Chain:** F: **PDB Molecule:**translation initiation factor eif-2b subunit gamma; **PDBTitle:** eukaryotic initiation factor eif2b in complex with isrib
90	c6qg2F_	Alignment	not modelled	99.0	12	**PDB header:**translation **Chain:** F: **PDB Molecule:**translation initiation factor eif-2b subunit gamma; **PDBTitle:** structure of eif2b-eif2 (phosphorylated at ser51) complex (model a)
91	d1fxja1	Alignment	not modelled	98.9	21	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**GlmU C-terminal domain-like
92	c2rijA_	Alignment	not modelled	98.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative 2,3,4,5-tetrahydropyridine-2-carboxylate n- **PDBTitle:** crystal structure of a putative 2,3,4,5-tetrahydropyridine-2-2 carboxylate n-succinyltransferase (cj1605c, dapd) from campylobacter3 jejuni at 1.90 a resolution
93	c1fwyA_	Alignment	not modelled	98.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine pyrophosphorylase; **PDBTitle:** crystal structure of n-acetylglucosamine 1-phosphate2 uridyltransferase bound to udp-glcnac
94	c5l6sF_	Alignment	not modelled	98.8	13	**PDB header:**transferase **Chain:** F: **PDB Molecule:**glucose-1-phosphate adenylyltransferase; **PDBTitle:** crystal structure of e. coli adp-glucose pyrophosphorylase (agpase) in2 complex with a positive allosteric regulator beta-fructose-1,6-3 diphosphate (fbp) - agpase*fbp
95	c3brkX_	Alignment	not modelled	98.6	18	**PDB header:**transferase **Chain:** X: **PDB Molecule:**glucose-1-phosphate adenylyltransferase; **PDBTitle:** crystal structure of adp-glucose pyrophosphorylase from agrobacterium2 tumefaciens
96	c5yysC_	Alignment	not modelled	47.8	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**l-fucokinase, l-fucose-1-p guanylyltransferase; **PDBTitle:** cryo-em structure of l-fucokinase, gdp-fucose pyrophosphorylase (fkp)2 in bacteroides fragilis
						PDB header:hydrolase

97	c5jxfA_	Alignment	not modelled	19.9	18	**Chain:** A: **PDB Molecule:**asp/glu-specific dipeptidyl-peptidase; **PDBTitle:** crystal structure of flavobacterium psychrophilum dpp11 in complex2 with dipeptide arg-asp
98	d2icya1	Alignment	not modelled	12.7	13	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**GlmU C-terminal domain-like
99	c3wolB_	Alignment	not modelled	11.6	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dipeptidyl aminopeptidase bii; **PDBTitle:** crystal structure of the dap bii dipeptide complex i