

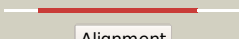

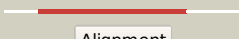











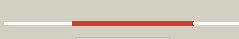
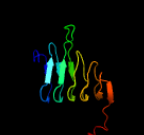



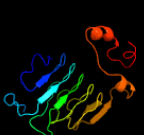
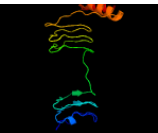
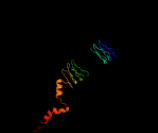
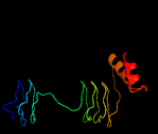



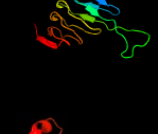

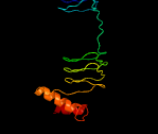


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2335_(cysE)_2609742_2610431
Date	Mon Aug 5 13:25:48 BST 2019
Unique Job ID	5e0390d75f622279

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1t3dB_	 Alignment		100.0	43	PDB header: transferase Chain: B: PDB Molecule: serine acetyltransferase; PDBTitle: crystal structure of serine acetyltransferase from e.coli at 2.2a
2	d1t3da_	 Alignment		100.0	43	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Serine acetyltransferase
3	d1ssqa_	 Alignment		100.0	43	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Serine acetyltransferase
4	c3mc4A_	 Alignment		100.0	48	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
5	c4n6bB_	 Alignment		100.0	49	PDB header: transferase Chain: B: PDB Molecule: serine acetyltransferase apoenzyme; PDBTitle: soybean serine acetyltransferase complexed with coa
6	c3q1xA_	 Alignment		100.0	49	PDB header: transferase Chain: A: PDB Molecule: serine acetyltransferase; PDBTitle: crystal structure of entamoeba histolytica serine acetyltransferase 12 in complex with l-serine
7	c3f1xA_	 Alignment		100.0	41	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.
8	c4e8IC_	 Alignment		100.0	27	PDB header: transferase Chain: C: PDB Molecule: virginiamycin a acetyltransferase; PDBTitle: crystal structure of streptogramin group a antibiotic2 acetyltransferase vata from staphylococcus aureus
9	d1krra_	 Alignment		100.0	28	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Galactoside acetyltransferase-like
10	d1locxa_	 Alignment		100.0	22	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Galactoside acetyltransferase-like
11	d1xata_	 Alignment		100.0	21	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Galactoside acetyltransferase-like

12	c5jxC	Alignment		100.0	25	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.
13	c2iu9C	Alignment		100.0	32	PDB header: transferase Chain: C: PDB Molecule: udp-3-o-[3-hydroxymyristoyl] glucosamine PDBTitle: chlamydia trachomatis lpxd with 100mm udpglcna (complex ii)
14	c5dg3D	Alignment		100.0	28	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)-glcna
15	c3r0sA	Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine o- PDBTitle: udp-n-acetylglucosamine acyltransferase from campylobacter jejuni
16	d1mr7a	Alignment		100.0	24	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Galactoside acetyltransferase-like
17	c2ic7A	Alignment		100.0	27	PDB header: transferase Chain: A: PDB Molecule: maltose transacetylase; PDBTitle: crystal structure of maltose transacetylase from geobacillus2 kaustophilus
18	c6mfkA	Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: chloramphenicol acetyltransferase; PDBTitle: crystal structure of chloramphenicol acetyltransferase from2 elizabethkingia anophelis
19	c4r36A	Alignment		100.0	31	PDB header: transferase Chain: A: PDB Molecule: putative acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine2 acyltransferase from bacteroides fragilis 9343
20	d1j2za	Alignment		99.9	32	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: UDP N-acetylglucosamine acyltransferase
21	c4eqyC	Alignment	not modelled	99.9	29	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
22	d2jf2a1	Alignment	not modelled	99.9	28	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: UDP N-acetylglucosamine acyltransferase
23	c3srtB	Alignment	not modelled	99.9	29	PDB header: transferase Chain: B: PDB Molecule: maltose o-acetyltransferase; PDBTitle: the crystal structure of a maltose o-acetyltransferase from2 clostridium difficile 630
24	c4e6tA	Alignment	not modelled	99.9	25	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)
25	c3fttA	Alignment	not modelled	99.9	26	PDB header: transferase Chain: A: PDB Molecule: putative acetyltransferase sacol2570; PDBTitle: crystal structure of the galactoside o-acetyltransferase from2 staphylococcus aureus
26	c5ux9D	Alignment	not modelled	99.9	28	PDB header: transferase Chain: D: PDB Molecule: chloramphenicol acetyltransferase; PDBTitle: the crystal structure of chloramphenicol acetyltransferase from vibrio2 fischeri es114
27	c3ectA	Alignment	not modelled	99.9	22	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
28	d3tdta	Alignment	not modelled	99.9	18	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Tetrahydrodipicolinate-N-succinyltransferase, THDP-

						succinyltransferase, DapD PDB header: transferase Chain: C: PDB Molecule: chloramphenicol acetyltransferase; PDBTitle: crystal structure of chloramphenicol acetyltransferase vca0300 from <i>Vibrio cholerae</i> O1 biovar eltor
29	c3eevC_	Alignment	not modelled	99.9	20	
30	c3jqyB_	Alignment	not modelled	99.9	22	PDB header: transferase Chain: B: PDB Molecule: polysialic acid o-acetyltransferase; PDBTitle: crystal structure of the polysialic acid specific acetyltransferase neuo
31	c5f42B_	Alignment	not modelled	99.9	23	PDB header: transferase Chain: B: PDB Molecule: acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine o- PDBTitle: activity and crystal structure of <i>Francisella novicida</i> udp-n-2 acetylglucosamine acyltransferase
32	c3i3aC_	Alignment	not modelled	99.9	25	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 <i>Leptospira interrogans</i> lpXA
33	c3pmoA_	Alignment	not modelled	99.9	22	PDB header: transferase Chain: A: PDB Molecule: udp-3-o-[3-hydroxymyristoyl] glucosamine n-acyltransferase; PDBTitle: the structure of lpXD from <i>Pseudomonas aeruginosa</i> at 1.3 Å resolution
34	c4mzuG_	Alignment	not modelled	99.9	32	PDB header: isomerase, transferase Chain: G: PDB Molecule: wxcm-like protein; PDBTitle: crystal structure of fdtd, a bifunctional ketoisomerase/n-2 acetyltransferase from <i>Shewanella denitrificans</i>
35	c3cj8B_	Alignment	not modelled	99.9	42	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 <i>Enterococcus faecalis</i> v583
36	c4m98A_	Alignment	not modelled	99.9	23	PDB header: transferase Chain: A: PDB Molecule: pilin glycosylation protein; PDBTitle: acetyltransferase domain of pglB from <i>Neisseria gonorrhoeae</i> fa1090
37	c3eh0C_	Alignment	not modelled	99.9	23	PDB header: transferase Chain: C: PDB Molecule: udp-3-o-[3-hydroxymyristoyl] glucosamine n- PDBTitle: crystal structure of lpXD from <i>Escherichia coli</i>
38	d3bswa1	Alignment	not modelled	99.9	25	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: PglD-like
39	c3r8yD_	Alignment	not modelled	99.9	38	PDB header: transferase Chain: D: PDB Molecule: 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n- PDBTitle: structure of the <i>Bacillus anthracis</i> tetrahydropicolinate2 succinyltransferase
40	c4ea8A_	Alignment	not modelled	99.9	25	PDB header: transferase Chain: A: PDB Molecule: perosamine n-acetyltransferase; PDBTitle: x-ray crystal structure of perB from <i>Caulobacter crescentus</i> in complex2 with coenzyme A and gdp-n-acetylperosamine at 1 Å resolution
41	c3fsbB_	Alignment	not modelled	99.9	40	PDB header: transferase Chain: B: PDB Molecule: qdtc; PDBTitle: crystal structure of qdtc, the dtdp-3-amino-3,6-dideoxy-d-2 glucose n-acetyl transferase from <i>Thermoanaerobacterium</i> 3 <i>thermosaccharolyticum</i> in complex with coa and dtdp-3-amino-4 quinovose
42	c3vbnA_	Alignment	not modelled	99.9	20	PDB header: transferase Chain: A: PDB Molecule: galactoside o-acetyltransferase; PDBTitle: crystal structure of the d94a mutant of antD, an n-acyltransferase2 from <i>Bacillus cereus</i> in complex with dtdp and coenzyme A
43	c3eg4A_	Alignment	not modelled	99.9	24	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 <i>Brucella melitensis</i> 3 biovar abortus 2308
44	c2wlgA_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: polysialic acid o-acetyltransferase; PDBTitle: crystallographic analysis of the polysialic acid o-2 acetyltransferase oatwy
45	c3mqhD_	Alignment	not modelled	99.9	34	PDB header: transferase Chain: D: PDB Molecule: lipopolysaccharides biosynthesis acetyltransferase; PDBTitle: crystal structure of the 3-n-acetyl transferase wlbB from <i>Bordetella pertussis</i> in complex with coa and udp-3-amino-2-acetamido-2,3-dideoxy3 glucuronic acid
46	c3t57A_	Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine o-acyltransferase domain-containing PDBTitle: activity and crystal structure of <i>Arabidopsis</i> udp-n-acetylglucosamine2 acyltransferase
47	c5e3pA_	Alignment	not modelled	99.9	21	PDB header: transferase Chain: A: PDB Molecule: 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n- PDBTitle: crystal structure of dapD from <i>Corynebacterium glutamicum</i>
48	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
49	c3d8vA_	Alignment	not modelled	99.9	26	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmU; PDBTitle: crystal structure of glmU from <i>Mycobacterium tuberculosis</i> 2 in complex with uridine-diphosphate-n-acetylglucosamine
50	c4e75A_	Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: udp-3-o-acylglucosamine n-acyltransferase; PDBTitle: structure of lpXD from <i>Acinetobacter baumannii</i> at 2.85 Å

					resolution2 (p21 form) PDB header: transferase Chain: C: PDB Molecule: bacterial transferase hexapeptide (three repeats) family PDBTitle: weei from acinetobacter baumannii aye
51	c4m9cC_	Alignment	not modelled	99.9	24 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
52	c6cktA_	Alignment	not modelled	99.9	18 PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: e.coli glmu in complex with an antibacterial inhibitor
53	c4aa7A_	Alignment	not modelled	99.9	22 PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of n-acetylglucosamine-1-phosphate2 uridylyltransferase (glmu) from mycobacterium tuberculosis in3 a cubic space group.
54	c3foqA_	Alignment	not modelled	99.9	27 PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine-1-phosphate uridylyltransferase; PDBTitle: crystal structure of s.pneumoniae n-acetylglucosamine-1-phosphate2 uridylyltransferase, glmu, bound to acetyl coenzyme a
55	c1hm8A_	Alignment	not modelled	99.9	23 Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: GlmU C-terminal domain-like
56	d2oi6a1	Alignment	not modelled	99.9	26 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 uridylyltransferase (glmu)
57	c2v0hA_	Alignment	not modelled	99.8	23 Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: gamma-carbonic anhydrase-like
58	d1v3wa_	Alignment	not modelled	99.8	30 PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: e. coli glmu- complex with udp-glcnac, coa and glcn-1-po4
59	c2oi6A_	Alignment	not modelled	99.8	21 Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: gamma-carbonic anhydrase-like
60	d1xhda_	Alignment	not modelled	99.8	25 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
61	c5vmkB_	Alignment	not modelled	99.8	24 PDB header: transferase Chain: A: PDB Molecule: hexapeptide transferase family protein; PDBTitle: crystal structure of hexapeptide transferase family protein from2 anaplasma phagocytophilum
62	c3ixcA_	Alignment	not modelled	99.8	22 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
63	c3fsyC_	Alignment	not modelled	99.8	28 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
64	c6iveA_	Alignment	not modelled	99.8	27 PDB header: motor protein Chain: V: PDB Molecule: dynactin; PDBTitle: cryo-em structure of dynein tail-dynactin-bicd2n complex
65	c5afuV_	Alignment	not modelled	99.8	17 PDB header: transferase Chain: D: PDB Molecule: bacterial transferase hexapeptide repeat; PDBTitle: x-ray structure of brucella abortus rica
66	c4n27D_	Alignment	not modelled	99.8	23 PDB header: transferase Chain: A: PDB Molecule: ferripyochelin binding protein; PDBTitle: structure of the yrdA ferripyochelin binding protein from salmonella2 enterica
67	c3r3rA_	Alignment	not modelled	99.8	22 PDB header: transferase Chain: A: PDB Molecule: tetrahydrodipicolinate n-succinyletransferase; PDBTitle: pseudomonas aeruginosa dapd (pa3666) apoprotein
68	c3r5dA_	Alignment	not modelled	99.8	19 PDB header: motor protein Chain: U: PDB Molecule: dynactin; PDBTitle: cryo-em structure of dynein tail-dynactin-bicd2n complex
69	c5afuU_	Alignment	not modelled	99.8	19 PDB header: transferase Chain: A: PDB Molecule: putative acyltransferase; PDBTitle: 2.0 angstrom resolution crystal structure of putative carbonic2 anhydrase from clostridium difficile.
70	c4mfgA_	Alignment	not modelled	99.8	25 PDB header: lyase Chain: A: PDB Molecule: carbonic anhydrase; PDBTitle: crystal structure of a carbonic anhydrase from a crude oil degrading2 psychrophilic library
71	c3r1wA_	Alignment	not modelled	99.7	16 PDB header: transferase Chain: A: PDB Molecule: 401aa long hypothetical glucose-1-phosphate PDBTitle: complex of hypothetical glucose-1-phosphate thymidyltransferase from2 sulfolobus tokodaii
72	c2gggA_	Alignment	not modelled	99.7	21 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
73	c3c8vA_	Alignment	not modelled	99.7	19 PDB header: transferase Chain: A: PDB Molecule: putative 2,3,4,5-tetrahydropyridine-2-

74	c2rijA_	Alignment	not modelled	99.6	25	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
75	c3tv0A_	Alignment	not modelled	99.6	23	PDB header: structural protein Chain: A: PDB Molecule: dynactin subunit 6; PDBTitle: structure of dynactin p27 subunit
76	c3kwcD_	Alignment	not modelled	99.4	24	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
77	d1qrea_	Alignment	not modelled	99.4	16	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: gamma-carbonic anhydrase-like
78	c1qreA_	Alignment	not modelled	99.4	16	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
79	d2f9ca1	Alignment	not modelled	99.4	13	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Ydck-like
80	c6i3mG_	Alignment	not modelled	99.3	18	PDB header: translation Chain: G: PDB Molecule: translation initiation factor eif-2b subunit epsilon; PDBTitle: eif2b:eif2 complex, phosphorylated on eif2 alpha serine 52.
81	c5b04I_	Alignment	not modelled	99.3	21	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
82	c6jlwJ_	Alignment	not modelled	99.2	14	PDB header: translation Chain: J: PDB Molecule: translation initiation factor eif-2b subunit epsilon; PDBTitle: eif2 - eif2b complex
83	d1fxja1	Alignment	not modelled	99.2	26	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: GlmU C-terminal domain-like
84	c2qkxA_	Alignment	not modelled	99.1	19	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: n-acetyl glucosamine 1-phosphate uridylyltransferase from mycobacterium2 tuberculosis complex with n-acetyl glucosamine 1-phosphate
85	c6ezoJ_	Alignment	not modelled	99.1	18	PDB header: membrane protein Chain: J: PDB Molecule: human eukaryotic initiation factor eif2b epsilon subunits; PDBTitle: eukaryotic initiation factor eif2b in complex with isrib
86	c5b04F_	Alignment	not modelled	99.1	19	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
87	d1yp2a1	Alignment	not modelled	99.0	16	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: GlmU C-terminal domain-like
88	c3kwdA_	Alignment	not modelled	99.0	25	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
89	c6ezoF_	Alignment	not modelled	99.0	22	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	c3d98A_	Alignment	not modelled	99.0	19	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
91	c1yp3C_	Alignment	not modelled	98.9	20	PDB header: transferase Chain: C: PDB Molecule: glucose-1-phosphate adenyllyltransferase small PDBTitle: crystal structure of potato tuber adp-glucose2 pyrophosphorylase in complex with atp
92	c5l6sF_	Alignment	not modelled	98.9	16	PDB header: transferase Chain: F: PDB Molecule: glucose-1-phosphate adenyllyltransferase; 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
93	c1fwyA_	Alignment	not modelled	98.9	26	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: crystal structure of n-acetylglucosamine 1-phosphate2 uridylyltransferase bound to udp-glnac
94	c6gg2F_	Alignment	not modelled	98.9	18	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)
95	c3brkX_	Alignment	not modelled	98.7	17	PDB header: transferase Chain: X: PDB Molecule: glucose-1-phosphate adenyllyltransferase; PDBTitle: crystal structure of adp-glucose pyrophosphorylase from agrobacterium2 tumefaciens
96	c5yysC_	Alignment	not modelled	39.5	20	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

97	c3gw6F_	Alignment	not modelled	29.0	16	PDB header: chaperone Chain: F; PDB Molecule: endo-n-acetylneuraminidase; PDBTitle: intramolecular chaperone
98	c4x0nB_	Alignment	not modelled	15.6	55	PDB header: hydrolase/hydrolase inhibitor Chain: B; PDB Molecule: helianthamide; PDBTitle: porcine pancreatic alpha-amylase in complex with helianthamide, a2 novel proteinaceous inhibitor
99	c6ria4_	Alignment	not modelled	11.9	20	PDB header: protein fibril Chain: 4; PDB Molecule: PDBTitle: bactofilin from thermus thermophilus, f105r mutant crystal structure