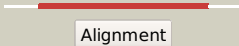
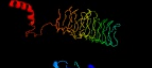

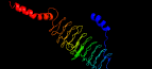
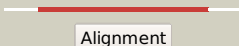

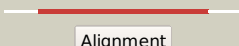
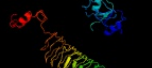
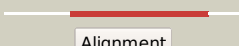

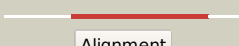

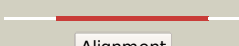
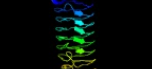










# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3034c (- )_3394030_3394932
Date	Thu Aug 8 16:20:20 BST 2019
Unique Job ID	c622b8aa4caa9846

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3pmoA_</a>	 Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-3-o-[3-hydroxymyristoyl] glucosamine n-acyltransferase; <b>PDBTitle:</b> the structure of lpxd from pseudomonas aeruginosa at 1.3 a resolution
2	<a href="#">c2iu9C_</a>	 Alignment		100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> udp-3-o-[3-hydroxymyristoyl] glucosamine <b>PDBTitle:</b> chlamydia trachomatis lpxd with 100mm udpglcnac (complex ii)
3	<a href="#">c3eh0C_</a>	 Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> udp-3-o-[3-hydroxymyristoyl] glucosamine n- <b>PDBTitle:</b> crystal structure of lpxd from escherichia coli
4	<a href="#">c4e75A_</a>	 Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-3-o-acylglucosamine n-acyltransferase; <b>PDBTitle:</b> structure of lpxd from acinetobacter baumannii at 2.85a resolution2 (p21 form)
5	<a href="#">d1j2za_</a>	 Alignment		100.0	15	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> UDP N-acetylglucosamine acyltransferase
6	<a href="#">c3i3aC_</a>	 Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> acyl-[acyl-carrier-protein]--udp-n- <b>PDBTitle:</b> structural basis for the sugar nucleotide and acyl chain2 selectivity of leptospira interrogans lpxa
7	<a href="#">c3t57A_</a>	 Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine o-acyltransferase domain-containing <b>PDBTitle:</b> activity and crystal structure of arabidopsis udp-n-acetylglucosamine2 acyltransferase
8	<a href="#">c4e6tA_</a>	 Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-[acyl-carrier-protein]--udp-n-acetylglucosamine o- <b>PDBTitle:</b> structure of lpxa from acinetobacter baumannii at 1.8a resolution2 (p212121 form)
9	<a href="#">d2jf2a1</a>	 Alignment		100.0	16	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> UDP N-acetylglucosamine acyltransferase
10	<a href="#">c4r36A_</a>	 Alignment		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative acyl-[acyl-carrier-protein]--udp-n- <b>PDBTitle:</b> crystal structure analysis of lpxa, a udp-n-acetylglucosamine2 acyltransferase from bacteroides fragilis 9343
11	<a href="#">c3r0sA_</a>	 Alignment		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-[acyl-carrier-protein]--udp-n-acetylglucosamine o- <b>PDBTitle:</b> udp-n-acetylglucosamine acyltransferase from campylobacter jejuni

12	<a href="#">c4eqyC_</a>	Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine o- <b>PDBTitle:</b> crystal structure of acyl-[acyl-carrier-protein]-udp-n-2 acetylglucosamine o-acyltransferase from burkholderia thailandensis
13	<a href="#">c5f42B_</a>	Alignment		100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine o- <b>PDBTitle:</b> activity and crystal structure of francisella novicida udp-n-2 acetylglucosamine acyltransferase
14	<a href="#">c5jxxC_</a>	Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine o- <b>PDBTitle:</b> crystal structure of udp-n-acetylglucosamine o-acyltransferase (lpxa)2 from moraxella catarrhalis rh4.
15	<a href="#">c5dg3D_</a>	Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine o- <b>PDBTitle:</b> structure of pseudomonas aeruginosa lpxa in complex with udp-3-o-(r-3-2 hydroxydecanoyl)-glcnae
16	<a href="#">c3d8vA_</a>	Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein glmu; <b>PDBTitle:</b> crystal structure of glmu from mycobacterium tuberculosis2 in complex with uridine-diphosphate-n-acetylglucosamine
17	<a href="#">c3jqyB_</a>	Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> polysialic acid o-acetyltransferase; <b>PDBTitle:</b> crystal strucutre of the polysia specific acetyltransferase neuo
18	<a href="#">c3vbnA_</a>	Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> galactoside o-acetyltransferase; <b>PDBTitle:</b> crystal structure of the d94a mutant of antd, an n-acyltransferase2 from bacillus cereus in complex with dtdp and coenzyme a
19	<a href="#">d1krra_</a>	Alignment		100.0	24	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> Galactoside acetyltransferase-like
20	<a href="#">c2wlgA_</a>	Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polysialic acid o-acetyltransferase; <b>PDBTitle:</b> crystallographic analysis of the polysialic acid o-2 acetyltransferase oatwy
21	<a href="#">c4aa7A_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein glmu; <b>PDBTitle:</b> e.coli glmu in complex with an antibacterial inhibitor
22	<a href="#">c3ectA_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hexapeptide-repeat containing-acetyltransferase; <b>PDBTitle:</b> crystal structure of the hexapeptide-repeat containing-2 acetyltransferase vca0836 from vibrio cholerae
23	<a href="#">d1g97a1</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> GlmU C-terminal domain-like
24	<a href="#">c3fttA_</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative acetyltransferase sacol2570; <b>PDBTitle:</b> crystal structure of the galactoside o-acetyltransferase from2 staphylococcus aureus
25	<a href="#">c4mzuG_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> isomerase, transferase <b>Chain:</b> G: <b>PDB Molecule:</b> wxcm-like protein; <b>PDBTitle:</b> crystal structure of fddt, a bifunctional ketoisomerase/n-2 acetyltransferase from shewanella dentrificans
26	<a href="#">c3srtB_</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> maltose o-acetyltransferase; <b>PDBTitle:</b> the crystal structure of a maltose o-acetyltransferase from2 clostridium difficile 630
27	<a href="#">c2ic7A_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> maltose transacetylase; <b>PDBTitle:</b> crystal structure of maltose transacetylase from geobacillus2 kaustophilus
28	<a href="#">c3mqhD_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> lipopolysaccharides biosynthesis acetyltransferase; <b>PDBTitle:</b> crystal structure of the 3-n-acetyl transferase wlb from bordetella2 petrii in complex with coa and udp-3-amino-2-

						acetamido-2,3-dideoxy3 glucuronic acid
29	<a href="#">d1mr7a_</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> Galactoside acetyltransferase-like
30	<a href="#">d2oi6a1</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> GlmU C-terminal domain-like
31	<a href="#">d1ocxa_</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> Galactoside acetyltransferase-like
32	<a href="#">c4e8lC_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> virginiamycin a acetyltransferase; <b>PDBTitle:</b> crystal structure of streptogramin group a antibiotic2 acetyltransferase vata from staphylococcus aureus
33	<a href="#">c3fsbB_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> qdtc; <b>PDBTitle:</b> crystal structure of qdtc, the dtdp-3-amino-3,6-dideoxy-d-2 glucose n-acetyl transferase from thermoanaerobacterium3 thermosaccharolyticum in complex with coa and dtdp-3-amino-4 quinovose
34	<a href="#">c6mfkA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> chloramphenicol acetyltransferase; <b>PDBTitle:</b> crystal structure of chloramphenicol acetyltransferase from2 elizabethkingia anophelis
35	<a href="#">c3eevC_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> chloramphenicol acetyltransferase; <b>PDBTitle:</b> crystal structure of chloramphenicol acetyltransferase vca0300 from2 vibrio cholerae o1 biovar eltor
36	<a href="#">d1xata_</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> Galactoside acetyltransferase-like
37	<a href="#">c1hm8A_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine-1-phosphate uridylyltransferase; <b>PDBTitle:</b> crystal structure of s.pneumoniae n-acetylglucosamine-1-phosphate2 uridylyltransferase, glmu, bound to acetyl coenzyme a
38	<a href="#">c3foqA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein glmu; <b>PDBTitle:</b> crystal structure of n-acetylglucosamine-1-phosphate2 uridylyltransferase (glmu) from mycobacterium tuberculosis in3 a cubic space group.
39	<a href="#">c5ux9D_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> chloramphenicol acetyltransferase; <b>PDBTitle:</b> the crystal structure of chloramphenicol acetyltransferase from vibrio2 fischeri es114
40	<a href="#">c5e3pA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n- <b>PDBTitle:</b> crystal structure of dapd from corynebacterium glutamicum
41	<a href="#">c3r3rA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ferripyochelin binding protein; <b>PDBTitle:</b> structure of the yrdA ferripyochelin binding protein from salmonella2 enterica
42	<a href="#">c4n27D_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> bacterial transferase hexapeptide repeat; <b>PDBTitle:</b> x-ray structure of brucella abortus rica
43	<a href="#">d1v3wa_</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> gamma-carbonic anhydrase-like
44	<a href="#">c4mfqA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative acyltransferase; <b>PDBTitle:</b> 2.0 angstrom resolution crystal structure of putative carbonic2 anhydrase from clostridium difficile.
45	<a href="#">c2v0hA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein glmu; <b>PDBTitle:</b> characterization of substrate binding and catalysis of the2 potential antibacterial target n-acetylglucosamine-1-3 phosphate uridylyltransferase (glmu)
46	<a href="#">c3ixcA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hexapeptide transferase family protein; <b>PDBTitle:</b> crystal structure of hexapeptide transferase family protein from2 anaplasma phagocytophilum
47	<a href="#">c2oi6A_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein glmu; <b>PDBTitle:</b> e. coli glmu- complex with udp-glcnac, coa and glcn-1-po4
48	<a href="#">c6iveA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ferripyochelin-binding protein; <b>PDBTitle:</b> molecular structure of a thermostable and a zinc ion binding gamma-2 class carbonic anhydrase
49	<a href="#">c3cj8B_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n- <b>PDBTitle:</b> crystal structure of 2,3,4,5-tetrahydropyridine-2-carboxylate n-2 succinyltransferase from enterococcus faecalis v583
50	<a href="#">c3r5dA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tetrahydrodipicolinate n-succinyletransferase; <b>PDBTitle:</b> pseudomonas aeruginosa dapd (pa3666) apoprotein
51	<a href="#">c3r1wA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> carbonic anhydrase; <b>PDBTitle:</b> crystal structure of a carbonic anhydrase from a crude oil degrading2 psychrophilic library
52	<a href="#">d1xhda_</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> gamma-carbonic anhydrase-like
						<b>Fold:</b> Single-stranded left-handed beta-helix

53	<a href="#">d1t3da_</a>	Alignment	not modelled	100.0	21	<b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> Serine acetyltransferase
54	<a href="#">c4m98A_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pilin glycosylation protein; <b>PDBTitle:</b> acetyltransferase domain of pglb from neisseria gonorrhoeae fa1090
55	<a href="#">c1t3dB_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine acetyltransferase; <b>PDBTitle:</b> crystal structure of serine acetyltransferase from e.coli at 2.2a
56	<a href="#">c3r8yD_</a>	Alignment	not modelled	99.9	28	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n- <b>PDBTitle:</b> structure of the bacillus anthracis tetrahydropicolinate2 succinyltransferase
57	<a href="#">d1ssga_</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> Serine acetyltransferase
58	<a href="#">c3c8vA_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative acetyltransferase; <b>PDBTitle:</b> crystal structure of putative acetyltransferase (yp_390128.1) from2 desulfovibrio desulfuricans g20 at 2.28 a resolution
59	<a href="#">d3bswa1</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> PglD-like
60	<a href="#">c5afuU_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> motor protein <b>Chain:</b> U: <b>PDB Molecule:</b> dynactin; <b>PDBTitle:</b> cryo-em structure of dynein tail-dynactin-bicd2n complex
61	<a href="#">c4ea8A_</a>	Alignment	not modelled	99.9	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> perosamine n-acetyltransferase; <b>PDBTitle:</b> x-ray crystal structure of perb from caulobacter crescentus in complex2 with coenzyme a and gdp-n-acetylperosamine at 1 angstrom resolution
62	<a href="#">c5afuV_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> motor protein <b>Chain:</b> V: <b>PDB Molecule:</b> dynactin; <b>PDBTitle:</b> cryo-em structure of dynein tail-dynactin-bicd2n complex
63	<a href="#">c4n6bB_</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine acetyltransferase apoenzyme; <b>PDBTitle:</b> soybean serine acetyltransferase complexed with coa
64	<a href="#">c3mc4A_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ww/rsp5/wwp domain:bacterial transferase hexapeptide <b>PDBTitle:</b> crystal structure of ww/rsp5/wwp domain: bacterial transferase2 hexapeptide repeat: serine o-acetyltransferase from brucella3 melitensis
65	<a href="#">c5vmkB_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein glmu; <b>PDBTitle:</b> crystal structure of a bifunctional glmu udp-n-acetylglucosamine2 diphosphorylase/glucosamine-1- phosphate n-acetyltransferase from3 acinetobacter baumannii
66	<a href="#">c1qreA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> carbonic anhydrase; <b>PDBTitle:</b> a closer look at the active site of gamma-carbonic anhydrases: high2 resolution crystallographic studies of the carbonic anhydrase from3 methanosarcina thermophila
67	<a href="#">d1qrea_</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> gamma-carbonic anhydrase-like
68	<a href="#">c3kwcD_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> lyase, protein binding, photosynthesis <b>Chain:</b> D: <b>PDB Molecule:</b> carbon dioxide concentrating mechanism protein; <b>PDBTitle:</b> oxidized, active structure of the beta-carboxysomal gamma-carbonic2 anhydrase, ccmm
69	<a href="#">c4m9cC_</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> bacterial transferase hexapeptide (three repeats) family <b>PDBTitle:</b> weei from acinetobacter baumannii aye
70	<a href="#">c3eg4A_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n- <b>PDBTitle:</b> crystal structure of 2,3,4,5-tetrahydropyridine-2,2 carboxylate n-succinyltransferase from brucella melitensis3 biovar abortus 2308
71	<a href="#">d3tdta_</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> Tetrahydrodipicolinate-N-succinyltransferase, THDP-succinyltransferase, DapD
72	<a href="#">c3tv0A_</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> dynactin subunit 6; <b>PDBTitle:</b> structure of dynactin p27 subunit
73	<a href="#">c6cktA_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n- <b>PDBTitle:</b> crystal structure of 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n-2 succinyltransferase from legionella pneumophila philadelphia 1
74	<a href="#">c3q1xA_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine acetyltransferase; <b>PDBTitle:</b> crystal structure of entamoeba histolytica serine acetyltransferase 12 in complex with l-serine
75	<a href="#">c5b04I_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> translation <b>Chain:</b> I: <b>PDB Molecule:</b> probable translation initiation factor eif-2b subunit <b>PDBTitle:</b> crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
						<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 401aa long hypothetical glucose-1-

76	<a href="#">c2gggA</a>	Alignment	not modelled	99.9	18	phosphate <b>PDBTitle:</b> complex of hypothetical glucose-1-phosphate thymidyltransferase from2 sulfobolus tokodaii
77	<a href="#">c3f1xA</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine acetyltransferase; <b>PDBTitle:</b> three dimensional structure of the serine acetyltransferase from2 bacteroides vulgatus, northeast structural genomics consortium target3 bvr62.
78	<a href="#">d2f9ca1</a>	Alignment	not modelled	99.8	11	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> YdcK-like
79	<a href="#">c3fsyC</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> tetrahydrodipicolinate n-succinyltransferase; <b>PDBTitle:</b> structure of tetrahydrodipicolinate n-succinyltransferase2 (rv1201c;dapd) in complex with succinyl-coa from mycobacterium3 tuberculosis
80	<a href="#">c3kwdA</a>	Alignment	not modelled	99.8	23	<b>PDB header:</b> lyase, protein binding, photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> carbon dioxide concentrating mechanism protein; <b>PDBTitle:</b> inactive truncation of the beta-carboxysomal gamma-carbonic anhydrase,2 ccmm, form 1
81	<a href="#">c3d98A</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein glmu; <b>PDBTitle:</b> crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
82	<a href="#">c6i3mG</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> translation <b>Chain:</b> G: <b>PDB Molecule:</b> translation initiation factor eif-2b subunit epsilon; <b>PDBTitle:</b> eif2b:eif2 complex, phosphorylated on eif2 alpha serine 52.
83	<a href="#">c6jlwJ</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> translation <b>Chain:</b> J: <b>PDB Molecule:</b> translation initiation factor eif-2b subunit epsilon; <b>PDBTitle:</b> eif2 - eif2b complex
84	<a href="#">c2qkxA</a>	Alignment	not modelled	99.6	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein glmu; <b>PDBTitle:</b> n-acetyl glucosamine 1-phosphate uridyltransferase from mycobacterium2 tuberculosis complex with n-acetyl glucosamine 1-phosphate
85	<a href="#">c6ezoJ</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> membrane protein <b>Chain:</b> J: <b>PDB Molecule:</b> human eukaryotic initiation factor eif2b epsilon subunits; <b>PDBTitle:</b> eukaryotic initiation factor eif2b in complex with isrib
86	<a href="#">d1yp2a1</a>	Alignment	not modelled	99.6	20	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> GlmU C-terminal domain-like
87	<a href="#">c2rijA</a>	Alignment	not modelled	99.5	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative 2,3,4,5-tetrahydropyridine-2-carboxylate n- <b>PDBTitle:</b> 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
88	<a href="#">c5b04F</a>	Alignment	not modelled	99.5	20	<b>PDB header:</b> translation <b>Chain:</b> F: <b>PDB Molecule:</b> probable translation initiation factor eif-2b subunit <b>PDBTitle:</b> crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
89	<a href="#">c1yp3C</a>	Alignment	not modelled	99.4	11	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> glucose-1-phosphate adenyltransferase small <b>PDBTitle:</b> crystal structure of potato tuber adp-glucose2 pyrophosphorylase in complex with atp
90	<a href="#">c6ezoF</a>	Alignment	not modelled	99.3	18	<b>PDB header:</b> membrane protein <b>Chain:</b> F: <b>PDB Molecule:</b> translation initiation factor eif-2b subunit gamma; <b>PDBTitle:</b> eukaryotic initiation factor eif2b in complex with isrib
91	<a href="#">c6qq2F</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> translation <b>Chain:</b> F: <b>PDB Molecule:</b> translation initiation factor eif-2b subunit gamma; <b>PDBTitle:</b> structure of eif2b-eif2 (phosphorylated at ser51) complex (model a)
92	<a href="#">c5l6sF</a>	Alignment	not modelled	99.3	13	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> glucose-1-phosphate adenyltransferase; <b>PDBTitle:</b> 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	<a href="#">d1fxja1</a>	Alignment	not modelled	99.2	19	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> GlmU C-terminal domain-like
94	<a href="#">c1fwyA</a>	Alignment	not modelled	99.1	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine pyrophosphorylase; <b>PDBTitle:</b> crystal structure of n-acetylglucosamine 1-phosphate2 uridyltransferase bound to udp-glnac
95	<a href="#">c3brkX</a>	Alignment	not modelled	99.1	12	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> glucose-1-phosphate adenyltransferase; <b>PDBTitle:</b> crystal structure of adp-glucose pyrophosphorylase from agrobacterium2 tumefaciens
96	<a href="#">c5yysC</a>	Alignment	not modelled	32.3	19	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> l-fucokinase, l-fucose-1-p guanylyltransferase; <b>PDBTitle:</b> cryo-em structure of l-fucokinase, gdp-fucose pyrophosphorylase (fkp)2 in bacteroides fragilis
97	<a href="#">c2n3dA</a>	Alignment	not modelled	25.6	13	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> bactofilin a; <b>PDBTitle:</b> atomic structure of the cytoskeletal bactofilin bac revealed by2 solid-state nmr
98	<a href="#">d2icya1</a>	Alignment	not modelled	22.2	18	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> GlmU C-terminal domain-like

99 [c4v1ao\\_](#)

Alignment

not modelled

14.9

36

**PDB header:**ribosome  
**Chain:** O: **PDB Molecule:**  
**PDBTitle:** structure of the large subunit of the mammalian mitoribosome, part 22 of 2