



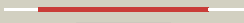
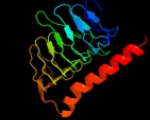









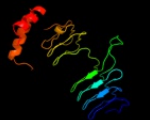



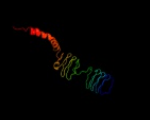



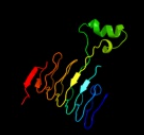






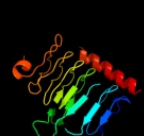


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3r3rA_</a>	 Alignment		100.0	88	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ferripyochelin binding protein; <b>PDBTitle:</b> structure of the yrdA ferripyochelin binding protein from salmonella2 enterica
2	<a href="#">c3r1wA_</a>	 Alignment		100.0	57	<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
3	<a href="#">d1v3wa_</a>	 Alignment		100.0	37	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> gamma-carbonic anhydrase-like
4	<a href="#">c3ixcA_</a>	 Alignment		100.0	41	<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
5	<a href="#">d1xhda_</a>	 Alignment		100.0	40	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> gamma-carbonic anhydrase-like
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="#">d2jf2a1</a>	 Alignment		99.9	18	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> UDP N-acetylglucosamine acyltransferase
8	<a href="#">d1j2za_</a>	 Alignment		99.9	20	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> UDP N-acetylglucosamine acyltransferase
9	<a href="#">c3r0sA_</a>	 Alignment		99.9	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
10	<a href="#">c2iu9C_</a>	 Alignment		99.9	22	<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)
11	<a href="#">c3pmoA_</a>	 Alignment		99.9	19	<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

12	<a href="#">d1krra_</a>	Alignment		99.9	23	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> Galactoside acetyltransferase-like
13	<a href="#">c3ectaA_</a>	Alignment		99.9	20	<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
14	<a href="#">c3eh0C_</a>	Alignment		99.9	20	<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
15	<a href="#">c3fttA_</a>	Alignment		99.9	22	<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-acetyltransferase2 from staphylococcus aureus
16	<a href="#">c3srtB_</a>	Alignment		99.9	21	<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
17	<a href="#">c3cj8B_</a>	Alignment		99.9	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 2,3,4,5-tetrahydropyridine-2-carboxylate n- <b>PDBTitle:</b> crystal structure of 2,3,4,5-tetrahydropyridine-2-carboxylate n-2 succinyltransferase from enterococcus faecalis v583
18	<a href="#">c2ic7A_</a>	Alignment		99.9	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> maltose transacetylase; <b>PDBTitle:</b> crystal structure of maltose transacetylase from2 geobacillus kaustophilus
19	<a href="#">c1qreA_</a>	Alignment		99.9	19	<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
20	<a href="#">d1qrea_</a>	Alignment		99.9	19	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> gamma-carbonic anhydrase-like
21	<a href="#">c3mqhD_</a>	Alignment	not modelled	99.9	21	<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 w1bb from bordetella2 petrii in complex with coa and udp-3-amino-2-acetamido-2,3-dideoxy3 glucuronic acid
22	<a href="#">d1mr7a_</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> Galactoside acetyltransferase-like
23	<a href="#">c3jqyB_</a>	Alignment	not modelled	99.9	21	<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
24	<a href="#">d1g97a1</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> Gl mU C-terminal domain-like
25	<a href="#">c3kwdA_</a>	Alignment	not modelled	99.9	24	<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 ccmh, form 1
26	<a href="#">c3eevC_</a>	Alignment	not modelled	99.9	18	<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
27	<a href="#">d1ocxa_</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> Galactoside acetyltransferase-like
28	<a href="#">d1xata_</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> Galactoside acetyltransferase-like
29	<a href="#">c3fsbB</a>	Alignment	not modelled	99.9	24	<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
30	<a href="#">c3c8vA</a>	Alignment	not modelled	99.9	14	<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
31	<a href="#">c2wlgA</a>	Alignment	not modelled	99.8	27	<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
32	<a href="#">d2oi6a1</a>	Alignment	not modelled	99.8	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
33	<a href="#">d3bswa1</a>	Alignment	not modelled	99.8	21	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> PglD-like
34	<a href="#">c1hm8A</a>	Alignment	not modelled	99.8	21	<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
35	<a href="#">d1t3da</a>	Alignment	not modelled	99.7	25	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> Serine acetyltransferase
36	<a href="#">c2oi6A</a>	Alignment	not modelled	99.7	23	<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-glcna, coa and glcn-1-po4
37	<a href="#">c1t3dB</a>	Alignment	not modelled	99.7	26	<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
38	<a href="#">c2v0hA</a>	Alignment	not modelled	99.7	25	<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)
39	<a href="#">d1ssqa</a>	Alignment	not modelled	99.7	24	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> Serine acetyltransferase
40	<a href="#">c3mc4A</a>	Alignment	not modelled	99.7	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ww/rsp5/wwp domain:bacterial transferase <b>PDBTitle:</b> crystal structure of ww/rsp5/wwp domain: bacterial2 transferase hexapeptide repeat: serine o-acetyltransferase3 from brucella melitensis
41	<a href="#">d3tdta</a>	Alignment	not modelled	99.7	19	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> Tetrahydroadipicinate-N-succinyltransferase, THDP-succinyltransferase, DapD
42	<a href="#">c3eg4A</a>	Alignment	not modelled	99.6	18	<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
43	<a href="#">c3q1xA</a>	Alignment	not modelled	99.5	23	<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
44	<a href="#">c3d98A</a>	Alignment	not modelled	99.5	16	<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
45	<a href="#">c3f1xA</a>	Alignment	not modelled	99.5	19	<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.
46	<a href="#">d2f9ca1</a>	Alignment	not modelled	99.4	19	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> Ydck-like
47	<a href="#">c2qkxA</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein glmu; <b>PDBTitle:</b> n-acetyl glucosamine 1-phosphate uridylyltransferase from mycobacterium2 tuberculosis complex with n-acetyl glucosamine 1-phosphate
48	<a href="#">c3fsyC</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> tetrahydroadipicinate n-succinyltransferase; <b>PDBTitle:</b> structure of tetrahydroadipicinate n-succinyltransferase2 (rv1201c;dapd) in complex with succinyl-coa from mycobacterium3 tuberculosis
49	<a href="#">d1yp2a1</a>	Alignment	not modelled	99.3	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
50	<a href="#">c2gggA</a>	Alignment	not modelled	99.2	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 401aa long hypothetical glucose-1-phosphate <b>PDBTitle:</b> complex of hypothetical glucose-1-phosphate thymidyltransferase from2 sulfolobus tokodaii
						<b>PDB header:</b> transferase

51	<a href="#">c1yp3C_</a>	Alignment	not modelled	99.1	16	<b>Chain:</b> C: <b>PDB Molecule:</b> glucose-1-phosphate adenylyltransferase small <b>PDBTitle:</b> crystal structure of potato tuber adp-glucose2 pyrophosphorylase in complex with atp
52	<a href="#">c1fwyA_</a>	Alignment	not modelled	98.6	25	<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 uridylyltransferase bound to udp-glcna
53	<a href="#">c2rijA_</a>	Alignment	not modelled	98.5	18	<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
54	<a href="#">d1fxja1</a>	Alignment	not modelled	98.5	25	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> GlmU C-terminal domain-like
55	<a href="#">c3brkX_</a>	Alignment	not modelled	98.2	12	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> glucose-1-phosphate adenylyltransferase; <b>PDBTitle:</b> crystal structure of adp-glucose pyrophosphorylase from2 agrobacterium tumefaciens
56	<a href="#">d1k3xa1</a>	Alignment	not modelled	16.4	6	<b>Fold:</b> S13-like H2TH domain <b>Superfamily:</b> S13-like H2TH domain <b>Family:</b> Middle domain of MutM-like DNA repair proteins
57	<a href="#">c2veaA_</a>	Alignment	not modelled	14.1	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phytochrome-like protein cph1; <b>PDBTitle:</b> the complete sensory module of the cyanobacterial2 phytochrome cph1 in the pr-state.
58	<a href="#">d1ee8a1</a>	Alignment	not modelled	13.3	26	<b>Fold:</b> S13-like H2TH domain <b>Superfamily:</b> S13-like H2TH domain <b>Family:</b> Middle domain of MutM-like DNA repair proteins
59	<a href="#">d1r2za1</a>	Alignment	not modelled	11.4	16	<b>Fold:</b> S13-like H2TH domain <b>Superfamily:</b> S13-like H2TH domain <b>Family:</b> Middle domain of MutM-like DNA repair proteins
60	<a href="#">d1k82a1</a>	Alignment	not modelled	11.1	19	<b>Fold:</b> S13-like H2TH domain <b>Superfamily:</b> S13-like H2TH domain <b>Family:</b> Middle domain of MutM-like DNA repair proteins
61	<a href="#">d1tdza1</a>	Alignment	not modelled	11.1	16	<b>Fold:</b> S13-like H2TH domain <b>Superfamily:</b> S13-like H2TH domain <b>Family:</b> Middle domain of MutM-like DNA repair proteins
62	<a href="#">d2icya1</a>	Alignment	not modelled	10.9	22	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> GlmU C-terminal domain-like
63	<a href="#">c2q0qa_</a>	Alignment	not modelled	9.0	4	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> at5g39720.1 protein; <b>PDBTitle:</b> solution structure of at5g39720.1 from arabidopsis thaliana
64	<a href="#">c3gueB_</a>	Alignment	not modelled	8.4	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> utp-glucose-1-phosphate uridylyltransferase 2; <b>PDBTitle:</b> crystal structure of udp-glucose phosphorylase from trypanosoma2 brucei, (tb10.389.0330)
65	<a href="#">d3c2wa2</a>	Alignment	not modelled	7.9	15	<b>Fold:</b> Profilin-like <b>Superfamily:</b> GAF domain-like <b>Family:</b> Phytochrome-specific domain
66	<a href="#">c3a46B_</a>	Alignment	not modelled	6.3	27	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> formamidopyrimidine-dna glycosylase; <b>PDBTitle:</b> crystal structure of mvnei1/thf complex
67	<a href="#">d1hyha2</a>	Alignment	not modelled	6.2	24	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
68	<a href="#">c1nnja_</a>	Alignment	not modelled	5.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> formamidopyrimidine-dna glycosylase; <b>PDBTitle:</b> crystal structure complex between the lactococcus lactis fpg and an2 abasic site containing dna
69	<a href="#">d1a5ja1</a>	Alignment	not modelled	5.6	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Myb/SANT domain