



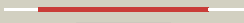




























#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3eh0C_</a>	 Alignment		100.0	100	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> udp-3-o-[3-hydroxymyristoyl] glucosamine n- <b>PDBTitle:</b> crystal structure of lpxd from escherichia coli
2	<a href="#">c3pmoA_</a>	 Alignment		100.0	51	<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
3	<a href="#">c2iu9C_</a>	 Alignment		100.0	33	<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)
4	<a href="#">d1j2za_</a>	 Alignment		100.0	24	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> UDP N-acetylglucosamine acyltransferase
5	<a href="#">c3i3aC_</a>	 Alignment		100.0	22	<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
6	<a href="#">d2jf2a1</a>	 Alignment		100.0	25	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> UDP N-acetylglucosamine acyltransferase
7	<a href="#">c3r0sA_</a>	 Alignment		100.0	28	<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
8	<a href="#">c3fsbB_</a>	 Alignment		100.0	25	<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
9	<a href="#">d2f9ca1</a>	 Alignment		100.0	13	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> YdcK-like
10	<a href="#">c3c8vA_</a>	 Alignment		100.0	15	<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
11	<a href="#">d2oi6a1</a>	 Alignment		100.0	21	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> GlmU C-terminal domain-like

12	<a href="#">dlg97a1</a>	Alignment		100.0	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
13	<a href="#">c3eg4A_</a>	Alignment		100.0	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
14	<a href="#">d3bswa1</a>	Alignment		100.0	22	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> PglD-like
15	<a href="#">d1mr7a_</a>	Alignment		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
16	<a href="#">c1hm8A_</a>	Alignment		100.0	20	<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
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 neuro
18	<a href="#">c3mqhD_</a>	Alignment		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
19	<a href="#">c2wlqA_</a>	Alignment		99.9	21	<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
20	<a href="#">c2v0hA_</a>	Alignment		99.9	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)
21	<a href="#">c3cj8B_</a>	Alignment	not modelled	99.9	22	<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
22	<a href="#">d1qrea_</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> gamma-carbonic anhydrase-like
23	<a href="#">c1qreA_</a>	Alignment	not modelled	99.9	17	<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
24	<a href="#">c3r3rA_</a>	Alignment	not modelled	99.9	19	<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
25	<a href="#">c2oi6A_</a>	Alignment	not modelled	99.9	20	<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
26	<a href="#">d1v3wa_</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> gamma-carbonic anhydrase-like
27	<a href="#">c3ecta_</a>	Alignment	not modelled	99.9	18	<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
						<b>Fold:</b> Single-stranded left-handed beta-helix

28	<a href="#">d1xata_</a>	Alignment	not modelled	99.9	13	<b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> Galactoside acetyltransferase-like
29	<a href="#">c3srtB_</a>	Alignment	not modelled	99.9	26	<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
30	<a href="#">d1krra_</a>	Alignment	not modelled	99.9	24	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> Galactoside acetyltransferase-like
31	<a href="#">c2ic7A_</a>	Alignment	not modelled	99.9	19	<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
32	<a href="#">c3fttA_</a>	Alignment	not modelled	99.9	32	<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
33	<a href="#">c3eevC_</a>	Alignment	not modelled	99.9	16	<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
34	<a href="#">d1xhda_</a>	Alignment	not modelled	99.9	25	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> gamma-carbonic anhydrase-like
35	<a href="#">d3tdta_</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> Tetrahydronicotinamide-N-succinyltransferase, THDP-succinyltransferase, DapD
36	<a href="#">d1ocxa_</a>	Alignment	not modelled	99.9	26	<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="#">c3rlwA_</a>	Alignment	not modelled	99.9	25	<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
38	<a href="#">c3ixcA_</a>	Alignment	not modelled	99.9	17	<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
39	<a href="#">d1t3da_</a>	Alignment	not modelled	99.9	26	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> Serine acetyltransferase
40	<a href="#">c1t3dB_</a>	Alignment	not modelled	99.9	28	<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
41	<a href="#">d1ssqa_</a>	Alignment	not modelled	99.8	24	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> Serine acetyltransferase
42	<a href="#">c2gggA_</a>	Alignment	not modelled	99.8	21	<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
43	<a href="#">c3mc4A_</a>	Alignment	not modelled	99.8	20	<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
44	<a href="#">c3q1xA_</a>	Alignment	not modelled	99.8	19	<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
45	<a href="#">c3kwdA_</a>	Alignment	not modelled	99.8	22	<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
46	<a href="#">c3f1xA_</a>	Alignment	not modelled	99.7	20	<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.
47	<a href="#">c3d98A_</a>	Alignment	not modelled	99.7	14	<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
48	<a href="#">c3fsyC_</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> tetrahydronicotinamide n-succinyltransferase; <b>PDBTitle:</b> structure of tetrahydronicotinamide n-succinyltransferase2 (rv1201c;dapd) in complex with succinyl-coa from mycobacterium3 tuberculosis
49	<a href="#">c2qkxA_</a>	Alignment	not modelled	99.7	14	<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
50	<a href="#">d1yp2a1</a>	Alignment	not modelled	99.6	16	<b>Fold:</b> Single-stranded left-handed beta-helix <b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> GlM U C-terminal domain-like
51	<a href="#">c1yp3C_</a>	Alignment	not modelled	99.4	16	<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
						<b>Fold:</b> Single-stranded left-handed beta-helix

52	<a href="#">d1fxja1</a>	Alignment	not modelled	99.3	31	<b>Superfamily:</b> Trimeric LpxA-like enzymes <b>Family:</b> GlmU C-terminal domain-like
53	<a href="#">c2rijA</a>	Alignment	not modelled	99.3	16	<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="#">c1fwyA</a>	Alignment	not modelled	99.2	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-glcnac
55	<a href="#">c3brkX</a>	Alignment	not modelled	99.0	14	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> glucose-1-phosphate adenyllyltransferase; <b>PDBTitle:</b> crystal structure of adp-glucose pyrophosphorylase from2 agrobacterium tumefaciens
56	<a href="#">d1gg4a3</a>	Alignment	not modelled	98.6	22	<b>Fold:</b> MurF and HprK N-domain-like <b>Superfamily:</b> MurE/MurF N-terminal domain <b>Family:</b> MurE/MurF N-terminal domain
57	<a href="#">c2wtzC</a>	Alignment	not modelled	98.1	24	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> udp-n-acetylmuramoyl-l-alanyl-d-glutamate- <b>PDBTitle:</b> mure ligase of mycobacterium tuberculosis
58	<a href="#">c1gg4A</a>	Alignment	not modelled	98.0	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramoylalanyl-d-glutamyl-2,6- <b>PDBTitle:</b> crystal structure of escherichia coli udpmurnac-tripeptide2 d-alanyl-d-alanine-adding enzyme (murf) at 2.3 angstrom3 resolution
59	<a href="#">c2am1A</a>	Alignment	not modelled	97.7	11	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramoylalanine-d-glutamyl-lysine-d-alanyl-d- <b>PDBTitle:</b> sp protein ligand 1
60	<a href="#">d1e8ca1</a>	Alignment	not modelled	96.4	9	<b>Fold:</b> MurF and HprK N-domain-like <b>Superfamily:</b> MurE/MurF N-terminal domain <b>Family:</b> MurE/MurF N-terminal domain
61	<a href="#">c1e8cB</a>	Alignment	not modelled	95.1	10	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-n-acetylmuramoylalanyl-d-glutamate--2,6- <b>PDBTitle:</b> structure of mure the udp-n-acetylmuramyl tripeptide2 synthetase from e. coli
62	<a href="#">c1cosC</a>	Alignment	not modelled	73.0	24	<b>PDB header:</b> alpha-helical bundle <b>Chain:</b> C: <b>PDB Molecule:</b> coiled serine; <b>PDBTitle:</b> crystal structure of a synthetic triple-stranded alpha-2 helical bundle
63	<a href="#">c1cosA</a>	Alignment	not modelled	69.1	24	<b>PDB header:</b> alpha-helical bundle <b>Chain:</b> A: <b>PDB Molecule:</b> coiled serine; <b>PDBTitle:</b> crystal structure of a synthetic triple-stranded alpha-2 helical bundle
64	<a href="#">c1cosB</a>	Alignment	not modelled	69.1	24	<b>PDB header:</b> alpha-helical bundle <b>Chain:</b> B: <b>PDB Molecule:</b> coiled serine; <b>PDBTitle:</b> crystal structure of a synthetic triple-stranded alpha-2 helical bundle
65	<a href="#">c3ci9B</a>	Alignment	not modelled	57.1	35	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> heat shock factor-binding protein 1; <b>PDBTitle:</b> crystal structure of the human hsbp1
66	<a href="#">c1by0A</a>	Alignment	not modelled	53.4	14	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein (hepatitis delta antigen); <b>PDBTitle:</b> n-terminal leucine-repeat region of hepatitis delta antigen
67	<a href="#">c2jgoA</a>	Alignment	not modelled	48.2	24	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> coil ser 19c; <b>PDBTitle:</b> structure of the arsenated de novo designed peptide coil ser2 19c
68	<a href="#">c2jgoC</a>	Alignment	not modelled	48.2	24	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> coil ser 19c; <b>PDBTitle:</b> structure of the arsenated de novo designed peptide coil ser2 19c
69	<a href="#">c3ljmC</a>	Alignment	not modelled	48.2	24	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> coil ser 19c; <b>PDBTitle:</b> structure of de novo designed apo peptide coil ser 19c
70	<a href="#">c2jgoB</a>	Alignment	not modelled	48.2	24	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> coil ser 19c; <b>PDBTitle:</b> structure of the arsenated de novo designed peptide coil ser2 19c
71	<a href="#">c3ljmA</a>	Alignment	not modelled	48.2	24	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> coil ser 19c; <b>PDBTitle:</b> structure of de novo designed apo peptide coil ser 19c
72	<a href="#">c3ljmB</a>	Alignment	not modelled	48.2	24	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> coil ser 19c; <b>PDBTitle:</b> structure of de novo designed apo peptide coil ser 19c
73	<a href="#">c1coiA</a>	Alignment	not modelled	42.0	24	<b>PDB header:</b> alpha-helical bundle <b>Chain:</b> A: <b>PDB Molecule:</b> coil-vald; <b>PDBTitle:</b> designed trimeric coiled coil-vald
74	<a href="#">d1lcda</a>	Alignment	not modelled	41.7	29	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
75	<a href="#">c3gw6F</a>	Alignment	not modelled	41.4	17	<b>PDB header:</b> chaperone <b>Chain:</b> F: <b>PDB Molecule:</b> endo-n-acetylneuraminidase; <b>PDBTitle:</b> intramolecular chaperone
76	<a href="#">c2nydB</a>	Alignment	not modelled	40.1	20	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> upf0135 protein sa1388; <b>PDBTitle:</b> crystal structure of staphylococcus aureus hypothetical protein sa1388

77	<a href="#">c1a92B_</a>	Alignment	not modelled	33.3	14	<b>PDB header:</b> leucine zipper <b>Chain:</b> B: <b>PDB Molecule:</b> delta antigen; <b>PDBTitle:</b> oligomerization domain of hepatitis delta antigen
78	<a href="#">c2x6pA_</a>	Alignment	not modelled	29.0	20	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> coil ser l19c; <b>PDBTitle:</b> crystal structure of coil ser l19c
79	<a href="#">c2x6pC_</a>	Alignment	not modelled	29.0	20	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> coil ser l19c; <b>PDBTitle:</b> crystal structure of coil ser l19c
80	<a href="#">c2x6pB_</a>	Alignment	not modelled	29.0	20	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> coil ser l19c; <b>PDBTitle:</b> crystal structure of coil ser l19c
81	<a href="#">c1lq7A_</a>	Alignment	not modelled	28.9	21	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> alpha3w; <b>PDBTitle:</b> de novo designed protein model of radical enzymes
82	<a href="#">c1aq5C_</a>	Alignment	not modelled	28.6	29	<b>PDB header:</b> coiled-coil <b>Chain:</b> C: <b>PDB Molecule:</b> cartilage matrix protein; <b>PDBTitle:</b> high-resolution solution nmr structure of the trimeric coiled-coil2 domain of chicken cartilage matrix protein, 20 structures
83	<a href="#">d2bjca1</a>	Alignment	not modelled	27.5	29	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
84	<a href="#">d2ioja1</a>	Alignment	not modelled	27.2	8	<b>Fold:</b> MurF and HprK N-domain-like <b>Superfamily:</b> HprK N-terminal domain-like <b>Family:</b> DRTGG domain
85	<a href="#">c1zvva_</a>	Alignment	not modelled	21.4	23	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-resistance amylase regulator; <b>PDBTitle:</b> crystal structure of a ccpa-crh-dna complex
86	<a href="#">c2wq1A_</a>	Alignment	not modelled	17.5	42	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4 leucine zipper mutant with three ixnbt motifs2 coordinating bromide
87	<a href="#">c2wq3A_</a>	Alignment	not modelled	17.5	42	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4 leucine zipper mutant with three ixnbt motifs2 coordinating chloride and nitrate
88	<a href="#">c2ergA_</a>	Alignment	not modelled	16.6	25	<b>PDB header:</b> transcription activator/dna <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein leu3; <b>PDBTitle:</b> crystal structure of leu3 dna-binding domain with a single2 h50c mutation complexed with a 15mer dna duplex
89	<a href="#">d2hh6a1</a>	Alignment	not modelled	16.6	11	<b>Fold:</b> Left-handed superhelix <b>Superfamily:</b> BH3980-like <b>Family:</b> BH3980-like
90	<a href="#">c2cwoD_</a>	Alignment	not modelled	15.5	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> rna silencing suppressor; <b>PDBTitle:</b> crystal structure of rna silencing suppressor p21 from beet yellows2 virus
91	<a href="#">d2o3la1</a>	Alignment	not modelled	15.0	15	<b>Fold:</b> Left-handed superhelix <b>Superfamily:</b> BH3980-like <b>Family:</b> BH3980-like
92	<a href="#">c1dipA_</a>	Alignment	not modelled	14.3	16	<b>PDB header:</b> acetylation <b>Chain:</b> A: <b>PDB Molecule:</b> delta-sleep-inducing peptide immunoreactive <b>PDBTitle:</b> the solution structure of porcine delta-sleep-inducing2 peptide immunoreactive peptide, nmr, 10 structures
93	<a href="#">c2xzfA_</a>	Alignment	not modelled	14.2	17	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> immunoglobulin-binding protein eibd; <b>PDBTitle:</b> escherichia coli immunoglobulin-binding protein eibd 391-438 fused2 to gcn4 adaptors
94	<a href="#">c1ry3A_</a>	Alignment	not modelled	14.1	15	<b>PDB header:</b> antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> bacteriocin carnobacteriocin b2; <b>PDBTitle:</b> nmr solution structure of the precursor for2 carnobacteriocin b2, an antimicrobial peptide from3 carnobacterium piscicola
95	<a href="#">c1ce0B_</a>	Alignment	not modelled	13.8	29	<b>PDB header:</b> hiv-1 envelope protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein (leucine zipper model h38-p1); <b>PDBTitle:</b> trimerization specificity in hiv-1 gp41: analysis with a2 gcn4 leucine zipper model
96	<a href="#">c2ccfA_</a>	Alignment	not modelled	12.2	33	<b>PDB header:</b> four helix bundle <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> antiparallel configuration of pli e20s
97	<a href="#">c1u9fa_</a>	Alignment	not modelled	12.2	33	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> heterocyclic peptide backbone modification in gcn4-pli based coiled2 coils: replacement of k(15)l(16)
98	<a href="#">c2wpzA_</a>	Alignment	not modelled	11.6	50	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4 leucine zipper mutant with two vxxnxxx motifs2 coordinating chloride
99	<a href="#">c1unwb_</a>	Alignment	not modelled	11.6	33	<b>PDB header:</b> four helix bundle <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> structure based engineering of internal molecular surfaces2 of four helix bundles