

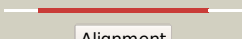

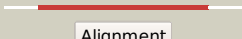



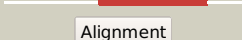
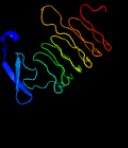

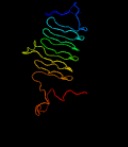
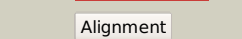
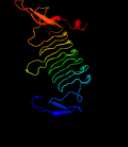
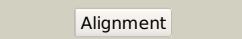

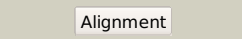

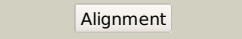
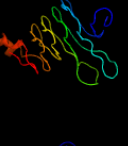
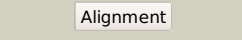
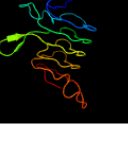


Phyre2

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|---------------|-------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD1201c_(-)_1344222_1345175 |
| Date | Wed Jul 31 22:05:29 BST 2019 |
| Unique Job ID | afbd63abadc97b31 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|---|
| 1 | c3fsyC_ |  Alignment |  | 100.0 | 100 | 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 |
| 2 | c2rijA_ |  Alignment |  | 100.0 | 40 | PDB header: transferase Chain: A: PDB Molecule: putative 2,3,4,5-tetrahydropyridine-2-carboxylate n- PDBTitle: crystal structure of a putative 2,3,4,5-tetrahydropyridine-2-2 carboxylate n-succinyltransferase (cj1605c, dapd) from campylobacter3 jejuni at 1.90 a resolution |
| 3 | c3r5dA_ |  Alignment |  | 100.0 | 49 | PDB header: transferase Chain: A: PDB Molecule: tetrahydrodipicolinate n-succinyltransferase; PDBTitle: pseudomonas aeruginosa dapd (pa3666) apoprotein |
| 4 | c5e3pA_ |  Alignment |  | 100.0 | 68 | PDB header: transferase Chain: A: PDB Molecule: 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n- PDBTitle: crystal strcuture of dapd from corynebacterium glutamicum |
| 5 | c3eg4A_ |  Alignment |  | 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 brucella melitensis3 biovar abortus 2308 |
| 6 | d3tdta_ |  Alignment |  | 99.9 | 25 | Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Tetrahydrodipicolinate-N-succinyltransferase, THDP-succinyltransferase, DapD |
| 7 | c6cktA_ |  Alignment |  | 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 |
| 8 | d1t3da_ |  Alignment |  | 99.9 | 18 | Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Serine acetyltransferase |
| 9 | c1t3dB_ |  Alignment |  | 99.9 | 18 | PDB header: transferase Chain: B: PDB Molecule: serine acetyltransferase; PDBTitle: crystal structure of serine acetyltransferase from e.coli at 2.2a |
| 10 | d1ssqa_ |  Alignment |  | 99.9 | 18 | Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Serine acetyltransferase |
| 11 | c4n6bB_ |  Alignment |  | 99.8 | 22 | PDB header: transferase Chain: B: PDB Molecule: serine acetyltransferase apoenzyme; PDBTitle: soybean serine acetyltransferase complexed with coa |

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|----|-------------------------|-----------|--------------|------|----|---|
| 12 | c3mc4A_ | Alignment | | 99.8 | 23 | 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 |
| 13 | c3q1xA_ | Alignment | | 99.8 | 14 | PDB header: transferase Chain: A: PDB Molecule: serine acetyltransferase; PDBTitle: crystal structure of entamoeba histolytica serine acetyltransferase 12 in complex with l-serine |
| 14 | c3cj8B_ | Alignment | | 99.8 | 19 | PDB header: transferase Chain: B: PDB Molecule: 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n- PDBTitle: crystal structure of 2,3,4,5-tetrahydropyridine-2-carboxylate n-2 succinyltransferase from enterococcus faecalis v583 |
| 15 | c3f1xA_ | Alignment | | 99.8 | 18 | 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. |
| 16 | d1krra_ | Alignment | | 99.8 | 15 | Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Galactoside acetyltransferase-like |
| 17 | c4mzuG_ | Alignment | | 99.8 | 18 | PDB header: isomerase, transferase Chain: G: PDB Molecule: wxcm-like protein; PDBTitle: crystal structure of fdtd, a bifunctional ketoisomerase/n-2 acetyltransferase from shewanella denitrificans |
| 18 | c2ic7A_ | Alignment | | 99.8 | 17 | PDB header: transferase Chain: A: PDB Molecule: maltose transacetylase; PDBTitle: crystal structure of maltose transacetylase from geobacillus2 kaustophilus |
| 19 | c2iu9C_ | Alignment | | 99.8 | 24 | PDB header: transferase Chain: C: PDB Molecule: udp-3-o-[3-hydroxymyristoyl] glucosamine PDBTitle: chlamydia trachomatis lpxd with 100mm udpglcnaC (complex ii) |
| 20 | c3i3aC_ | Alignment | | 99.8 | 20 | PDB header: transferase Chain: C: PDB Molecule: acyl-[acyl-carrier-protein]-udp-n- PDBTitle: structural basis for the sugar nucleotide and acyl chain2 selectivity of leptospira interrogans lpxa |
| 21 | c3eh0C_ | Alignment | not modelled | 99.8 | 23 | PDB header: transferase Chain: C: PDB Molecule: udp-3-o-[3-hydroxymyristoyl] glucosamine n- PDBTitle: crystal structure of lpxd from escherichia coli |
| 22 | c4m98A_ | Alignment | not modelled | 99.8 | 12 | PDB header: transferase Chain: A: PDB Molecule: pilin glycosylation protein; PDBTitle: acetyltransferase domain of pglb from neisseria gonorrhoeae fa1090 |
| 23 | c3srtB_ | Alignment | not modelled | 99.8 | 20 | PDB header: transferase Chain: B: PDB Molecule: maltose o-acetyltransferase; PDBTitle: the crystal structure of a maltose o-acetyltransferase from2 clostridium difficile 630 |
| 24 | c4e75A_ | Alignment | not modelled | 99.8 | 22 | PDB header: transferase Chain: A: PDB Molecule: udp-3-o-acylglucosamine n-acyltransferase; PDBTitle: structure of lpxd from acinetobacter baumannii at 2.85a resolution2 (p21 form) |
| 25 | c3d8vA_ | Alignment | not modelled | 99.7 | 16 | PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of glmu from mycobacterium tuberculosis2 in complex with uridine-diphosphate-n-acetylglucosamine |
| 26 | c3ectA_ | Alignment | not modelled | 99.7 | 20 | 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 |
| 27 | c5jxxC_ | Alignment | not modelled | 99.7 | 23 | PDB header: transferase Chain: C: PDB Molecule: acyl-[acyl-carrier-protein]-udp-n-acylglucosamine o- PDBTitle: crystal structure of udp-n-acetylglucosamine o-acyltransferase (lpxa)2 from moraxella catarrhalis rh4. |

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|----|-------------------------|-----------|--------------|------|----|---|
| 28 | d2jf2a1 | Alignment | not modelled | 99.7 | 19 | Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: UDP N-acetylglucosamine acyltransferase |
| 29 | c3fttA | Alignment | not modelled | 99.7 | 19 | PDB header: transferase Chain: A: PDB Molecule: putative acetyltransferase sacol2570; PDBTitle: crystal structure of the galactoside o-acetyltransferase from2 staphylococcus aureus |
| 30 | c4r36A | Alignment | not modelled | 99.7 | 21 | PDB header: transferase Chain: A: PDB Molecule: putative acyl-[acyl-carrier-protein]-udp-n- PDBTitle: crystal structure analysis of lpxa, a udp-n-acetylglucosamine2 acyltransferase from bacteroides fragilis 9343 |
| 31 | c4eqyC | Alignment | not modelled | 99.7 | 25 | 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 |
| 32 | c4e6tA | Alignment | not modelled | 99.7 | 17 | 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) |
| 33 | c3r8yD | Alignment | not modelled | 99.7 | 23 | PDB header: transferase Chain: D: PDB Molecule: 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n- PDBTitle: structure of the bacillus anthracis tetrahydropicolinate2 succinyltransferase |
| 34 | d1ocxa | Alignment | not modelled | 99.7 | 13 | Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Galactoside acetyltransferase-like |
| 35 | d1mr7a | Alignment | not modelled | 99.7 | 15 | Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Galactoside acetyltransferase-like |
| 36 | c3c8vA | Alignment | not modelled | 99.7 | 18 | 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 |
| 37 | c5f42B | Alignment | not modelled | 99.7 | 17 | PDB header: transferase Chain: B: PDB Molecule: acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine o- PDBTitle: activity and crystal structure of francisella novicida udp-n-2 acetylglucosamine acyltransferase |
| 38 | c3r0sA | Alignment | not modelled | 99.7 | 19 | PDB header: transferase Chain: A: PDB Molecule: acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine o- PDBTitle: udp-n-acetylglucosamine acyltransferase from campylobacter jejuni |
| 39 | c5dg3D | Alignment | not modelled | 99.7 | 17 | 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)-glcnaac |
| 40 | c3vbnA | Alignment | not modelled | 99.7 | 12 | PDB header: transferase Chain: A: PDB Molecule: galactoside o-acetyltransferase; PDBTitle: crystal structure of the d94a mutant of antd, an n-acyltransferase2 from bacillus cereus in complex with dtdp and coenzyme a |
| 41 | c3jqyB | Alignment | not modelled | 99.7 | 17 | PDB header: transferase Chain: B: PDB Molecule: polysialic acid o-acetyltransferase; PDBTitle: crystal structure of the polysia specific acetyltransferase neuo |
| 42 | d1j2za | Alignment | not modelled | 99.7 | 16 | Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: UDP N-acetylglucosamine acyltransferase |
| 43 | c4ea8A | Alignment | not modelled | 99.7 | 23 | PDB header: transferase Chain: A: PDB Molecule: perosamine n-acetyltransferase; PDBTitle: x-ray crystal structure of perb from caulobacter crescentus in complex2 with coenzyme a and gdp-n-acetylperosamine at 1 angstrom resolution |
| 44 | c3t57A | Alignment | not modelled | 99.7 | 19 | PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine o-acyltransferase domain-containing PDBTitle: activity and crystal structure of arabidopsis udp-n-acetylglucosamine2 acyltransferase |
| 45 | c3pmoA | Alignment | not modelled | 99.7 | 21 | PDB header: transferase Chain: A: PDB Molecule: udp-3-o-[3-hydroxymyristoyl] glucosamine n-acyltransferase; PDBTitle: the structure of lpxd from pseudomonas aeruginosa at 1.3 a resolution |
| 46 | c4e8lC | Alignment | not modelled | 99.7 | 21 | PDB header: transferase Chain: C: PDB Molecule: virginiamycin a acetyltransferase; PDBTitle: crystal structure of streptogramin group a antibiotic2 acetyltransferase vata from staphylococcus aureus |
| 47 | c3foqA | Alignment | not modelled | 99.7 | 15 | PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu1; PDBTitle: crystal structure of n-acetylglucosamine-1-phosphate2 uridylyltransferase (glmu) from mycobacterium tuberculosis in3 a cubic space group. |
| 48 | c3mqhD | Alignment | not modelled | 99.7 | 18 | PDB header: transferase Chain: D: PDB Molecule: lipopolysaccharides biosynthesis acetyltransferase; PDBTitle: crystal structure of the 3-n-acetyl transferase wlbb from bordetella2 petrii in complex with coa and udp-3-amino-2-acetamido-2,3-dideoxy3 glucuronic acid |
| 49 | d3bswa1 | Alignment | not modelled | 99.6 | 22 | Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: PgID-like |
| 50 | c2v0hA | Alignment | not modelled | 99.6 | 21 | PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: characterization of substrate binding and catalysis of the2 |

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|----|-------------------------|-----------|--------------|------|----|---|
| | | | | | | potential antibacterial target n-acetylglucosamine-1-3 phosphate uridylyltransferase (glmu) |
| 51 | c3fsbB | Alignment | not modelled | 99.6 | 19 | 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 thermoanaerobacterium3 thermosaccharolyticum in complex with coa and dtdp-3-amino-4 quinovose |
| 52 | c6mfkA | Alignment | not modelled | 99.6 | 16 | PDB header: transferase Chain: A: PDB Molecule: chloramphenicol acetyltransferase; PDBTitle: crystal structure of chloramphenicol acetyltransferase from2 elizabethkingia anophelis |
| 53 | c2oi6A | Alignment | not modelled | 99.6 | 21 | PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: e. coli glmu- complex with udp-glcnac, coa and glcn-1-po4 |
| 54 | c4aa7A | Alignment | not modelled | 99.6 | 19 | PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: e.coli glmu in complex with an antibacterial inhibitor |
| 55 | c1hm8A | Alignment | not modelled | 99.6 | 18 | 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 |
| 56 | c2wlgA | Alignment | not modelled | 99.6 | 18 | PDB header: transferase Chain: A: PDB Molecule: polysialic acid o-acetyltransferase; PDBTitle: crystallographic analysis of the polysialic acid o-2 acetyltransferase oatwy |
| 57 | d1g97a1 | Alignment | not modelled | 99.6 | 20 | Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: GlmU C-terminal domain-like |
| 58 | c4m9cC | Alignment | not modelled | 99.6 | 22 | PDB header: transferase Chain: C: PDB Molecule: bacterial transferase hexapeptide (three repeats) family PDBTitle: weei from acinetobacter baumannii aye |
| 59 | d1xata | Alignment | not modelled | 99.6 | 16 | Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: Galactoside acetyltransferase-like |
| 60 | c5b04I | Alignment | not modelled | 99.6 | 15 | 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 |
| 61 | c3kwcD | Alignment | not modelled | 99.6 | 16 | 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 |
| 62 | d1v3wa | Alignment | not modelled | 99.5 | 17 | Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: gamma-carbonic anhydrase-like |
| 63 | c5vmkB | Alignment | not modelled | 99.5 | 23 | 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 |
| 64 | d2oi6a1 | Alignment | not modelled | 99.5 | 19 | Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: GlmU C-terminal domain-like |
| 65 | c3eevC | Alignment | not modelled | 99.5 | 12 | PDB header: transferase Chain: C: PDB Molecule: chloramphenicol acetyltransferase; PDBTitle: crystal structure of chloramphenicol acetyltransferase vca0300 from2 vibrio cholerae o1 biovar eltor |
| 66 | d1xhda | Alignment | not modelled | 99.5 | 16 | Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: gamma-carbonic anhydrase-like |
| 67 | c5ux9D | Alignment | not modelled | 99.5 | 17 | PDB header: transferase Chain: D: PDB Molecule: chloramphenicol acetyltransferase; PDBTitle: the crystal structure of chloramphenicol acetyltransferase from vibrio2 fischeri es114 |
| 68 | c4mfgA | Alignment | not modelled | 99.4 | 18 | PDB header: transferase Chain: A: PDB Molecule: putative acyltransferase; PDBTitle: 2.0 angstrom resolution crystal structure of putative carbonic2 anhydrase from clostridium difficile. |
| 69 | c6i3mG | Alignment | not modelled | 99.4 | 20 | PDB header: translation Chain: G: PDB Molecule: translation initiation factor eif-2b subunit epsilon; PDBTitle: eif2b:eif2 complex, phosphorylated on eif2 alpha serine 52. |
| 70 | c3r3rA | Alignment | not modelled | 99.4 | 22 | PDB header: transferase Chain: A: PDB Molecule: ferripyochelin binding protein; PDBTitle: structure of the yrda ferripyochelin binding protein from salmonella2 enterica |
| 71 | c3ixcA | Alignment | not modelled | 99.4 | 14 | PDB header: transferase Chain: A: PDB Molecule: hexapeptide transferase family protein; PDBTitle: crystal structure of hexapeptide transferase family protein from2 anaplasma phagocytophilum |
| 72 | c4n27D | Alignment | not modelled | 99.4 | 19 | PDB header: transferase Chain: D: PDB Molecule: bacterial transferase hexapeptide repeat; PDBTitle: x-ray structure of brucella abortus rica |
| 73 | c5afuU | Alignment | not modelled | 99.4 | 13 | PDB header: motor protein Chain: U: PDB Molecule: dynactin; PDBTitle: cryo-em structure of dynein tail-dynactin-bicd2n complex |
| 74 | c6iveA | Alignment | not modelled | 99.4 | 20 | 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 PDB header: lyase |

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|----|-------------------------|-----------|--------------|------|----|--|
| 75 | c3r1wA_ | Alignment | not modelled | 99.4 | 22 | Chain: A: PDB Molecule: carbonic anhydrase; PDBTitle: crystal structure of a carbonic anhydrase from a crude oil degrading2 psychrophilic library |
| 76 | c3tv0A_ | Alignment | not modelled | 99.3 | 16 | PDB header: structural protein Chain: A: PDB Molecule: dynactin subunit 6; PDBTitle: structure of dynactin p27 subunit |
| 77 | d1qrea_ | Alignment | not modelled | 99.3 | 22 | Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: gamma-carbonic anhydrase-like |
| 78 | c1qreA_ | Alignment | not modelled | 99.3 | 22 | 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 | c2ggqA_ | Alignment | not modelled | 99.3 | 15 | PDB header: transferase Chain: A: PDB Molecule: 401aa long hypothetical glucose-1-phosphate PDBTitle: complex of hypothetical glucose-1-phosphate thymidyltransferase from2 sulfobolus tokodaii |
| 80 | c6jlwJ_ | Alignment | not modelled | 99.3 | 17 | PDB header: translation Chain: J: PDB Molecule: translation initiation factor eif-2b subunit epsilon; PDBTitle: eif2 - eif2b complex |
| 81 | c2qkxA_ | Alignment | not modelled | 99.3 | 18 | PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: n-acetyl glucosamine 1-phosphate uridytransferase from mycobacterium2 tuberculosis complex with n-acetyl glucosamine 1-phosphate |
| 82 | c6ezoJ_ | Alignment | not modelled | 99.3 | 17 | PDB header: membrane protein Chain: J: PDB Molecule: human eukaryotic initiation factor eif2b epsilon subunits; PDBTitle: eukaryotic initiation factor eif2b in complex with isrib |
| 83 | c5afuV_ | Alignment | not modelled | 99.2 | 15 | PDB header: motor protein Chain: V: PDB Molecule: dynactin; PDBTitle: cryo-em structure of dynein tail-dynactin-bicd2n complex |
| 84 | c3d98A_ | Alignment | not modelled | 99.2 | 18 | PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form |
| 85 | c5b04F_ | Alignment | not modelled | 99.2 | 18 | 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 |
| 86 | c3kwdA_ | Alignment | not modelled | 99.2 | 14 | 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 |
| 87 | c3brkX_ | Alignment | not modelled | 99.1 | 11 | PDB header: transferase Chain: X: PDB Molecule: glucose-1-phosphate adenyltransferase; PDBTitle: crystal structure of adp-glucose pyrophosphorylase from agrobacterium2 tumefaciens |
| 88 | c5l6sF_ | Alignment | not modelled | 99.0 | 15 | PDB header: transferase Chain: F: PDB Molecule: glucose-1-phosphate adenyltransferase; 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 |
| 89 | c6ezoF_ | Alignment | not modelled | 99.0 | 8 | 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 | c6gq2F_ | Alignment | not modelled | 98.9 | 17 | PDB header: translation Chain: F: PDB Molecule: translation initiation factor eif-2b subunit gamma; PDBTitle: structure of eif2b-eif2 (phosphorylated at ser51) complex (model a) |
| 91 | d2f9ca1 | Alignment | not modelled | 98.9 | 17 | Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: YdcK-like |
| 92 | c1yp3C_ | Alignment | not modelled | 98.9 | 16 | PDB header: transferase Chain: C: PDB Molecule: glucose-1-phosphate adenyltransferase small PDBTitle: crystal structure of potato tuber adp-glucose2 pyrophosphorylase in complex with atp |
| 93 | d1fxja1 | Alignment | not modelled | 98.8 | 23 | Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: GlmU C-terminal domain-like |
| 94 | d1yp2a1 | Alignment | not modelled | 98.8 | 5 | Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: GlmU C-terminal domain-like |
| 95 | c1fwyA_ | Alignment | not modelled | 98.7 | 17 | PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: crystal structure of n-acetylglucosamine 1-phosphate2 uridytransferase bound to udp-glnac |
| 96 | c6djpB_ | Alignment | not modelled | 21.3 | 19 | PDB header: membrane protein Chain: B: PDB Molecule: integrin beta-8; PDBTitle: integrin alpha-v beta-8 in complex with the fabs 8b8 and 68 |
| 97 | c5xynC_ | Alignment | not modelled | 20.1 | 19 | PDB header: dna binding protein Chain: C: PDB Molecule: suppressor of hu sensitivity involved in recombination PDBTitle: the crystal structure of csm2-psy3-shu1-shu2 complex from budding2 yeast |
| 98 | c4um9D_ | Alignment | not modelled | 18.4 | 18 | PDB header: immune system Chain: D: PDB Molecule: integrin beta-6; PDBTitle: crystal structure of alpha v beta 6 with peptide |

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|----|------------------------|-----------|--------------|------|----|--|
| 99 | c2n3dA | Alignment | not modelled | 16.3 | 18 | PDB header: structural protein Chain: A: PDB Molecule: bactofilin a; PDBTitle: atomic structure of the cytoskeletal bactofilin bac revealed by 2 solid-state nmr |
|----|------------------------|-----------|--------------|------|----|--|