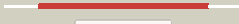























Phyre2

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|---------------|----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0998 (-) _1114752_1115753 |
| Date | Wed Jul 31 22:05:06 BST 2019 |
| Unique Job ID | 15fb315c79e7d46a |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c4avcA_ |  Alignment |  | 100.0 | 97 | PDB header: transferase Chain: A; PDB Molecule: lysine acetyltransferase; PDBTitle: crystal structure of protein lysine acetyltransferase rv09982 in complex with acetyl coa and camp |
| 2 | c4orfA_ |  Alignment |  | 100.0 | 57 | PDB header: transferase Chain: A; PDB Molecule: acetyltransferase pat; PDBTitle: camp-binding acyltransferase from mycobacterium smegmatis, mutant r95k |
| 3 | c5jonA_ |  Alignment |  | 99.9 | 18 | PDB header: transport protein Chain: A; PDB Molecule: maltose-binding periplasmic protein.potassium/sodium PDBTitle: crystal structure of the unliganded form of hcn2 cnbd |
| 4 | c4u5yA_ |  Alignment |  | 99.9 | 34 | PDB header: ligase Chain: A; PDB Molecule: acyl-coa synthetase; PDBTitle: crystal structure of the complex between the gnat domain of s.2 lividans pat and the acetyl-coa synthetase c-terminal domain of s.3 enterica |
| 5 | c4chwB_ |  Alignment |  | 99.9 | 28 | PDB header: transport protein Chain: B; PDB Molecule: cyclic nucleotide-gated potassium channel ml3241; PDBTitle: the electron crystallography structure of the camp-free potassium2 channel ml0k1 |
| 6 | c3gydA_ |  Alignment |  | 99.9 | 23 | PDB header: dna binding protein Chain: A; PDB Molecule: cyclic nucleotide-binding domain; PDBTitle: crystal structure of a cyclic nucleotide-binding domain (mfla_1926)2 from methylobacillus flagellatus kt at 1.79 a resolution |
| 7 | c3j4qC_ |  Alignment |  | 99.9 | 18 | PDB header: transferase Chain: C; PDB Molecule: camp-dependent protein kinase type ii-alpha regulatory PDBTitle: pseudo-atomic model of the akap18-pka complex in a bent conformation2 derived from electron microscopy |
| 8 | c5h3oA_ |  Alignment |  | 99.9 | 22 | PDB header: transport protein Chain: A; PDB Molecule: cyclic nucleotide-gated cation channel; PDBTitle: structure of a eukaryotic cyclic nucleotide-gated channel |
| 9 | d1zyba2 |  Alignment |  | 99.9 | 11 | Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain |
| 10 | c4myiA_ |  Alignment |  | 99.9 | 23 | PDB header: transferase Chain: A; PDB Molecule: cgmp-dependent protein kinase, putative; PDBTitle: crystal structure of pvx_084705 |
| 11 | d1cx4a1 |  Alignment |  | 99.9 | 19 | Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain |

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|----|-------------------------|-----------|--------------|------|----|--|
| 12 | c2pqqD_ | Alignment | | 99.9 | 26 | PDB header: transcription Chain: D: PDB Molecule: putative transcriptional regulator; PDBTitle: structural genomics, the crystal structure of the n-terminal domain of 2 a transcriptional regulator from streptomyces coelicolor a3(2) |
| 13 | c3mdpA_ | Alignment | | 99.9 | 16 | PDB header: nucleotide binding protein Chain: A: PDB Molecule: cyclic nucleotide-binding domain (cnmpbd) protein; PDBTitle: crystal structure of a putative cyclic nucleotide-binding protein2 (gmet_1532) from geobacter metallireducens gs-15 at 1.90 a resolution |
| 14 | d1ne6a2 | Alignment | | 99.9 | 27 | Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain |
| 15 | d1cx4a2 | Alignment | | 99.9 | 22 | Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain |
| 16 | c5v4sB_ | Alignment | | 99.9 | 23 | PDB header: transport protein Chain: B: PDB Molecule: transporter, cation channel family / cyclic nucleotide- PDBTitle: cryoem structure of a prokaryotic cyclic nucleotide-gated ion channel |
| 17 | c5v30B_ | Alignment | | 99.9 | 17 | PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of the sensor domain of the transcriptional2 regulator hcpr from porphyromonas gingivalis |
| 18 | c5k71A_ | Alignment | | 99.9 | 19 | PDB header: metal transport/calcium binding protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily h member 1; PDBTitle: single particle cryo-em structure of the voltage-gated k+ channel eag12 bound to the channel inhibitor calmodulin |
| 19 | c5u6pA_ | Alignment | | 99.9 | 18 | PDB header: transport protein Chain: A: PDB Molecule: potassium/sodium hyperpolarization-activated cyclic PDBTitle: structure of the human hcn1 hyperpolarization-activated cyclic2 nucleotide-gated ion channel in complex with camp |
| 20 | c3idcB_ | Alignment | | 99.9 | 20 | PDB header: transferase Chain: B: PDB Molecule: camp-dependent protein kinase type ii-beta regulatory PDBTitle: crystal structure of (102-265)riib:c holoenzyme of camp-dependent2 protein kinase |
| 21 | c2byvE_ | Alignment | not modelled | 99.9 | 20 | PDB header: regulation Chain: E: PDB Molecule: rap guanine nucleotide exchange factor 4; PDBTitle: structure of the camp responsive exchange factor epac2 in2 its auto-inhibited state |
| 22 | c2ptmA_ | Alignment | not modelled | 99.9 | 18 | PDB header: transport protein Chain: A: PDB Molecule: hyperpolarization-activated (ih) channel; PDBTitle: structure and rearrangements in the carboxy-terminal region of spih2 channels |
| 23 | c5va1A_ | Alignment | not modelled | 99.9 | 20 | PDB header: transport protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily h member 2; PDBTitle: cryo-em structure of the human ether-a-go-go related k+ channel |
| 24 | d1ne6a1 | Alignment | not modelled | 99.8 | 19 | Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain |
| 25 | c5bv6A_ | Alignment | not modelled | 99.8 | 18 | PDB header: transferase Chain: A: PDB Molecule: cgmp-dependent protein kinase 2; PDBTitle: pkg ii's carboxyl terminal cyclic nucleotide binding domain (cnb-b) in2 a complex with cgmp |
| 26 | c5t3nB_ | Alignment | not modelled | 99.8 | 20 | PDB header: transferase Chain: B: PDB Molecule: camp-dependent protein kinase regulatory subunit; PDBTitle: sp-2cl-camps bound to pkar cbd2 |
| 27 | c3pvbB_ | Alignment | not modelled | 99.8 | 20 | PDB header: transferase Chain: B: PDB Molecule: camp-dependent protein kinase type i-alpha regulatory PDBTitle: crystal structure of (73-244)ria:c holoenzyme of camp-dependent2 protein kinase |
| 28 | c6cjtB_ | Alignment | not modelled | 99.8 | 22 | PDB header: transport protein Chain: B: PDB Molecule: sthk cyclic nucleotide-gated potassium channel; PDBTitle: structure of the sthk cyclic nucleotide-gated potassium |

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|----|-------------------------|-----------|--------------|------|--|
| | | | | | channel in2 complex with cgmp PDB header: unknown function Chain: B: PDB Molecule: cyclic nucleotide-binding protein; PDBTitle: structure of cyclic nucleotide-binding-like protein from brucella2 abortus bv. 1 str. 9-941 |
| 29 | c5d1lB_ | Alignment | not modelled | 99.8 | 26 |
| 30 | c3fx3A_ | Alignment | not modelled | 99.8 | 17 |
| 31 | c3cf6E_ | Alignment | not modelled | 99.8 | 23 |
| 32 | c1o7fA_ | Alignment | not modelled | 99.8 | 21 |
| 33 | c2z69A_ | Alignment | not modelled | 99.8 | 20 |
| 34 | c3otfA_ | Alignment | not modelled | 99.8 | 19 |
| 35 | d1wgpA_ | Alignment | not modelled | 99.8 | 15 |
| 36 | c3dn7A_ | Alignment | not modelled | 99.8 | 15 |
| 37 | c5j3uA_ | Alignment | not modelled | 99.8 | 24 |
| 38 | c3ogjD_ | Alignment | not modelled | 99.8 | 21 |
| 39 | c5kbfA_ | Alignment | not modelled | 99.8 | 21 |
| 40 | c1zybA_ | Alignment | not modelled | 99.8 | 11 |
| 41 | c4d7sB_ | Alignment | not modelled | 99.8 | 22 |
| 42 | d2gaua2 | Alignment | not modelled | 99.8 | 15 |
| 43 | d1vp6a_ | Alignment | not modelled | 99.8 | 27 |
| 44 | c4ev0A_ | Alignment | not modelled | 99.8 | 23 |
| 45 | c4f8aA_ | Alignment | not modelled | 99.8 | 20 |
| 46 | d1q3ea_ | Alignment | not modelled | 99.8 | 18 |
| 47 | c5c8wB_ | Alignment | not modelled | 99.8 | 20 |
| 48 | c4dinB_ | Alignment | not modelled | 99.8 | 24 |
| 49 | d3e5ua2 | Alignment | not modelled | 99.8 | 14 |
| 50 | c3uknC_ | Alignment | not modelled | 99.8 | 20 |
| 51 | d1o7fa3 | Alignment | not modelled | 99.8 | 23 |
| 52 | d1o7fa2 | Alignment | not modelled | 99.8 | 20 |
| 53 | c4lloE_ | Alignment | not modelled | 99.8 | 20 |

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|----|-------------------------|-----------|--------------|------|----|---|
| | | | | | | PDBTitle: structure of the eag domain-cnbhd complex of the mouse eag1 channel |
| 54 | c3e97A_ | Alignment | not modelled | 99.8 | 22 | PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, crp/fnr family; PDBTitle: crystal structure of transcriptional regulator of crp/fnr family2 (yp_604437.1) from deinococcus geothermalis dsm 11300 at 1.86 a3 resolution |
| 55 | d1ft9a2 | Alignment | not modelled | 99.8 | 11 | Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: CO-sensing protein CooA, N-terminal domain |
| 56 | c6ftfB_ | Alignment | not modelled | 99.8 | 19 | PDB header: signaling protein Chain: B: PDB Molecule: protein kinase a regulatory subunit, putative; PDBTitle: regulatory subunit of a camp-independent protein kinase a from2 trypanosoma cruzi at 1.09 a resolution |
| 57 | c1rgsA_ | Alignment | not modelled | 99.8 | 34 | PDB header: kinase Chain: A: PDB Molecule: camp dependent protein kinase; PDBTitle: regulatory subunit of camp dependent protein kinase |
| 58 | d2h6ca2 | Alignment | not modelled | 99.8 | 14 | Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain |
| 59 | c3of1A_ | Alignment | not modelled | 99.8 | 27 | PDB header: transferase Chain: A: PDB Molecule: camp-dependent protein kinase regulatory subunit; PDBTitle: crystal structure of bcy1, the yeast regulatory subunit of pka |
| 60 | c3iwzB_ | Alignment | not modelled | 99.8 | 19 | PDB header: transcription Chain: B: PDB Molecule: catabolite activation-like protein; PDBTitle: the c-di-gmp responsive global regulator clp links cell-cell signaling2 to virulence gene expression in xanthomonas campestris |
| 61 | c4kg1A_ | Alignment | not modelled | 99.8 | 25 | PDB header: lyase Chain: A: PDB Molecule: diguanylate cyclase; PDBTitle: cgmp-responsive diguanylate cyclase |
| 62 | c1cx4A_ | Alignment | not modelled | 99.8 | 19 | PDB header: signaling protein Chain: A: PDB Molecule: camp-dependent protein kinase regulatory subunit PDBTitle: crystal structure of a deletion mutant of the type ii beta2 regulatory subunit of camp-dependent protein kinase |
| 63 | c3dv8A_ | Alignment | not modelled | 99.8 | 11 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, crp/fnr family; PDBTitle: crystal structure of a putative transcriptional regulator of the2 crp/fnr family (eubrec_1222) from eubacterium rectale atcc 33656 at3 2.55 a resolution |
| 64 | d1i5za2 | Alignment | not modelled | 99.8 | 22 | Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain |
| 65 | d2oz6a2 | Alignment | not modelled | 99.8 | 22 | Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain |
| 66 | c3shrA_ | Alignment | not modelled | 99.8 | 25 | PDB header: transferase Chain: A: PDB Molecule: cgmp-dependent protein kinase 1; PDBTitle: crystal structure of cgmp-dependent protein kinase reveals novel site2 of interchain communication |
| 67 | c1o51A_ | Alignment | not modelled | 99.8 | 16 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, crp family; PDBTitle: crystal structure of transcriptional regulator (tm1171) from2 thermotoga maritima at 2.30 a resolution |
| 68 | d1o51a1 | Alignment | not modelled | 99.8 | 16 | Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain |
| 69 | c2n7gA_ | Alignment | not modelled | 99.7 | 20 | PDB header: membrane protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily h member 2; PDBTitle: structure of the cyclic nucleotide-binding homology domain of the herg2 channel |
| 70 | c3f8kA_ | Alignment | not modelled | 99.7 | 23 | PDB header: transferase Chain: A: PDB Molecule: protein acetyltransferase; PDBTitle: crystal structure of protein acetyltransferase (pat) from sulfolobus2 solfataricus |
| 71 | c4l11A_ | Alignment | not modelled | 99.7 | 15 | PDB header: metal transport Chain: A: PDB Molecule: agap007709-pa; PDBTitle: structure of the c-linker/cnbhd of agerg channels |
| 72 | c3d3sA_ | Alignment | not modelled | 99.7 | 17 | PDB header: transferase Chain: A: PDB Molecule: l-2,4-diaminobutyric acid acetyltransferase; PDBTitle: crystal structure of l-2,4-diaminobutyric acid acetyltransferase from2 bordetella parapertussis |
| 73 | c5w5aB_ | Alignment | not modelled | 99.7 | 22 | PDB header: transcription Chain: B: PDB Molecule: hth-type transcriptional regulator cmr; PDBTitle: crystal structure of mycobacterium tuberculosis crp-fnr family2 transcription factor cmr (rv1675c) |
| 74 | c3d0sA_ | Alignment | not modelled | 99.7 | 27 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein; PDBTitle: camp receptor protein from m.tuberculosis, camp-free form |
| 75 | c3g8wB_ | Alignment | not modelled | 99.7 | 9 | PDB header: transferase Chain: B: PDB Molecule: lactococcal prophage ps3 protein 05; PDBTitle: crystal structure of a probable acetyltransferase from staphylococcus2 epidermidis atcc 12228 |
| 76 | c3tnqA_ | Alignment | not modelled | 99.7 | 19 | PDB header: transferase Chain: A: PDB Molecule: camp-dependent protein kinase type ii-beta regulatory PDBTitle: structure and allostery of the pka riib tetrameric holoenzyme |
| 77 | c2d93A_ | Alignment | not modelled | 99.7 | 16 | PDB header: signaling protein Chain: A: PDB Molecule: rap guanine nucleotide exchange factor 6; PDBTitle: solution structure of the cnmp_binding domain of human |

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|-----|-------------------------|-----------|--------------|------|----|---|
| | | | | | | rap2 guanine nucleotide exchange factor 6 PDB header: transferase Chain: B: PDB Molecule: ynca; PDBTitle: structure of ynca, a putative acetyltransferase from salmonella2 typhimurium with its cofactor acetyl-coa |
| 78 | c3dr8B_ | Alignment | not modelled | 99.7 | 17 | PDB header: transferase Chain: A: PDB Molecule: putative d-alanine n-acetyltransferase of gnat family; PDBTitle: crystal structure of a putative acetyltransferase of the gnat family2 (dde_3044) from desulfovibrio desulfuricans subsp. at 1.85 a3 resolution |
| 79 | c2r7hA_ | Alignment | not modelled | 99.7 | 17 | Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain |
| 80 | d2coha2 | Alignment | not modelled | 99.7 | 20 | PDB header: transferase Chain: A: PDB Molecule: acetyltransferase; PDBTitle: the human o-glcnacase c-terminal domain is a pseudo histone2 acetyltransferase |
| 81 | c3zj0A_ | Alignment | not modelled | 99.7 | 13 | Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT |
| 82 | d2i6ca1 | Alignment | not modelled | 99.7 | 20 | PDB header: transferase Chain: D: PDB Molecule: phosphinothricin n-acetyltransferase; PDBTitle: crystal structure of streptomyces hygrosopicus biaphos resistance2 (bar) protein in complex with coenzyme a and l-phosphinothricin |
| 83 | c5t7eD_ | Alignment | not modelled | 99.7 | 14 | PDB header: transcription regulator Chain: B: PDB Molecule: dnr protein; PDBTitle: crystal structure of dnr from pseudomonas aeruginosa. |
| 84 | c3dkwB_ | Alignment | not modelled | 99.7 | 22 | PDB header: metal transport Chain: H: PDB Molecule: metal transporter cnm4; PDBTitle: crystal structure of the cnm4 binding domain of the magnesium2 transporter cnm4 |
| 85 | c6g52H_ | Alignment | not modelled | 99.7 | 16 | Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT |
| 86 | d2beia1 | Alignment | not modelled | 99.7 | 19 | PDB header: transcription Chain: A: PDB Molecule: prfa; PDBTitle: prfa-g145s, a constitutive active mutant of the2 transcriptional regulator in l.monocytogenes |
| 87 | c2bgcA_ | Alignment | not modelled | 99.7 | 9 | PDB header: transferase Chain: A: PDB Molecule: probable acetyltransferase; PDBTitle: crystal structure of acetyltransferase from thermus thermophilus hb8 |
| 88 | c3exnA_ | Alignment | not modelled | 99.7 | 20 | Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT |
| 89 | d1yvoa1 | Alignment | not modelled | 99.7 | 15 | Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT |
| 90 | d1s7ka1 | Alignment | not modelled | 99.7 | 15 | Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT |
| 91 | c2vzza_ | Alignment | not modelled | 99.7 | 14 | PDB header: transferase Chain: A: PDB Molecule: rv0802c; PDBTitle: crystal structure of rv0802c from mycobacterium2 tuberculosis in complex with succinyl-coa |
| 92 | c4jxqA_ | Alignment | not modelled | 99.7 | 12 | PDB header: transferase Chain: A: PDB Molecule: acetyltransferase; PDBTitle: crystal structure of a gnat superfamily phosphinothricin2 acetyltransferase (pat) from sinorhizobium meliloti 1021 |
| 93 | c2pswA_ | Alignment | not modelled | 99.7 | 14 | PDB header: transferase Chain: A: PDB Molecule: n-acetyltransferase 13; PDBTitle: human mak3 homolog in complex with coa |
| 94 | c4h89A_ | Alignment | not modelled | 99.7 | 15 | PDB header: transferase Chain: A: PDB Molecule: gcn5-related n-acetyltransferase; PDBTitle: the structure of a gcn5-related n-acetyltransferase from kribbella2 flavida |
| 95 | d1qsmA_ | Alignment | not modelled | 99.7 | 15 | Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT |
| 96 | d2ae6a1 | Alignment | not modelled | 99.7 | 17 | Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT |
| 97 | d1vhsa_ | Alignment | not modelled | 99.6 | 17 | Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT |
| 98 | c2i79B_ | Alignment | not modelled | 99.6 | 14 | PDB header: transferase Chain: B: PDB Molecule: acetyltransferase, gnat family; PDBTitle: the crystal structure of the acetyltransferase of gnat family from2 streptococcus pneumoniae |
| 99 | c5jtfB_ | Alignment | not modelled | 99.6 | 17 | PDB header: transferase Chain: B: PDB Molecule: putative phosphinothricin n-acetyltransferase; PDBTitle: crystal structure of arsn n-acetyltransferase from pseudomonas putida2 kt2440 |
| 100 | d1tiqa_ | Alignment | not modelled | 99.6 | 12 | Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT |
| 101 | c3kccA_ | Alignment | not modelled | 99.6 | 23 | PDB header: transcription Chain: A: PDB Molecule: catabolite gene activator; PDBTitle: crystal structure of d138l mutant of catabolite gene activator protein |
| 102 | c3pp9B_ | Alignment | not modelled | 99.6 | 14 | PDB header: transferase Chain: B: PDB Molecule: putative streptothricin acetyltransferase; PDBTitle: 1.6 angstrom resolution crystal structure of putative streptothricin2 acetyltransferase from bacillus anthracis str. ames in complex with3 acetyl coenzyme a |

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|-----|-------------------------|-----------|--------------|------|----|---|
| 103 | c5e44A_ | Alignment | not modelled | 99.6 | 15 | PDB header: transcription Chain: A: PDB Molecule: fnr regulator; PDBTitle: crystal structure of holo-fnr of a. fischeri |
| 104 | c6c37A_ | Alignment | not modelled | 99.6 | 16 | PDB header: transferase Chain: A: PDB Molecule: acetyltransferase, gnat family protein; PDBTitle: mycobacterium smegmatis rimj in complex with coa-disulfide |
| 105 | c4rfaA_ | Alignment | not modelled | 99.6 | 17 | PDB header: transcription regulator Chain: A: PDB Molecule: lmo0740 protein; PDBTitle: crystal structure of cyclic nucleotide-binding domain containing2 protein from listeria monocytogenes egd-e |
| 106 | c2r1iB_ | Alignment | not modelled | 99.6 | 17 | PDB header: transferase Chain: B: PDB Molecule: gcn5-related n-acetyltransferase; PDBTitle: crystal structure of putative acetyltransferase (yp_831484.1) from2 arthrobacter sp. fb24 at 1.65 a resolution |
| 107 | d1yr0a1 | Alignment | not modelled | 99.6 | 16 | Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT |
| 108 | c5hmnE_ | Alignment | not modelled | 99.6 | 18 | PDB header: transferase Chain: E: PDB Molecule: aac3-i; PDBTitle: crystal structure of an aminoglycoside acetyltransferase hmb0005 from2 an uncultured soil metagenomic sample, unknown active site density3 modeled as polyethylene glycol |
| 109 | c3w6sA_ | Alignment | not modelled | 99.6 | 13 | PDB header: transferase Chain: A: PDB Molecule: mpr1 protein; PDBTitle: yeast n-acetyltransferase mpr1 involved in oxidative stress tolerance2 via proline metabolism |
| 110 | c4mbuB_ | Alignment | not modelled | 99.6 | 15 | PDB header: transferase Chain: B: PDB Molecule: similar to n-acetyltransferase; PDBTitle: crystal structure of n-acetyltransferase from staphylococcus aureus2 mu50 |
| 111 | d1mk4a_ | Alignment | not modelled | 99.6 | 13 | Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT |
| 112 | c3fixA_ | Alignment | not modelled | 99.6 | 11 | PDB header: transferase Chain: A: PDB Molecule: n-acetyltransferase; PDBTitle: crystal structure of a putative n-acetyltransferase (ta0374) from2 thermoplasma acidophilum |
| 113 | c4bmhA_ | Alignment | not modelled | 99.6 | 22 | PDB header: transferase Chain: A: PDB Molecule: acetyltransferase; PDBTitle: crystal structure of sshot |
| 114 | c4e0aB_ | Alignment | not modelled | 99.6 | 18 | PDB header: transferase Chain: B: PDB Molecule: bh1408 protein; PDBTitle: crystal structure of the mutant f44r bh1408 protein from bacillus2 halodurans, northeast structural genomics consortium (nesg) target3 bhr182 |
| 115 | c3c26A_ | Alignment | not modelled | 99.6 | 18 | PDB header: transferase Chain: A: PDB Molecule: putative acetyltransferase ta0821; PDBTitle: crystal structure of a putative acetyltransferase (np_394282.1) from2 thermoplasma acidophilum at 2.00 a resolution |
| 116 | c3e6dA_ | Alignment | not modelled | 99.6 | 16 | PDB header: transcription regulation Chain: A: PDB Molecule: cyclic nucleotide-binding protein; PDBTitle: crystal structure of cprk c200s |
| 117 | d1yk3a1 | Alignment | not modelled | 99.6 | 13 | Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT |
| 118 | c3r95A_ | Alignment | not modelled | 99.6 | 15 | PDB header: transferase Chain: A: PDB Molecule: mcce protein; PDBTitle: crystal structure of microcin c7 self immunity acetyltransferase mcce2 in complex with acetyl-coa |
| 119 | c3eo4A_ | Alignment | not modelled | 99.6 | 10 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein mj1062; PDBTitle: the crystal structure of a domain from methanocaldococcus jannaschii2 dsm 2661 |
| 120 | c4ubrA_ | Alignment | not modelled | 99.6 | 12 | PDB header: transferase Chain: A: PDB Molecule: putative acetyltransferase; PDBTitle: crystal structure of pseudomonas aeruginosa n-acetyltransferase pa4534 |