

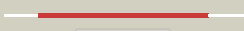














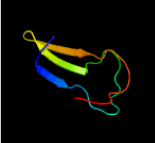

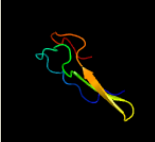

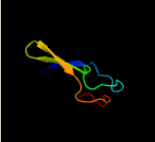


Phyre2

| | |
|---------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD1826_(gcvH)_2071959_2072363 |
| Date | Fri Aug 2 13:30:43 BST 2019 |
| Unique Job ID | 1a54f9e99388682e |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|---|
| 1 | c3iftA_ |  Alignment |  | 100.0 | 100 | PDB header: oxidoreductase Chain: A: PDB Molecule: glycine cleavage system h protein; PDBTitle: crystal structure of glycine cleavage system protein h from2 mycobacterium tuberculosis, using x-rays from the compact light3 source. |
| 2 | c2edgA_ |  Alignment |  | 100.0 | 42 | PDB header: biosynthetic protein Chain: A: PDB Molecule: glycine cleavage system h protein; PDBTitle: solution structure of the gcv_h domain from mouse glycine |
| 3 | c3a8jF_ |  Alignment |  | 100.0 | 48 | PDB header: transferase/transport protein Chain: F: PDB Molecule: glycine cleavage system h protein; PDBTitle: crystal structure of et-ehred complex |
| 4 | d1onla_ |  Alignment |  | 100.0 | 54 | Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains |
| 5 | d1hpca_ |  Alignment |  | 100.0 | 48 | Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains |
| 6 | c2ka7A_ |  Alignment |  | 100.0 | 45 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: glycine cleavage system h protein; PDBTitle: nmr solution structure of tm0212 at 40 c |
| 7 | c3mxuA_ |  Alignment |  | 100.0 | 44 | PDB header: oxidoreductase Chain: A: PDB Molecule: glycine cleavage system h protein; PDBTitle: crystal structure of glycine cleavage system protein h from bartonella2 henselae |
| 8 | c5a35A_ |  Alignment |  | 100.0 | 24 | PDB header: transport protein Chain: A: PDB Molecule: glycine cleavage system h protein; PDBTitle: crystal structure of glycine cleavage protein h-like (gcvh-l)2 from streptococcus pyogenes |
| 9 | c5ks8D_ |  Alignment |  | 97.9 | 30 | PDB header: ligase Chain: D: PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus |
| 10 | c2b8gA_ |  Alignment |  | 97.9 | 30 | PDB header: biosynthetic protein Chain: A: PDB Molecule: biotin/lipoyl attachment protein; PDBTitle: solution structure of bacillus subtilis blap biotinylated-2 form (energy minimized mean structure) |
| 11 | d1dcza_ |  Alignment |  | 97.8 | 34 | Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|--|
| 12 | c3n6rK_ | Alignment | | 97.8 | 30 | PDB header: ligase Chain: K: PDB Molecule: propionyl-coa carboxylase, alpha subunit; PDBTitle: crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc) |
| 13 | c5ks8F_ | Alignment | | 97.8 | 30 | PDB header: ligase Chain: F: PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus |
| 14 | d1k8ma_ | Alignment | | 97.8 | 24 | Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains |
| 15 | d1bdoa_ | Alignment | | 97.7 | 29 | Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains |
| 16 | c2ejmA_ | Alignment | | 97.7 | 25 | PDB header: ligase Chain: A: PDB Molecule: methylcrotonoyl-coa carboxylase subunit alpha; PDBTitle: solution structure of ruh-072, an apo-biotnly domain form2 human acetyl coenzyme a carboxylase |
| 17 | c3bg5B_ | Alignment | | 97.7 | 28 | PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate carboxylase |
| 18 | c3hblA_ | Alignment | | 97.7 | 28 | PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of s. aureus pyruvate carboxylase t908a mutant |
| 19 | c5vz0D_ | Alignment | | 97.7 | 22 | PDB header: ligase Chain: D: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of lactococcus lactis pyruvate carboxylase g746a2 mutant in complex with cyclic-di-amp |
| 20 | c4hnbB_ | Alignment | | 97.6 | 27 | PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of r54e mutant of s. aureus pyruvate carboxylase |
| 21 | d1ghja_ | Alignment | not modelled | 97.6 | 26 | Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains |
| 22 | c4qskB_ | Alignment | not modelled | 97.6 | 30 | PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of l. monocytogenes pyruvate carboxylase in complex2 with cyclic-di-amp |
| 23 | c2l5tA_ | Alignment | not modelled | 97.6 | 21 | PDB header: transferase Chain: A: PDB Molecule: lipoamide acyltransferase; PDBTitle: solution nmr structure of e2 lipoyl domain from thermoplasma2 acidophilum |
| 24 | c2dneA_ | Alignment | not modelled | 97.6 | 16 | PDB header: transferase Chain: A: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase PDBTitle: solution structure of rsgi ruh-058, a lipoyl domain of2 human 2-oxoacid dehydrogenase |
| 25 | d1qjoa_ | Alignment | not modelled | 97.6 | 29 | Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains |
| 26 | c2q8iB_ | Alignment | not modelled | 97.5 | 16 | PDB header: transferase Chain: B: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase component of PDBTitle: pyruvate dehydrogenase kinase isoform 3 in complex with antitumor drug2 radicicol |
| 27 | d1iyua_ | Alignment | not modelled | 97.5 | 23 | Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains |
| 28 | c2einD_ | Alignment | not modelled | 97.5 | 24 | PDB header: ligase Chain: D: PDB Molecule: 149aa long hypothetical methylmalonyl-coa decarboxylase |

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|----|-------------------------|-----------|--------------|------|----|---|
| 28 | c2ejgD | Alignment | not modelled | 97.5 | 24 | PDBTitle: crystal structure of the biotin protein ligase (mutation r48a) and2 biotin carboxyl carrier protein complex from pyrococcus horikoshii3 ot3 PDB header: transferase Chain: A: PDB Molecule: pyruvate dehydrogenase protein x component; PDBTitle: solution structure of rsgi ruh-054, a lipoyl domain from2 human 2-oxoacid dehydrogenase |
| 29 | c2dncA | Alignment | not modelled | 97.5 | 35 | PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase, mitochondrial; PDBTitle: crystal structure of human pyruvate carboxylase (missing the biotin2 carboxylase domain at the n-terminus) |
| 30 | c3bg3A | Alignment | not modelled | 97.5 | 24 | Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains |
| 31 | d2pnrc1 | Alignment | not modelled | 97.5 | 16 | Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains |
| 32 | d1y8ob1 | Alignment | not modelled | 97.5 | 16 | Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains |
| 33 | d1o78a | Alignment | not modelled | 97.4 | 34 | Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains |
| 34 | d1laba | Alignment | not modelled | 97.4 | 29 | Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains |
| 35 | d1qjxa | Alignment | not modelled | 97.4 | 26 | Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains |
| 36 | c3va7A | Alignment | not modelled | 97.3 | 28 | PDB header: ligase Chain: A: PDB Molecule: klla0e08119p; PDBTitle: crystal structure of the kluyveromyces lactis urea carboxylase |
| 37 | c2kccA | Alignment | not modelled | 97.2 | 26 | PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: solution structure of biotinoyl domain from human acetyl-2 coa carboxylase 2 |
| 38 | c2dn8A | Alignment | not modelled | 97.2 | 27 | PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: solution structure of rsgi ruh-053, an apo-biotin carboxy2 carrier protein from human transcarboxylase |
| 39 | c3u9sA | Alignment | not modelled | 97.1 | 32 | PDB header: ligase Chain: A: PDB Molecule: methylcrotonyl-coa carboxylase, alpha-subunit; PDBTitle: crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex |
| 40 | d1pmra | Alignment | not modelled | 97.0 | 29 | Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains |
| 41 | c4rcnA | Alignment | not modelled | 96.7 | 33 | PDB header: ligase Chain: A: PDB Molecule: long-chain acyl-coa carboxylase; PDBTitle: structure and function of a single-chain, multi-domain long-chain2 acyl-coa carboxylase |
| 42 | c3d4rE | Alignment | not modelled | 96.6 | 28 | PDB header: unknown function Chain: E: PDB Molecule: domain of unknown function from the pfam-b_34464 family; PDBTitle: crystal structure of a duf2118 family protein (mmp0046) from2 methanococcus maripaludis at 2.20 a resolution |
| 43 | c6g2dC | Alignment | not modelled | 96.6 | 33 | PDB header: ligase Chain: C: PDB Molecule: acetyl-coa carboxylase 1; PDBTitle: citrate-induced acetyl-coa carboxylase (acc-cit) filament at 5.4 a2 resolution |
| 44 | c5csiA | Alignment | not modelled | 96.4 | 23 | PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of the 500 kd yeast acetyl-coa carboxylase2 holoenzyme dimer |
| 45 | c5csaA | Alignment | not modelled | 95.6 | 23 | PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of domains bt-bccp-ac1-ac5 of yeast acetyl-coa2 carboxylase |
| 46 | c4p6vA | Alignment | not modelled | 94.9 | 30 | PDB header: oxidoreductase Chain: A: PDB Molecule: na(+)-translocating nadh-quinone reductase subunit a; PDBTitle: crystal structure of the na+-translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae |
| 47 | c2k33A | Alignment | not modelled | 94.6 | 30 | PDB header: membrane protein, transport protein Chain: A: PDB Molecule: acra; PDBTitle: solution structure of an n-glycosylated protein using in2 vitro glycosylation |
| 48 | c2qf7A | Alignment | not modelled | 93.6 | 24 | PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase protein; PDBTitle: crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli |
| 49 | c2qj8B | Alignment | not modelled | 91.9 | 19 | PDB header: hydrolase Chain: B: PDB Molecule: mlr6093 protein; PDBTitle: crystal structure of an aspartoacylase family protein (mlr6093) from2 mesorhizobium loti maff303099 at 2.00 a resolution |
| 50 | c3tw6B | Alignment | not modelled | 91.7 | 29 | PDB header: ligase/activator Chain: B: PDB Molecule: pyruvate carboxylase protein; PDBTitle: structure of rhizobium etli pyruvate carboxylase t882a with the2 allosteric activator, acetyl coenzyme-a |
| 51 | c3na6A | Alignment | not modelled | 89.3 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: succinylglutamate desuccinylase/aspartoacylase; PDBTitle: crystal structure of a succinylglutamate desuccinylase (tm1040_2694)2 from silicibacter sp. tm1040 at 2.00 a resolution |
| 52 | c3fmcC | Alignment | not modelled | 86.1 | 17 | PDB header: hydrolase Chain: C: PDB Molecule: putative succinylglutamate desuccinylase / aspartoacylase; PDBTitle: crystal structure of a putative succinylglutamate desuccinylase /2 aspartoacylase family protein (sama_0604) from |

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|----|-------------------------|-----------|--------------|------|----|---|
| | | | | | | shewanella amazonensis3 sb2b at 1.80 a resolution |
| 53 | c4kkuD | Alignment | not modelled | 81.8 | 24 | PDB header: membrane protein Chain: D: PDB Molecule: membrane fusion protein; PDBTitle: structure of besa (selenomethionone derivative - p212121) |
| 54 | c3cdxB | Alignment | not modelled | 79.9 | 24 | PDB header: hydrolase Chain: B: PDB Molecule: succinylglutamatedesuccinylase/aspartoacylase; PDBTitle: crystal structure of succinylglutamatedesuccinylase/aspartoacylase2 from rhodobacter sphaeroides |
| 55 | c3t51C | Alignment | not modelled | 74.1 | 24 | PDB header: transport protein Chain: C: PDB Molecule: cation efflux system protein cusb; PDBTitle: crystal structures of the pre-extrusion and extrusion states of the2 cusba adaptor-transporter complex |
| 56 | c2jkuA | Alignment | not modelled | 68.1 | 36 | PDB header: ligase Chain: A: PDB Molecule: propionyl-coa carboxylase alpha chain, mitochondrial; PDBTitle: crystal structure of the n-terminal region of the biotin acceptor2 domain of human propionyl-coa carboxylase |
| 57 | c3h9iB | Alignment | not modelled | 67.0 | 24 | PDB header: transport protein Chain: B: PDB Molecule: cation efflux system protein cusb; PDBTitle: crystal structure of the membrane fusion protein cusb from escherichia2 coli |
| 58 | d1brw3 | Alignment | not modelled | 63.0 | 29 | Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain |
| 59 | d1uoua3 | Alignment | not modelled | 59.5 | 19 | Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain |
| 60 | d2tpt3 | Alignment | not modelled | 54.3 | 10 | Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain |
| 61 | c5xu0B | Alignment | not modelled | 41.3 | 24 | PDB header: transport protein Chain: B: PDB Molecule: membrane-fusion protein; PDBTitle: structure of the membrane fusion protein spr0693 from streptococcus2 pneumoniae r6 |
| 62 | c5c22A | Alignment | not modelled | 39.3 | 15 | PDB header: protein transport Chain: A: PDB Molecule: chromosomal hemolysin d; PDBTitle: crystal structure of zn-bound hlyd from e. coli |
| 63 | c2f1mA | Alignment | not modelled | 35.1 | 16 | PDB header: transport protein Chain: A: PDB Molecule: acriflavine resistance protein a; PDBTitle: conformational flexibility in the multidrug efflux system protein acra |
| 64 | c3lnnB | Alignment | not modelled | 33.7 | 28 | PDB header: metal transport Chain: B: PDB Molecule: membrane fusion protein (mfp) heavy metal cation efflux PDBTitle: crystal structure of zneb from cupriavidus metallidurans |
| 65 | c3h5qA | Alignment | not modelled | 33.6 | 29 | PDB header: transferase Chain: A: PDB Molecule: pyrimidine-nucleoside phosphorylase; PDBTitle: crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus |
| 66 | c5nenA | Alignment | not modelled | 33.0 | 33 | PDB header: hydrolase Chain: A: PDB Molecule: lipase c; PDBTitle: crystal structure of the soluble domain of lipc, a membrane fusion2 protein of a type i secretion system |
| 67 | c2dsjA | Alignment | not modelled | 32.6 | 29 | PDB header: transferase Chain: A: PDB Molecule: pyrimidine-nucleoside (thymidine) phosphorylase; PDBTitle: crystal structure of project id tt0128 from thermus thermophilus hb8 |
| 68 | c1brwB | Alignment | not modelled | 32.6 | 29 | PDB header: transferase Chain: B: PDB Molecule: protein (pyrimidine nucleoside phosphorylase); PDBTitle: the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation |
| 69 | c1t5eB | Alignment | not modelled | 31.8 | 24 | PDB header: transport protein Chain: B: PDB Molecule: multidrug resistance protein mexa; PDBTitle: the structure of mexa |
| 70 | c2j0fC | Alignment | not modelled | 31.2 | 19 | PDB header: transferase Chain: C: PDB Molecule: thymidine phosphorylase; PDBTitle: structural basis for non-competitive product inhibition in2 human thymidine phosphorylase: implication for drug design |
| 71 | c1otpA | Alignment | not modelled | 30.9 | 10 | PDB header: phosphorylase Chain: A: PDB Molecule: thymidine phosphorylase; PDBTitle: structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase |
| 72 | c5nbbA | Alignment | not modelled | 29.1 | 21 | PDB header: chaperone Chain: A: PDB Molecule: rna chaperone proq; PDBTitle: structure of the c-terminal domain of the escherichia coli proq rna2 binding protein |
| 73 | c4ga5H | Alignment | not modelled | 28.8 | 14 | PDB header: transferase Chain: H: PDB Molecule: putative thymidine phosphorylase; PDBTitle: crystal structure of amp phosphorylase c-terminal deletion mutant in2 the apo-form |
| 74 | d1vf7a | Alignment | not modelled | 28.0 | 20 | Fold: HlyD-like secretion proteins Superfamily: HlyD-like secretion proteins Family: HlyD-like secretion proteins |
| 75 | c2aukA | Alignment | not modelled | 27.8 | 25 | PDB header: transferase Chain: A: PDB Molecule: dna-directed rna polymerase beta' chain; PDBTitle: structure of e. coli rna polymerase beta' g/g' insert |
| 76 | c4l8jA | Alignment | not modelled | 27.0 | 20 | PDB header: transport protein Chain: A: PDB Molecule: putative efflux transporter; PDBTitle: crystal structure of a putative efflux transporter (bacegg_01895) from2 bacteroides eggerthii dsm 20697 at 2.06 a resolution |

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|----|-------------------------|-----------|--------------|------|----|--|
| 77 | c5nilG_ | Alignment | not modelled | 27.0 | 20 | PDB header: transport protein Chain: G; PDB Molecule: macrolide export protein maca; PDBTitle: structure of the macab-tolc abc-type tripartite multidrug efflux pump-2 macb section |
| 78 | c4tkoB_ | Alignment | not modelled | 25.0 | 28 | PDB header: membrane protein Chain: B; PDB Molecule: emra; PDBTitle: structure of the periplasmic adaptor protein emra |
| 79 | d1v95a_ | Alignment | not modelled | 21.0 | 17 | Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS |
| 80 | d2f3ga_ | Alignment | not modelled | 18.7 | 24 | Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like |
| 81 | d2gpra_ | Alignment | not modelled | 18.6 | 16 | Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like |
| 82 | d1gpra_ | Alignment | not modelled | 17.2 | 22 | Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like |
| 83 | c5v5sH_ | Alignment | not modelled | 16.7 | 16 | PDB header: membrane protein Chain: H; PDB Molecule: multidrug efflux pump subunit acra; PDBTitle: multi-drug efflux; membrane transport; rnd superfamily; drug2 resistance |
| 84 | d1ci3m2 | Alignment | not modelled | 16.4 | 29 | Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain |
| 85 | d1qapa2 | Alignment | not modelled | 16.2 | 27 | Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like |
| 86 | d2p84a1 | Alignment | not modelled | 15.1 | 20 | Fold: YopX-like Superfamily: YopX-like Family: YopX-like |
| 87 | c5b0hB_ | Alignment | not modelled | 14.4 | 14 | PDB header: metal binding protein Chain: B; PDB Molecule: leukocyte cell-derived chemotaxin-2; PDBTitle: crystal structure of human leukocyte cell-derived chemotaxin 2 |
| 88 | c4cg4D_ | Alignment | not modelled | 13.9 | 10 | PDB header: actin-binding protein Chain: D; PDB Molecule: pyrin; PDBTitle: crystal structure of the chs-b30.2 domains of trim20 |
| 89 | c3sdzA_ | Alignment | not modelled | 13.5 | 30 | PDB header: hydrolase Chain: A; PDB Molecule: v-type atp synthase alpha chain; PDBTitle: structural characterization of the subunit a mutant f427w of the a-atp2 synthase from pyrococcus horikoshii |
| 90 | c4dk0A_ | Alignment | not modelled | 13.0 | 24 | PDB header: membrane protein Chain: A; PDB Molecule: putative maca; PDBTitle: crystal structure of maca from actinobacillus actinomycetemcomitans |
| 91 | c3fppB_ | Alignment | not modelled | 13.0 | 26 | PDB header: membrane protein Chain: B; PDB Molecule: macrolide-specific efflux protein maca; PDBTitle: crystal structure of e.coli maca |
| 92 | c3lnnA_ | Alignment | not modelled | 12.2 | 28 | PDB header: metal transport Chain: A; PDB Molecule: membrane fusion protein (mfp) heavy metal cation efflux PDBTitle: crystal structure of zneb from cupriavidus metallidurans |
| 93 | c4dk1B_ | Alignment | not modelled | 12.2 | 20 | PDB header: membrane protein Chain: B; PDB Molecule: putative maca, multidrug resistance protein mexa; PDBTitle: crystal structure of maca-mexa chimeric protein, containing the2 pseudomonas aeruginosa mexa alpha-hairpin domain. |
| 94 | d1m1fa_ | Alignment | not modelled | 11.9 | 25 | Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Kid/PemK |
| 95 | c6fnE_ | Alignment | not modelled | 11.8 | 29 | PDB header: protein binding Chain: E; PDB Molecule: e3 ubiquitin/isg15 ligase trim25; PDBTitle: crystal structure of the human trim25 coiled-coil and pryspry domains |
| 96 | d1glaf_ | Alignment | not modelled | 11.6 | 24 | Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like |
| 97 | c3pajA_ | Alignment | not modelled | 9.9 | 24 | PDB header: transferase Chain: A; PDB Molecule: nicotinate-nucleotide pyrophosphorylase, carboxylating; PDBTitle: 2.00 angstrom resolution crystal structure of a quinolinate2 phosphoribosyltransferase from vibrio cholerae o1 biovar eltor str.3 n16961 |
| 98 | c4zhbA_ | Alignment | not modelled | 9.7 | 57 | PDB header: structural genomics, unknown function Chain: A; PDB Molecule: ankyrin repeat-containing protein; PDBTitle: n-terminal structure of ankyrin repeat-containing protein lega11 from2 legionella pneumophila |
| 99 | d1o4ua2 | Alignment | not modelled | 9.5 | 16 | Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like |