







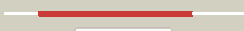
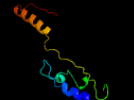














Phyre2

| | |
|---------------|------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD1466_(-)_1653237_1653584 |
| Date | Fri Aug 2 13:30:04 BST 2019 |
| Unique Job ID | 6b555977b43a5d19 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c5irdA_ |  Alignment |  | 100.0 | 100 | PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of rv1466 from mycobacterium tuberculosis, a2 protein associated with [fe-s] complex assembly and repair - seattle3 structural genomics center for infectious disease target4 mytud.17486.a |
| 2 | c3lnoA_ |  Alignment |  | 100.0 | 34 | PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of domain of unknown function duf59 from2 bacillus anthracis |
| 3 | d1uwda_ |  Alignment |  | 100.0 | 33 | Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: PaaD-like |
| 4 | d2cu6a1 |  Alignment |  | 100.0 | 36 | Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: PaaD-like |
| 5 | c3ux2A_ |  Alignment |  | 99.8 | 26 | PDB header: immune system Chain: A: PDB Molecule: mip18 family protein fam96a; PDBTitle: crystal structure of domain-swapped fam96a major dimer |
| 6 | d1xhja_ |  Alignment |  | 95.2 | 18 | Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: NifU C-terminal domain-like |
| 7 | d1veha_ |  Alignment |  | 92.0 | 15 | Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: NifU C-terminal domain-like |
| 8 | c2z51A_ |  Alignment |  | 87.4 | 16 | PDB header: metal transport Chain: A: PDB Molecule: nifu-like protein 2, chloroplast; PDBTitle: crystal structure of arabidopsis cnfu involved in iron-sulfur cluster2 biosynthesis |
| 9 | c1yg0A_ |  Alignment |  | 87.4 | 21 | PDB header: metal transport Chain: A: PDB Molecule: cop associated protein; PDBTitle: solution structure of apo-copp from helicobacter pylori |
| 10 | c2l3mA_ |  Alignment |  | 85.3 | 11 | PDB header: metal binding protein Chain: A: PDB Molecule: copper-ion-binding protein; PDBTitle: solution structure of the putative copper-ion-binding protein from2 bacillus anthracis str. ames |
| 11 | c2jnvA_ |  Alignment |  | 84.2 | 19 | PDB header: metal transport Chain: A: PDB Molecule: nifu-like protein 1, chloroplast; PDBTitle: solution structure of c-terminal domain of nifu-like2 protein from oryza sativa |

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|----|-------------------------|-----------|--------------|------|----|--|
| 12 | c2ofgX_ | Alignment | | 83.6 | 19 | PDB header: hydrolase, membrane protein Chain: X: PDB Molecule: zinc-transporting atpase; PDBTitle: solution structure of the n-terminal domain of the zinc(ii) atpase2 ziaa in its apo form |
| 13 | d2qifa1 | Alignment | | 83.2 | 13 | Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain |
| 14 | c2kkhA_ | Alignment | | 82.9 | 8 | PDB header: metal transport Chain: A: PDB Molecule: putative heavy metal transporter; PDBTitle: structure of the zinc binding domain of the atpase hma4 |
| 15 | c2kt2A_ | Alignment | | 81.4 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: mercuric reductase; PDBTitle: structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase |
| 16 | d1osda_ | Alignment | | 79.9 | 8 | Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain |
| 17 | c4u9rA_ | Alignment | | 79.6 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: czcp cation efflux p1-atpase; PDBTitle: structure of the n-terminal extension from cupriavidus metallidurans2 czcp |
| 18 | c2lqba_ | Alignment | | 79.4 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: metal binding repeat 2 of the wilson disease protein (atp7b) |
| 19 | d1th5a1 | Alignment | | 79.1 | 13 | Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: NifU C-terminal domain-like |
| 20 | d1afia_ | Alignment | | 78.5 | 10 | Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain |
| 21 | c2ropA_ | Alignment | not modelled | 78.4 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: solution structure of domains 3 and 4 of human atp7b |
| 22 | d1q8la_ | Alignment | not modelled | 77.4 | 18 | Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain |
| 23 | c2ew9A_ | Alignment | not modelled | 77.1 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: solution structure of apowln5-6 |
| 24 | d1p6ta2 | Alignment | not modelled | 76.6 | 15 | Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain |
| 25 | c4y2ia_ | Alignment | not modelled | 76.0 | 11 | PDB header: metal transport Chain: A: PDB Molecule: putative metal-binding transport protein; PDBTitle: gold ion bound to golb |
| 26 | d1kvja_ | Alignment | not modelled | 75.6 | 14 | Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain |
| 27 | c2ofhX_ | Alignment | not modelled | 74.3 | 21 | PDB header: hydrolase, membrane protein Chain: X: PDB Molecule: zinc-transporting atpase; PDBTitle: solution structure of the n-terminal domain of the zinc(ii) atpase2 ziaa in its apo form |
| 28 | d1sb6a_ | Alignment | not modelled | 74.3 | 15 | Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain |
| 29 | c2ldia_ | Alignment | not modelled | 73.2 | 23 | PDB header: hydrolase Chain: A: PDB Molecule: zinc-transporting atpase; |

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|----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | PDBTitle: nmr solution structure of ziaan sub mutant |
| 30 | c2n7yA_ | Alignment | not modelled | 72.5 | 11 | PDB header: metal binding protein Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: nmr structure of metal-binding domain 1 of atp7b |
| 31 | d1p6ta1 | Alignment | not modelled | 71.8 | 20 | Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain |
| 32 | d1mwza_ | Alignment | not modelled | 71.6 | 9 | Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain |
| 33 | d1qupa2 | Alignment | not modelled | 71.3 | 8 | Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain |
| 34 | d1s6ua_ | Alignment | not modelled | 70.9 | 11 | Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain |
| 35 | c2k2pA_ | Alignment | not modelled | 69.4 | 16 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu1203; PDBTitle: solution nmr structure of protein atu1203 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att10, ontario center for structural proteomics target atc1183 |
| 36 | c1y3kA_ | Alignment | not modelled | 69.4 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 1; PDBTitle: solution structure of the apo form of the fifth domain of2 menkes protein |
| 37 | c3dxxX_ | Alignment | not modelled | 68.2 | 20 | PDB header: hydrolase Chain: X: PDB Molecule: copper-transporting atpase ran1; PDBTitle: crystal structure of a copper binding domain from hma7, a p-2 type atpase |
| 38 | d2ggpb1 | Alignment | not modelled | 66.0 | 15 | Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain |
| 39 | c6ff2A_ | Alignment | not modelled | 64.6 | 14 | PDB header: chaperone Chain: A: PDB Molecule: copper chaperone copz; PDBTitle: copz metallochaperone |
| 40 | c1yjrA_ | Alignment | not modelled | 64.5 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 1; PDBTitle: solution structure of the apo form of the sixth soluble2 domain a69p mutant of menkes protein |
| 41 | d2aw0a_ | Alignment | not modelled | 63.6 | 20 | Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain |
| 42 | c3j1zP_ | Alignment | not modelled | 62.8 | 11 | PDB header: metal transport Chain: P: PDB Molecule: cation efflux family protein; PDBTitle: inward-facing conformation of the zinc transporter yiiip revealed by2 cryo-electron microscopy |
| 43 | c2rogA_ | Alignment | not modelled | 61.9 | 12 | PDB header: metal binding protein Chain: A: PDB Molecule: heavy metal binding protein; PDBTitle: solution structure of thermus thermophilus hb8 ttha17182 protein in living e. coli cells |
| 44 | c4mt1A_ | Alignment | not modelled | 61.1 | 17 | PDB header: membrane protein, tranport protein Chain: A: PDB Molecule: drug efflux protein; PDBTitle: crystal structure of the neisseria gonorrhoeae mtrd inner membrane2 multidrug efflux pump |
| 45 | c1jk9D_ | Alignment | not modelled | 60.7 | 8 | PDB header: oxidoreductase Chain: D: PDB Molecule: copper chaperone for superoxide dismutase; PDBTitle: heterodimer between h48f-ysoD1 and yccs |
| 46 | d1cc8a_ | Alignment | not modelled | 59.3 | 16 | Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain |
| 47 | c2gcfA_ | Alignment | not modelled | 57.4 | 12 | PDB header: hydrolase Chain: A: PDB Molecule: cation-transporting atpase pacs; PDBTitle: solution structure of the n-terminal domain of the copppe(i) atpase2 pacs in its apo form |
| 48 | c6gzbD_ | Alignment | not modelled | 56.4 | 11 | PDB header: structural protein Chain: D: PDB Molecule: spore germination protein germ; PDBTitle: tandem germn domains of the sporulation protein germ from bacillus2 subtilis |
| 49 | c1qupA_ | Alignment | not modelled | 52.7 | 8 | PDB header: chaperone Chain: A: PDB Molecule: superoxide dismutase 1 copper chaperone; PDBTitle: crystal structure of the copper chaperone for superoxide dismutase |
| 50 | c3w66A_ | Alignment | not modelled | 51.4 | 17 | PDB header: metal transport Chain: A: PDB Molecule: magnetosome protein mamm; PDBTitle: mamm-ctd d249a and h285a |
| 51 | d1ttza_ | Alignment | not modelled | 49.5 | 20 | Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase |
| 52 | c2rmlA_ | Alignment | not modelled | 47.5 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting p-type atpase copa; PDBTitle: solution structure of the n-terminal soluble domains of2 bacillus subtilis copa |
| 53 | d2dyja1 | Alignment | not modelled | 45.7 | 21 | Fold: Alpha-lytic protease prodomain-like Superfamily: Ribosome-binding factor A, RbFA Family: Ribosome-binding factor A, RbFA |
| 54 | c2aj1A_ | Alignment | not modelled | 44.8 | 9 | PDB header: hydrolase Chain: A: PDB Molecule: probable cadmium-transporting atpase; PDBTitle: solution structure of apocada |
| 55 | c1oy8A_ | Alignment | not modelled | 43.9 | 20 | PDB header: membrane protein Chain: A: PDB Molecule: acriflavine resistance protein b; PDBTitle: structural basis of multiple drug binding capacity of the |

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|----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | acrb2 multidrug efflux pump |
| 56 | c5lq3F_ | Alignment | not modelled | 42.2 | 19 | PDB header: transport protein Chain: F; PDB Molecule: cmcb; PDBTitle: structures and transport dynamics of the campylobacter jejuni2 multidrug efflux pump cmcb |
| 57 | c2v50A_ | Alignment | not modelled | 42.1 | 17 | PDB header: membrane protein Chain: A; PDB Molecule: multidrug resistance protein mexb; PDBTitle: the missing part of the bacterial mexab-oprm system: structural2 determination of the multidrug exporter mexb |
| 58 | c3io1B_ | Alignment | not modelled | 41.5 | 10 | PDB header: hydrolase Chain: B; PDB Molecule: aminobenzoyl-glutamate utilization protein; PDBTitle: crystal structure of aminobenzoyl-glutamate utilization2 protein from klebsiella pneumoniae |
| 59 | c4mnnA_ | Alignment | not modelled | 39.4 | 6 | PDB header: oxidoreductase Chain: A; PDB Molecule: glutaredoxin related protein; PDBTitle: the crystal structure of sso1120 from sulfolobus solfataricus |
| 60 | c2kyzA_ | Alignment | not modelled | 37.6 | 12 | PDB header: metal binding protein Chain: A; PDB Molecule: heavy metal binding protein; PDBTitle: nmr structure of heavy metal binding protein tm0320 from thermotoga2 maritima |
| 61 | c1hyuA_ | Alignment | not modelled | 37.5 | 15 | PDB header: oxidoreductase Chain: A; PDB Molecule: alkyl hydroperoxide reductase subunit f; PDBTitle: crystal structure of intact ahpf |
| 62 | c6h3cC_ | Alignment | not modelled | 33.5 | 10 | PDB header: signaling protein Chain: C; PDB Molecule: brisc and brca1-a complex member 2; PDBTitle: cryo-em structure of the brisc complex bound to shmt2 |
| 63 | c2ga7A_ | Alignment | not modelled | 30.6 | 14 | PDB header: hydrolase Chain: A; PDB Molecule: copper-transporting atpase 1; PDBTitle: solution structure of the copper(i) form of the third metal-2 binding domain of atp7a protein (menkes disease protein) |
| 64 | c3j09A_ | Alignment | not modelled | 30.3 | 15 | PDB header: hydrolase, metal transport Chain: A; PDB Molecule: copper-exporting p-type atpase a; PDBTitle: high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa |
| 65 | d1w4ha1 | Alignment | not modelled | 30.1 | 15 | Fold: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Superfamily: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Family: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex |
| 66 | c2qfiB_ | Alignment | not modelled | 29.8 | 14 | PDB header: transport protein Chain: B; PDB Molecule: ferrous-iron efflux pump fief; PDBTitle: structure of the zinc transporter ylip |
| 67 | c6csxA_ | Alignment | not modelled | 28.9 | 20 | PDB header: transport protein Chain: A; PDB Molecule: multidrug efflux pump subunit acrb; PDBTitle: single particles cryo-em structure of acrb d407a associated with lipid2 bilayer at 3.0 angstrom |
| 68 | c2kzfA_ | Alignment | not modelled | 28.1 | 15 | PDB header: ribosomal protein Chain: A; PDB Molecule: ribosome-binding factor a; PDBTitle: solution nmr structure of the thermotoga maritima protein tm0855 a2 putative ribosome binding factor a |
| 69 | d1iloa_ | Alignment | not modelled | 27.1 | 18 | Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase |
| 70 | c2fgxA_ | Alignment | not modelled | 26.8 | 18 | PDB header: structural genomics, unknown function Chain: A; PDB Molecule: putative thioredoxin; PDBTitle: solution nmr structure of protein ne2328 from nitrosomonas2 europaea. northeast structural genomics consortium target3 net3. |
| 71 | d1cpza_ | Alignment | not modelled | 26.1 | 9 | Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain |
| 72 | c6b71A_ | Alignment | not modelled | 25.5 | 23 | PDB header: unknown function Chain: A; PDB Molecule: immune modulator a; PDBTitle: aeromonas veronii immune modulator a |
| 73 | d1fe0a_ | Alignment | not modelled | 24.8 | 18 | Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain |
| 74 | c3qxbB_ | Alignment | not modelled | 24.6 | 17 | PDB header: isomerase Chain: B; PDB Molecule: putative xylose isomerase; PDBTitle: crystal structure of a putative xylose isomerase (yp_426450.1) from2 rhodospirillum rubrum atcc 11170 at 1.90 a resolution |
| 75 | c5tp4B_ | Alignment | not modelled | 24.1 | 10 | PDB header: hydrolase Chain: B; PDB Molecule: amidase, hydantoinase/carbamoylase family; PDBTitle: crystal structure of a hydantoinase/carbamoylase family amidase from2 burkholderia ambifaria |
| 76 | c6fp6X_ | Alignment | not modelled | 22.9 | 24 | PDB header: metal binding protein Chain: X; PDB Molecule: copper chaperone for superoxide dismutase; PDBTitle: complex of human cu,zn sod1 with the human copper chaperone for sod12 in a compact conformation |
| 77 | d1t4aa_ | Alignment | not modelled | 22.8 | 16 | Fold: PurS-like Superfamily: PurS-like Family: PurS subunit of FGAM synthetase |
| 78 | d1tz9a_ | Alignment | not modelled | 21.9 | 10 | Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: UxuA-like |
| 79 | d2cya1 | Alignment | not modelled | 21.7 | 13 | Fold: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Superfamily: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Family: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex |

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|----|-------------------------|-----------|--------------|------|----|--|
| 80 | c5ho5D_ | Alignment | not modelled | 21.7 | 19 | PDB header: metal transport Chain: D: PDB Molecule: magnetosome protein mamb; PDBTitle: mamb |
| 81 | c2cr1A_ | Alignment | not modelled | 21.5 | 24 | PDB header: chaperone Chain: A: PDB Molecule: copper chaperone for superoxide dismutase; PDBTitle: the apo form of hma domain of copper chaperone for2 superoxide dismutase |
| 82 | c3hd5A_ | Alignment | not modelled | 21.4 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsba; PDBTitle: crystal structure of a thiol:disulfide interchange protein2 dsba from bordetella parapertussis |
| 83 | d2qfia1 | Alignment | not modelled | 21.3 | 19 | Fold: Alpha-lytic protease prodomain-like Superfamily: Cation efflux protein cytoplasmic domain-like Family: Cation efflux protein cytoplasmic domain-like |
| 84 | c3fryB_ | Alignment | not modelled | 21.1 | 11 | PDB header: hydrolase Chain: B: PDB Molecule: probable copper-exporting p-type atpase a; PDBTitle: crystal structure of the copa c-terminal metal binding domain |
| 85 | d1w85i_ | Alignment | not modelled | 20.6 | 19 | Fold: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Superfamily: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Family: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex |
| 86 | c1zwvA_ | Alignment | not modelled | 19.6 | 12 | PDB header: transferase Chain: A: PDB Molecule: lipamide acyltransferase component of branched- PDBTitle: solution structure of the subunit binding domain (hbsbd) of2 the human mitochondrial branched-chain alpha-ketoacid3 dehydrogenase |
| 87 | d1z6ma1 | Alignment | not modelled | 19.3 | 12 | Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbA-like |
| 88 | d1vq3a_ | Alignment | not modelled | 19.2 | 16 | Fold: PurS-like Superfamily: PurS-like Family: PurS subunit of FGAM synthetase |
| 89 | c2vxob_ | Alignment | not modelled | 18.9 | 7 | PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: human gmp synthetase in complex with xmp |
| 90 | c3dv0l_ | Alignment | not modelled | 18.9 | 19 | PDB header: oxidoreductase/transferase Chain: I: PDB Molecule: dihydropolyllysine-residue acetyltransferase PDBTitle: snapshots of catalysis in the e1 subunit of the pyruvate2 dehydrogenase multi-enzyme complex |
| 91 | d1r7ha_ | Alignment | not modelled | 18.7 | 19 | Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase |
| 92 | d1josa_ | Alignment | not modelled | 18.4 | 21 | Fold: Alpha-lytic protease prodomain-like Superfamily: Ribosome-binding factor A, RbfA Family: Ribosome-binding factor A, RbfA |
| 93 | d3bypa1 | Alignment | not modelled | 18.2 | 15 | Fold: Alpha-lytic protease prodomain-like Superfamily: Cation efflux protein cytoplasmic domain-like Family: Cation efflux protein cytoplasmic domain-like |
| 94 | c1zy8M_ | Alignment | not modelled | 17.9 | 13 | PDB header: oxidoreductase Chain: M: PDB Molecule: pyruvate dehydrogenase protein x component, PDBTitle: the crystal structure of dihydrolipoamide dehydrogenase and2 dihydrolipoamide dehydrogenase-binding protein (didomain)3 subcomplex of human pyruvate dehydrogenase complex. |
| 95 | c4xvwK_ | Alignment | not modelled | 17.6 | 12 | PDB header: isomerase Chain: K: PDB Molecule: dsba-like protein; PDBTitle: crystal structure of proteus mirabilis scsc in a compact conformation |
| 96 | d2d4pa1 | Alignment | not modelled | 17.1 | 22 | Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT |
| 97 | c2eq7C_ | Alignment | not modelled | 17.1 | 7 | PDB header: oxidoreductase Chain: C: PDB Molecule: 2-oxoglutarate dehydrogenase e2 component; PDBTitle: crystal structure of lipamide dehydrogenase from thermus thermophilus2 hb8 with psbdo |
| 98 | c4j1jA_ | Alignment | not modelled | 17.1 | 23 | PDB header: viral protein/dna Chain: A: PDB Molecule: nucleocapsid; PDBTitle: leanyer orthobunyavirus nucleoprotein-ssdna complex |
| 99 | c4euyA_ | Alignment | not modelled | 17.0 | 21 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of thioredoxin-like protein bce_0499 from bacillus2 cereus atcc 10987 |