



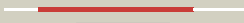










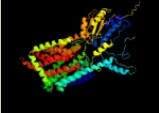





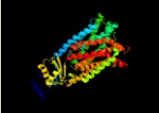


Phyre2

| | |
|---------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0206c_(mmpL3)_244484_247318 |
| Date | Tue Jul 23 14:50:26 BST 2019 |
| Unique Job ID | c42b6a40c1cbf2a3 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|--|
| 1 | c6ajjA_ |  Alignment |  | 100.0 | 72 | PDB header: membrane protein, hydrolase Chain: A: PDB Molecule: drug exporters of the rnd superfamily-like protein, PDBTitle: crystal structure of mycolic acid transporter mmpL3 from mycobacterium2 smegmatis complexed with ica38 |
| 2 | c5khnB_ |  Alignment |  | 100.0 | 15 | PDB header: membrane protein Chain: B: PDB Molecule: rnd transporter; PDBTitle: crystal structures of the burkholderia multivorans hopanoid2 transporter hpnn |
| 3 | c6dmoA_ |  Alignment |  | 100.0 | 15 | PDB header: protein binding Chain: A: PDB Molecule: protein patched homolog 1; PDBTitle: cryo-em structure of human ptch1 with three mutations2 l282q/t500f/p504l |
| 4 | c3jd8A_ |  Alignment |  | 100.0 | 13 | PDB header: membrane protein Chain: A: PDB Molecule: niemann-pick c1 protein; PDBTitle: cryo-em structure of the full-length human npc1 at 4.4 angstrom |
| 5 | c5lq3F_ |  Alignment |  | 100.0 | 17 | PDB header: transport protein Chain: F: PDB Molecule: cmeb; PDBTitle: structures and transport dynamics of the campylobacter jejuni2 multidrug efflux pump cmeb |
| 6 | c4mt1A_ |  Alignment |  | 100.0 | 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 |
| 7 | c6owsB_ |  Alignment |  | 100.0 | 17 | PDB header: membrane protein Chain: B: PDB Molecule: efflux pump membrane transporter; PDBTitle: cryo-em structure of an acinetobacter baumannii multidrug efflux pump |
| 8 | c3k07A_ |  Alignment |  | 100.0 | 21 | PDB header: transport protein Chain: A: PDB Molecule: cation efflux system protein cusa; PDBTitle: crystal structure of cusa |
| 9 | c2v50A_ |  Alignment |  | 100.0 | 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 |
| 10 | c5xamA_ |  Alignment |  | 100.0 | 14 | PDB header: membrane protein Chain: A: PDB Molecule: protein translocase subunit secdf; PDBTitle: crystal structure of secdf in i form at 4 a resolution |
| 11 | c3aqpB_ |  Alignment |  | 100.0 | 12 | PDB header: membrane protein Chain: B: PDB Molecule: probable secdf protein-export membrane protein; PDBTitle: crystal structure of secdf, a translocon-associated membrane protein,2 from thermus thrmophilus |

| | | | | | | |
|----|-------------------------|-----------|--------------|-------|----|--|
| 12 | c1oy8A_ | Alignment | | 100.0 | 18 | PDB header: membrane protein Chain: A: PDB Molecule: acriflavine resistance protein b; PDBTitle: structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump |
| 13 | c4k0eA_ | Alignment | | 100.0 | 22 | PDB header: transport protein Chain: A: PDB Molecule: heavy metal cation tricomponent efflux pump znea(czca- PDBTitle: x-ray crystal structure of a heavy metal efflux pump, crystal form ii |
| 14 | c4k0eC_ | Alignment | | 100.0 | 20 | PDB header: transport protein Chain: C: PDB Molecule: heavy metal cation tricomponent efflux pump znea(czca- PDBTitle: x-ray crystal structure of a heavy metal efflux pump, crystal form ii |
| 15 | c6csxA_ | Alignment | | 100.0 | 13 | 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 |
| 16 | c5mg3F_ | Alignment | | 100.0 | 15 | PDB header: chaperone Chain: F: PDB Molecule: protein translocase subunit secf; PDBTitle: em fitted model of bacterial holo-translocon |
| 17 | c5mg3D_ | Alignment | | 100.0 | 16 | PDB header: chaperone Chain: D: PDB Molecule: protein translocase subunit secd; PDBTitle: em fitted model of bacterial holo-translocon |
| 18 | d1iwga7 | Alignment | | 100.0 | 16 | Fold: Multidrug efflux transporter AcrB transmembrane domain Superfamily: Multidrug efflux transporter AcrB transmembrane domain Family: Multidrug efflux transporter AcrB transmembrane domain |
| 19 | d1iwga8 | Alignment | | 100.0 | 15 | Fold: Multidrug efflux transporter AcrB transmembrane domain Superfamily: Multidrug efflux transporter AcrB transmembrane domain Family: Multidrug efflux transporter AcrB transmembrane domain |
| 20 | c2yvxD_ | Alignment | | 95.0 | 16 | PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte |
| 21 | c4av3A_ | Alignment | not modelled | 54.2 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: k(+)-stimulated pyrophosphate-energized sodium pump; PDBTitle: crystal structure of thermotoga maritima sodium pumping membrane2 integral pyrophosphatase with metal ions in active site |
| 22 | c4ev6E_ | Alignment | not modelled | 38.9 | 10 | PDB header: metal transport Chain: E: PDB Molecule: magnesium transport protein cora; PDBTitle: the complete structure of cora magnesium transporter from2 methanocaldococcus jannaschii |
| 23 | c1p58E_ | Alignment | not modelled | 37.8 | 16 | PDB header: virus Chain: E: PDB Molecule: envelope protein m; PDBTitle: complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction |
| 24 | d1iwga3 | Alignment | not modelled | 32.8 | 14 | Fold: Ferredoxin-like Superfamily: Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains Family: Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains |
| 25 | d2yvxa3 | Alignment | not modelled | 32.2 | 14 | Fold: MgtE membrane domain-like Superfamily: MgtE membrane domain-like Family: MgtE membrane domain-like |
| 26 | c6hwhb_ | Alignment | not modelled | 31.7 | 14 | PDB header: electron transport Chain: B: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis |
| 27 | c5lm4A_ | Alignment | not modelled | 29.5 | 17 | PDB header: transport protein Chain: A: PDB Molecule: excitatory amino acid transporter 1,neutral amino acid PDBTitle: structure of the thermostabilized eaat1 cryst-ii mutant in complex2 with l-asp and the allosteric inhibitor ucph101 |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|---|
| 28 | c5m87A_ | Alignment | not modelled | 28.6 | 19 | PDB header: transport protein Chain: A: PDB Molecule: divalent metal cation transporter mnth; PDBTitle: crystal structure of eremococcus coleocola manganese transporter |
| 29 | c5n9yB_ | Alignment | not modelled | 21.6 | 15 | PDB header: membrane protein Chain: B: PDB Molecule: zinc transport protein zntb; PDBTitle: the full-length structure of zntb |
| 30 | c6b2zf_ | Alignment | not modelled | 20.1 | 24 | PDB header: membrane protein Chain: F: PDB Molecule: atp synthase subunit c, mitochondrial; PDBTitle: cryo-em structure of the dimeric fo region of yeast mitochondrial atp2 synthase |
| 31 | c6b8ht_ | Alignment | not modelled | 20.1 | 24 | PDB header: membrane protein Chain: T: PDB Molecule: atp synthase subunit 9, mitochondrial; PDBTitle: mosaic model of yeast mitochondrial atp synthase monomer |
| 32 | d3bzka3 | Alignment | not modelled | 20.0 | 9 | Fold: Tex N-terminal region-like Superfamily: Tex N-terminal region-like Family: Tex N-terminal region-like |
| 33 | c2bbjB_ | Alignment | not modelled | 18.8 | 15 | PDB header: metal transport/membrane protein Chain: B: PDB Molecule: divalent cation transport-related protein; PDBTitle: crystal structure of the cora mg2+ transporter |
| 34 | c6gctA_ | Alignment | not modelled | 14.7 | 23 | PDB header: membrane protein Chain: A: PDB Molecule: neutral amino acid transporter b(0); PDBTitle: cryo-em structure of the human neutral amino acid transporter asct2 |
| 35 | c2oceA_ | Alignment | not modelled | 14.5 | 9 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pa5201; PDBTitle: crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa |
| 36 | c1p58F_ | Alignment | not modelled | 13.2 | 10 | PDB header: virus Chain: F: PDB Molecule: envelope protein m; PDBTitle: complex organization of dengue virus membrane proteins as revealed by 2 9.5 angstrom cryo-em reconstruction |
| 37 | d1iwg4 | Alignment | not modelled | 13.0 | 8 | Fold: Ferredoxin-like Superfamily: Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains Family: Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains |
| 38 | c4p6vE_ | Alignment | not modelled | 12.3 | 11 | PDB header: oxidoreductase Chain: E: PDB Molecule: na(+)-translocating nadh-quinone reductase subunit e; PDBTitle: crystal structure of the na+-translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae |
| 39 | c3j2pD_ | Alignment | not modelled | 11.5 | 10 | PDB header: viral protein Chain: D: PDB Molecule: small envelope protein m; PDBTitle: cryoem structure of dengue virus envelope protein heterotetramer |
| 40 | c6mctE_ | Alignment | not modelled | 11.1 | 18 | PDB header: de novo protein Chain: E: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction |
| 41 | c6mctF_ | Alignment | not modelled | 11.1 | 18 | PDB header: de novo protein Chain: F: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction |
| 42 | c6mctN_ | Alignment | not modelled | 11.1 | 18 | PDB header: de novo protein Chain: N: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction |
| 43 | c6mpwA_ | Alignment | not modelled | 11.1 | 18 | PDB header: de novo protein Chain: A: PDB Molecule: mini-evgl membrane protein; PDBTitle: de novo design of membrane protein--mini-evgl membrane protein, c22212 form-1 |
| 44 | c6mctM_ | Alignment | not modelled | 11.1 | 18 | PDB header: de novo protein Chain: M: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction |
| 45 | c6mctL_ | Alignment | not modelled | 11.1 | 18 | PDB header: de novo protein Chain: L: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction |
| 46 | c6mctJ_ | Alignment | not modelled | 11.1 | 18 | PDB header: de novo protein Chain: J: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction |
| 47 | c6mctO_ | Alignment | not modelled | 11.1 | 18 | PDB header: de novo protein Chain: O: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction |
| 48 | c6mctH_ | Alignment | not modelled | 11.1 | 18 | PDB header: de novo protein Chain: H: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction |
| 49 | c6mq2D_ | Alignment | not modelled | 11.1 | 18 | PDB header: de novo protein Chain: D: PDB Molecule: mini-evgl membrane protein; PDBTitle: de novo design of membrane protein--mini-evgl membrane protein, c22212 form-2 |
| 50 | c6mctD_ | Alignment | not modelled | 11.1 | 18 | PDB header: de novo protein Chain: D: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction |
| 51 | c6mctB_ | Alignment | not modelled | 11.1 | 18 | PDB header: de novo protein Chain: B: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction |
| 52 | c6mctC_ | Alignment | not modelled | 11.1 | 18 | PDB header: de novo protein Chain: C: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction |
| 53 | c6mctK_ | Alignment | not modelled | 11.1 | 18 | PDB header: de novo protein Chain: K: PDB Molecule: mini-evgl membrane protein; |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|--|
| 53 | c6mctK | Alignment | not modelled | 11.1 | 18 | PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction PDB header: de novo protein |
| 54 | c6mctG | Alignment | not modelled | 11.1 | 18 | Chain: G; PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction |
| 55 | c6mctA | Alignment | not modelled | 11.1 | 18 | PDB header: de novo protein Chain: A; PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction |
| 56 | c6mctI | Alignment | not modelled | 11.1 | 18 | PDB header: de novo protein Chain: I; PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction |
| 57 | c6m97A | Alignment | not modelled | 11.0 | 12 | PDB header: transport protein Chain: A; PDB Molecule: chimera protein of high affinity copper uptake protein 1 PDBTitle: crystal structure of the high-affinity copper transporter ctr1 |
| 58 | c6mq2B | Alignment | not modelled | 10.8 | 18 | PDB header: de novo protein Chain: B; PDB Molecule: mini-evgl membrane protein; PDBTitle: de novo design of membrane protein--mini-evgl membrane protein, c22212 form-2 |
| 59 | c6mpwD | Alignment | not modelled | 10.8 | 18 | PDB header: de novo protein Chain: D; PDB Molecule: mini-evgl membrane protein; PDBTitle: de novo design of membrane protein--mini-evgl membrane protein, c22212 form-1 |
| 60 | c6mpwE | Alignment | not modelled | 10.8 | 18 | PDB header: de novo protein Chain: E; PDB Molecule: mini-evgl membrane protein; PDBTitle: de novo design of membrane protein--mini-evgl membrane protein, c22212 form-1 |
| 61 | c6mq2E | Alignment | not modelled | 10.8 | 18 | PDB header: de novo protein Chain: E; PDB Molecule: mini-evgl membrane protein; PDBTitle: de novo design of membrane protein--mini-evgl membrane protein, c22212 form-2 |
| 62 | c6mq2A | Alignment | not modelled | 10.8 | 18 | PDB header: de novo protein Chain: A; PDB Molecule: mini-evgl membrane protein; PDBTitle: de novo design of membrane protein--mini-evgl membrane protein, c22212 form-2 |
| 63 | c6mq2C | Alignment | not modelled | 10.8 | 18 | PDB header: de novo protein Chain: C; PDB Molecule: mini-evgl membrane protein; PDBTitle: de novo design of membrane protein--mini-evgl membrane protein, c22212 form-2 |
| 64 | c6mpwC | Alignment | not modelled | 10.8 | 18 | PDB header: de novo protein Chain: C; PDB Molecule: mini-evgl membrane protein; PDBTitle: de novo design of membrane protein--mini-evgl membrane protein, c22212 form-1 |
| 65 | c6mpwB | Alignment | not modelled | 10.8 | 18 | PDB header: de novo protein Chain: B; PDB Molecule: mini-evgl membrane protein; PDBTitle: de novo design of membrane protein--mini-evgl membrane protein, c22212 form-1 |
| 66 | c4gn0D | Alignment | not modelled | 10.7 | 13 | PDB header: signaling protein Chain: D; PDB Molecule: hamp domain of af1503; PDBTitle: de novo phasing of a hamp-complex using an improved arcimboldo method |
| 67 | d1a87a | Alignment | not modelled | 10.7 | 17 | Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin |
| 68 | c1a87A | Alignment | not modelled | 10.7 | 17 | PDB header: bacteriocin Chain: A; PDB Molecule: colicin n; PDBTitle: colicin n |
| 69 | c2na9A | Alignment | not modelled | 10.5 | 33 | PDB header: signaling protein Chain: A; PDB Molecule: cytokine receptor common subunit beta; PDBTitle: transmembrane structure of the p441a mutant of the cytokine receptor2 common subunit beta |
| 70 | c2na8A | Alignment | not modelled | 10.4 | 33 | PDB header: membrane protein Chain: A; PDB Molecule: cytokine receptor common subunit beta; PDBTitle: transmembrane structure of the cytokine receptor common subunit beta |
| 71 | d2r8ca2 | Alignment | not modelled | 10.4 | 23 | Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like |
| 72 | c5b16C | Alignment | not modelled | 9.8 | 21 | PDB header: hydrolase Chain: C; PDB Molecule: microprocessor complex subunit dgcr8; PDBTitle: x-ray structure of drosha in complex with the c-terminal tail of2 dgcr8. |
| 73 | c2m67A | Alignment | not modelled | 9.7 | 16 | PDB header: transport protein Chain: A; PDB Molecule: merf; PDBTitle: full-length mercury transporter protein merf in lipid bilayer2 membranes |
| 74 | d2nwwa1 | Alignment | not modelled | 9.5 | 11 | Fold: Proton glutamate symport protein Superfamily: Proton glutamate symport protein Family: Proton glutamate symport protein |
| 75 | c5oonA | Alignment | not modelled | 9.5 | 9 | PDB header: membrane protein Chain: A; PDB Molecule: undecaprenyl-diphosphatase; PDBTitle: structure of undecaprenyl-pyrophosphate phosphatase, baca |
| 76 | c5b16B | Alignment | not modelled | 9.4 | 21 | PDB header: hydrolase Chain: B; PDB Molecule: microprocessor complex subunit dgcr8; PDBTitle: x-ray structure of drosha in complex with the c-terminal tail of2 dgcr8. |
| 77 | d3ehbb2 | Alignment | not modelled | 8.6 | 16 | Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region |
| 78 | c6nbxG | Alignment | not modelled | 8.6 | 11 | PDB header: oxidoreductase Chain: G; PDB Molecule: nadh-quinone oxidoreductase subunit j; PDBTitle: t.elongatus ndh (data-set 2) |
| | | | | | | PDB header: unknown function |

| | | | | | | |
|----|-------------------------|-----------|--------------|-----|----|--|
| 79 | c3ut7A_ | Alignment | not modelled | 8.6 | 29 | Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: structural view of a non pfam singleton and crystal packing analysis |
| 80 | c5ireD_ | Alignment | not modelled | 8.4 | 5 | PDB header: virus Chain: D: PDB Molecule: m protein; PDBTitle: the cryo-em structure of zika virus |
| 81 | c5gasN_ | Alignment | not modelled | 8.2 | 12 | PDB header: hydrolase Chain: N: PDB Molecule: archaeal/vacuolar-type h+-atpase subunit i; PDBTitle: thermus thermophilus v/a-atpase, conformation 2 |
| 82 | c5xu1M_ | Alignment | not modelled | 8.0 | 7 | PDB header: transport protein Chain: M: PDB Molecule: abc transporter permease; PDBTitle: structure of a non-canonical abc transporter from streptococcus2 pneumoniae r6 |
| 83 | c6c08F_ | Alignment | not modelled | 7.9 | 19 | PDB header: membrane protein Chain: F: PDB Molecule: sodium-coupled neutral amino acid transporter 9; PDBTitle: zebrafish slc38a9 with arginine bound in the cytosol open state |
| 84 | c4cbfB_ | Alignment | not modelled | 7.9 | 5 | PDB header: virus Chain: B: PDB Molecule: m protein; PDBTitle: near-atomic resolution cryo-em structure of dengue serotype 4 virus |
| 85 | c2wse3_ | Alignment | not modelled | 7.8 | 15 | PDB header: photosynthesis Chain: 3: PDB Molecule: lhca3; PDBTitle: improved model of plant photosystem i |
| 86 | c6o7xa_ | Alignment | not modelled | 7.8 | 13 | PDB header: membrane protein Chain: A: PDB Molecule: vacuolar atp synthase catalytic subunit a; PDBTitle: saccharomyces cerevisiae v-atpase stv1-v1vo state 3 |
| 87 | c3pmiC_ | Alignment | not modelled | 7.8 | 14 | PDB header: protein binding Chain: C: PDB Molecule: pwpp domain-containing protein mum1; PDBTitle: pwpp domain of human mutated melanoma-associated antigen 1 |
| 88 | c5wsnD_ | Alignment | not modelled | 7.6 | 10 | PDB header: virus Chain: D: PDB Molecule: m protein; PDBTitle: structure of japanese encephalitis virus |
| 89 | c2mudA_ | Alignment | not modelled | 7.6 | 33 | PDB header: membrane protein Chain: A: PDB Molecule: variant-specific surface protein; PDBTitle: structural modifications to a high-activity binding peptide located2 within the pfemp1 nts domain induce protection against p. falciparum3 malaria in aotus monkeys |
| 90 | c6o7ua_ | Alignment | not modelled | 7.5 | 15 | PDB header: membrane protein Chain: A: PDB Molecule: PDBTitle: saccharomyces cerevisiae v-atpase stv1-vo |
| 91 | d1cia1 | Alignment | not modelled | 7.3 | 15 | Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin |
| 92 | c4a01B_ | Alignment | not modelled | 7.3 | 16 | PDB header: hydrolase Chain: B: PDB Molecule: proton pyrophosphatase; PDBTitle: crystal structure of the h-translocating pyrophosphatase |
| 93 | c2n4xA_ | Alignment | not modelled | 7.1 | 12 | PDB header: membrane protein Chain: A: PDB Molecule: cytochrome c-type biogenesis protein (ccda); PDBTitle: structure of the transmembrane electron transporter ccda |
| 94 | c4p6vD_ | Alignment | not modelled | 7.1 | 17 | PDB header: oxidoreductase Chain: D: PDB Molecule: na(+)-translocating nadh-quinone reductase subunit d; PDBTitle: crystal structure of the na+-translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae |
| 95 | c1agqB_ | Alignment | not modelled | 7.0 | 0 | PDB header: growth factor Chain: B: PDB Molecule: glial cell-derived neurotrophic factor; PDBTitle: glial cell-derived neurotrophic factor from rat |
| 96 | c3abnA_ | Alignment | not modelled | 6.9 | 27 | PDB header: structural protein Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)4-hyp-asp-gly-(pro-pro-gly)4 at 1.022 a |
| 97 | d1ebfa2 | Alignment | not modelled | 6.9 | 0 | Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Homoserine dehydrogenase-like |
| 98 | d3dtub2 | Alignment | not modelled | 6.7 | 13 | Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region |
| 99 | c6mitC_ | Alignment | not modelled | 6.7 | 20 | PDB header: lipid transport Chain: C: PDB Molecule: lipopolysaccharide export system protein lptc; PDBTitle: lptbfgc from enterobacter cloacae |