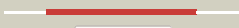
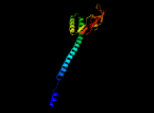

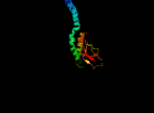






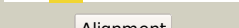

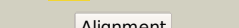
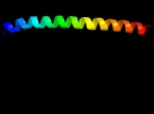
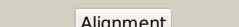
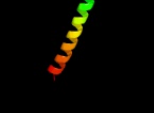
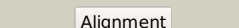
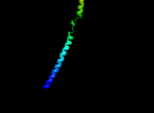
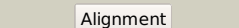
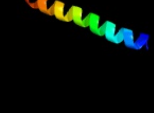




Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0351_(grpE)_421709_422416
 Date Tue Jul 23 14:50:42 BST 2019
 Unique Job ID 248642459379d170

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c1dkgB_ |  Alignment |  | 100.0 | 22 | PDB header: complex (hsp24/hsp70) Chain: B: PDB Molecule: nucleotide exchange factor grpe; PDBTitle: crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak |
| 2 | c4aniA_ |  Alignment |  | 100.0 | 35 | PDB header: chaperone Chain: A: PDB Molecule: protein grpe; PDBTitle: structural basis for the intermolecular communication between2 dnak and grpe in the dnak chaperone system from3 geobacillus kaustophilus hta426 |
| 3 | c3a6mB_ |  Alignment |  | 100.0 | 30 | PDB header: chaperone Chain: B: PDB Molecule: protein grpe; PDBTitle: crystal structure of grpe from thermus thermophilus hb8 |
| 4 | d1dkga1 |  Alignment |  | 99.8 | 21 | Fold: Head domain of nucleotide exchange factor GrpE Superfamily: Head domain of nucleotide exchange factor GrpE Family: Head domain of nucleotide exchange factor GrpE |
| 5 | c5dolB_ |  Alignment |  | 87.0 | 16 | PDB header: replication Chain: B: PDB Molecule: initiation-control protein yaba; PDBTitle: crystal structure of yaba amino-terminal domain from bacillus subtilis |
| 6 | c3mkxC_ |  Alignment |  | 71.0 | 19 | PDB header: antiviral protein Chain: C: PDB Molecule: bone marrow stromal antigen 2; PDBTitle: crystal structure of bst2/tetherin |
| 7 | c3swfA_ |  Alignment |  | 70.3 | 12 | PDB header: transport protein Chain: A: PDB Molecule: cgmp-gated cation channel alpha-1; PDBTitle: cnga1 621-690 containing clz domain |
| 8 | c2yy0D_ |  Alignment |  | 67.6 | 5 | PDB header: transcription Chain: D: PDB Molecule: c-myc-binding protein; PDBTitle: crystal structure of ms0802, c-myc-1 binding protein domain2 from homo sapiens |
| 9 | c5mg8B_ |  Alignment |  | 67.3 | 11 | PDB header: recombination Chain: B: PDB Molecule: structural maintenance of chromosomes protein 6; PDBTitle: crystal structure of the s.pombe smc5/6 hinge domain |
| 10 | c1m7IA_ |  Alignment |  | 53.3 | 34 | PDB header: sugar binding protein Chain: A: PDB Molecule: pulmonary surfactant-associated protein d; PDBTitle: solution structure of the coiled-coil trimerization domain2 from lung surfactant protein d |
| 11 | c3swyB_ |  Alignment |  | 52.5 | 10 | PDB header: transport protein Chain: B: PDB Molecule: cyclic nucleotide-gated cation channel alpha-3; PDBTitle: cnga3 626-672 containing clz domain |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|---|
| 12 | c3m9bK_ | Alignment | | 49.0 | 15 | PDB header: chaperone Chain: K: PDB Molecule: proteasome-associated atpase; PDBTitle: crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa |
| 13 | c2x7aB_ | Alignment | | 46.9 | 19 | PDB header: immune system Chain: B: PDB Molecule: bone marrow stromal antigen 2; PDBTitle: structural basis of hiv-1 tethering to membranes by the2 bst2-tetherin ectodomain |
| 14 | c5fv8B_ | Alignment | | 44.6 | 9 | PDB header: structural protein Chain: B: PDB Molecule: fosw; PDBTitle: structure of cjun-fosw coiled coil complex. |
| 15 | c5fv8A_ | Alignment | | 44.1 | 9 | PDB header: structural protein Chain: A: PDB Molecule: fosw; PDBTitle: structure of cjun-fosw coiled coil complex. |
| 16 | c1gk6B_ | Alignment | | 32.1 | 9 | PDB header: structural protein Chain: B: PDB Molecule: vimentin; PDBTitle: human vimentin coil 2b fragment linked to gcn4 leucine zipper (z2b) |
| 17 | c4y66D_ | Alignment | | 30.6 | 15 | PDB header: cell cycle Chain: D: PDB Molecule: putative tbpip family protein; PDBTitle: crystal structure of giardia lamblia hop2-mnd1 complex |
| 18 | c4jzlA_ | Alignment | | 29.2 | 20 | PDB header: apoptosis, transport protein Chain: A: PDB Molecule: b-cell receptor-associated protein 31; PDBTitle: crystal structure of bap31 vded at alkaline ph |
| 19 | c5j10A_ | Alignment | | 29.2 | 21 | PDB header: de novo protein Chain: A: PDB Molecule: peptide design 214hc2_24; PDBTitle: de novo design of protein homo-oligomers with modular hydrogen bond2 network-mediated specificity |
| 20 | c4w7yB_ | Alignment | | 28.8 | 14 | PDB header: transport protein Chain: B: PDB Molecule: b-cell receptor-associated protein 29; PDBTitle: dimeric bap29 vded with disulfide bonds in crystal contacts |
| 21 | c1u2mC_ | Alignment | not modelled | 24.5 | 11 | PDB header: chaperone Chain: C: PDB Molecule: histone-like protein hlp-1; PDBTitle: crystal structure of skp |
| 22 | c4kqtA_ | Alignment | not modelled | 24.1 | 17 | PDB header: chaperone Chain: A: PDB Molecule: putative outer membrane chaperone (omph-like); PDBTitle: crystal structure of a putative outer membrane chaperone (omph-like)2 (cc_1914) from caulobacter crescentus cb15 at 2.83 a resolution (psi3 community target, shapiro) |
| 23 | c3j0xl_ | Alignment | not modelled | 23.1 | 16 | PDB header: ribosome Chain: I: PDB Molecule: 30s ribosomal protein s6; PDBTitle: structural characterization of mrna-trna translocation intermediates2 (30s ribosome of class 4b of the six classes) |
| 24 | c2xv5A_ | Alignment | not modelled | 21.3 | 18 | PDB header: structural protein Chain: A: PDB Molecule: lamin-a/c; PDBTitle: human lamin a coil 2b fragment |
| 25 | c3k8zD_ | Alignment | not modelled | 20.5 | 16 | PDB header: oxidoreductase Chain: D: PDB Molecule: nad-specific glutamate dehydrogenase; PDBTitle: crystal structure of gudb1 a decrypted secondary glutamate2 dehydrogenase from b. subtilis |
| 26 | c5vgzC_ | Alignment | not modelled | 19.4 | 13 | PDB header: hydrolase Chain: C: PDB Molecule: 26s proteasome regulatory subunit 8; PDBTitle: conformational landscape of the p28-bound human proteasome regulatory2 particle |
| 27 | c4wvmA_ | Alignment | not modelled | 18.3 | 9 | PDB header: toxin Chain: A: PDB Molecule: stonustoxin subunit alpha; PDBTitle: stonustoxin structure |
| 28 | d1ep5a_ | Alignment | not modelled | 17.9 | 23 | Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases PDB header: viral protein |

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|----|-------------------------|-----------|--------------|------|----|--|
| 29 | c1kxfA_ | Alignment | not modelled | 17.7 | 15 | Chain: A: PDB Molecule: sindbis virus capsid protein; PDBTitle: sindbis virus capsid, (wild-type) residues 1-264, tetragonal crystal2 form (form ii) |
| 30 | d1wyka_ | Alignment | not modelled | 17.1 | 15 | Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases |
| 31 | c4qdyA_ | Alignment | not modelled | 16.6 | 9 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of a ybbr-like protein (sp_1560) from streptococcus2 pneumoniae tigr4 at 2.74 a resolution |
| 32 | c2kxyA_ | Alignment | not modelled | 16.3 | 9 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of sur18c from streptococcus thermophilus.2 northeast structural genomics consortium target sur18c |
| 33 | c3ni0A_ | Alignment | not modelled | 16.3 | 15 | PDB header: immune system Chain: A: PDB Molecule: bone marrow stromal antigen 2; PDBTitle: crystal structure of mouse bst-2/tetherin ectodomain |
| 34 | c2gl2B_ | Alignment | not modelled | 15.8 | 4 | PDB header: cell adhesion Chain: B: PDB Molecule: adhesion a; PDBTitle: crystal structure of the tetra mutant (t66g,r67g,f68g,y69g) of2 bacterial adhesin fada |
| 35 | d2qeec1 | Alignment | not modelled | 14.8 | 14 | Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Uronate isomerase-like |
| 36 | c3nmdA_ | Alignment | not modelled | 14.7 | 21 | PDB header: transferase Chain: A: PDB Molecule: cgmp dependent protein kinase; PDBTitle: crystal structure of the leucine zipper domain of cgmp dependent2 protein kinase i beta |
| 37 | d1wi8a_ | Alignment | not modelled | 14.6 | 16 | Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD |
| 38 | d1vcpa_ | Alignment | not modelled | 14.6 | 33 | Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases |
| 39 | d1ttea1 | Alignment | not modelled | 14.3 | 28 | Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain |
| 40 | d1j2za_ | Alignment | not modelled | 14.0 | 11 | Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: UDP N-acetylglucosamine acyltransferase |
| 41 | c5yzlA_ | Alignment | not modelled | 13.7 | 40 | PDB header: chaperone Chain: A: PDB Molecule: protein archease; PDBTitle: crystal structure of human archease d178a |
| 42 | d1k4ta1 | Alignment | not modelled | 13.5 | 14 | Fold: Long alpha-hairpin Superfamily: Eukaryotic DNA topoisomerase I, dispensable insert domain Family: Eukaryotic DNA topoisomerase I, dispensable insert domain |
| 43 | c5fiyE_ | Alignment | not modelled | 13.3 | 18 | PDB header: apoptosis Chain: E: PDB Molecule: prkc apoptosis wt1 regulator protein; PDBTitle: crystal structure of coiled coil domain of pawr |
| 44 | d2cpia1 | Alignment | not modelled | 13.2 | 8 | Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD |
| 45 | c6cfzG_ | Alignment | not modelled | 12.5 | 18 | PDB header: nuclear protein Chain: G: PDB Molecule: hsk3; PDBTitle: structure of the dash/dam1 complex shows its role at the yeast2 kinetochore-microtubule interface |
| 46 | c1dipA_ | Alignment | not modelled | 12.5 | 7 | PDB header: acetylation Chain: A: PDB Molecule: delta-sleep-inducing peptide immunoreactive PDBTitle: the solution structure of porcine delta-sleep-inducing2 peptide immunoreactive peptide, nmr, 10 structures |
| 47 | d2d6fa1 | Alignment | not modelled | 12.5 | 13 | Fold: Sm-like fold Superfamily: GatD N-terminal domain-like Family: GatD N-terminal domain-like |
| 48 | c2marA_ | Alignment | not modelled | 12.4 | 16 | PDB header: unknown function Chain: A: PDB Molecule: sxp/ral-2 family protein; PDBTitle: solution structure of ani s 5 anisakis simplex allergen |
| 49 | c4fzsB_ | Alignment | not modelled | 12.3 | 12 | PDB header: protein transport Chain: B: PDB Molecule: sorting nexin-1; PDBTitle: structure of human snx1 bar domain |
| 50 | c3zfa_ | Alignment | not modelled | 12.2 | 17 | PDB header: zinc-binding protein Chain: A: PDB Molecule: pneumococcal histidine triad protein d; PDBTitle: n-terminal domain of pneumococcal phtd protein with bound2 zn(ii) |
| 51 | d2choa1 | Alignment | not modelled | 12.2 | 10 | Fold: Hyaluronidase domain-like Superfamily: Hyaluronidase post-catalytic domain-like Family: Hyaluronidase post-catalytic domain-like |
| 52 | d1rk8a_ | Alignment | not modelled | 11.2 | 8 | Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD |
| 53 | c6mx7C_ | Alignment | not modelled | 11.1 | 23 | PDB header: virus Chain: C: PDB Molecule: capsid; PDBTitle: cryoem structure of chimeric eastern equine encephalitis virus:2 genome-binding capsid n-terminal domain |
| 54 | c2oszA_ | Alignment | not modelled | 10.9 | 12 | PDB header: structural protein Chain: A: PDB Molecule: nucleoporin p58/p45; PDBTitle: structure of nup58/45 suggests flexible nuclear pore diameter by2 intermolecular sliding |
| 55 | c4n2pC_ | Alignment | not modelled | 10.8 | 50 | PDB header: chaperone Chain: C: PDB Molecule: protein archease; |

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|----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | PDBTitle: structure of archease from pyrococcus horikoshii |
| 56 | c5w3dB_ | Alignment | not modelled | 10.8 | 8 | PDB header: motor protein Chain: B: PDB Molecule: protein claret segregational; PDBTitle: the structure of kinesin-14 wild-type ncd- adp dimer |
| 57 | c3kltB_ | Alignment | not modelled | 10.4 | 7 | PDB header: structural protein Chain: B: PDB Molecule: vimentin; PDBTitle: crystal structure of a vimentin fragment |
| 58 | c5szwA_ | Alignment | not modelled | 10.2 | 14 | PDB header: rna binding protein Chain: A: PDB Molecule: elav-like protein 1; PDBTitle: nmr solution structure of the rrm1 domain of the post-transcriptional2 regulator hur |
| 59 | c4uqtA_ | Alignment | not modelled | 10.2 | 12 | PDB header: translation Chain: A: PDB Molecule: u2 snrnp component ist3; PDBTitle: rrm-peptide structure in res complex |
| 60 | c2wt7B_ | Alignment | not modelled | 10.1 | 11 | PDB header: transcription Chain: B: PDB Molecule: transcription factor mafb; PDBTitle: crystal structure of the bzip heterodimeric complex mafb:cfos bound to2 dna |
| 61 | c3ssuB_ | Alignment | not modelled | 10.1 | 22 | PDB header: structural protein Chain: B: PDB Molecule: vimentin; PDBTitle: crystal structure of vimentin coil1a/1b fragment |
| 62 | c3cvfA_ | Alignment | not modelled | 10.0 | 16 | PDB header: signaling protein Chain: A: PDB Molecule: homer protein homolog 3; PDBTitle: crystal structure of the carboxy terminus of homer3 |
| 63 | c6h7wO_ | Alignment | not modelled | 9.9 | 8 | PDB header: protein transport Chain: O: PDB Molecule: putative vacuolar protein sorting-associated protein; PDBTitle: model of retromer-vps5 complex assembled on membrane. |
| 64 | c5vgzF_ | Alignment | not modelled | 9.8 | 7 | PDB header: hydrolase Chain: F: PDB Molecule: 26s proteasome regulatory subunit 6a; PDBTitle: conformational landscape of the p28-bound human proteasome regulatory2 particle |
| 65 | c3nwiC_ | Alignment | not modelled | 9.6 | 15 | PDB header: transport protein Chain: C: PDB Molecule: zinc transport protein zntb; PDBTitle: the soluble domain structure of the zntb zn2+ efflux system |
| 66 | c2x6rA_ | Alignment | not modelled | 9.6 | 8 | PDB header: isomerase Chain: A: PDB Molecule: trehalose-synthase tret; PDBTitle: crystal structure of trehalose synthase tret from p.2 horikoshi produced by soaking in trehalose |
| 67 | c2yewG_ | Alignment | not modelled | 9.5 | 33 | PDB header: virus Chain: G: PDB Molecule: capsid protein; PDBTitle: modeling barmah forest virus structural proteins |
| 68 | d1huwa_ | Alignment | not modelled | 9.5 | 15 | Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Long-chain cytokines |
| 69 | c4tq1B_ | Alignment | not modelled | 9.5 | 17 | PDB header: protein binding Chain: B: PDB Molecule: tectonin beta-propeller repeat-containing protein 1; PDBTitle: crystal structure of human atg5-tecair |
| 70 | c3ipkA_ | Alignment | not modelled | 9.4 | 8 | PDB header: cell adhesion Chain: A: PDB Molecule: agi/ii; PDBTitle: crystal structure of a3vp1 of agi/ii of streptococcus mutans |
| 71 | d2cbia1 | Alignment | not modelled | 9.3 | 10 | Fold: Hyaluronidase domain-like Superfamily: Hyaluronidase post-catalytic domain-like Family: Hyaluronidase post-catalytic domain-like |
| 72 | c6dt0D_ | Alignment | not modelled | 9.3 | 4 | PDB header: transport protein Chain: D: PDB Molecule: mitochondrial calcium uniporter; PDBTitle: cryo-em structure of a mitochondrial calcium uniporter |
| 73 | d1fxla1 | Alignment | not modelled | 9.2 | 8 | Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD |
| 74 | d1gc5a_ | Alignment | not modelled | 8.6 | 19 | Fold: Ribokinase-like Superfamily: Ribokinase-like Family: ADP-specific Phosphofructokinase/Glucokinase |
| 75 | c2cbjA_ | Alignment | not modelled | 8.5 | 11 | PDB header: hydrolase Chain: A: PDB Molecule: hyaluronidase; PDBTitle: structure of the clostridium perfringens nagj family 84 glycoside2 hydrolase, a homologue of human o-glcnacase in complex with pugnac |
| 76 | d1hcia1 | Alignment | not modelled | 8.5 | 14 | Fold: Spectrin repeat-like Superfamily: Spectrin repeat Family: Spectrin repeat |
| 77 | d1weya_ | Alignment | not modelled | 8.4 | 7 | Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD |
| 78 | d1ykhb1 | Alignment | not modelled | 8.3 | 8 | Fold: Mediator hinge subcomplex-like Superfamily: Mediator hinge subcomplex-like Family: CSE2-like |
| 79 | d1rsoa_ | Alignment | not modelled | 8.1 | 19 | Fold: L27 domain Superfamily: L27 domain Family: L27 domain |
| 80 | c4lpqA_ | Alignment | not modelled | 8.1 | 30 | PDB header: transferase Chain: A: PDB Molecule: erfk/ybis/ycfs/ynhg family protein; PDBTitle: crystal structure of the l,d-transpeptidase (residues 123-326) from2 xylanimonas cellulositytica dsm 15894 |
| 81 | c3ghgK_ | Alignment | not modelled | 8.1 | 9 | PDB header: blood clotting Chain: K: PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of human fibrinogen |

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|----|-------------------------|-----------|--------------|-----|----|---|
| 82 | c1x8yA_ | Alignment | not modelled | 8.0 | 19 | PDB header: structural protein Chain: A: PDB Molecule: lamin a/c; PDBTitle: human lamin coil 2b |
| 83 | d2j01s1 | Alignment | not modelled | 8.0 | 30 | Fold: Ribonuclease H-like motif Superfamily: Translational machinery components Family: Ribosomal protein L18 and S11 |
| 84 | c5mmjv_ | Alignment | not modelled | 8.0 | 10 | PDB header: ribosome Chain: V: PDB Molecule: PDBTitle: structure of the small subunit of the chloroplast ribosome |
| 85 | c2xmpB_ | Alignment | not modelled | 7.9 | 8 | PDB header: sugar binding protein Chain: B: PDB Molecule: trehalose-synthase tret; PDBTitle: crystal structure of trehalose synthase tret mutant e326a2 from p.horishiki in complex with udp |
| 86 | c6o7xa_ | Alignment | not modelled | 7.7 | 9 | PDB header: membrane protein Chain: A: PDB Molecule: vacuolar atp synthase catalytic subunit a; PDBTitle: saccharomyces cerevisiae v-atpase stv1-v1vo state 3 |
| 87 | c4gc5A_ | Alignment | not modelled | 7.7 | 19 | PDB header: transferase Chain: A: PDB Molecule: dimethyladenosine transferase 1, mitochondrial; PDBTitle: crystal structure of murine tfb1m |
| 88 | c6ejjA_ | Alignment | not modelled | 7.6 | 15 | PDB header: transferase Chain: A: PDB Molecule: wlac protein; PDBTitle: structure of a glycosyltransferase |
| 89 | c2choA_ | Alignment | not modelled | 7.6 | 8 | PDB header: hydrolase Chain: A: PDB Molecule: glucosaminidase; PDBTitle: bacteroides thetaiotaomicron hexosaminidase with o-2 glcnacase activity |
| 90 | d2pq6a1 | Alignment | not modelled | 7.6 | 22 | Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like |
| 91 | d2vy4a1 | Alignment | not modelled | 7.6 | 29 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: CHHC finger |
| 92 | c6h9mA_ | Alignment | not modelled | 7.6 | 8 | PDB header: membrane protein Chain: A: PDB Molecule: coiled-coil domain-containing protein 90b, mitochondrial, PDBTitle: coiled-coil domain-containing protein 90b residues 43-125 from homo2 sapiens fused to a gcn4 adaptor |
| 93 | c3nmdB_ | Alignment | not modelled | 7.5 | 19 | PDB header: transferase Chain: B: PDB Molecule: cgmp dependent protein kinase; PDBTitle: crystal structure of the leucine zipper domain of cgmp dependent2 protein kinase i beta |
| 94 | c5jvpC_ | Alignment | not modelled | 7.5 | 7 | PDB header: motor protein Chain: C: PDB Molecule: chimera protein of centromere-associated protein e and PDBTitle: the neck-linker and alpha 7 helix of homo sapiens cenp-e |
| 95 | d1gpia_ | Alignment | not modelled | 7.4 | 14 | Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Glycosyl hydrolase family 7 catalytic core |
| 96 | c2gejA_ | Alignment | not modelled | 7.3 | 15 | PDB header: transferase Chain: A: PDB Molecule: phosphatidylinositol mannosyltransferase (pima); PDBTitle: crystal structure of phosphatidylinositol mannosyltransferase (pima)2 from mycobacterium smegmatis in complex with gdp-man |
| 97 | c3pltB_ | Alignment | not modelled | 7.3 | 11 | PDB header: structural protein Chain: B: PDB Molecule: sphingolipid long chain base-responsive protein lsp1; PDBTitle: crystal structure of lsp1 from saccharomyces cerevisiae |
| 98 | c1qoyA_ | Alignment | not modelled | 7.3 | 11 | PDB header: toxin Chain: A: PDB Molecule: hemolysin e; PDBTitle: e.coli hemolysin e (hlye, clya, shea) |
| 99 | c6dnfA_ | Alignment | not modelled | 7.3 | 8 | PDB header: membrane protein Chain: A: PDB Molecule: mitochondrial calcium uniporter mcu; PDBTitle: cryo-em structure of the mitochondrial calcium uniporter mcu from the2 fungus cyphellophora europaea |