














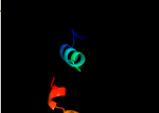



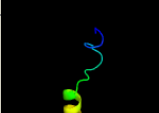




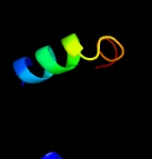


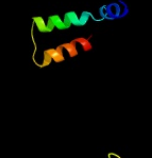

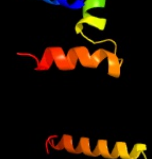
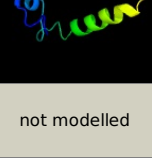


Phyre2

| | |
|---------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0203 (-) _241514_241924 |
| Date | Tue Jul 23 14:50:26 BST 2019 |
| Unique Job ID | 4786db5e1290b5ff |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|--|
| 1 | c3mayE_ |  Alignment |  | 100.0 | 100 | PDB header: heme-binding protein Chain: E: PDB Molecule: possible exported protein; PDBTitle: crystal structure of a secreted mycobacterium tuberculosis heme-2 binding protein |
| 2 | d1mo6a2 |  Alignment |  | 55.0 | 14 | Fold: Anti-LPS factor/recA domain Superfamily: RecA protein, C-terminal domain Family: RecA protein, C-terminal domain |
| 3 | d1ubea2 |  Alignment |  | 53.6 | 14 | Fold: Anti-LPS factor/recA domain Superfamily: RecA protein, C-terminal domain Family: RecA protein, C-terminal domain |
| 4 | d1xp8a2 |  Alignment |  | 53.3 | 9 | Fold: Anti-LPS factor/recA domain Superfamily: RecA protein, C-terminal domain Family: RecA protein, C-terminal domain |
| 5 | d1u94a2 |  Alignment |  | 53.1 | 23 | Fold: Anti-LPS factor/recA domain Superfamily: RecA protein, C-terminal domain Family: RecA protein, C-terminal domain |
| 6 | c3qc7A_ |  Alignment |  | 40.2 | 20 | PDB header: viral protein Chain: A: PDB Molecule: head fiber protein; PDBTitle: the structure of bacteriophage phi29 head fibers has a supercoiled2 triple repeating helix-turn-helix motif |
| 7 | c2llwA_ |  Alignment |  | 32.4 | 26 | PDB header: chaperone Chain: A: PDB Molecule: heat shock protein sti1; PDBTitle: solution structure of the yeast sti1 dp2 domain |
| 8 | c3l6gA_ |  Alignment |  | 31.2 | 22 | PDB header: glycine betaine-binding protein Chain: A: PDB Molecule: betaine abc transporter permease and substrate binding PDBTitle: crystal structure of lactococcal opuac in its open conformation |
| 9 | c3eywA_ |  Alignment |  | 29.3 | 22 | PDB header: transport protein Chain: A: PDB Molecule: c-terminal domain of glutathione-regulated potassium-efflux PDBTitle: crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff |
| 10 | c2yy0D_ |  Alignment |  | 29.1 | 21 | 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 |
| 11 | c4w66A_ |  Alignment |  | 24.5 | 17 | PDB header: transferase Chain: A: PDB Molecule: glutathione s-transferase domain protein; PDBTitle: crystal structure of glutathione s-transferase domain protein from2 haliangium ochraceum dsm 14365 |

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|----|-------------------------|-----------|---|------|----|--|
| 12 | d1m0ua1 | Alignment |  | 23.4 | 33 | Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain |
| 13 | d2pnwa1 | Alignment |  | 23.1 | 11 | Fold: Double psi beta-barrel Superfamily: Barwin-like endoglucanases Family: MLTA-like |
| 14 | d2g5da1 | Alignment |  | 21.6 | 26 | Fold: Double psi beta-barrel Superfamily: Barwin-like endoglucanases Family: MLTA-like |
| 15 | c3g36D_ | Alignment |  | 21.5 | 12 | PDB header: nuclear protein Chain: D: PDB Molecule: protein dpy-30 homolog; PDBTitle: crystal structure of the human dpy-30-like c-terminal domain |
| 16 | d1gr0a1 | Alignment |  | 21.0 | 28 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 17 | c6chgE_ | Alignment |  | 20.7 | 13 | PDB header: transferase Chain: E: PDB Molecule: klla0e03521p; PDBTitle: crystal structure of the yeast compass catalytic module |
| 18 | c3vptA_ | Alignment |  | 19.8 | 28 | PDB header: transferase Chain: A: PDB Molecule: glutathione s-transferase sigma; PDBTitle: crystal structure of bombyx mori sigma-class glutathione transferase2 in apo form |
| 19 | d1tw9a1 | Alignment |  | 19.3 | 23 | Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain |
| 20 | c4uiqA_ | Alignment |  | 19.2 | 17 | PDB header: transferase Chain: A: PDB Molecule: globin-coupled sensor with diguanylate cyclase activity; PDBTitle: isolated globin domain of the bordetella pertussis globin-2 coupled sensor with a heme at the dimer interface |
| 21 | c2k7hA_ | Alignment | not modelled | 18.4 | 35 | PDB header: allergen Chain: A: PDB Molecule: stress-induced protein sam22; PDBTitle: nmr solution structure of soybean allergen gly m 4 |
| 22 | c2x7pA_ | Alignment | not modelled | 18.3 | 9 | PDB header: unknown function Chain: A: PDB Molecule: possible thiamine biosynthesis enzyme; PDBTitle: the conserved candida albicans ca3427 gene product defines a new2 family of proteins exhibiting the generic periplasmic binding3 protein structural fold |
| 23 | c3tl4X_ | Alignment | not modelled | 18.2 | 10 | PDB header: ligase Chain: X: PDB Molecule: glutaminyl-trna synthetase; PDBTitle: crystal structure of the trna binding domain of glutaminyl-trna2 synthetase from saccharomyces cerevisiae |
| 24 | c6bx3N_ | Alignment | not modelled | 14.2 | 21 | PDB header: gene regulation/transferase Chain: N: PDB Molecule: compass component sdc1; PDBTitle: structure of histone h3k4 methyltransferase |
| 25 | d1okta1 | Alignment | not modelled | 14.2 | 10 | Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain |
| 26 | c4r7qA_ | Alignment | not modelled | 14.0 | 17 | PDB header: signaling protein Chain: A: PDB Molecule: sensor histidine kinase; PDBTitle: the structure of a sensor domain of a histidine kinase from vibrio2 cholerae o1 biovar eltor str. n16961 |
| 27 | c2wlvA_ | Alignment | not modelled | 13.2 | 15 | PDB header: viral protein Chain: A: PDB Molecule: gag polyprotein; PDBTitle: structure of the n-terminal capsid domain of hiv-2 |
| 28 | d1r9la_ | Alignment | not modelled | 13.0 | 10 | Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like PDB header: transferase |

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|----|-------------------------|-----------|--------------|------|----|---|
| 29 | c2hnlB_ | Alignment | not modelled | 11.9 | 12 | Chain: B; PDB Molecule: glutathione s-transferase 1; PDBTitle: structure of the prostaglandin d synthase from the parasitic nematode2 onchocerca volvulus |
| 30 | c2mqkA_ | Alignment | not modelled | 11.9 | 9 | PDB header: hydrolase Chain: A; PDB Molecule: atp-dependent target dna activator b; PDBTitle: solution structure of n terminal domain of the nub aaa+ atpase |
| 31 | c4kvuC_ | Alignment | not modelled | 11.6 | 31 | PDB header: de novo protein Chain: C; PDB Molecule: 6-helix coiled coil cc-hex-I17c-w224bf; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-I17c-w224bf |
| 32 | c5h5IA_ | Alignment | not modelled | 11.5 | 25 | PDB header: transferase Chain: A; PDB Molecule: glutathione s-transferase s2; PDBTitle: structure of prostaglandin synthase d of nilaparvata lugens |
| 33 | d1hsta_ | Alignment | not modelled | 11.2 | 25 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Linker histone H1/H5 |
| 34 | d1yqaa1 | Alignment | not modelled | 11.1 | 16 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Linker histone H1/H5 |
| 35 | c2gsqA_ | Alignment | not modelled | 10.7 | 16 | PDB header: transferase Chain: A; PDB Molecule: glutathione s-transferase; PDBTitle: glutathione s-transferase from squid digestive gland complexed with s-2 (3-iodobenzyl)glutathione |
| 36 | c4kvuA_ | Alignment | not modelled | 10.5 | 31 | PDB header: de novo protein Chain: A; PDB Molecule: 6-helix coiled coil cc-hex-I17c-w224bf; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-I17c-w224bf |
| 37 | c4kvuB_ | Alignment | not modelled | 10.4 | 31 | PDB header: de novo protein Chain: B; PDB Molecule: 6-helix coiled coil cc-hex-I17c-w224bf; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-I17c-w224bf |
| 38 | c2q2kB_ | Alignment | not modelled | 10.4 | 13 | PDB header: dna binding protein/dna Chain: B; PDB Molecule: hypothetical protein; PDBTitle: structure of nucleic-acid binding protein |
| 39 | d1pd211 | Alignment | not modelled | 10.3 | 20 | Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain |
| 40 | c4h67D_ | Alignment | not modelled | 10.2 | 17 | PDB header: transferase Chain: D; PDB Molecule: pyrimidine precursor biosynthesis enzyme thi5; PDBTitle: crystal structure of hmp synthase thi5 from s. cerevisiae |
| 41 | d1or4a_ | Alignment | not modelled | 10.2 | 10 | Fold: Globin-like Superfamily: Globin-like Family: Globins |
| 42 | d1kja1 | Alignment | not modelled | 10.0 | 26 | Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: DNA gyrase/MutL, second domain |
| 43 | d1su3a1 | Alignment | not modelled | 9.9 | 43 | Fold: PGBD-like Superfamily: PGBD-like Family: MMP N-terminal domain |
| 44 | c1gr0A_ | Alignment | not modelled | 9.8 | 21 | PDB header: isomerase Chain: A; PDB Molecule: inositol-3-phosphate synthase; PDBTitle: myo-inositol 1-phosphate synthase from mycobacterium2 tuberculosis in complex with nad and zinc. |
| 45 | c6gq9A_ | Alignment | not modelled | 9.8 | 14 | PDB header: allergen Chain: A; PDB Molecule: major allergen cor a 1.0401; PDBTitle: solution structure of the hazel allergen cor a 1.0401 |
| 46 | d1xdfa1 | Alignment | not modelled | 9.7 | 29 | Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like |
| 47 | c3czbA_ | Alignment | not modelled | 9.7 | 6 | PDB header: structural genomics, unknown function Chain: A; PDB Molecule: putative transglycosylase; PDBTitle: crystal structure of putative transglycosylase from caulobacter2 crescentus |
| 48 | c4ps2A_ | Alignment | not modelled | 9.6 | 25 | PDB header: contractile protein Chain: A; PDB Molecule: putative type vi secretion protein; PDBTitle: structure of the c-terminal fragment (87-165) of e.coli eaec tssb2 molecule |
| 49 | c2k5jB_ | Alignment | not modelled | 9.4 | 0 | PDB header: structural genomics, unknown function Chain: B; PDB Molecule: uncharacterized protein yiif; PDBTitle: solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1 |
| 50 | d1f3ba1 | Alignment | not modelled | 9.4 | 14 | Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain |
| 51 | c1iyiA_ | Alignment | not modelled | 9.4 | 24 | PDB header: isomerase Chain: A; PDB Molecule: hematopoietic prostaglandin d synthase; PDBTitle: crystal structure of hematopoietic prostaglandin d synthase |
| 52 | c5wd9A_ | Alignment | not modelled | 9.3 | 14 | PDB header: protein binding Chain: A; PDB Molecule: lem22; PDBTitle: crystal structure of legionella pneumophila effector lpg2328 |
| 53 | d1ml6a1 | Alignment | not modelled | 9.2 | 14 | Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain |
| 54 | d1slma1 | Alignment | not modelled | 9.1 | 43 | Fold: PGBD-like Superfamily: PGBD-like Family: MMP N-terminal domain |
| 55 | c3g80B_ | Alianment | not modelled | 8.9 | 30 | PDB header: viral protein Chain: B; PDB Molecule: protein b2; |

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|----|-------------------------|-----------|--------------|-----|----|--|
| | | | | | | PDBTitle: nodamura virus protein b2, rna-binding domain |
| 56 | c2lnbA | Alignment | not modelled | 8.6 | 35 | PDB header: immune system Chain: A: PDB Molecule: z-dna-binding protein 1; PDBTitle: solution nmr structure of n-terminal domain (6-74) of human zbp12 protein, northeast structural genomics consortium target hr8174a. |
| 57 | c2de4B | Alignment | not modelled | 8.4 | 14 | PDB header: hydrolase Chain: B: PDB Molecule: dibenzothiophene desulfurization enzyme b; PDBTitle: crystal structure of dszb c27s mutant in complex with biphenyl-2-2 sulfinic acid |
| 58 | d1ussa | Alignment | not modelled | 8.4 | 19 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Linker histone H1/H5 |
| 59 | c2lnmA | Alignment | not modelled | 8.2 | 11 | PDB header: protein transport Chain: A: PDB Molecule: protein tic 40, chloroplastic; PDBTitle: solution structure of the c-terminal np-repeat domain of tic40, a co-2 chaperone during protein import into chloroplasts |
| 60 | c2rqpA | Alignment | not modelled | 8.1 | 13 | PDB header: gene regulation Chain: A: PDB Molecule: heterochromatin protein 1-binding protein 3; PDBTitle: the solution structure of heterochromatin protein 1-binding2 protein 74 histone h1 like domain |
| 61 | c2q2kA | Alignment | not modelled | 8.1 | 13 | PDB header: dna binding protein/dna Chain: A: PDB Molecule: hypothetical protein; PDBTitle: structure of nucleic-acid binding protein |
| 62 | d1gpqa | Alignment | not modelled | 8.0 | 25 | Fold: Inhibitor of vertebrate lysozyme, lvy Superfamily: Inhibitor of vertebrate lysozyme, lvy Family: Inhibitor of vertebrate lysozyme, lvy |
| 63 | d1l6ja1 | Alignment | not modelled | 7.9 | 43 | Fold: PGBD-like Superfamily: PGBD-like Family: MMP N-terminal domain |
| 64 | c6n39A | Alignment | not modelled | 7.8 | 15 | PDB header: transferase Chain: A: PDB Molecule: dephospho-coa kinase; PDBTitle: crystal structure of an dephospho-coa kinase coae from mycobacterium2 paratuberculosis |
| 65 | d1eaka1 | Alignment | not modelled | 7.8 | 43 | Fold: PGBD-like Superfamily: PGBD-like Family: MMP N-terminal domain |
| 66 | d1hyoa1 | Alignment | not modelled | 7.8 | 23 | Fold: SH3-like barrel Superfamily: Fumarylacetoacetate hydrolase, FAH, N-terminal domain Family: Fumarylacetoacetate hydrolase, FAH, N-terminal domain |
| 67 | d1icxa | Alignment | not modelled | 7.6 | 24 | Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like |
| 68 | d2eiaa2 | Alignment | not modelled | 7.5 | 8 | Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain |
| 69 | c2rejA | Alignment | not modelled | 7.3 | 17 | PDB header: choline-binding protein Chain: A: PDB Molecule: putative glycine betaine abc transporter protein; PDBTitle: abc-transporter choline binding protein in unliganded semi-2 closed conformation |
| 70 | d1s16a1 | Alignment | not modelled | 7.2 | 16 | Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: DNA gyrase/MutL, second domain |
| 71 | d1m9dc | Alignment | not modelled | 7.2 | 21 | Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain |
| 72 | d1b8xa1 | Alignment | not modelled | 7.1 | 11 | Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain |
| 73 | d1v4aa2 | Alignment | not modelled | 7.1 | 16 | Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: GlnE-like domain |
| 74 | d1m9fd | Alignment | not modelled | 6.8 | 19 | Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain |
| 75 | d1e09a | Alignment | not modelled | 6.7 | 14 | Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like |
| 76 | d2gsqa1 | Alignment | not modelled | 6.7 | 21 | Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain |
| 77 | d2cvda1 | Alignment | not modelled | 6.7 | 24 | Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain |
| 78 | c6iuiC | Alignment | not modelled | 6.6 | 29 | PDB header: protein binding Chain: C: PDB Molecule: paxillin; PDBTitle: crystal structure of git1 pbd domain in complex with paxillin ld42 motif |
| 79 | c6iuiD | Alignment | not modelled | 6.5 | 29 | PDB header: protein binding Chain: D: PDB Molecule: paxillin; PDBTitle: crystal structure of git1 pbd domain in complex with paxillin ld42 motif |
| 80 | c2pijB | Alignment | not modelled | 6.5 | 20 | PDB header: transcription Chain: B: PDB Molecule: prophage pfl 6 cro; PDBTitle: structure of the cro protein from prophage pfl 6 in pseudomonas2 fluorescens pf-5 |
| 81 | d2pxrc1 | Alignment | not modelled | 6.4 | 21 | Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain |

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|----|-------------------------|-----------|--------------|-----|----|---|
| | | | | | | Family: Retrovirus capsid protein, N-terminal core domain |
| 82 | c5x90B_ | Alignment | not modelled | 6.4 | 29 | PDB header: protein transport Chain: B: PDB Molecule: icmw; PDBTitle: structure of dotl(656-783)-icms-icmw-lvga derived from legionella2 pneumophila |
| 83 | d1ei1a1 | Alignment | not modelled | 6.4 | 16 | Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: DNA gyrase/MutL, second domain |
| 84 | c2ws2B_ | Alignment | not modelled | 6.3 | 34 | PDB header: transferase Chain: B: PDB Molecule: glutathione s-transferase; PDBTitle: the 2 angstrom structure of a nu-class gst from haemonchus contortus |
| 85 | d1k3ya1 | Alignment | not modelled | 6.2 | 16 | Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain |
| 86 | c5i6hA_ | Alignment | not modelled | 6.2 | 14 | PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase-like protein; PDBTitle: crystal structure of cd-ct domains of chaetomium thermophilum acetyl-2 coa carboxylase |
| 87 | c1m0uB_ | Alignment | not modelled | 6.1 | 34 | PDB header: transferase Chain: B: PDB Molecule: gst2 gene product; PDBTitle: crystal structure of the drosophila glutathione s-transferase-2 in2 complex with glutathione |
| 88 | c4esxA_ | Alignment | not modelled | 6.1 | 11 | PDB header: transferase Chain: A: PDB Molecule: pyrimidine biosynthesis enzyme thi13; PDBTitle: crystal structure of c. albicans thi5 complexed with plp |
| 89 | c1l6nA_ | Alignment | not modelled | 6.1 | 28 | PDB header: viral protein Chain: A: PDB Molecule: gag polyprotein; PDBTitle: structure of the n-terminal 283-residue fragment of the hiv-2 1 gag polyprotein |
| 90 | c3chgB_ | Alignment | not modelled | 5.9 | 5 | PDB header: ligand binding protein Chain: B: PDB Molecule: glycine betaine-binding protein; PDBTitle: the compatible solute-binding protein opuac from bacillus2 subtilis in complex with dmsa |
| 91 | c3f2eA_ | Alignment | not modelled | 5.9 | 19 | PDB header: viral protein Chain: A: PDB Molecule: sirv coat protein; PDBTitle: crystal structure of yellowstone sirv coat protein c-terminus |
| 92 | d1wjfa_ | Alignment | not modelled | 5.9 | 11 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: N-terminal Zn binding domain of HIV integrase Family: N-terminal Zn binding domain of HIV integrase |
| 93 | c5i0cA_ | Alignment | not modelled | 5.9 | 21 | PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein yjdj; PDBTitle: crystal structure of predicted acyltransferase yjdj with acyl-coa n-2 acyltransferase domain from escherichia coli str. k-12 |
| 94 | c3jqhA_ | Alignment | not modelled | 5.9 | 32 | PDB header: sugar binding protein Chain: A: PDB Molecule: c-type lectin domain family 4 member m; PDBTitle: structure of the neck region of the glycan-binding receptor dc-signr |
| 95 | d1ixsa_ | Alignment | not modelled | 5.8 | 19 | Fold: RuvA C-terminal domain-like Superfamily: DNA helicase RuvA subunit, C-terminal domain Family: DNA helicase RuvA subunit, C-terminal domain |
| 96 | d1r5aa1 | Alignment | not modelled | 5.8 | 15 | Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain |
| 97 | d1wiwa_ | Alignment | not modelled | 5.6 | 10 | Fold: SIS domain Superfamily: SIS domain Family: double-SIS domain |
| 98 | c3tmgA_ | Alignment | not modelled | 5.6 | 8 | PDB header: transport protein Chain: A: PDB Molecule: glycine betaine, l-proline abc transporter, PDBTitle: crystal structure of glycine betaine, l-proline abc transporter,2 glycine/betaine/l-proline-binding protein (prox) from borrelia3 burgdorferi |
| 99 | c4deyB_ | Alignment | not modelled | 5.4 | 18 | PDB header: transport protein Chain: B: PDB Molecule: voltage-dependent l-type calcium channel subunit alpha-1c; PDBTitle: crystal structure of the voltage dependent calcium channel beta-22 subunit in complex with the cav1.2 i-ii linker. |