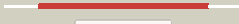



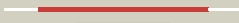








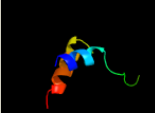
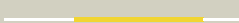






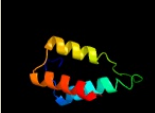
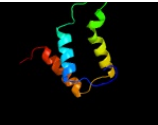



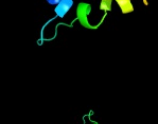
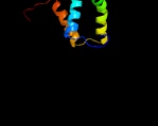

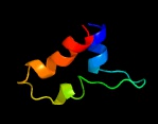
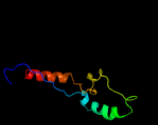


Phyre2

| | |
|---------------|-------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD3046c (-)_3407325_3407699 |
| Date | Thu Aug 8 16:20:22 BST 2019 |
| Unique Job ID | 2f3b5d90a0b841dd |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c2lkyA_ |  Alignment |  | 100.0 | 38 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of msmeq_1053, the second duf3349 annotated protein2 in the genome of mycobacterium smegmatis, seattle structural genomics3 center for infectious disease target myma.17112.b |
| 2 | c2kvcA_ |  Alignment |  | 100.0 | 38 | PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a |
| 3 | c3ol4B_ |  Alignment |  | 100.0 | 37 | PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c |
| 4 | c2m0nA_ |  Alignment |  | 100.0 | 54 | PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of a duf3349 annotated protein from mycobacterium2 abscessus, mab_3403c. seattle structural genomics center for3 infectious disease target myaba.17112.a.a2 |
| 5 | d1khda1 |  Alignment |  | 86.2 | 20 | Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain |
| 6 | d1o17a1 |  Alignment |  | 86.1 | 9 | Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain |
| 7 | d1hj3a1 |  Alignment |  | 83.0 | 30 | Fold: Cytochrome c Superfamily: Cytochrome c Family: N-terminal (heme c) domain of cytochrome cd1-nitrite reductase |
| 8 | d1v8ga1 |  Alignment |  | 79.4 | 20 | Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain |
| 9 | d1qksa1 |  Alignment |  | 79.3 | 21 | Fold: Cytochrome c Superfamily: Cytochrome c Family: N-terminal (heme c) domain of cytochrome cd1-nitrite reductase |
| 10 | d1uoua1 |  Alignment |  | 76.9 | 18 | Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain |
| 11 | d2tpta1 |  Alignment |  | 73.0 | 18 | Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain |

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|----|--------------------------|-----------|---|------|----|---|
| 12 | d1brwa1 | Alignment |  | 71.8 | 20 | Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain |
| 13 | c3mk7F_ | Alignment |  | 61.6 | 9 | PDB header: oxidoreductase Chain: F: PDB Molecule: cytochrome c oxidase, cbb3-type, subunit p; PDBTitle: the structure of cbb3 cytochrome oxidase |
| 14 | c1o17A_ | Alignment |  | 61.2 | 8 | PDB header: transferase Chain: A: PDB Molecule: anthranilate phosphoribosyltransferase; PDBTitle: anthranilate phosphoribosyl-transferase (trpd) |
| 15 | d1e2rb1 | Alignment |  | 58.7 | 16 | Fold: Cytochrome c Superfamily: Cytochrome c Family: N-terminal (heme c) domain of cytochrome cd1-nitrite reductase |
| 16 | c4hkmA_ | Alignment |  | 57.2 | 6 | PDB header: transferase Chain: A: PDB Molecule: anthranilate phosphoribosyltransferase; PDBTitle: crystal structure of an anthranilate phosphoribosyltransferase (target2 id nysgrc-016600) from xanthomonas campestris |
| 17 | c1ta9A_ | Alignment |  | 57.1 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase from schizosaccharomyces pombe |
| 18 | d1nira1 | Alignment |  | 54.0 | 26 | Fold: Cytochrome c Superfamily: Cytochrome c Family: N-terminal (heme c) domain of cytochrome cd1-nitrite reductase |
| 19 | d1t1ea2 | Alignment |  | 51.6 | 21 | Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Subtilase propeptides/inhibitors |
| 20 | c3ee6A_ | Alignment |  | 50.3 | 21 | PDB header: hydrolase Chain: A: PDB Molecule: tripeptidyl-peptidase 1; PDBTitle: crystal structure analysis of tripeptidyl peptidase -i |
| 21 | d2c8sa1 | Alignment | not modelled | 50.1 | 13 | Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c |
| 22 | c2m29A_ | Alignment | not modelled | 49.0 | 16 | PDB header: metal binding protein Chain: A: PDB Molecule: calcium-binding protein 4; PDBTitle: nmr structure of ca2+ bound cabp4 n-domain |
| 23 | c3ek7A_ | Alignment | not modelled | 47.6 | 26 | PDB header: fluorescent protein Chain: A: PDB Molecule: myosin light chain kinase, green fluorescent protein, PDBTitle: calcium-saturated gcamp2 dimer |
| 24 | c3gr0D_ | Alignment | not modelled | 46.9 | 18 | PDB header: membrane protein Chain: D: PDB Molecule: protein prgh; PDBTitle: periplasmic domain of the t3ss inner membrane protein prgh from2 s.typhimurium (fragment 170-362) |
| 25 | d1lavsa_ | Alignment | not modelled | 46.2 | 18 | Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like |
| 26 | c3edyA_ | Alignment | not modelled | 44.9 | 22 | PDB header: hydrolase Chain: A: PDB Molecule: tripeptidyl-peptidase 1; PDBTitle: crystal structure of the precursor form of human tripeptidyl-peptidase2 1 |
| 27 | c4oy4A_ | Alignment | not modelled | 44.6 | 23 | PDB header: calcium binding, fluorescent, transferas Chain: A: PDB Molecule: chimera protein of calmodulin, gpf-like protein eosfp, and PDBTitle: calcium-free campari v0.2 |
| 28 | d1ng6a_ | Alignment | not modelled | 44.4 | 15 | Fold: GatB/YqeY motif Superfamily: GatB/YqeY motif Family: GatB/YqeY domain |
| 29 | c2k7ba_ | Alignment | not modelled | 43.9 | 12 | PDB header: metal binding protein Chain: A: PDB Molecule: calcium-binding protein 1; PDBTitle: nmr structure of mg2+-bound cabp1 n-domain |

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|----|-------------------------|-----------|--------------|------|----|---|
| 30 | c1khdD | Alignment | not modelled | 42.5 | 17 | PDB header: transferase Chain: D: PDB Molecule: anthranilate phosphoribosyltransferase; PDBTitle: crystal structure analysis of the anthranilate2 phosphoribosyltransferase from erwinia carotovora at 1.9 resolution3 (current name, pectobacterium carotovorum) |
| 31 | c4muoB | Alignment | not modelled | 41.1 | 8 | PDB header: dna binding protein Chain: B: PDB Molecule: uncharacterized protein ybib; PDBTitle: the trpd2 enzyme from e.coli: ybib |
| 32 | d1h9xa1 | Alignment | not modelled | 40.9 | 18 | Fold: Cytochrome c Superfamily: Cytochrome c Family: N-terminal (heme c) domain of cytochrome cd1-nitrite reductase |
| 33 | d2pq3a1 | Alignment | not modelled | 40.3 | 25 | Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like |
| 34 | c2ktgA | Alignment | not modelled | 40.2 | 13 | PDB header: ca-binding protein Chain: A: PDB Molecule: calmodulin, putative; PDBTitle: calmodulin like protein from entamoeba histolytica: solution structure2 and calcium binding properties of a partially folded protein |
| 35 | c1tleA | Alignment | not modelled | 39.9 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: kumamolisin; PDBTitle: high resolution crystal structure of the intact pro-2 kumamolisin, a sedolisin type proteinase (previously3 called kumamolysin or kscp) |
| 36 | c6ge2A | Alignment | not modelled | 39.4 | 26 | PDB header: hormone Chain: A: PDB Molecule: exendin-4; PDBTitle: exendin-4 based dual glp-1/glucagon receptor agonist |
| 37 | c2zxyA | Alignment | not modelled | 38.8 | 12 | PDB header: oxygen binding, transport protein Chain: A: PDB Molecule: cytochrome c552; PDBTitle: crystal structure of cytochrome c555 from aquifex aeolicus |
| 38 | c3u0kA | Alignment | not modelled | 37.8 | 18 | PDB header: fluorescent protein Chain: A: PDB Molecule: rcamp; PDBTitle: crystal structure of the genetically encoded calcium indicator rcamp |
| 39 | c1brwB | Alignment | not modelled | 37.4 | 20 | PDB header: transferase Chain: B: PDB Molecule: protein (pyrimidine nucleoside phosphorylase); PDBTitle: the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation |
| 40 | d1hzua1 | Alignment | not modelled | 36.7 | 26 | Fold: Cytochrome c Superfamily: Cytochrome c Family: N-terminal (heme c) domain of cytochrome cd1-nitrite reductase |
| 41 | c2dsjA | Alignment | not modelled | 36.2 | 10 | PDB header: transferase Chain: A: PDB Molecule: pyrimidine-nucleoside (thymidine) phosphorylase; PDBTitle: crystal structure of project id tt0128 from thermus thermophilus hb8 |
| 42 | c1jrjA | Alignment | not modelled | 35.9 | 42 | PDB header: hormone/growth factor Chain: A: PDB Molecule: exendin-4; PDBTitle: solution structure of exendin-4 in 30-vol% trifluoroethanol |
| 43 | c2xtsD | Alignment | not modelled | 33.8 | 14 | PDB header: oxidoreductase/electron transport Chain: D: PDB Molecule: cytochrome; PDBTitle: crystal structure of the sulfane dehydrogenase soxcd from paracoccus2 pantotrophus |
| 44 | c5n1tB | Alignment | not modelled | 33.6 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome c; PDBTitle: crystal structure of complex between flavocytochrome c and copper2 chaperone copc from t. paradoxus |
| 45 | c3cuqD | Alignment | not modelled | 33.2 | 27 | PDB header: protein transport Chain: D: PDB Molecule: vacuolar protein-sorting-associated protein 25; PDBTitle: integrated structural and functional model of the human escrt-ii2 complex |
| 46 | c2zmeD | Alignment | not modelled | 33.2 | 27 | PDB header: protein transport Chain: D: PDB Molecule: vacuolar protein-sorting-associated protein 25; PDBTitle: integrated structural and functional model of the human escrt-ii2 complex |
| 47 | c5mwwA | Alignment | not modelled | 32.4 | 25 | PDB header: transferase Chain: A: PDB Molecule: rna polymerase sigma factor siga; PDBTitle: sigma1.1 domain of sigmaa from bacillus subtilis |
| 48 | d1dvha | Alignment | not modelled | 31.5 | 9 | Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c |
| 49 | c1h1oA | Alignment | not modelled | 30.5 | 14 | PDB header: electron transport Chain: A: PDB Molecule: cytochrome c-552; PDBTitle: acidithiobacillus ferrooxidans cytochrome c4 structure2 supports a complex-induced tuning of electron transfer |
| 50 | c1wvoA | Alignment | not modelled | 30.4 | 41 | PDB header: transferase Chain: A: PDB Molecule: sialic acid synthase; PDBTitle: solution structure of rsgi ruh-029, an antifreeze protein2 like domain in human n-acetylneuraminic acid phosphate3 synthase gene. |
| 51 | c4n6cB | Alignment | not modelled | 29.6 | 17 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the b1rzq2 protein from streptococcus pneumoniae.2 northeast structural genomics consortium (nesg) target spr36. |
| 52 | c5zorA | Alignment | not modelled | 29.3 | 29 | PDB header: metal binding protein Chain: A: PDB Molecule: centrin, putative; PDBTitle: solution structure of centrin4 from trypanosoma brucei |
| 53 | c6jtdB | Alignment | not modelled | 29.2 | 12 | PDB header: transferase Chain: B: PDB Molecule: c-glycosyltransferase; PDBTitle: crystal structure of tccg1 in complex with udp |

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|----|--------------------------|-----------|--------------|------|----|---|
| 54 | c4ga5H_ | Alignment | not modelled | 27.4 | 18 | PDB header: transferase Chain: H: PDB Molecule: putative thymidine phosphorylase; PDBTitle: crystal structure of amp phosphorylase c-terminal deletion mutant in2 the apo-form |
| 55 | c1c8aA_ | Alignment | not modelled | 27.3 | 22 | PDB header: antifreeze protein Chain: A: PDB Molecule: protein (antifreeze protein type iii); PDBTitle: nmr structure of intramolecular dimer antifreeze protein2 rd3, 40 sa structures |
| 56 | c3h5qA_ | Alignment | not modelled | 26.9 | 13 | PDB header: transferase Chain: A: PDB Molecule: pyrimidine-nucleoside phosphorylase; PDBTitle: crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus |
| 57 | c4i66A_ | Alignment | not modelled | 26.5 | 13 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein hoch_4089; PDBTitle: crystal structure of hoch_4089 protein from haliangium ochraceum |
| 58 | d3nlaa_ | Alignment | not modelled | 26.4 | 28 | Fold: beta-clip Superfamily: AFP III-like domain Family: AFP III-like domain |
| 59 | d1c8aa2_ | Alignment | not modelled | 26.2 | 22 | Fold: beta-clip Superfamily: AFP III-like domain Family: AFP III-like domain |
| 60 | d1xb4a1_ | Alignment | not modelled | 25.1 | 18 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain |
| 61 | c5tdyD_ | Alignment | not modelled | 25.0 | 23 | PDB header: motor protein Chain: D: PDB Molecule: flagellar motor switch protein flig; PDBTitle: structure of cofolded flifc:flign complex from thermotoga maritima |
| 62 | c5xj0Y_ | Alignment | not modelled | 24.9 | 33 | PDB header: transferase/transcription Chain: Y: PDB Molecule: gp76; PDBTitle: t. thermophilus rna polymerase holoenzyme bound with gp39 and gp76 |
| 63 | d2vcha1_ | Alignment | not modelled | 24.8 | 7 | Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like |
| 64 | c2k6xA_ | Alignment | not modelled | 24.6 | 17 | PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma factor rpod; PDBTitle: autoregulation of a group 1 bacterial sigma factor involves2 the formation of a region 1.1- induced compacted structure |
| 65 | c2bpqB_ | Alignment | not modelled | 24.2 | 16 | PDB header: transferase Chain: B: PDB Molecule: anthranilate phosphoribosyltransferase; PDBTitle: anthranilate phosphoribosyltransferase (trpd) from2 mycobacterium tuberculosis (apo structure) |
| 66 | c3kblA_ | Alignment | not modelled | 24.1 | 36 | PDB header: protein binding Chain: A: PDB Molecule: female germline-specific tumor suppressor gld-1; PDBTitle: crystal structure of the gld-1 homodimerization domain from2 caenorhabditis elegans n169a mutant at 2.28 a resolution |
| 67 | d1fcdc1_ | Alignment | not modelled | 23.9 | 16 | Fold: Cytochrome c Superfamily: Cytochrome c Family: Two-domain cytochrome c |
| 68 | c2j0fC_ | Alignment | not modelled | 23.9 | 16 | PDB header: transferase Chain: C: PDB Molecule: thymidine phosphorylase; PDBTitle: structural basis for non-competitive product inhibition in2 human thymidine phosphorylase: implication for drug design |
| 69 | c4j20B_ | Alignment | not modelled | 23.8 | 29 | PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome c-555; PDBTitle: x-ray structure of the cytochrome c-554 from chlorobaculum tepidum |
| 70 | c1vquB_ | Alignment | not modelled | 23.7 | 12 | PDB header: transferase Chain: B: PDB Molecule: anthranilate phosphoribosyltransferase 2; PDBTitle: crystal structure of anthranilate phosphoribosyltransferase 22 (17130499) from nostoc sp. at 1.85 a resolution |
| 71 | c3ecjC_ | Alignment | not modelled | 23.5 | 13 | PDB header: oxidoreductase Chain: C: PDB Molecule: protein (homoprotocatechuate 2,3-dioxygenase); PDBTitle: structure of e323l mutant of homoprotocatechuate 2,3-dioxygenase from2 brevibacterium fuscum at 1.65a resolution |
| 72 | c1zswA_ | Alignment | not modelled | 23.3 | 9 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: glyoxalase family protein; PDBTitle: crystal structure of bacillus cereus metallo protein from glyoxalase2 family |
| 73 | d1c53a_ | Alignment | not modelled | 23.2 | 13 | Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c |
| 74 | d1c75a_ | Alignment | not modelled | 23.2 | 21 | Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c |
| 75 | c4dnnB_ | Alignment | not modelled | 22.7 | 36 | PDB header: splicing Chain: B: PDB Molecule: protein quaking; PDBTitle: crystal structure of the quaking qua1 homodimerization domain |
| 76 | d2acva1_ | Alignment | not modelled | 22.5 | 18 | Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like |
| 77 | c3deeA_ | Alignment | not modelled | 22.4 | 8 | PDB header: transcription Chain: A: PDB Molecule: putative regulatory protein; PDBTitle: crystal structure of a putative regulatory protein involved in2 transcription (ngo1945) from neisseria gonorrhoeae fa 1090 at 2.25 a3 resolution |
| 78 | c4i2yB_ | Alignment | not modelled | 22.3 | 24 | PDB header: fluorescent protein Chain: B: PDB Molecule: rgeco1; PDBTitle: crystal structure of the genetically encoded calcium indicator rgeco1 |

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|----|-------------------------|-----------|--------------|------|----|--|
| 79 | c2zszW | Alignment | not modelled | 22.3 | 14 | PDB header: electron transport Chain: W: PDB Molecule: PDBTitle: crystal structure of cytochrome c554 from vibrio2 parahaemolyticus strain rimd2210633 |
| 80 | c2zooA | Alignment | not modelled | 22.0 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: probable nitrite reductase; PDBTitle: crystal structure of nitrite reductase from pseudoalteromonas2 haloplanktis tac125 |
| 81 | d1zaca | Alignment | not modelled | 22.0 | 19 | Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like |
| 82 | c3omdB | Alignment | not modelled | 21.8 | 11 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of unknown function protein from leptospirillum2 rubarum |
| 83 | c6hwhj | Alignment | not modelled | 21.8 | 21 | PDB header: electron transport Chain: J: PDB Molecule: co-purified unknown peptide built as polyala; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis |
| 84 | d1opsa | Alignment | not modelled | 21.4 | 28 | Fold: beta-clip Superfamily: AFP III-like domain Family: AFP III-like domain |
| 85 | d1a56a | Alignment | not modelled | 21.4 | 9 | Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c |
| 86 | c2lv7A | Alignment | not modelled | 21.4 | 13 | PDB header: metal binding protein Chain: A: PDB Molecule: calcium-binding protein 7; PDBTitle: solution structure of ca2+-bound cabp7 n-terminal doman |
| 87 | d1zswa2 | Alignment | not modelled | 21.1 | 9 | Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: BC1024-like |
| 88 | c4ax3A | Alignment | not modelled | 21.0 | 6 | PDB header: oxidoreductase Chain: A: PDB Molecule: copper-containing nitrite reductase; PDBTitle: structure of three-domain heme-cu nitrite reductase from ralstonia2 pickettii at 1.6 a resolution |
| 89 | d1m70a2 | Alignment | not modelled | 20.3 | 11 | Fold: Cytochrome c Superfamily: Cytochrome c Family: Two-domain cytochrome c |
| 90 | c2ybvN | Alignment | not modelled | 20.0 | 28 | PDB header: lyase Chain: N: PDB Molecule: ribulose bisphosphate carboxylase small subunit; PDBTitle: structure of rubisco from thermosynechococcus elongatus |
| 91 | c6adqC | Alignment | not modelled | 19.9 | 18 | PDB header: electron transport Chain: C: PDB Molecule: cytochrome bc1 complex cytochrome c subunit; PDBTitle: respiratory complex ciii2civ2sod2 from mycobacterium smegmatis |
| 92 | c2n39A | Alignment | not modelled | 19.9 | 27 | PDB header: dna binding protein Chain: A: PDB Molecule: chromodomain-helicase-dna-binding protein 1; PDBTitle: nmr solution structure of a c-terminal domain of the chromodomain2 helicase dna-binding protein 1 |
| 93 | c5v2kA | Alignment | not modelled | 19.8 | 12 | PDB header: transferase Chain: A: PDB Molecule: udp-glucosyltransferase 74f2; PDBTitle: crystal structure of udp-glucosyltransferase, ugt74f2 (t15a), with udp2 and 2-bromobenzoic acid |
| 94 | c4pwaA | Alignment | not modelled | 19.8 | 24 | PDB header: electron transport Chain: A: PDB Molecule: putative cytochrome c; PDBTitle: crystal structure of the c-type cytochrome soru from sinorhizobium2 meliloti |
| 95 | d1rbli | Alignment | not modelled | 19.8 | 32 | Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit |
| 96 | c2i2rK | Alignment | not modelled | 19.7 | 40 | PDB header: transport protein Chain: K: PDB Molecule: potassium voltage-gated channel subfamily d member 3; PDBTitle: crystal structure of the kchip1/kv4.3 t1 complex |
| 97 | d1f54a | Alignment | not modelled | 19.5 | 23 | Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like |
| 98 | d2ji7a1 | Alignment | not modelled | 19.2 | 22 | Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain |
| 99 | d2ns0a1 | Alignment | not modelled | 19.1 | 22 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: RHA1 ro06458-like |