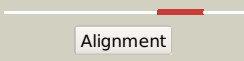

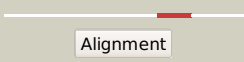

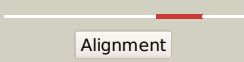

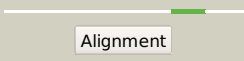
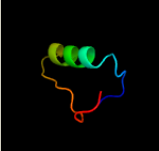
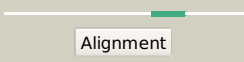
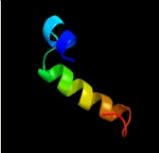
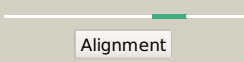
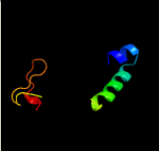
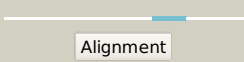
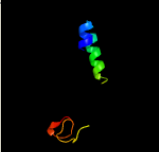
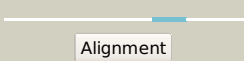

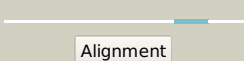

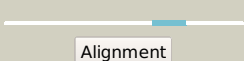
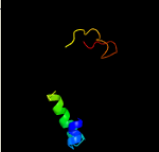
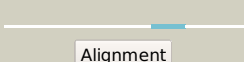
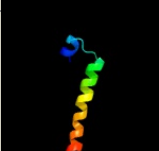

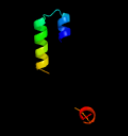

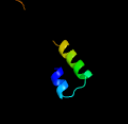
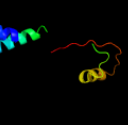
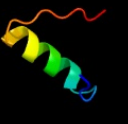
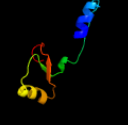




Phyre2

| | |
|---------------|------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0862c_(-)_960345_962615 |
| Date | Fri Jul 26 01:50:45 BST 2019 |
| Unique Job ID | 887956da345ffac0 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c6nmiA_ |  Alignment |  | 98.7 | 21 | PDB header: transcription Chain: A: PDB Molecule: general transcription and dna repair factor iih helicase PDBTitle: cryo-em structure of the human tfiih core complex |
| 2 | c6nmiD_ |  Alignment |  | 97.6 | 19 | PDB header: transcription Chain: D: PDB Molecule: general transcription factor iih subunit 4, p52; PDBTitle: cryo-em structure of the human tfiih core complex |
| 3 | c6ro4A_ |  Alignment |  | 97.2 | 20 | PDB header: translocase Chain: A: PDB Molecule: general transcription and dna repair factor iih helicase PDBTitle: structure of the core tfiih-xpa-dna complex |
| 4 | c3fryB_ |  Alignment |  | 55.6 | 16 | PDB header: hydrolase Chain: B: PDB Molecule: probable copper-exporting p-type atpase a; PDBTitle: crystal structure of the copa c-terminal metal binding domain |
| 5 | c4g9qA_ |  Alignment |  | 42.5 | 12 | PDB header: lyase Chain: A: PDB Molecule: 4-carboxymuconolactone decarboxylase; PDBTitle: crystal structure of a 4-carboxymuconolactone decarboxylase |
| 6 | c3pl5A_ |  Alignment |  | 40.4 | 26 | PDB header: lipid binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: fatty acid binding protein |
| 7 | d1pzxa_ |  Alignment |  | 39.6 | 18 | Fold: DAK1/DegV-like Superfamily: DAK1/DegV-like Family: DegV-like |
| 8 | d2ga1a1 |  Alignment |  | 37.7 | 9 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Alr1493-like |
| 9 | c2r8rB_ |  Alignment |  | 36.0 | 24 | PDB header: transferase Chain: B: PDB Molecule: sensor protein; PDBTitle: crystal structure of the n-terminal region (19..243) of sensor protein2 kdpd from pseudomonas syringae pv. tomato str. dc3000 |
| 10 | c6cngA_ |  Alignment |  | 34.0 | 23 | PDB header: transferase Chain: A: PDB Molecule: fatty acid kinase (fak) b3 protein; PDBTitle: the x-ray crystal structure of the streptococcus pneumoniae fatty acid2 kinase (fak) b3 protein loaded with linoleic acid to 1.47 angstrom3 resolution |
| 11 | d2q0ta1 |  Alignment |  | 31.3 | 24 | Fold: AhpD-like Superfamily: AhpD-like Family: AhpD |

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|----|-------------------------|-----------|---|------|----|--|
| 12 | d2af7a1 | Alignment |  | 31.1 | 24 | Fold: AhpD-like Superfamily: AhpD-like Family: CMD-like |
| 13 | c2g7zB_ | Alignment |  | 31.0 | 11 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved hypothetical protein spy1493; PDBTitle: conserved degv-like protein of unknown function from streptococcus2 pyogenes m1 gas binds long-chain fatty acids |
| 14 | c4a6dA_ | Alignment |  | 27.8 | 12 | PDB header: transferase Chain: A: PDB Molecule: hydroxyindole o-methyltransferase; PDBTitle: crystal structure of human n-acetylserotonin2 methyltransferase (asmt) in complex with sam |
| 15 | c6dj6B_ | Alignment |  | 27.2 | 11 | PDB header: transferase Chain: B: PDB Molecule: fatty acid kinase (fak) b2 protein (spr1019); PDBTitle: the x-ray crystal structure of the streptococcus pneumoniae fatty acid2 kinase (fak) b2 protein loaded with cis-oleic acid to 1.9 angstrom3 resolution |
| 16 | c5utoB_ | Alignment |  | 25.3 | 13 | PDB header: transport protein Chain: B: PDB Molecule: edd domain protein, degv family; PDBTitle: the crystal structure of the staphylococcus aureus fatty acid kinase2 (fak) b1 protein loaded with palmitic acid to 1.83 angstrom3 resolution |
| 17 | c1zhvA_ | Alignment |  | 24.1 | 20 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein atu0741; PDBTitle: x-ray crystal structure protein atu0741 from agobacterium tumefaciens.2 northeast structural genomics consortium target atr8. |
| 18 | d2p0la1 | Alignment |  | 22.9 | 14 | Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: LplA-like |
| 19 | d3bz6a2 | Alignment |  | 22.4 | 23 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PSPTO2686-like |
| 20 | d1mgpa_ | Alignment |  | 21.7 | 20 | Fold: DAK1/DegV-like Superfamily: DAK1/DegV-like Family: DegV-like |
| 21 | c1mgpA_ | Alignment | not modelled | 21.7 | 20 | PDB header: lipid binding protein Chain: A: PDB Molecule: hypothetical protein tm841; PDBTitle: hypothetical protein tm841 from thermotoga maritima reveals2 fatty acid binding function |
| 22 | c2dt8A_ | Alignment | not modelled | 21.0 | 14 | PDB header: lipid binding protein Chain: A: PDB Molecule: degv family protein; PDBTitle: fatty acid binding of a degv family protein from thermus thermophilus |
| 23 | c5tmxA_ | Alignment | not modelled | 20.4 | 13 | PDB header: transcription regulator Chain: A: PDB Molecule: protein sini; PDBTitle: solution structure of sini, antagonist to the master biofilm-regulator2 sinr in bacillus subtilis |
| 24 | c3lstB | Alignment | not modelled | 19.3 | 20 | PDB header: transferase Chain: B: PDB Molecule: calo1 methyltransferase; PDBTitle: crystal structure of calo1, methyltransferase in calicheamicin2 biosynthesis, sah bound form |
| 25 | c3nyiA_ | Alignment | not modelled | 19.0 | 17 | PDB header: lipid binding protein Chain: A: PDB Molecule: fat acid-binding protein; PDBTitle: the crystal structure of a fat acid (stearic acid)-binding protein2 from eubacterium ventriosum atcc 27560. |
| 26 | c3iuoA_ | Alignment | not modelled | 18.7 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent dna helicase recq; PDBTitle: the crystal structure of the c-terminal domain of the atp-dependent2 dna helicase recq from porphyromonas gingivalis to 1.6a |
| 27 | c2xvcA_ | Alignment | not modelled | 18.1 | 27 | PDB header: cell cycle Chain: A: PDB Molecule: escrt-iii; PDBTitle: molecular and structural basis of escrt-iii recruitment to membranes2 during archaeal cell division |
| 28 | c3fdjA_ | Alignment | not modelled | 17.7 | 11 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: degv family protein; PDBTitle: the structure of a degv family protein from eubacterium |

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|----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | eligens. |
| 29 | c3bz6A_ | Alignment | not modelled | 17.2 | 23 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0502 protein pspto_2686; PDBTitle: crystal structure of a conserved protein of unknown function from2 pseudomonas syringae pv. tomato str. dc3000 |
| 30 | c2k2pA_ | Alignment | not modelled | 17.0 | 18 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu1203; PDBTitle: solution nmr structure of protein atu1203 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att10, ontario center for structural proteomics target atc1183 |
| 31 | c2va0E_ | Alignment | not modelled | 16.7 | 35 | PDB header: transferase Chain: E: PDB Molecule: abfs arabinofuranosidase two component system sensor PDBTitle: differential regulation of the xylan degrading apparatus of2 cellvibrio japonicus by a novel two component system |
| 32 | d1rj9a1 | Alignment | not modelled | 16.5 | 38 | Fold: Four-helical up-and-down bundle Superfamily: Domain of the SRP/SRP receptor G-proteins Family: Domain of the SRP/SRP receptor G-proteins |
| 33 | c4x9xA_ | Alignment | not modelled | 16.4 | 17 | PDB header: transferase Chain: A: PDB Molecule: degv domain-containing protein mw1315; PDBTitle: biochemical roles for conserved residues in the bacterial fatty acid2 binding protein family |
| 34 | d1zhva2 | Alignment | not modelled | 15.7 | 19 | Fold: Ferredoxin-like Superfamily: ACT-like Family: Atu0741-like |
| 35 | c2hcnA_ | Alignment | not modelled | 15.6 | 30 | PDB header: transferase Chain: A: PDB Molecule: rna-directed rna polymerase (ns5); PDBTitle: crystal structure of rna dependent rna polymerase domain from west2 Nile virus |
| 36 | c3dp7B_ | Alignment | not modelled | 15.6 | 13 | PDB header: transferase Chain: B: PDB Molecule: sam-dependent methyltransferase; PDBTitle: crystal structure of sam-dependent methyltransferase from bacteroides2 vulgatus atcc 8482 |
| 37 | d1wmhb_ | Alignment | not modelled | 14.7 | 29 | Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain |
| 38 | c3pzfA_ | Alignment | not modelled | 14.4 | 16 | PDB header: hydrolase inhibitor Chain: A: PDB Molecule: serpin 2; PDBTitle: 1.75a resolution structure of serpin-2 from anopheles gambiae |
| 39 | d1b0na1 | Alignment | not modelled | 14.4 | 33 | Fold: Dimerisation interlock Superfamily: SinR repressor dimerisation domain-like Family: SinR repressor dimerisation domain-like |
| 40 | c3oq9C_ | Alignment | not modelled | 14.3 | 22 | PDB header: apoptosis Chain: C: PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: structure of the fas/fadd death domain assembly |
| 41 | d2p5ia1 | Alignment | not modelled | 13.2 | 23 | Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: LplA-like |
| 42 | c4gysA_ | Alignment | not modelled | 12.5 | 22 | PDB header: hydrolase Chain: A: PDB Molecule: allophanate hydrolase; PDBTitle: granulibacter bethesdensis allophanate hydrolase co-crystallized with2 malonate |
| 43 | c3wvqA_ | Alignment | not modelled | 12.4 | 16 | PDB header: biosynthetic protein Chain: A: PDB Molecule: pgm1; PDBTitle: structure of atp grasp protein |
| 44 | d2ikba1 | Alignment | not modelled | 12.3 | 11 | Fold: Lysozyme-like Superfamily: Lysozyme-like Family: NMB1012-like |
| 45 | c3jr7A_ | Alignment | not modelled | 11.9 | 14 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized egv family protein cog1307; PDBTitle: the crystal structure of the protein of degv family cog1307 with2 unknown function from ruminococcus gnavus atcc 29149 |
| 46 | d1jg5a_ | Alignment | not modelled | 11.5 | 23 | Fold: GTP cyclohydrolase I feedback regulatory protein, GFRP Superfamily: GTP cyclohydrolase I feedback regulatory protein, GFRP Family: GTP cyclohydrolase I feedback regulatory protein, GFRP |
| 47 | c2hl7A_ | Alignment | not modelled | 11.2 | 25 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome c-type biogenesis protein ccmh; PDBTitle: crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa |
| 48 | c1y3kA_ | Alignment | not modelled | 11.0 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 1; PDBTitle: solution structure of the apo form of the fifth domain of2 menkes protein |
| 49 | c6dkeA_ | Alignment | not modelled | 10.9 | 17 | PDB header: transferase Chain: A: PDB Molecule: fatty acid kinase (fak) b1 protein; PDBTitle: the x-ray crystal structure of streptococcus pneumoniae fatty acid2 kinase (fak) b1 protein loaded with palmitic acid (c16:0) to 1.763 angstrom resolution |
| 50 | c1dmIF_ | Alignment | not modelled | 10.9 | 35 | PDB header: dna binding protein/transferase Chain: F: PDB Molecule: dna polymerase; PDBTitle: crystal structure of herpes simplex ul42 bound to the c-terminus of2 hsv pol |
| 51 | c1dmIH_ | Alignment | not modelled | 10.9 | 35 | PDB header: dna binding protein/transferase Chain: H: PDB Molecule: dna polymerase; PDBTitle: crystal structure of herpes simplex ul42 bound to the c-terminus of2 hsv pol |
| 52 | c1dmID_ | Alignment | not modelled | 10.9 | 35 | PDB header: dna binding protein/transferase Chain: D: PDB Molecule: dna polymerase; PDBTitle: crystal structure of herpes simplex ul42 bound to the c-terminus of2 hsv pol |
| | | | | | | PDB header: dna binding protein/transferase |

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|----|-------------------------|-----------|--------------|------|----|---|
| 53 | c1dmIB | Alignment | not modelled | 10.9 | 35 | Chain: B: PDB Molecule: dna polymerase; PDBTitle: crystal structure of herpes simplex ul42 bound to the c-terminus of2 hsv pol |
| 54 | d1m6ya1 | Alignment | not modelled | 10.8 | 19 | Fold: SAM domain-like Superfamily: Putative methyltransferase TM0872, insert domain Family: Putative methyltransferase TM0872, insert domain |
| 55 | c5tn2B | Alignment | not modelled | 10.7 | 33 | PDB header: transcription Chain: B: PDB Molecule: hth-type transcriptional regulator sinr; PDBTitle: solution structure of the c-terminal multimerization domain of the2 master biofilm-regulator sinr from bacillus subtilis |
| 56 | d1qzza1 | Alignment | not modelled | 10.3 | 24 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Plant O-methyltransferase, N-terminal domain |
| 57 | d1z0xa2 | Alignment | not modelled | 10.3 | 40 | Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain |
| 58 | c3lupA | Alignment | not modelled | 10.2 | 14 | PDB header: structure genomics, unknown function Chain: A: PDB Molecule: degv family protein; PDBTitle: crystal structure of fatty acid binding degv family protein sag13422 from streptococcus agalactiae |
| 59 | c2ygwB | Alignment | not modelled | 10.0 | 35 | PDB header: lyase Chain: B: PDB Molecule: malonyl-coa decarboxylase, mitochondrial; PDBTitle: crystal structure of human mcd |
| 60 | c2kw0A | Alignment | not modelled | 9.9 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: ccmh protein; PDBTitle: solution structure of n-terminal domain of ccmh from escherichia.coli |
| 61 | c2zc3F | Alignment | not modelled | 9.8 | 11 | PDB header: biosynthetic protein Chain: F: PDB Molecule: penicillin-binding protein 2x; PDBTitle: penicillin-binding protein 2x (pbp 2x) acyl-enzyme complex2 (biapenem) from streptococcus pneumoniae |
| 62 | d1s6ua | Alignment | not modelled | 9.7 | 15 | Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain |
| 63 | c3ghfA | Alignment | not modelled | 9.6 | 22 | PDB header: cell cycle Chain: A: PDB Molecule: septum site-determining protein minc; PDBTitle: crystal structure of the septum site-determining protein minc from2 salmonella typhimurium |
| 64 | d1kvja | Alignment | not modelled | 9.4 | 8 | Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain |
| 65 | c5u8jA | Alignment | not modelled | 8.9 | 21 | PDB header: unknown function Chain: A: PDB Molecule: upf0502 protein bfj73_07745; PDBTitle: crystal structure of a protein of unknown function ec_l_02571 involved2 in membrane biogenesis from enterobacter cloacae |
| 66 | d1pyya1 | Alignment | not modelled | 8.9 | 11 | Fold: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Superfamily: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Family: Penicillin-binding protein 2x (pbp-2x), c-terminal domain |
| 67 | c4qvgC | Alignment | not modelled | 8.7 | 14 | PDB header: transferase Chain: C: PDB Molecule: sib1; PDBTitle: crystal structure of s-adenosylmethionine-dependent methyltransferase2 sib1 in its apo form |
| 68 | d1ddfa | Alignment | not modelled | 8.7 | 15 | Fold: DEATH domain Superfamily: DEATH domain Family: DEATH domain, DD |
| 69 | c3o59X | Alignment | not modelled | 8.6 | 40 | PDB header: transferase Chain: X: PDB Molecule: dna polymerase ii large subunit; PDBTitle: dna polymerase d large subunit dp2(1-300) from pyrococcus horikoshii |
| 70 | c4u4hA | Alignment | not modelled | 8.3 | 23 | PDB header: viral protein Chain: A: PDB Molecule: tegument protein ul21; PDBTitle: crystal structure of hsv-1 ul21 n-terminal domain |
| 71 | c1u3eM | Alignment | not modelled | 8.3 | 17 | PDB header: dna binding protein/dna Chain: M: PDB Molecule: hnh homing endonuclease; PDBTitle: dna binding and cleavage by the hnh homing endonuclease i-hmui |
| 72 | c2o1uA | Alignment | not modelled | 8.2 | 29 | PDB header: chaperone Chain: A: PDB Molecule: endoplasmic; PDBTitle: structure of full length grp94 with amp-pnp bound |
| 73 | d1wg8a1 | Alignment | not modelled | 8.0 | 25 | Fold: SAM domain-like Superfamily: Putative methyltransferase TM0872, insert domain Family: Putative methyltransferase TM0872, insert domain |
| 74 | d1k25a1 | Alignment | not modelled | 7.9 | 11 | Fold: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Superfamily: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Family: Penicillin-binding protein 2x (pbp-2x), c-terminal domain |
| 75 | c2ip2B | Alignment | not modelled | 7.9 | 19 | PDB header: transferase Chain: B: PDB Molecule: probable phenazine-specific methyltransferase; PDBTitle: structure of the pyocyanin biosynthetic protein phzm |
| 76 | d1tw3a1 | Alignment | not modelled | 7.6 | 31 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Plant O-methyltransferase, N-terminal domain |
| 77 | c5lltB | Alignment | not modelled | 7.6 | 18 | PDB header: transferase Chain: B: PDB Molecule: nicotinate-nucleotide adenyllyltransferase; PDBTitle: plasmodium falciparum nicotinic acid mononucleotide2 adenyllyltransferase complexed with naad |
| 78 | c6h45B | Alignment | not modelled | 7.6 | 16 | PDB header: transferase Chain: B: PDB Molecule: queuine trna-ribosyltransferase catalytic subunit 1; PDBTitle: crystal structure of the human tgt catalytic subunit qtrt1 in complex2 with queuine |
| | | | | | | Fold: DNA/RNA-binding 3-helical bundle |

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|----|-------------------------|-----------|--------------|-----|----|--|
| 79 | d1g3wa1 | Alignment | not modelled | 7.5 | 12 | Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein |
| 80 | c5zzaP | Alignment | not modelled | 7.5 | 29 | PDB header: structural protein Chain: P: PDB Molecule: uncharacterized protein; PDBTitle: odinprofilin/rabbit actin complex |
| 81 | c4z2yA | Alignment | not modelled | 7.3 | 23 | PDB header: transferase Chain: A: PDB Molecule: calo6; PDBTitle: crystal structure of methyltransferase calo6 |
| 82 | c4e6kl | Alignment | not modelled | 7.1 | 30 | PDB header: metal binding protein/electron transport Chain: I: PDB Molecule: bacterioferritin-associated ferredoxin; PDBTitle: 2.0 a resolution structure of pseudomonas aeruginosa bacterioferritin2 (bfrb) in complex with bacterioferritin associated ferredoxin (bfd) |
| 83 | c3mwmA | Alignment | not modelled | 7.1 | 20 | PDB header: transcription Chain: A: PDB Molecule: putative metal uptake regulation protein; PDBTitle: graded expression of zinc-responsive genes through two regulatory2 zinc-binding sites in zur |
| 84 | c3omdB | Alignment | not modelled | 7.1 | 7 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of unknown function protein from leptospirillum2 rubarum |
| 85 | c3fpnA | Alignment | not modelled | 7.0 | 17 | PDB header: dna binding protein Chain: A: PDB Molecule: geobacillus stearothermophilus uvra interaction domain; PDBTitle: crystal structure of uvra-uvrb interaction domains |
| 86 | d1qpa2 | Alignment | not modelled | 7.0 | 22 | Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain |
| 87 | c2kt7A | Alignment | not modelled | 7.0 | 31 | PDB header: cell adhesion, membrane protein Chain: A: PDB Molecule: putative peptidoglycan bound protein (lpxtg) PDBTitle: solution nmr structure of mucin-binding domain of protein2 lmo0835 from listeria monocytogenes, northeast structural3 genomics consortium target lmr64a |
| 88 | d1u5ta2 | Alignment | not modelled | 7.0 | 13 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain |
| 89 | d1pzqa | Alignment | not modelled | 6.9 | 30 | Fold: Dimerisation interlock Superfamily: Docking domain A of the erythromycin polyketide synthase (DEBS) Family: Docking domain A of the erythromycin polyketide synthase (DEBS) |
| 90 | c1tw3A | Alignment | not modelled | 6.8 | 28 | PDB header: transferase Chain: A: PDB Molecule: carinomycin 4-o-methyltransferase; PDBTitle: crystal structure of carinomycin-4-o-methyltransferase (dnrk) in2 complex with s-adenosyl-l-homocystein (sah) and 4-methoxy-e-3 rhodomycin t (m-et) |
| 91 | c1wsuA | Alignment | not modelled | 6.7 | 20 | PDB header: translation/rna Chain: A: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: c-terminal domain of elongation factor selb complexed with2 secis rna |
| 92 | c2x4hA | Alignment | not modelled | 6.7 | 14 | PDB header: transcription Chain: A: PDB Molecule: hypothetical protein sso2273; PDBTitle: crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus |
| 93 | c1xduA | Alignment | not modelled | 6.6 | 21 | PDB header: transferase Chain: A: PDB Molecule: protein rdmb; PDBTitle: crystal structure of aclacinomycin-10-hydroxylase (rdmb) in complex2 with sinefungin (sfg) |
| 94 | c3gxgA | Alignment | not modelled | 6.6 | 26 | PDB header: hydrolase Chain: A: PDB Molecule: putative phosphatase (duf442); PDBTitle: crystal structure of putative phosphatase (duf442) (yp_001181608.1)2 from shewanella putrefaciens cn-32 at 1.60 a resolution |
| 95 | c1af7A | Alignment | not modelled | 6.5 | 20 | PDB header: methyltransferase Chain: A: PDB Molecule: chemotaxis receptor methyltransferase cher; PDBTitle: cher from salmonella typhimurium |
| 96 | c3fysA | Alignment | not modelled | 6.5 | 20 | PDB header: fatty acid-binding protein Chain: A: PDB Molecule: protein degv; PDBTitle: crystal structure of degv, a fatty acid binding protein2 from bacillus subtilis |
| 97 | c6ff2A | Alignment | not modelled | 6.4 | 15 | PDB header: chaperone Chain: A: PDB Molecule: copper chaperone copz; PDBTitle: copz metallochaperone |
| 98 | d2fi0a1 | Alignment | not modelled | 6.4 | 23 | Fold: SP0561-like Superfamily: SP0561-like Family: SP0561-like |
| 99 | c2j7uA | Alignment | not modelled | 6.4 | 24 | PDB header: viral protein Chain: A: PDB Molecule: rna dependent rna polymerase; PDBTitle: dengue virus ns5 rna dependent rna polymerase domain |