



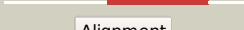
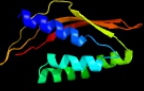
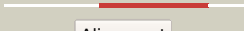
















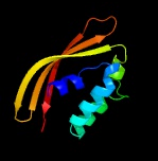
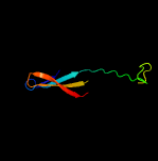
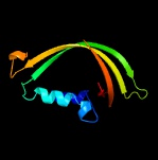




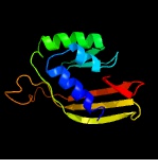


Phyre2




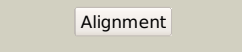
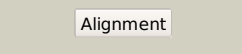
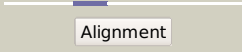
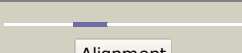

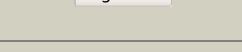

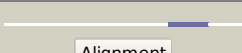


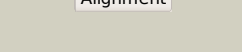
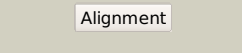
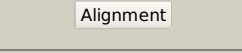
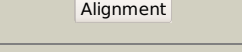
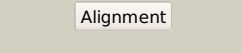
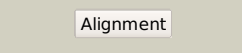


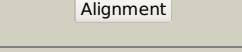
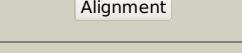
| | |
|------------------|-----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD3493c (-)_3911126_3911854 |
| Date | Fri Aug 9 18:20:17 BST 2019 |
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Detailed template
information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|-----------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------------|--------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1 | d3d9ra1 |  Alignment |  | 96.7 | 7 | Fold: Cystatin-like Superfamily: NTF2-like Family: ECA1476-like |
| 2 | c5cn1A_ |  Alignment |  | 96.5 | 8 | PDB header: protein transport Chain: A: PDB Molecule: icml-like; PDBTitle: crystal structure of an icml-like type iv secretion system protein2 (lpg0120) from legionella pneumophila subsp. pneumophila str.3 philadelphia 1 at 2.65 a resolution |
| 3 | c3wz4F_ |  Alignment |  | 96.1 | 11 | PDB header: unknown function Chain: F: PDB Molecule: doti; PDBTitle: structure of the periplasmic domain of doti (crystal form i) |
| 4 | c3wz3A_ |  Alignment |  | 96.0 | 9 | PDB header: unknown function Chain: A: PDB Molecule: tram protein; PDBTitle: structure of a periplasmic fragment of tram |
| 5 | c3robC_ |  Alignment |  | 95.7 | 9 | PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized conserved protein; PDBTitle: the crystal structure of a conserved protein from planctomyces2 limnophilus dsm 3776 |
| 6 | c5u9oD_ |  Alignment |  | 95.3 | 12 | PDB header: cell cycle Chain: D: PDB Molecule: plastid division protein cdp1, chloroplastic,plastid PDBTitle: cocrystal structure of the intermembrane space region of the plastid2 division proteins parc6 and pdv1 |
| 7 | c3hx8A_ |  Alignment |  | 94.5 | 11 | PDB header: isomerase Chain: A: PDB Molecule: putative ketosteroid isomerase; PDBTitle: crystal structure of putative ketosteroid isomerase (np_103587.1) from2 mesorhizobium loti at 1.45 a resolution |
| 8 | c3a76B_ |  Alignment |  | 93.6 | 9 | PDB header: lyase Chain: B: PDB Molecule: gamma-hexachlorocyclohexane dehydrochlorinase; PDBTitle: the crystal structure of lina |
| 9 | c5i97C_ |  Alignment |  | 91.8 | 13 | PDB header: protein transport Chain: C: PDB Molecule: conjugal transfer protein; PDBTitle: structural analysis and inhibition of trae from the pkm101 type iv2 secretion system |
| 10 | d2ux0a1 |  Alignment |  | 91.7 | 10 | Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A |
| 11 | c3h51A_ |  Alignment |  | 91.1 | 10 | PDB header: protein binding Chain: A: PDB Molecule: putative calcium/calmodulin dependent protein kinase ii PDBTitle: crystal structure of putative calcium/calmodulin dependent protein2 kinase ii association domain (np_636218.1) from xanthomonas3 campestris at 1.70 a resolution |

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|----|-------------------------|-----------|-------------------------------------------------------------------------------------|------|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 12 | d2f86b1 | Alignment |  | 90.8 | 12 | Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A |
| 13 | d2cc3a1 | Alignment |  | 90.8 | 14 | Fold: Cystatin-like Superfamily: NTF2-like Family: VirB8-like |
| 14 | d3stda | Alignment |  | 89.5 | 13 | Fold: Cystatin-like Superfamily: NTF2-like Family: Scytalone dehydratase |
| 15 | c5d9rA | Alignment |  | 89.4 | 10 | PDB header: biosynthetic protein Chain: A: PDB Molecule: protein accumulation and replication of chloroplasts 6, PDBTitle: crystal structure of a conserved domain in the intermembrane space2 region of the plastid division protein arc6 |
| 16 | c4nhfF | Alignment |  | 88.0 | 14 | PDB header: protein transport Chain: F: PDB Molecule: trwg protein; PDBTitle: crystal structure of the soluble domain of trwg type iv secretion2 machinery from bartonella grahamii |
| 17 | c5uwaB | Alignment |  | 87.9 | 26 | PDB header: transport protein Chain: B: PDB Molecule: probable phospholipid-binding protein mlac; PDBTitle: structure of e. coli phospholipid binding protein mlac |
| 18 | d3ebya1 | Alignment |  | 87.6 | 16 | Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit |
| 19 | d3b8la1 | Alignment |  | 86.0 | 17 | Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like |
| 20 | c4ovmE | Alignment |  | 85.9 | 8 | PDB header: unknown function Chain: E: PDB Molecule: uncharacterized protein sgcj; PDBTitle: crystal structure of sgcj protein from streptomyces carzinostaticus |
| 21 | c3gzaA | Alignment | not modelled | 85.2 | 6 | PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein with a ntf2-like fold; PDBTitle: crystal structure of an uncharacterized protein with a cystatin-like2 fold (cc_2572) from caulobacter vibrioides at 1.40 a resolution |
| 22 | c5ig4A | Alignment | not modelled | 84.4 | 12 | PDB header: transferase Chain: A: PDB Molecule: predicted protein; PDBTitle: crystal structure of n. vectensis camkii-a hub |
| 23 | d1hkxa | Alignment | not modelled | 82.6 | 10 | Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A |
| 24 | c5ig5E | Alignment | not modelled | 82.1 | 9 | PDB header: transferase Chain: E: PDB Molecule: camkii-b hub; PDBTitle: crystal structure of n. vectensis camkii-b hub at ph 4.2 |
| 25 | d3cu3a1 | Alignment | not modelled | 80.4 | 10 | Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like |
| 26 | c4i4kB | Alignment | not modelled | 78.5 | 13 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein sgcj; PDBTitle: streptomyces globisporus c-1027 9-membered enediyne conserved protein2 sgce6 |
| 27 | d2rfra1 | Alignment | not modelled | 77.2 | 10 | Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like |
| 28 | c3soyA | Alignment | not modelled | 75.5 | 13 | PDB header: membrane protein Chain: A: PDB Molecule: ntf2-like superfamily protein; PDBTitle: nuclear transport factor 2 (ntf2-like) superfamily protein from2 salmonella enterica subsp. enterica serovar typhimurium str. |

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|----|-------------------------|-----------|--------------|------|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| | | | | | | lt2 |
| 29 | c3bb9D_ | Alignment | not modelled | 74.1 | 8 | PDB header: unknown function Chain: D: PDB Molecule: putative orphan protein; PDBTitle: crystal structure of a putative ketosteroid isomerase (sfri_1973) from <i>Shewanella frigidimarina</i> ncimb 400 at 1.80 a resolution |
| 30 | d3ef8a1 | Alignment | not modelled | 71.1 | 8 | Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like |
| 31 | d3bb9a1 | Alignment | not modelled | 68.2 | 5 | Fold: Cystatin-like Superfamily: NTF2-like Family: SO0125-like |
| 32 | c4fczB_ | Alignment | not modelled | 67.3 | 23 | PDB header: transport protein Chain: B: PDB Molecule: toluene-tolerance protein; PDBTitle: crystal structure of toluene-tolerance protein from <i>Pseudomonas putida</i> 2 (strain kt2440), northeast structural genomics consortium (nesg)3 target ppr99 |
| 33 | c3f7sA_ | Alignment | not modelled | 66.6 | 6 | PDB header: unknown function Chain: A: PDB Molecule: uncharacterized ntf2-like protein; PDBTitle: crystal structure of a ntf2-like protein of unknown function (pp_4556)2 from <i>Pseudomonas putida</i> kt2440 at 2.11 a resolution |
| 34 | c4lehA_ | Alignment | not modelled | 66.5 | 7 | PDB header: lyase Chain: A: PDB Molecule: bile acid 7-alpha dehydratase, baie; PDBTitle: crystal structure of a bile-acid 7-alpha dehydratase (closci_03134)2 from <i>Clostridium scindens</i> atcc 35704 at 2.90 a resolution |
| 35 | c4meiA_ | Alignment | not modelled | 65.1 | 12 | PDB header: protein transport Chain: A: PDB Molecule: virb8 protein; PDBTitle: crystal structure of a virb8 type iv secretion system machinery2 soluble domain from <i>Bartonella tribocorum</i> |
| 36 | c2bhmE_ | Alignment | not modelled | 64.3 | 14 | PDB header: bacterial protein Chain: E: PDB Molecule: type iv secretion system protein virb8; PDBTitle: crystal structure of virb8 from <i>Brucella suis</i> |
| 37 | c6of9G_ | Alignment | not modelled | 59.1 | 14 | PDB header: unknown function Chain: G: PDB Molecule: camkii hub; PDBTitle: structure of the <i>Chlamydomonas reinhardtii</i> camkii hub homology domain |
| 38 | d2r4ia1 | Alignment | not modelled | 58.3 | 11 | Fold: Cystatin-like Superfamily: NTF2-like Family: CHU142-like |
| 39 | d3blza1 | Alignment | not modelled | 57.5 | 12 | Fold: Cystatin-like Superfamily: NTF2-like Family: Sbal0622-like |
| 40 | d1ldpa_ | Alignment | not modelled | 49.8 | 13 | Fold: Cystatin-like Superfamily: NTF2-like Family: Scytalone dehydratase |
| 41 | d2bhma1 | Alignment | not modelled | 49.6 | 9 | Fold: Cystatin-like Superfamily: NTF2-like Family: VirB8-like |
| 42 | d2chca1 | Alignment | not modelled | 45.7 | 17 | Fold: Cystatin-like Superfamily: NTF2-like Family: Rv3472-like |
| 43 | c2qguA_ | Alignment | not modelled | 44.4 | 21 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: probable signal peptide protein; PDBTitle: three-dimensional structure of the phospholipid-binding protein from <i>Ralstonia solanacearum</i> q8xv73_ralsq in complex with a phospholipid at3 the resolution 1.53 a. northeast structural genomics consortium4 target rsr89 |
| 44 | d3b7ca1 | Alignment | not modelled | 43.9 | 10 | Fold: Cystatin-like Superfamily: NTF2-like Family: SO0125-like |
| 45 | d2rgqa1 | Alignment | not modelled | 42.8 | 13 | Fold: Cystatin-like Superfamily: NTF2-like Family: Rv3472-like |
| 46 | c5ig0A_ | Alignment | not modelled | 42.1 | 12 | PDB header: transferase Chain: A: PDB Molecule: camk/camk2 protein kinase; PDBTitle: crystal structure of <i>S. rosetta</i> camkii hub |
| 47 | c4hzbE_ | Alignment | not modelled | 41.9 | 7 | PDB header: hydrolase Chain: E: PDB Molecule: putative periplasmic protein; PDBTitle: crystal structure of the type vi semet effector-immunity complex tae3-2 tai3 from <i>Ralstonia pickettii</i> |
| 48 | c4o3vA_ | Alignment | not modelled | 34.2 | 15 | PDB header: protein transport Chain: A: PDB Molecule: virb8-like protein of type iv secretion system; PDBTitle: crystal structure of a virb8-like protein of type iv secretion system2 from <i>Rickettsia typhi</i> |
| 49 | c4r4gA_ | Alignment | not modelled | 31.9 | 8 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative lipoprotein ycdA; PDBTitle: crystal structure of a putative lipoprotein (ycda) from <i>Bacillus subtilis</i> subsp. <i>subtilis</i> str. 168 at 2.62 a resolution |
| 50 | c3k7cC_ | Alignment | not modelled | 29.5 | 13 | PDB header: protein binding Chain: C: PDB Molecule: putative ntf2-like transpeptidase; PDBTitle: crystal structure of putative ntf2-like transpeptidase (np_281412.1)2 from <i>Campylobacter jejuni</i> at 2.00 a resolution |
| 51 | d3cnxa1 | Alignment | not modelled | 26.6 | 11 | Fold: Cystatin-like Superfamily: NTF2-like Family: SAV4671-like |
| 52 | d2b1xb1 | Alignment | not modelled | 26.2 | 5 | Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit |
| 53 | c4gb5A_ | Alignment | not modelled | 22.0 | 14 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of kfla4162 protein from <i>Kribbella flavida</i> |

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|----|-------------------------|-----------------------------------------------------------------------------------------------|--------------|------|----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 54 | c2ls01_ |  Alignment | not modelled | 21.3 | 22 | PDB header: hydrolase Chain: 1: PDB Molecule: zoozin a endopeptidase; PDB Fragment: unp residues 170-285; PDBTitle: solution structure of the target recognition domain of zoozin a |
| 55 | c4a4iA_ |  Alignment | not modelled | 20.8 | 13 | PDB header: rna binding protein Chain: A: PDB Molecule: protein lin-28 homolog b; PDBTitle: crystal structure of the human lin28b cold shock domain |
| 56 | c6f0kA_ |  Alignment | not modelled | 17.2 | 16 | PDB header: membrane protein Chain: A: PDB Molecule: cytochrome c family protein; PDBTitle: alternative complex iii |
| 57 | c5up5A_ |  Alignment | not modelled | 15.0 | 54 | PDB header: de novo protein Chain: A: PDB Molecule: ehee_rd1_0284; PDBTitle: solution structure of the de novo mini protein ehee_rd1_0284 |
| 58 | c3efyB_ |  Alignment | not modelled | 14.5 | 27 | PDB header: cell cycle Chain: B: PDB Molecule: cif (cell cycle inhibiting factor); PDBTitle: structure of the cyclomodulin cif from pathogenic2 escherichia coli |
| 59 | c6nhyA_ |  Alignment | not modelled | 14.1 | 16 | PDB header: immune system Chain: A: PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 mutant2 (g217y) - trimer only |
| 60 | c6nhyC_ |  Alignment | not modelled | 14.1 | 16 | PDB header: immune system Chain: C: PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 mutant2 (g217y) - trimer only |
| 61 | c6nhyB_ |  Alignment | not modelled | 14.1 | 16 | PDB header: immune system Chain: B: PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 mutant2 (g217y) - trimer only |
| 62 | c3gwrA_ |  Alignment | not modelled | 13.9 | 12 | PDB header: protein binding Chain: A: PDB Molecule: putative calcium/calmodulin-dependent protein kinase type PDBTitle: crystal structure of putative calcium/calmodulin-dependent protein2 kinase type ii association domain (yp_315894.1) from thiobacillus3 denitrificans atcc 25259 at 2.00 a resolution |
| 63 | c3ke7A_ |  Alignment | not modelled | 13.2 | 3 | PDB header: isomerase Chain: A: PDB Molecule: putative ketosteroid isomerase; PDBTitle: crystal structure of putative ketosteroid isomerase (yp_001303366.1)2 from parabacteroides distazonis atcc 8503 at 1.45 a resolution |
| 64 | c5x9kA_ |  Alignment | not modelled | 12.0 | 19 | PDB header: isomerase Chain: A: PDB Molecule: austinol synthesis protein h; PDBTitle: structre of aush from aspergillus nidulans |
| 65 | c3kspA_ |  Alignment | not modelled | 11.4 | 7 | PDB header: unknown function Chain: A: PDB Molecule: calcium/calmodulin-dependent kinase ii association domain; PDBTitle: crystal structure of a putative ca/calmodulin-dependent kinase ii2 association domain (exig_1688) from exiguobacterium sibiricum 255-153 at 2.59 a resolution |
| 66 | c3j6vl_ |  Alignment | not modelled | 10.6 | 26 | PDB header: ribosome Chain: I: PDB Molecule: 28s ribosomal protein s9, mitochondrial; PDBTitle: cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome |
| 67 | d2gxfa1 |  Alignment | not modelled | 10.4 | 16 | Fold: Cystatin-like Superfamily: NTF2-like Family: YybH-like |
| 68 | d1jz8a1 |  Alignment | not modelled | 10.3 | 20 | Fold: Immunoglobulin-like beta-sandwich Superfamily: beta-Galactosidase/glucuronidase domain Family: beta-Galactosidase/glucuronidase domain |
| 69 | c3klqB_ |  Alignment | not modelled | 9.9 | 16 | PDB header: cell adhesion Chain: B: PDB Molecule: putative pilus anchoring protein; PDBTitle: crystal structure of the minor pilin fctb from streptococcus pyogenes2 90/306s |
| 70 | c2rujA_ |  Alignment | not modelled | 9.5 | 30 | PDB header: protein binding Chain: A: PDB Molecule: stress-activated map kinase-interacting protein 1; PDBTitle: solution structure of mtsl spin-labeled schizosaccharomyces pombe sin12 crim domain |
| 71 | c1nm3B_ |  Alignment | not modelled | 9.4 | 21 | PDB header: electron transport Chain: B: PDB Molecule: protein hi0572; PDBTitle: crystal structure of heamophilus influenza hybrid-prx5 |
| 72 | d2cw9a1 |  Alignment | not modelled | 8.9 | 9 | Fold: Cystatin-like Superfamily: NTF2-like Family: TIM44-like |
| 73 | c5wdaL_ |  Alignment | not modelled | 8.6 | 8 | PDB header: protein transport Chain: L: PDB Molecule: general secretion pathway protein g; PDBTitle: structure of the pulg pseudopilus |
| 74 | c3r2cJ_ |  Alignment | not modelled | 8.4 | 20 | PDB header: transcription/rna Chain: J: PDB Molecule: 30s ribosomal protein s10; PDBTitle: crystal structure of antitermination factors nusB and nusE in complex2 with boxA rna |
| 75 | c2kd2A_ |  Alignment | not modelled | 8.2 | 36 | PDB header: apoptosis Chain: A: PDB Molecule: fas apoptotic inhibitory molecule 1; PDBTitle: nmr structure of faim-ctd |
| 76 | c5wqhE_ |  Alignment | not modelled | 7.8 | 14 | PDB header: isomerase Chain: E: PDB Molecule: isomerase trt14; PDBTitle: structure of fungal meroterpenoid isomerase trt14 complexed with2 substrate analog and endo-terretonin d |
| 77 | c2ytyA_ |  Alignment | not modelled | 7.8 | 5 | PDB header: rna binding protein Chain: A: PDB Molecule: cold shock domain-containing protein e1; PDBTitle: solution structure of the fourth cold-shock domain of the human2 kiaa0885 protein (unr protein) |

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|----|-------------------------|-----------|--------------|-----|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 78 | c2gbxF_ | Alignment | not modelled | 7.6 | 6 | PDB header: oxidoreductase Chain: F; PDB Molecule: biphenyl 2,3-dioxygenase beta subunit; PDBTitle: crystal structure of biphenyl 2,3-dioxygenase from sphingomonas2 yanoikuyae b1 bound to biphenyl |
| 79 | c6nhwB_ | Alignment | not modelled | 7.5 | 16 | PDB header: immune system Chain: B; PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer |
| 80 | c6nhwF_ | Alignment | not modelled | 7.5 | 16 | PDB header: immune system Chain: F; PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer |
| 81 | c6nhwD_ | Alignment | not modelled | 7.5 | 16 | PDB header: immune system Chain: D; PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer |
| 82 | c6nhwE_ | Alignment | not modelled | 7.5 | 16 | PDB header: immune system Chain: E; PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer |
| 83 | c6nhwC_ | Alignment | not modelled | 7.5 | 16 | PDB header: immune system Chain: C; PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer |
| 84 | c6nhwA_ | Alignment | not modelled | 7.5 | 16 | PDB header: immune system Chain: A; PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer |
| 85 | c6oegY_ | Alignment | not modelled | 7.3 | 13 | PDB header: translocase Chain: Y; PDB Molecule: type iv secretion system apparatus protein cagx; PDBTitle: structure of cagx from a cryo-em reconstruction of a t4ss |
| 86 | c2n6uA_ | Alignment | not modelled | 7.1 | 29 | PDB header: unknown function Chain: A; PDB Molecule: astexin2-dc4; PDBTitle: solution study of astexin2-dc4 |
| 87 | d2iafa1 | Alignment | not modelled | 7.0 | 23 | Fold: FwdE/GAPDH domain-like Superfamily: Serine metabolism enzymes domain Family: Serine dehydratase beta chain-like |
| 88 | c2lcnA_ | Alignment | not modelled | 6.8 | 41 | PDB header: membrane protein Chain: A; PDB Molecule: walp19-p10 peptide; PDBTitle: 1h and 15n assignments of walp19-p10 peptide in sds micelles |
| 89 | d3ejva1 | Alignment | not modelled | 6.7 | 17 | Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like |
| 90 | d2h1ta1 | Alignment | not modelled | 6.1 | 13 | Fold: Spiral beta-roll Superfamily: PA1994-like Family: PA1994-like |
| 91 | c1xt5A_ | Alignment | not modelled | 6.0 | 19 | PDB header: immune system Chain: A; PDB Molecule: variable region-containing chitin-binding PDBTitle: crystal structure of vcbp3, domain 1, from branchiostoma2 floridae |
| 92 | c2lcoA_ | Alignment | not modelled | 5.9 | 47 | PDB header: membrane protein Chain: A; PDB Molecule: walp19-p8 peptide; PDBTitle: 1h and 15n assignments of walp19-p8 peptide in sds micelles |
| 93 | d1omha_ | Alignment | not modelled | 5.9 | 3 | Fold: Origin of replication-binding domain, RBD-like Superfamily: Origin of replication-binding domain, RBD-like Family: Relaxase domain |
| 94 | d2ngra1 | Alignment | not modelled | 5.8 | 9 | Fold: beta-clip Superfamily: MoeA C-terminal domain-like Family: MoeA C-terminal domain-like |
| 95 | c3dukD_ | Alignment | not modelled | 5.6 | 16 | PDB header: unknown function Chain: D; PDB Molecule: ntf2-like protein of unknown function; PDBTitle: crystal structure of a ntf2-like protein of unknown function2 (mfla_0564) from methylobacillus flagellatus kt at 2.200 a resolution |
| 96 | c1cwxA_ | Alignment | not modelled | 5.4 | 56 | PDB header: viral protein Chain: A; PDB Molecule: hepatitis c virus capsid protein; PDBTitle: solution structure of the hepatitis c virus n-terminal2 capsid protein 2-45 [c-hcv(2-45)] |
| 97 | c2k9yB_ | Alignment | not modelled | 5.4 | 19 | PDB header: transferase Chain: B; PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0 |
| 98 | c2k9yA_ | Alignment | not modelled | 5.4 | 19 | PDB header: transferase Chain: A; PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0 |
| 99 | d2pila_ | Alignment | not modelled | 5.3 | 16 | Fold: Pili subunits Superfamily: Pili subunits Family: Pilin |