
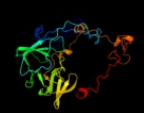






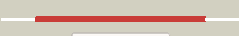













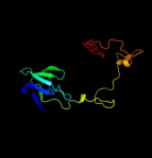


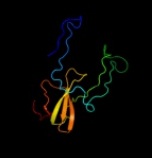
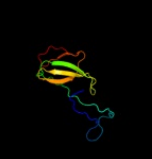

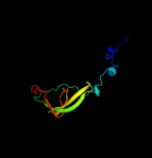
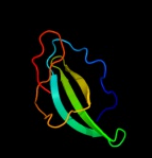



Phyre2

| | |
|---------------|------------------------------|
| Email | l.a.kelley@imperial.ac.uk |
| Description | P60430 |
| Date | Tue Jul 17 17:05:11 BST 2012 |
| Unique Job ID | ae3ba034564e9902 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c3d5bD_ | Alignment  |  | 100.0 | 65 | PDB header: ribosome Chain: D: PDB Molecule: 50s ribosomal protein L2; PDBTitle: structural basis for translation termination on the 70s ribosome. this2 file contains the 50s subunit of one 70s ribosome. the entire crystal3 structure contains two 70s ribosomes as described in remark 400. |
| 2 | c2z4lC_ | Alignment  |  | 100.0 | 58 | PDB header: ribosome Chain: C: PDB Molecule: 50s ribosomal protein L2; PDBTitle: crystal structure of the bacterial ribosome from escherichia2 coli in complex with paromomycin and ribosome recycling3 factor (rrf). this file contains the 50s subunit of the4 first 70s ribosome, with paromomycin and rrf bound. the5 entire crystal structure contains two 70s ribosomes and is6 described in remark 400. |
| 3 | c3bboE_ | Alignment  |  | 100.0 | 54 | PDB header: ribosome Chain: E: PDB Molecule: ribosomal protein L2; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome |
| 4 | c2gyaA_ | Alignment  |  | 100.0 | 62 | PDB header: ribosome Chain: A: PDB Molecule: 50s ribosomal protein L2; PDBTitle: structure of the 50s subunit of a pre-translocational e.2 coli ribosome obtained by fitting atomic models for rna and3 protein components into cryo-em map emd-1056 |
| 5 | c4a1cA_ | Alignment  |  | 100.0 | 36 | PDB header: ribosome Chain: A: PDB Molecule: rpl8; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4. |
| 6 | c2zkra_ | Alignment  |  | 100.0 | 36 | PDB header: ribosomal protein/rna Chain: A: PDB Molecule: rna expansion segment es3; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map |
| 7 | c1kqsA_ | Alignment  |  | 100.0 | 39 | PDB header: ribosome Chain: A: PDB Molecule: ribosomal protein L2; PDBTitle: the haloarcula marismortui 50s complexed with a2 pretranslocational intermediate in protein synthesis |
| 8 | c2b66D_ | Alignment  |  | 100.0 | 68 | PDB header: ribosome Chain: D: PDB Molecule: 50s ribosomal protein L2; PDBTitle: 50s ribosomal subunit from a crystal structure of release factor rf1,2 trnas and mrna bound to the ribosome. this file contains the 50s3 subunit from a crystal structure of release factor rf1, trnas and4 mrna bound to the ribosome and is described in remark 400 |
| 9 | d2j01d1 | Alignment  |  | 100.0 | 63 | Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: C-terminal domain of ribosomal protein L2 |
| 10 | d2zjra1 | Alignment  |  | 100.0 | 65 | Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: C-terminal domain of ribosomal protein L2 |
| 11 | d2qamc1 | Alignment  |  | 100.0 | 60 | Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: C-terminal domain of ribosomal protein L2 |

| | | | | | | |
|----|-------------------------|-----------|---|-------|----|---|
| 12 | d1vqoa1 | Alignment |  | 100.0 | 39 | Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: C-terminal domain of ribosomal protein L2 |
| 13 | c1rl2A_ | Alignment |  | 100.0 | 75 | PDB header: ribosomal protein Chain: A: PDB Molecule: protein (ribosomal protein l2); PDBTitle: ribosomal protein l2 rna-binding domain from bacillus2 stearotherophilus |
| 14 | c2ftcB_ | Alignment |  | 100.0 | 40 | PDB header: ribosome Chain: B: PDB Molecule: mitochondrial ribosomal protein l2; PDBTitle: structural model for the large subunit of the mammalian mitochondrial2 ribosome |
| 15 | d2j01d2 | Alignment |  | 100.0 | 68 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 16 | d2zjra2 | Alignment |  | 100.0 | 66 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 17 | d1rl2a1 | Alignment |  | 99.9 | 79 | Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: C-terminal domain of ribosomal protein L2 |
| 18 | d1vqoa2 | Alignment |  | 99.9 | 31 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 19 | d1rl2a2 | Alignment |  | 99.8 | 71 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 20 | d2qamc2 | Alignment |  | 99.8 | 67 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 21 | c3peiA_ | Alignment | not modelled | 88.5 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: cytosol aminopeptidase; PDBTitle: crystal structure of cytosol aminopeptidase from francisella2 tularensis |
| 22 | d2dy1a1 | Alignment | not modelled | 81.8 | 23 | Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Elongation factors |
| 23 | c3ij3A_ | Alignment | not modelled | 68.1 | 26 | PDB header: hydrolase Chain: A: PDB Molecule: cytosol aminopeptidase; PDBTitle: 1.8 angstrom resolution crystal structure of cytosol aminopeptidase2 from coxiella burnetii |
| 24 | c1lanA_ | Alignment | not modelled | 62.0 | 22 | PDB header: hydrolase Chain: A: PDB Molecule: leucine aminopeptidase; PDBTitle: leucine aminopeptidase complex with l-leucinal |
| 25 | c3h8gC_ | Alignment | not modelled | 54.2 | 22 | PDB header: hydrolase Chain: C: PDB Molecule: cytosol aminopeptidase; PDBTitle: bestatin complex structure of leucine aminopeptidase from pseudomonas2 putida |
| 26 | c3kzwD_ | Alignment | not modelled | 48.1 | 21 | PDB header: hydrolase Chain: D: PDB Molecule: cytosol aminopeptidase; PDBTitle: crystal structure of cytosol aminopeptidase from staphylococcus aureus2 col |
| 27 | d2bv3a1 | Alignment | not modelled | 46.0 | 24 | Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Elongation factors |
| 28 | d1lama1 | Alignment | not modelled | 43.7 | 22 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Leucine aminopeptidase, C-terminal domain |
| | | | | | | PDB header: hydrolase |

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|----|-------------------------|-----------|--------------|------|----|---|
| 29 | c3jruB | Alignment | not modelled | 43.6 | 21 | Chain: B: PDB Molecule: probable cytosol aminopeptidase; PDBTitle: crystal structure of leucyl aminopeptidase (pepa) from xoo0834,2 xanthomonas oryzae pv. oryzae kacc10331 |
| 30 | c2jmzA | Alignment | not modelled | 41.6 | 13 | PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein mj0781; PDBTitle: solution structure of a klba intein precursor from2 methanococcus jannaschii |
| 31 | d2cqaa1 | Alignment | not modelled | 36.4 | 23 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: TIP49 domain |
| 32 | d1ulva4 | Alignment | not modelled | 34.6 | 21 | Fold: Supersandwich Superfamily: Galactose mutarotase-like Family: Bacterial glucoamylase N-terminal domain-like |
| 33 | c1gytG | Alignment | not modelled | 34.5 | 25 | PDB header: hydrolase Chain: G: PDB Molecule: cytosol aminopeptidase; PDBTitle: e. coli aminopeptidase a (pepa) |
| 34 | d1gyta2 | Alignment | not modelled | 29.4 | 26 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Leucine aminopeptidase, C-terminal domain |
| 35 | c1x65A | Alignment | not modelled | 27.5 | 27 | PDB header: rna binding protein Chain: A: PDB Molecule: unr protein; PDBTitle: solution structure of the third cold-shock domain of the human2 kiaa0885 protein (unr protein) |
| 36 | c2kcyA | Alignment | not modelled | 24.3 | 22 | PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s8e; PDBTitle: solution structure of ribosomal protein s8e from2 methanothermobacter thermautotrophicus,3 northeaststructural genomics consortium (nseg) target tr71d |
| 37 | c2xzn2 | Alignment | not modelled | 21.4 | 28 | PDB header: ribosome Chain: 2: PDB Molecule: 40s ribosomal protein s8; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2 |
| 38 | c3u5cl | Alignment | not modelled | 20.7 | 25 | PDB header: ribosome Chain: I: PDB Molecule: 40s ribosomal protein s8-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome a |
| 39 | c4efdF | Alignment | not modelled | 19.5 | 17 | PDB header: hydrolase Chain: F: PDB Molecule: aminopeptidase; PDBTitle: crystal structure of an m17 aminopeptidase from trypanosoma brucei,2 tb427tmp.02.4440 |
| 40 | d2pi2e1 | Alignment | not modelled | 19.2 | 21 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB |
| 41 | c2pqaB | Alignment | not modelled | 18.8 | 21 | PDB header: replication Chain: B: PDB Molecule: replication protein a 14 kda subunit; PDBTitle: crystal structure of full-length human rpa 14/32 heterodimer |
| 42 | c3d3rA | Alignment | not modelled | 17.0 | 20 | PDB header: chaperone Chain: A: PDB Molecule: hydrogenase assembly chaperone hycp/hupf; PDBTitle: crystal structure of the hydrogenase assembly chaperone hycp/hupf2 family protein from shewanella oneidensis mr-1 |
| 43 | c2ns2A | Alignment | not modelled | 16.6 | 28 | PDB header: cell cycle Chain: A: PDB Molecule: spindlin-1; PDBTitle: crystal structure of spindlin1 |
| 44 | d1lf6a2 | Alignment | not modelled | 16.5 | 22 | Fold: Supersandwich Superfamily: Galactose mutarotase-like Family: Bacterial glucoamylase N-terminal domain-like |
| 45 | c2j5uB | Alignment | not modelled | 15.7 | 22 | PDB header: cell shape regulation Chain: B: PDB Molecule: mrec protein; PDBTitle: mrec lysteria monocytogenes |
| 46 | c3r6oA | Alignment | not modelled | 14.5 | 25 | PDB header: isomerase Chain: A: PDB Molecule: 2-hydroxyhepta-2,4-diene-1, 7-dioate isomerase; PDBTitle: crystal structure of a probable 2-hydroxyhepta-2,4-diene-1, 7-2 dioate isomerase from mycobacterium abscessus |
| 47 | c3f1zF | Alignment | not modelled | 14.4 | 38 | PDB header: dna binding protein Chain: F: PDB Molecule: putative nucleic acid-binding lipoprotein; PDBTitle: crystal structure of putative nucleic acid-binding lipoprotein2 (yp_001337197.1) from klebsiella pneumoniae subsp. pneumoniae mgh3 78578 at 2.46 a resolution |
| 48 | c2jz8A | Alignment | not modelled | 13.9 | 56 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bh09830; PDBTitle: solution nmr structure of bh09830 from bartonella henselae2 modeled with one zn+2 bound. northeast structural genomics3 consortium target bnr55 |
| 49 | c1gyca | Alignment | not modelled | 13.8 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: laccase 2; PDBTitle: crystal structure determination at room temperature of a2 laccase from trametes versicolor in its oxidised form3 containing a full complement of copper ions |
| 50 | c2kkga | Alignment | not modelled | 13.0 | 48 | PDB header: membrane protein Chain: A: PDB Molecule: major prion protein; PDBTitle: nmr structure of the octarepeat region of prion protein2 bound to pentosan polysulfate |
| 51 | c2dfuB | Alignment | not modelled | 12.6 | 28 | PDB header: isomerase Chain: B: PDB Molecule: probable 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase; PDBTitle: crystal structure of the 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase2 from thermus thermophilus hb8 |
| 52 | d1yoxa1 | Alignment | not modelled | 12.3 | 16 | Fold: Double-stranded beta-helix Superfamily: TRAP-like Family: PA3696/SPS0176-like |
| 53 | c1i7oC | Alignment | not modelled | 11.7 | 26 | PDB header: isomerase, lyase Chain: C: PDB Molecule: 4-hydroxyphenylacetate degradation |

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|----|-------------------------|-----------|--------------|------|----|--|
| 53 | c1f70c_ | Alignment | not modelled | 11.7 | 20 | bifunctional PDB header: crystal structure of hpce |
| 54 | c2cbjA_ | Alignment | not modelled | 11.5 | 17 | Chain: A; PDB Molecule: hyaluronidase; PDBTitle: structure of the clostridium perfringens nagj family 842 glycoside hydrolase, a homologue of human o-glcnacase in3 complex with pugnac |
| 55 | d1k28a3 | Alignment | not modelled | 11.4 | 31 | Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Phage lysozyme |
| 56 | d1g03a_ | Alignment | not modelled | 11.2 | 71 | Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain |
| 57 | c2kjpA_ | Alignment | not modelled | 11.0 | 27 | PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein ylbl; PDBTitle: solution structure of protein ylbl (bsu15050) from bacillus2 subtilis, northeast structural genomics consortium target3 sr713a |
| 58 | c4e2uA_ | Alignment | not modelled | 10.7 | 12 | PDB header: unknown function Chain: A; PDB Molecule: pho rada intein; PDBTitle: crystal structures of radamin intein from pyrococcus horikoshii |
| 59 | c2kcoA_ | Alignment | not modelled | 10.7 | 22 | PDB header: ribosomal protein Chain: A; PDB Molecule: 30s ribosomal protein s8e; PDBTitle: solution nmr structure of ribosomal protein sso0164 from2 sulfobolus solfataricus. northeast structural genomics3 consortium (nesg) target sst4. |
| 60 | d3d3ra1 | Alignment | not modelled | 10.6 | 19 | Fold: OB-fold Superfamily: HupF/HypC-like Family: HupF/HypC-like |
| 61 | d1sawa_ | Alignment | not modelled | 10.1 | 18 | Fold: FAH Superfamily: FAH Family: FAH |
| 62 | d1hxma2 | Alignment | not modelled | 9.8 | 20 | Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like) |
| 63 | d1s3sg_ | Alignment | not modelled | 9.7 | 21 | Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: UBX domain |
| 64 | c1wzoC_ | Alignment | not modelled | 9.4 | 21 | PDB header: isomerase Chain: C; PDB Molecule: hpce; PDBTitle: crystal structure of the hpce from thermus thermophilus hb8 |
| 65 | d1o6aa_ | Alignment | not modelled | 8.9 | 11 | Fold: Surface presentation of antigens (SPOA) Superfamily: Surface presentation of antigens (SPOA) Family: Surface presentation of antigens (SPOA) |
| 66 | d1i42a_ | Alignment | not modelled | 8.8 | 21 | Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: UBX domain |
| 67 | c3a5zF_ | Alignment | not modelled | 8.8 | 31 | PDB header: ligase Chain: F; PDB Molecule: elongation factor p; PDBTitle: crystal structure of escherichia coli genx in complex with elongation2 factor p |
| 68 | c2hbpA_ | Alignment | not modelled | 8.7 | 11 | PDB header: endocytosis, protein binding Chain: A; PDB Molecule: cytoskeleton assembly control protein sla1; PDBTitle: solution structure of sla1 homology domain 1 |
| 69 | c2knrA_ | Alignment | not modelled | 8.5 | 32 | PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein atc0905; PDBTitle: solution structure of protein atu0922 from a. tumefaciens. northeast2 structural genomics consortium target att13. ontario center for3 structural proteomics target atc0905 |
| 70 | d1o9ya_ | Alignment | not modelled | 8.4 | 13 | Fold: Surface presentation of antigens (SPOA) Superfamily: Surface presentation of antigens (SPOA) Family: Surface presentation of antigens (SPOA) |
| 71 | d1q1ca2 | Alignment | not modelled | 8.2 | 17 | Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase |
| 72 | c3j1aE_ | Alignment | not modelled | 8.0 | 63 | PDB header: virus Chain: E; PDB Molecule: capsid protein; PDBTitle: hk97-like fold fitted into 3d reconstruction of bacteriophage cw02 |
| 73 | c2qx2A_ | Alignment | not modelled | 7.9 | 18 | PDB header: structural genomics, unknown function Chain: A; PDB Molecule: sex pheromone staph-cam373; PDBTitle: structure of the c-terminal domain of sex pheromone staph-cam3732 precursor from staphylococcus aureus |
| 74 | c2jy9A_ | Alignment | not modelled | 7.7 | 24 | PDB header: hydrolase Chain: A; PDB Molecule: putative trna hydrolase domain; PDBTitle: nmr structure of putative trna hydrolase domain from2 salmonella typhimurium. northeast structural genomics3 consortium target str220 |
| 75 | d1m06g_ | Alignment | not modelled | 7.5 | 17 | Fold: Nucl eoplasm in-like/VP (viral coat and capsid proteins) Superfamily: ssDNA viruses Family: Microviridae-like VP |
| 76 | c2q1dX_ | Alignment | not modelled | 7.5 | 19 | PDB header: lyase Chain: X; PDB Molecule: 2-keto-3-deoxy-d-arabinonate dehydratase; PDBTitle: 2-keto-3-deoxy-d-arabinonate dehydratase complexed with magnesium and2 2,5-dioxopentanoate |
| 77 | c2hc9A_ | Alignment | not modelled | 7.5 | 17 | PDB header: hydrolase Chain: A; PDB Molecule: leucine aminopeptidase 1; PDBTitle: structure of caenorhabditis elegans leucine aminopeptidase-zinc2 complex (lap1) |
| 78 | d1qtta2 | Alignment | not modelled | 7.5 | 24 | Fold: FAH Superfamily: FAH |

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|----|-------------------------|-----------|--------------|-----|----|---|
| | | | | | | Family: FAH |
| 79 | d1gta1 | Alignment | not modelled | 7.4 | 14 | Fold: FAH Superfamily: FAH Family: FAH |
| 80 | d1c9ha | Alignment | not modelled | 7.4 | 22 | Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase |
| 81 | c2dzkA | Alignment | not modelled | 7.2 | 16 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ubx domain-containing protein 2; PDBTitle: structure of the ubx domain in mouse ubx domain-containing2 protein 2 |
| 82 | c2k4yA | Alignment | not modelled | 7.2 | 23 | PDB header: metal transport Chain: A: PDB Molecule: feoa-like protein; PDBTitle: nmr structure of feoa-like protein from clostridium2 acetobutylicum: northeast structural genomics consortium3 target car178 |
| 83 | d2cr5a1 | Alignment | not modelled | 7.2 | 18 | Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: UBX domain |
| 84 | c3kr5E | Alignment | not modelled | 7.2 | 24 | PDB header: hydrolase Chain: E: PDB Molecule: m17 leucyl aminopeptidase; PDBTitle: structure of a protease 4 |
| 85 | c3j0cH | Alignment | not modelled | 7.1 | 16 | PDB header: virus Chain: H: PDB Molecule: e2 envelope glycoprotein; PDBTitle: models of e1, e2 and cp of venezuelan equine encephalitis virus tc-832 strain restrained by a near atomic resolution cryo-em map |
| 86 | c3lzkC | Alignment | not modelled | 7.0 | 22 | PDB header: hydrolase Chain: C: PDB Molecule: fumarylacetoacetate hydrolase family protein; PDBTitle: the crystal structure of a probably aromatic amino acid2 degradation protein from sinorhizobium meliloti 1021 |
| 87 | c2qf4A | Alignment | not modelled | 6.9 | 27 | PDB header: structural protein Chain: A: PDB Molecule: cell shape determining protein mrec; PDBTitle: high resolution structure of the major periplasmic domain from the2 cell shape-determining filament mrec (orthorhombic form) |
| 88 | c3l0wB | Alignment | not modelled | 6.7 | 18 | PDB header: replication Chain: B: PDB Molecule: monoubiquitinated proliferating cell nuclear PDBTitle: structure of split monoubiquitinated pcna with ubiquitin in2 position two |
| 89 | c3uepB | Alignment | not modelled | 6.7 | 13 | PDB header: protein transport Chain: B: PDB Molecule: yscq-c, type iii secretion protein; PDBTitle: crystal structure of yscq-c from yersinia pseudotuberculosis |
| 90 | c3hshA | Alignment | not modelled | 6.6 | 18 | PDB header: protein binding Chain: A: PDB Molecule: collagen alpha-1(xviii) chain; PDBTitle: crystal structure of human collagen xviii trimerization domain2 (tetragonal crystal form) |
| 91 | d2lbaa2 | Alignment | not modelled | 6.4 | 43 | Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: Urate oxidase (uricase) |
| 92 | d1gff2 | Alignment | not modelled | 6.4 | 26 | Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: ssDNA viruses Family: Microviridae-like VP |
| 93 | d1dq3a1 | Alignment | not modelled | 6.3 | 15 | Fold: Hedgehog/intein (Hint) domain Superfamily: Hedgehog/intein (Hint) domain Family: Intein (protein splicing domain) |
| 94 | c2zkqm | Alignment | not modelled | 6.3 | 23 | PDB header: ribosomal protein/rna Chain: M: PDB Molecule: PDBTitle: structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map |
| 95 | c3mhxB | Alignment | not modelled | 6.1 | 18 | PDB header: metal transport Chain: B: PDB Molecule: putative ferrous iron transport protein a; PDBTitle: crystal structure of stentrophomonas maltophilia feoa complexed with2 zinc: a unique procaryotic sh3 domain protein possibly acting as a3 bacterial ferrous iron transport activating factor |
| 96 | d2d6fa1 | Alignment | not modelled | 6.1 | 18 | Fold: Sm-like fold Superfamily: GatD N-terminal domain-like Family: GatD N-terminal domain-like |
| 97 | c2xfbl | Alignment | not modelled | 5.9 | 17 | PDB header: virus Chain: I: PDB Molecule: e2 envelope glycoprotein; PDBTitle: the chikungunya e1 e2 envelope glycoprotein complex fit into2 the sindbis virus cryo-em map |
| 98 | c3n43B | Alignment | not modelled | 5.9 | 17 | PDB header: viral protein Chain: B: PDB Molecule: e2 envelope glycoprotein; PDBTitle: crystal structures of the mature envelope glycoprotein complex2 (trypsin cleavage) of chikungunya virus. |
| 99 | c3iefA | Alignment | not modelled | 5.8 | 67 | PDB header: transferase, rna binding protein Chain: A: PDB Molecule: trna (guanine-n(1)-)-methyltransferase; PDBTitle: crystal structure of trna guanine-n1-methyltransferase from2 bartonella henselae using mpcs. |