













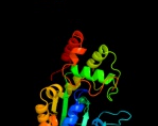






Phyre2

| | |
|---------------|------------------------------|
| Email | I.a.kelley@imperial.ac.uk |
| Description | Q2TBF2 |
| Date | Thu Apr 26 09:35:20 BST 2012 |
| Unique Job ID | 3b70eea1c5a9c35f |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|---|
| 1 | d1fmja_ |  Alignment |  | 100.0 | 22 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase |
| 2 | d1q44a_ |  Alignment |  | 100.0 | 21 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase |
| 3 | c2h8kA_ |  Alignment |  | 100.0 | 20 | PDB header: transferase Chain: A: PDB Molecule: sult1c3 splice variant d; PDBTitle: human sulfotranferase sult1c3 in complex with pap |
| 4 | d1q20a_ |  Alignment |  | 100.0 | 21 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase |
| 5 | d1g3ma_ |  Alignment |  | 100.0 | 19 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase |
| 6 | d1xv1a_ |  Alignment |  | 100.0 | 17 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase |
| 7 | c2zvpX_ |  Alignment |  | 100.0 | 18 | PDB header: transferase Chain: X: PDB Molecule: tyrosine-ester sulfotransferase; PDBTitle: crystal structure of mouse cytosolic sulfotransferase msult1d1 complex2 with pap and p-nitrophenol |
| 8 | d1ls6a_ |  Alignment |  | 100.0 | 15 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase |
| 9 | c3u3oA_ |  Alignment |  | 100.0 | 15 | PDB header: transferase Chain: A: PDB Molecule: sulfotransferase 1a1; PDBTitle: crystal structure of human sult1a1 bound to pap and two 3-cyano-7-2 hydroxycoumarin |
| 10 | d1aqua_ |  Alignment |  | 100.0 | 17 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase |
| 11 | d2a3ra1 |  Alignment |  | 100.0 | 15 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase |

| | | | | | | |
|----|-------------------------|-----------|---|-------|----|--|
| 12 | c1q1qA_ | Alignment |  | 100.0 | 19 | PDB header: transferase Chain: A: PDB Molecule: sulfotransferase family, cytosolic, 2b, member 1 PDBTitle: crystal structure of human pregnenolone sulfotransferase2 (sult2b1a) in the presence of pap |
| 13 | c1zd1B_ | Alignment |  | 100.0 | 17 | PDB header: transferase Chain: B: PDB Molecule: sulfotransferase 4a1; PDBTitle: human sulfortransferase sult4a1 |
| 14 | d1j99a_ | Alignment |  | 100.0 | 17 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase |
| 15 | d3bfxa1 | Alignment |  | 100.0 | 17 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase |
| 16 | c2gwhA_ | Alignment |  | 100.0 | 18 | PDB header: transferase Chain: A: PDB Molecule: sulfotransferase 1c2; PDBTitle: human sulfotranferase sult1c2 in complex with pap and2 pentachlorophenol |
| 17 | c3mgbA_ | Alignment |  | 100.0 | 18 | PDB header: transferase/antibiotic Chain: A: PDB Molecule: teg12; PDBTitle: teg 12 ternary structure complexed with pap and the teicoplanin2 aglycone |
| 18 | c3mg9A_ | Alignment |  | 100.0 | 18 | PDB header: transferase/antibiotic Chain: A: PDB Molecule: teg12; PDBTitle: teg 12 binary structure complexed with the teicoplanin aglycone |
| 19 | c2ovfA_ | Alignment |  | 100.0 | 18 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: stal; PDBTitle: crystal structure of stal-pap complex |
| 20 | c3ap3A_ | Alignment |  | 99.9 | 16 | PDB header: transferase Chain: A: PDB Molecule: protein-tyrosine sulfotransferase 2; PDBTitle: crystal structure of human tyrosylprotein sulfotransferase-2 complexed2 with pap |
| 21 | d1t8ta_ | Alignment | not modelled | 99.9 | 14 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase |
| 22 | c1vkjA_ | Alignment | not modelled | 99.9 | 13 | PDB header: transferase Chain: A: PDB Molecule: heparan sulfate (glucosamine) 3-o-sulfotransferase2 isoform 1 in the presence of pap PDBTitle: crystal structure of heparan sulfate 3-o-sulfotransferase2 isoform 1 in the presence of pap |
| 23 | d1vkja_ | Alignment | not modelled | 99.9 | 13 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase |
| 24 | c1nstA_ | Alignment | not modelled | 99.9 | 15 | PDB header: sulfotransferase Chain: A: PDB Molecule: heparan sulfate n-deacetylase/n-sulfotransferase; PDBTitle: the sulfotransferase domain of human haparin sulfate n-2 deacetylase/n-sulfotransferase |
| 25 | d1nsta_ | Alignment | not modelled | 99.9 | 15 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase |
| 26 | c3rnlA_ | Alignment | not modelled | 99.8 | 14 | PDB header: transferase Chain: A: PDB Molecule: sulfotransferase; PDBTitle: crystal structure of sulfotransferase from alicyclobacillus2 acidocaldarius |
| 27 | c3bd9A_ | Alignment | not modelled | 99.8 | 10 | PDB header: transferase Chain: A: PDB Molecule: heparan sulfate glucosamine 3-o-sulfotransferase PDBTitle: human 3-o-sulfotransferase isoform 5 with bound pap |
| 28 | c2z6vA_ | Alignment | not modelled | 99.7 | 14 | PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of sulfotransferase stf9 from2 mycobacterium avium |
| | | | | | | PDB header: transferase |

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|----|-------------------------|-----------|--------------|------|----|--|
| 29 | c2zq5A | Alignment | not modelled | 99.6 | 12 | Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of sulfotransferase stf1 from2 mycobacterium tuberculosis h37rv (type1 form) |
| 30 | d1texa | Alignment | not modelled | 99.5 | 12 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase |
| 31 | c3f5fA | Alignment | not modelled | 94.7 | 15 | PDB header: transport, transferase Chain: A: PDB Molecule: maltose-binding periplasmic protein, heparan PDBTitle: crystal structure of heparan sulfate 2-o-sulfotransferase2 from gallus gallus as a maltose binding protein fusion. |
| 32 | d2cbia2 | Alignment | not modelled | 64.0 | 23 | Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: alpha-D-glucuronidase/Hyaluronidase catalytic domain |
| 33 | c1nijA | Alignment | not modelled | 52.7 | 25 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein yjia; PDBTitle: yjia protein |
| 34 | c2xsbA | Alignment | not modelled | 48.2 | 23 | PDB header: hydrolase Chain: A: PDB Molecule: hyaluronoglucosaminidase; PDBTitle: ogoga pugnac complex |
| 35 | d1qgva | Alignment | not modelled | 45.6 | 18 | Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: spliceosomal protein U5-15Kd |
| 36 | d1nija1 | Alignment | not modelled | 41.8 | 26 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like |
| 37 | d1s2xa | Alignment | not modelled | 37.0 | 25 | Fold: STAT-like Superfamily: Cag-Z Family: Cag-Z |
| 38 | c1s2xA | Alignment | not modelled | 37.0 | 25 | PDB header: unknown function Chain: A: PDB Molecule: cag-z; PDBTitle: crystal structure of cag-z from helicobacter pylori |
| 39 | d2choa2 | Alignment | not modelled | 36.8 | 14 | Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: alpha-D-glucuronidase/Hyaluronidase catalytic domain |
| 40 | c1ti5A | Alignment | not modelled | 35.9 | 27 | PDB header: plant protein Chain: A: PDB Molecule: plant defensin; PDBTitle: solution structure of plant defensin |
| 41 | d1jkza | Alignment | not modelled | 35.1 | 24 | Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Plant defensins |
| 42 | c2cbjA | Alignment | not modelled | 28.1 | 23 | PDB header: hydrolase 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 |
| 43 | c1yj5B | Alignment | not modelled | 27.6 | 22 | PDB header: transferase Chain: B: PDB Molecule: 5' polynucleotide kinase-3' phosphatase catalytic domain; PDBTitle: molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme |
| 44 | c3zvmA | Alignment | not modelled | 24.7 | 27 | PDB header: hydrolase/transferase/dna Chain: A: PDB Molecule: bifunctional polynucleotide phosphatase/kinase; PDBTitle: the structural basis for substrate recognition by mammalian2 polynucleotide kinase 3' phosphatase |
| 45 | d1wiza | Alignment | not modelled | 24.0 | 17 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: CUT domain |
| 46 | d1j09a2 | Alignment | not modelled | 22.4 | 13 | Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain |
| 47 | c3c52B | Alignment | not modelled | 21.2 | 23 | PDB header: lyase Chain: B: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: class ii fructose-1,6-bisphosphate aldolase from2 helicobacter pylori in complex with3 phosphoglycolohydroxamic acid, a competitive inhibitor |
| 48 | c2j8lA | Alignment | not modelled | 19.8 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: coagulation factor xi; PDBTitle: fxi apple 4 domain loop-out conformation |
| 49 | d1dx5i3 | Alignment | not modelled | 18.9 | 26 | Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: EGF/Laminin Family: EGF-type module |
| 50 | d1l3ya | Alignment | not modelled | 18.5 | 41 | Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: EGF/Laminin Family: Integrin beta EGF-like domains |
| 51 | c1wxnA | Alignment | not modelled | 17.6 | 46 | PDB header: toxin Chain: A: PDB Molecule: toxin apetx2; PDBTitle: solution structure of apetx2, a specific peptide inhibitor2 of ASIC3 proton-gated channels |
| 52 | d1ppid1 | Alignment | not modelled | 16.3 | 27 | Fold: Cytochrome c Superfamily: Cytochrome c Family: Cytochrome bc1 domain |
| 53 | d1rz3a | Alignment | not modelled | 16.3 | 10 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Phosphoribulokinase/pantothenate kinase |
| 54 | d1pvza | Alignment | not modelled | 15.4 | 27 | Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like |

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|----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | Family: Short-chain scorpion toxins |
| 55 | c2j8jB_ | Alignment | not modelled | 15.2 | 19 | PDB header: hydrolase Chain: B: PDB Molecule: coagulation factor xi; PDBTitle: solution structure of the a4 domain of blood coagulation2 factor xi |
| 56 | c1wqkA_ | Alignment | not modelled | 14.2 | 55 | PDB header: toxin Chain: A: PDB Molecule: toxin apetx1; PDBTitle: solution structure of apetx1, a specific peptide inhibitor2 of human ether-a-go-go-related gene potassium channels3 from the venom of the sea anemone anthopleura4 elegantissima: a new fold for an herg toxin |
| 57 | c2j8lB_ | Alignment | not modelled | 12.5 | 19 | PDB header: hydrolase Chain: B: PDB Molecule: coagulation factor xi; PDBTitle: fxi apple 4 domain loop-out conformation |
| 58 | c2choA_ | Alignment | not modelled | 12.5 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: glucosaminidase; PDBTitle: bacteroides thetaiotaomicron hexosaminidase with o-2 glcnacase activity |
| 59 | c2j8jA_ | Alignment | not modelled | 12.1 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: coagulation factor xi; PDBTitle: solution structure of the a4 domain of blood coagulation2 factor xi |
| 60 | d1cfza_ | Alignment | not modelled | 11.4 | 17 | Fold: Phosphorylase/hydrolase-like Superfamily: HybD-like Family: Hydrogenase maturing endopeptidase HybD |
| 61 | d1esfa1 | Alignment | not modelled | 11.0 | 25 | Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Superantigen toxins, N-terminal domain |
| 62 | c3pesA_ | Alignment | not modelled | 11.0 | 23 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein gp49; PDBTitle: crystal structure of uncharacterized protein from pseudomonas phage2 yua |
| 63 | d1ekga_ | Alignment | not modelled | 10.8 | 31 | Fold: N domain of copper amine oxidase-like Superfamily: Fratxin/Nqo15-like Family: Fratxin-like |
| 64 | c3cwbQ_ | Alignment | not modelled | 10.4 | 34 | PDB header: oxidoreductase Chain: Q: PDB Molecule: mitochondrial cytochrome c1, heme protein; PDBTitle: chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d |
| 65 | d1tafb_ | Alignment | not modelled | 10.2 | 20 | Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs |
| 66 | c1p84D_ | Alignment | not modelled | 10.2 | 17 | PDB header: oxidoreductase Chain: D: PDB Molecule: cytochrome c1, heme protein; PDBTitle: hdbt inhibited yeast cytochrome bc1 complex |
| 67 | d1s6ya2 | Alignment | not modelled | 10.2 | 17 | Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: AgIA-like glucosidase |
| 68 | c1ly1A_ | Alignment | not modelled | 9.8 | 43 | PDB header: transferase Chain: A: PDB Molecule: polynucleotide kinase; PDBTitle: structure and mechanism of t4 polynucleotide kinase |
| 69 | d1ly1a_ | Alignment | not modelled | 9.8 | 43 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases |
| 70 | c2kp0A_ | Alignment | not modelled | 9.2 | 22 | PDB header: de novo protein Chain: A: PDB Molecule: nasonin-1m; PDBTitle: solution structure of nasonin-1m |
| 71 | c3izcw_ | Alignment | not modelled | 9.1 | 15 | PDB header: ribosome Chain: W: PDB Molecule: 60s ribosomal protein rpl22 (l22e); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome |
| 72 | c2w1oA_ | Alignment | not modelled | 8.7 | 23 | PDB header: translation Chain: A: PDB Molecule: 60s acidic ribosomal protein p2; PDBTitle: nmr structure of dimerization domain of human ribosomal2 protein p2 |
| 73 | d1h9ji_ | Alignment | not modelled | 8.5 | 25 | Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Plant inhibitors of proteinases and amylases Family: Plant inhibitors of proteinases and amylases |
| 74 | c2a45L_ | Alignment | not modelled | 8.1 | 38 | PDB header: hydrolase/hydrolase inhibitor Chain: L: PDB Molecule: fibrinogen gamma chain; PDBTitle: crystal structure of the complex between thrombin and the central "e"2 region of fibrin |
| 75 | d1ozza_ | Alignment | not modelled | 8.1 | 29 | Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Insect defensins |
| 76 | c1yseA_ | Alignment | not modelled | 8.0 | 20 | PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding protein satb1; PDBTitle: solution structure of the mar-binding domain of satb1 |
| 77 | c3iz5w_ | Alignment | not modelled | 7.9 | 19 | PDB header: ribosome Chain: W: PDB Molecule: 60s ribosomal protein l22 (l22e); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome |
| 78 | c3enoC_ | Alignment | not modelled | 7.9 | 29 | PDB header: hydrolase/unknown function Chain: C: PDB Molecule: uncharacterized protein pf2011; PDBTitle: crystal structure of pyrococcus furiosus pcc1 in complex2 with thermoplasma acidophilum kae1 |
| 79 | d1iwea_ | Alignment | not modelled | 7.9 | 28 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like |
| | | | | | | PDB header: transcription, cell cycle |

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|----|--------------------------|-----------|--------------|-----|----|---|
| 80 | c1xbsA_ | Alignment | not modelled | 7.9 | 20 | Chain: A: PDB Molecule: dim1-like protein; PDBTitle: crystal structure of human dim2: a dim1-like protein |
| 81 | c2c1eB_ | Alignment | not modelled | 7.8 | 30 | PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: caspase-3 subunit p12; PDBTitle: crystal structures of caspase-3 in complex with aza-peptide michael2 acceptor inhibitors. |
| 82 | d1yj5a2 | Alignment | not modelled | 7.8 | 28 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases |
| 83 | c2f1rA_ | Alignment | not modelled | 7.8 | 13 | PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis PDBTitle: crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobb) |
| 84 | d1myna_ | Alignment | not modelled | 7.8 | 23 | Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Insect defensins |
| 85 | c3bs3A_ | Alignment | not modelled | 7.7 | 23 | PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of a putative dna-binding protein from bacteroides2 fragilis |
| 86 | c3dnlG_ | Alignment | not modelled | 7.2 | 25 | PDB header: viral protein Chain: G: PDB Molecule: hiv-1 envelope glycoprotein gp120; PDBTitle: molecular structure for the hiv-1 gp120 trimer in the b12-2 bound state |
| 87 | d1sisa_ | Alignment | not modelled | 7.1 | 38 | Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Short-chain scorpion toxins |
| 88 | d1q90a3 | Alignment | not modelled | 6.8 | 16 | Fold: Single transmembrane helix Superfamily: Cytochrome f subunit of the cytochrome b6f complex, transmembrane anchor Family: Cytochrome f subunit of the cytochrome b6f complex, transmembrane anchor |
| 89 | d2ga5a1 | Alignment | not modelled | 6.8 | 38 | Fold: N domain of copper amine oxidase-like Superfamily: Frataxin/Nqo15-like Family: Frataxin-like |
| 90 | c2e3eA_ | Alignment | not modelled | 6.8 | 17 | PDB header: antimicrobial protein Chain: A: PDB Molecule: defensin, mutant def-bbb; PDBTitle: nmr structure of def-bbb, a mutant of anopheles defensin2 def-aaa |
| 91 | c2kz5A_ | Alignment | not modelled | 6.7 | 18 | PDB header: transcription Chain: A: PDB Molecule: transcription factor nf-e2 45 kda subunit; PDBTitle: solution nmr structure of transcription factor nf-e2 subunit's dna2 binding domain from homo sapiens, northeast structural genomics3 consortium target hr4653b |
| 92 | d1m8pa3 | Alignment | not modelled | 6.6 | 14 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ATP sulfurylase C-terminal domain |
| 93 | cliweB_ | Alignment | not modelled | 6.5 | 28 | PDB header: ligase Chain: B: PDB Molecule: adenylosuccinate synthetase; PDBTitle: imp complex of the recombinant mouse-muscle2 adenylosuccinate synthetase |
| 94 | d1mb3_ | Alignment | not modelled | 6.5 | 11 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors |
| 95 | c3b85A_ | Alignment | not modelled | 6.4 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: phosphate starvation-inducible protein; PDBTitle: crystal structure of predicted phosphate starvation-induced atpase2 pho2 from corynebacterium glutamicum |
| 96 | c2nz3A_ | Alignment | not modelled | 6.4 | 30 | PDB header: antimicrobial protein Chain: A: PDB Molecule: defensin, mutant def-aaa; PDBTitle: nmr structure of def-aaa, a mutant of anopheles defensin2 def-aaa |
| 97 | d1licaa_ | Alignment | not modelled | 6.3 | 26 | Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Insect defensins |
| 98 | d1zela1 | Alignment | not modelled | 6.3 | 32 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Rv2827c N-terminal domain-like |
| 99 | c3m1eA_ | Alignment | not modelled | 6.2 | 13 | PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: crystal structure of benm_dbd |