
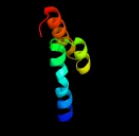


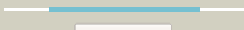






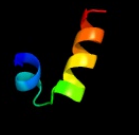





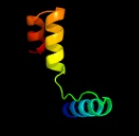






Phyre2

| | |
|---------------|------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD2271_(-)_2545342_2545641 |
| Date | Mon Aug 5 13:25:41 BST 2019 |
| Unique Job ID | aa7ff64f8835e6d1 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c5u9oD_ |  Alignment |  | 55.8 | 17 | PDB header: cell cycle Chain: D: PDB Molecule: plastid division protein cdp1, chloroplastic,plastid PDBTitle: cocystal structure of the intermembrane space region of the plastid2 division proteins parc6 and pdv1 |
| 2 | d1lvaa4 |  Alignment |  | 50.9 | 16 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: C-terminal fragment of elongation factor SelB |
| 3 | c4jrbA_ |  Alignment |  | 34.2 | 17 | PDB header: lipid binding protein Chain: A: PDB Molecule: green fluorescent protein; PDBTitle: structure of cockroach allergen bla g 1 tandem repeat as a egfp fusion |
| 4 | c3uxuA_ |  Alignment |  | 33.4 | 2 | PDB header: recombination Chain: A: PDB Molecule: probable integrase; PDBTitle: the structure of the catalytic domain of the sulfobolus spindle-shaped2 viral integrase reveals an evolutionarily conserved catalytic core3 and supports a mechanism of dna cleavage in trans |
| 5 | c3lacA_ |  Alignment |  | 31.1 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: pyrrolidone-carboxylate peptidase; PDBTitle: crystal structure of bacillus anthracis pyrrolidone-carboxylate2 peptidase, pcp |
| 6 | c1wsuA_ |  Alignment |  | 27.5 | 22 | PDB header: translation/rna Chain: A: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: c-terminal domain of elongation factor selb complexed with2 secis rna |
| 7 | c2xvcA_ |  Alignment |  | 26.6 | 29 | 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 |
| 8 | c2pjpA_ |  Alignment |  | 26.2 | 22 | PDB header: translation/rna Chain: A: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: structure of the mrna-binding domain of elongation factor2 selb from e.coli in complex with secis rna |
| 9 | c1z1bA_ |  Alignment |  | 26.1 | 12 | PDB header: dna binding protein/dna Chain: A: PDB Molecule: integrase; PDBTitle: crystal structure of a lambda integrase dimer bound to a2 coc' core site |
| 10 | c1lvaA_ |  Alignment |  | 25.7 | 22 | PDB header: translation Chain: A: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: crystal structure of a c-terminal fragment of moorella2 thermoacetica elongation factor selb |
| 11 | c4j5mA_ |  Alignment |  | 24.8 | 12 | PDB header: protein transport Chain: A: PDB Molecule: unconventional myosin-vb; PDBTitle: structure of the cargo binding domain from human myosin vb |

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|----|-------------------------|-----------|--------------|------|----|---|
| 12 | c3nijA_ | Alignment | | 22.3 | 67 | PDB header: metal binding protein Chain: A; PDB Molecule: e3 ubiquitin-protein ligase ubr1; PDBTitle: the structure of ubr box (h1aa) |
| 13 | c3hy4A_ | Alignment | | 22.3 | 15 | PDB header: ligase Chain: A; PDB Molecule: 5-formyltetrahydrofolate cyclo-ligase; PDBTitle: structure of human mthfs with n5-iminium phosphate |
| 14 | c5d9rA_ | Alignment | | 21.7 | 14 | 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 |
| 15 | c5oatF_ | Alignment | | 21.0 | 7 | PDB header: kinase Chain: F; PDB Molecule: serine/threonine-protein kinase pink1, mitochondrial-like PDBTitle: pink1 structure |
| 16 | c2plyB_ | Alignment | | 21.0 | 22 | PDB header: translation/rna Chain: B; PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: structure of the mrna binding fragment of elongation factor2 selb in complex with secis rna. |
| 17 | c5dcaA_ | Alignment | | 20.5 | 14 | PDB header: recombination Chain: A; PDB Molecule: tyrosine recombinase xerd,dna translocase ftsk; PDBTitle: c-terminal domain of xerd recombinase in complex with gamma domain of ftsk |
| 18 | c3bhpA_ | Alignment | | 20.2 | 30 | PDB header: structural genomics, unknown function Chain: A; PDB Molecule: upf0291 protein yncz; PDBTitle: crystal structure of upf0291 protein yncz from bacillus2 subtilis at resolution 2.0 a. northeast structural3 genomics consortium target sr384 |
| 19 | c2kfvA_ | Alignment | | 19.7 | 22 | PDB header: isomerase Chain: A; PDB Molecule: fk506-binding protein 3; PDBTitle: structure of the amino-terminal domain of human fk506-2 binding protein 3 / northeast structural genomics3 consortium target ht99a |
| 20 | c2f6hX_ | Alignment | | 19.5 | 16 | PDB header: structural protein Chain: X; PDB Molecule: myosin-2; PDBTitle: myosin v cargo binding domain |
| 21 | c2csdB_ | Alignment | not modelled | 19.1 | 33 | PDB header: isomerase Chain: B; PDB Molecule: topoisomerase v; PDBTitle: crystal structure of topoisomerase v (61 kda fragment) |
| 22 | c5aonB_ | Alignment | not modelled | 18.3 | 18 | PDB header: signaling protein Chain: B; PDB Molecule: peroxin 14; PDBTitle: crystal structure of the conserved n-terminal domain of pex14 from trypanosoma brucei |
| 23 | c5zrzB_ | Alignment | not modelled | 17.7 | 20 | PDB header: protein binding Chain: B; PDB Molecule: sterile alpha motif domain-containing protein 5; PDBTitle: crystal structure of epha5/samd5 complex |
| 24 | c3wb8H_ | Alignment | not modelled | 17.2 | 12 | PDB header: motor protein Chain: H; PDB Molecule: unconventional myosin-va; PDBTitle: crystal structure of myova-gtd |
| 25 | c3hilB_ | Alignment | not modelled | 16.8 | 27 | PDB header: transferase Chain: B; PDB Molecule: ephrin type-a receptor 1; PDBTitle: sam domain of human ephrin type-a receptor 1 (epha1) |
| 26 | c2w85A_ | Alignment | not modelled | 16.3 | 15 | PDB header: protein transport Chain: A; PDB Molecule: peroxisomal membrane anchor protein pex14; PDBTitle: structure of pex14 in complex with pex19 |
| 27 | c4l8tA_ | Alignment | not modelled | 16.2 | 13 | PDB header: protein transport Chain: A; PDB Molecule: unconventional myosin-vc; PDBTitle: structure of the cargo binding domain from human myosin vc |
| 28 | c4b2vA_ | Alignment | not modelled | 16.2 | 67 | PDB header: toxin Chain: A; PDB Molecule: s64; PDBTitle: s64, a spider venom toxin peptide from sicarius dolichocephalus |
| | | | | | | Fold: DNA breaking-rejoining enzymes |

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|----|-------------------------|-----------|--------------|------|----|---|
| 29 | d1p7da_ | Alignment | not modelled | 15.3 | 16 | Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core |
| 30 | c5n9jA_ | Alignment | not modelled | 15.3 | 12 | PDB header: transcription Chain: A: PDB Molecule: mediator of rna polymerase ii transcription subunit 14; PDBTitle: core mediator of transcriptional regulation |
| 31 | c1pscA_ | Alignment | not modelled | 15.1 | 9 | PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase; PDBTitle: phosphotriesterase from pseudomonas diminuta |
| 32 | c2lh0B_ | Alignment | not modelled | 14.9 | 23 | PDB header: chaperone Chain: B: PDB Molecule: histone chaperone rtt106; PDBTitle: nmr structure of the histone-interacting n-terminal homodimeric region2 of rtt106 |
| 33 | d1j5ja_ | Alignment | not modelled | 14.2 | 80 | Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Short-chain scorpion toxins |
| 34 | c5z47A_ | Alignment | not modelled | 14.1 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: pyrrolidone-carboxylate peptidase; PDBTitle: crystal structure of pyrrolidone carboxylate peptidase i with2 disordered loop a from deinococcus radiodurans r1 |
| 35 | c5vmdA_ | Alignment | not modelled | 14.1 | 43 | PDB header: ligase Chain: A: PDB Molecule: f-box only protein 11; PDBTitle: crystal structure of ubr-box from ubr6 in a domain-swapping2 conformation |
| 36 | c3hy5A_ | Alignment | not modelled | 13.6 | 13 | PDB header: transport protein Chain: A: PDB Molecule: retinaldehyde-binding protein 1; PDBTitle: crystal structure of cralbp |
| 37 | c3pk1A_ | Alignment | not modelled | 13.4 | 25 | PDB header: apoptosis/apoptosis regulator Chain: A: PDB Molecule: induced myeloid leukemia cell differentiation protein mcl- PDBTitle: crystal structure of mcl-1 in complex with the baxbh3 domain |
| 38 | c6gfmA_ | Alignment | not modelled | 13.3 | 30 | PDB header: hydrolase Chain: A: PDB Molecule: pyrimidine/purine nucleotide 5'-monophosphate nucleosidase; PDBTitle: crystal structure of the escherichia coli nucleosidase ppnn (ppgpp-2 form) |
| 39 | d1olma1 | Alignment | not modelled | 13.2 | 13 | Fold: RuvA C-terminal domain-like Superfamily: CRAL/TRIO N-terminal domain Family: CRAL/TRIO N-terminal domain |
| 40 | c3ny1B_ | Alignment | not modelled | 13.1 | 83 | PDB header: ligase Chain: B: PDB Molecule: e3 ubiquitin-protein ligase ubr1; PDBTitle: structure of the ubr-box of the ubr1 ubiquitin ligase |
| 41 | c3ebnD_ | Alignment | not modelled | 12.9 | 17 | PDB header: hydrolase Chain: D: PDB Molecule: replicase polyprotein 1ab; PDBTitle: a special dimerization of sars-cov main protease c-terminal2 domain due to domain-swapping |
| 42 | c2vofA_ | Alignment | not modelled | 12.9 | 25 | PDB header: apoptosis Chain: A: PDB Molecule: bcl-2-related protein a1; PDBTitle: structure of mouse a1 bound to the puma bh3-domain |
| 43 | c3omdB_ | Alignment | not modelled | 12.7 | 11 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of unknown function protein from leptospirillum2 rubarum |
| 44 | c5vmdC_ | Alignment | not modelled | 12.6 | 43 | PDB header: ligase Chain: C: PDB Molecule: f-box only protein 11; PDBTitle: crystal structure of ubr-box from ubr6 in a domain-swapping2 conformation |
| 45 | d1dx5i3 | Alignment | not modelled | 12.5 | 67 | Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: EGF/Laminin Family: EGF-type module |
| 46 | c5l87A_ | Alignment | not modelled | 12.4 | 18 | PDB header: membrane protein Chain: A: PDB Molecule: peroxin 14; PDBTitle: targeting the pex14-pex5 interaction by small molecules provides novel2 therapeutic routes to treat trypanosomiasis. |
| 47 | d1v38a_ | Alignment | not modelled | 12.3 | 19 | Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain |
| 48 | c3nkhB_ | Alignment | not modelled | 12.1 | 10 | PDB header: recombination Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of integrase from mrsa strain staphylococcus aureus |
| 49 | c3ikoC_ | Alignment | not modelled | 12.0 | 13 | PDB header: structural protein, protein transport Chain: C: PDB Molecule: nucleoporin nup84; PDBTitle: crystal structure of the heterotrimeric sec13-nup145c-nup842 nucleoporin complex |
| 50 | c2vm6A_ | Alignment | not modelled | 11.6 | 25 | PDB header: immune system Chain: A: PDB Molecule: bcl-2-related protein a1; PDBTitle: human bcl2-a1 in complex with bim-bh3 peptide |
| 51 | c2a3vA_ | Alignment | not modelled | 11.4 | 18 | PDB header: recombination Chain: A: PDB Molecule: site-specific recombinase inti4; PDBTitle: structural basis for broad dna-specificity in integron recombination |
| 52 | c2k89A_ | Alignment | not modelled | 11.3 | 12 | PDB header: protein binding Chain: A: PDB Molecule: phospholipase a-2-activating protein; PDBTitle: solution structure of a novel ubiquitin-binding domain from2 human plaa (pfuc, gly76-pro77 cis isomer) |
| 53 | d1iyka1 | Alignment | not modelled | 11.3 | 25 | Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-myristoyl transferase, NMT |
| 54 | c5w63A_ | Alignment | not modelled | 11.2 | 33 | PDB header: apoptosis Chain: A: PDB Molecule: apoptosis regulator bax; PDBTitle: crystal structure of channel catfish bax |
| | | | | | | Fold: Zincin-like |

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|----|--------------------------|-----------|--------------|------|----|--|
| 55 | d1k9xa_ | Alignment | not modelled | 11.0 | 8 | Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Neurolysin-like |
| 56 | c5wddA_ | Alignment | not modelled | 10.8 | 42 | PDB header: apoptosis Chain: A: PDB Molecule: bcl-2-related ovarian killer protein; PDBTitle: crystal structure of chicken bok |
| 57 | c2hqhE_ | Alignment | not modelled | 10.8 | 67 | PDB header: structural protein, protein binding Chain: E: PDB Molecule: restin; PDBTitle: crystal structure of p150glued and clip-170 |
| 58 | c3e2uE_ | Alignment | not modelled | 10.8 | 67 | PDB header: protein binding Chain: E: PDB Molecule: scap-gly domain-containing linker protein 1; PDBTitle: crystal structure of the zink-knuckle 2 domain of human clip-170 in2 complex with cap-gly domain of human dynactin-1 (p150-glued) |
| 59 | c3e2uF_ | Alignment | not modelled | 10.8 | 67 | PDB header: protein binding Chain: F: PDB Molecule: scap-gly domain-containing linker protein 1; PDBTitle: crystal structure of the zink-knuckle 2 domain of human clip-170 in2 complex with cap-gly domain of human dynactin-1 (p150-glued) |
| 60 | c5wosA_ | Alignment | not modelled | 10.8 | 8 | PDB header: viral protein Chain: A: PDB Molecule: cnpv058 bcl-2 like protein; PDBTitle: structural and functional insights into canarypox virus crnp0582 regulation of apoptosis |
| 61 | d1g5ma_ | Alignment | not modelled | 10.4 | 33 | Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death |
| 62 | c3e2uH_ | Alignment | not modelled | 10.3 | 67 | PDB header: protein binding Chain: H: PDB Molecule: scap-gly domain-containing linker protein 1; PDBTitle: crystal structure of the zink-knuckle 2 domain of human clip-170 in2 complex with cap-gly domain of human dynactin-1 (p150-glued) |
| 63 | d2d2ja1 | Alignment | not modelled | 10.3 | 11 | Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like |
| 64 | c2vc7A_ | Alignment | not modelled | 10.2 | 10 | PDB header: hydrolase Chain: A: PDB Molecule: aryldialkylphosphatase; PDBTitle: structural basis for natural lactonase and promiscuous2 phosphotriesterase activities |
| 65 | c3kkaD_ | Alignment | not modelled | 10.1 | 26 | PDB header: transferase Chain: D: PDB Molecule: ephrin type-a receptor 2; PDBTitle: co-crystal structure of the sam domains of epha1 and epha2 |
| 66 | c2yv6A_ | Alignment | not modelled | 10.1 | 30 | PDB header: apoptosis Chain: A: PDB Molecule: bcl-2 homologous antagonist/killer; PDBTitle: crystal structure of human bcl-2 family protein bak |
| 67 | c2k9uB_ | Alignment | not modelled | 10.0 | 43 | PDB header: structural protein Chain: B: PDB Molecule: filamin-binding lim protein 1; PDBTitle: solution nmr structure of the filamin-migfilin complex |
| 68 | d1q59a_ | Alignment | not modelled | 10.0 | 27 | Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death |
| 69 | c3mmiB_ | Alignment | not modelled | 9.9 | 11 | PDB header: motor protein Chain: B: PDB Molecule: myosin-4; PDBTitle: crystal structure of the globular tail of myo4p |
| 70 | d1g1xb_ | Alignment | not modelled | 9.9 | 15 | Fold: S15/NS1 RNA-binding domain Superfamily: S15/NS1 RNA-binding domain Family: Ribosomal protein S15 |
| 71 | c5tzipA_ | Alignment | not modelled | 9.7 | 0 | PDB header: apoptosis Chain: A: PDB Molecule: bcl-2-like protein fpv039; PDBTitle: crystal structure of fpv039:bik bh3 complex |
| 72 | c5ua4A_ | Alignment | not modelled | 9.6 | 25 | PDB header: apoptosis Chain: A: PDB Molecule: 5-hl; PDBTitle: crystal structure of a179l:bid bh3 complex |
| 73 | c3c1dA_ | Alignment | not modelled | 9.6 | 17 | PDB header: recombination, dna binding protein Chain: A: PDB Molecule: regulatory protein recx; PDBTitle: x-ray crystal structure of recx |
| 74 | c6j4pB_ | Alignment | not modelled | 9.5 | 22 | PDB header: hydrolase Chain: B: PDB Molecule: small vasohibin-binding protein; PDBTitle: structural basis of tubulin detyrosination by vasohibins-svbp enzyme2 complex and functional implications |
| 75 | c2xa0A_ | Alignment | not modelled | 9.4 | 33 | PDB header: apoptosis Chain: A: PDB Molecule: apoptosis regulator bcl-2; PDBTitle: crystal structure of bcl-2 in complex with a bax bh32 peptide |
| 76 | d1o0la_ | Alignment | not modelled | 9.3 | 33 | Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death |
| 77 | c5vmnA_ | Alignment | not modelled | 9.3 | 16 | PDB header: viral protein Chain: A: PDB Molecule: bak protein; PDBTitle: crystal structure of grouper iridovirus giv66 |
| 78 | d2ponb1 | Alignment | not modelled | 9.1 | 42 | Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death |
| 79 | d1zyla1 | Alignment | not modelled | 9.0 | 26 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: APH phosphotransferases |
| 80 | c6exxA_ | Alignment | not modelled | 8.9 | 10 | PDB header: rna binding protein Chain: A: PDB Molecule: protein pes4; PDBTitle: crystal structure of pes4 rrm4 |
| | | | | | | Fold: SP0561-like |

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|----|-------------------------|-----------|--------------|-----|----|---|
| 81 | d2fi0a1 | Alignment | not modelled | 8.9 | 11 | Superfamily: SP0561-like Family: SP0561-like |
| 82 | d2d8ca1 | Alignment | not modelled | 8.8 | 25 | Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain |
| 83 | c1v85A_ | Alignment | not modelled | 8.6 | 17 | PDB header: apoptosis Chain: A: PDB Molecule: similar to ring finger protein 36; PDBTitle: sterile alpha motif (sam) domain of mouse bifunctional2 apoptosis regulator |
| 84 | d1wgnA_ | Alignment | not modelled | 8.5 | 13 | Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain |
| 85 | c3d5IA_ | Alignment | not modelled | 8.5 | 17 | PDB header: signaling protein Chain: A: PDB Molecule: regulatory protein recx; PDBTitle: crystal structure of regulatory protein recx |
| 86 | d1qjta_ | Alignment | not modelled | 8.5 | 15 | Fold: EF Hand-like Superfamily: EF-hand Family: Eps15 homology domain (EH domain) |
| 87 | c3qbrA_ | Alignment | not modelled | 8.4 | 25 | PDB header: apoptosis Chain: A: PDB Molecule: sjchgc06286 protein; PDBTitle: bakbh3 in complex with sja |
| 88 | c6mafC_ | Alignment | not modelled | 8.4 | 29 | PDB header: hydrolase Chain: C: PDB Molecule: bbvci endonuclease subunit 2; PDBTitle: native bbvci a2b2 tetramer at low resolution |
| 89 | d1zo0a1 | Alignment | not modelled | 8.4 | 35 | Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: Ornithine decarboxylase antizyme-like |
| 90 | c3bs7A_ | Alignment | not modelled | 8.3 | 6 | PDB header: signaling protein Chain: A: PDB Molecule: protein aveugle; PDBTitle: crystal structure of the sterile alpha motif (sam) domain2 of hyphen/aveugle |
| 91 | c6jxaA_ | Alignment | not modelled | 8.3 | 10 | PDB header: transferase Chain: A: PDB Molecule: serine/threonine-protein kinase tel1; PDBTitle: tel1 kinase compact monomer |
| 92 | d1pqla_ | Alignment | not modelled | 8.2 | 42 | Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death |
| 93 | c2o2fA_ | Alignment | not modelled | 8.1 | 40 | PDB header: apoptosis Chain: A: PDB Molecule: apoptosis regulator bcl-2; PDBTitle: solution structure of the anti-apoptotic protein bcl-2 in2 complex with an acyl-sulfonamide-based ligand |
| 94 | d1iica1 | Alignment | not modelled | 8.1 | 19 | Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-myristoyl transferase, NMT |
| 95 | c3smtA_ | Alignment | not modelled | 8.1 | 19 | PDB header: transferase Chain: A: PDB Molecule: histone-lysine n-methyltransferase setd3; PDBTitle: crystal structure of human set domain-containing protein3 |
| 96 | d2vl8a1 | Alignment | not modelled | 8.0 | 28 | Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Glycosylating toxin catalytic domain-like |
| 97 | c5hxyE_ | Alignment | not modelled | 7.9 | 16 | PDB header: recombination Chain: E: PDB Molecule: tyrosine recombinase xera; PDBTitle: crystal structure of xera recombinase |
| 98 | d1ysga1 | Alignment | not modelled | 7.9 | 50 | Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death |
| 99 | d1aoya_ | Alignment | not modelled | 7.8 | 15 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain |