

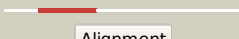

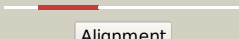



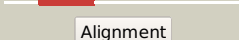

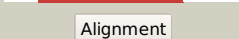

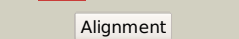

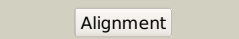

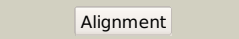









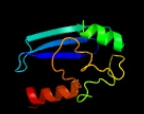






Phyre2

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|---------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0797 (-) _890391_891485 |
| Date | Fri Jul 26 01:50:38 BST 2019 |
| Unique Job ID | 72f2e28e0894e779 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|---|
| 1 | c4ep5A_ |  Alignment |  | 97.4 | 16 | PDB header: hydrolase Chain: A; PDB Molecule: crossover junction endodeoxyribonuclease ruvc; PDBTitle: thermus thermophilus ruvc structure |
| 2 | c2e2pA_ |  Alignment |  | 97.3 | 22 | PDB header: transferase Chain: A; PDB Molecule: hexokinase; PDBTitle: crystal structure of sulfobolus tokodaii hexokinase in2 complex with adp |
| 3 | d1hjrA_ |  Alignment |  | 97.1 | 17 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: RuvC resolvase |
| 4 | c2nnwC_ |  Alignment |  | 96.9 | 16 | PDB header: transferase Chain: C; PDB Molecule: nop5/nop56 related protein; PDBTitle: alternative conformations of nop56/58-fibrillar complex and2 implication for induced-fit assenly of box c/d rnps |
| 5 | c5nckA_ |  Alignment |  | 96.8 | 14 | PDB header: transferase Chain: A; PDB Molecule: n-acetylmannosamine kinase; PDBTitle: the crystal structure of n-acetylmannosamine kinase in fusobacterium2 nucleatum |
| 6 | c3psfA_ |  Alignment |  | 96.7 | 13 | PDB header: transcription Chain: A; PDB Molecule: transcription elongation factor spt6; PDBTitle: crystal structure of the spt6 core domain from saccharomyces2 cerevisiae, form spt6(236-1259) |
| 7 | d1iv0a_ |  Alignment |  | 96.6 | 18 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX |
| 8 | c3eo3B_ |  Alignment |  | 96.5 | 14 | PDB header: isomerase, transferase Chain: B; PDB Molecule: bifunctional udp-n-acetylglucosamine 2-epimerase/n- PDBTitle: crystal structure of the n-acetylmannosamine kinase domain of human2 gne protein |
| 9 | c2oceA_ |  Alignment |  | 96.3 | 20 | PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein pa5201; PDBTitle: crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa |
| 10 | c1xc3A_ |  Alignment |  | 96.2 | 11 | PDB header: transferase Chain: A; PDB Molecule: putative fructokinase; PDBTitle: structure of a putative fructokinase from bacillus subtilis |
| 11 | d2ap1a2 |  Alignment |  | 96.0 | 17 | Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK |

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|----|-------------------------|-----------|---|------|----|--|
| 12 | d1xc3a1 | Alignment |  | 95.9 | 10 | Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK |
| 13 | c3c6aA | Alignment |  | 95.7 | 13 | PDB header: viral protein Chain: A: PDB Molecule: terminase large subunit; PDBTitle: crystal structure of the rb49 gp17 nuclease domain |
| 14 | d1pu6a | Alignment |  | 95.7 | 10 | Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: 3-Methyladenine DNA glycosylase III (MagIII) |
| 15 | c5o9zH | Alignment |  | 95.7 | 18 | PDB header: splicing Chain: H: PDB Molecule: u4/u6 small nuclear ribonucleoprotein prp31; PDBTitle: cryo-em structure of a pre-catalytic human spliceosome primed for2 activation (b complex) |
| 16 | d1z05a3 | Alignment |  | 95.7 | 10 | Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK |
| 17 | d2ozbb1 | Alignment |  | 95.7 | 20 | Fold: Nop domain Superfamily: Nop domain Family: Nop domain |
| 18 | c3h1qB | Alignment |  | 95.7 | 18 | PDB header: structural protein Chain: B: PDB Molecule: ethanolamine utilization protein eutj; PDBTitle: crystal structure of the ethanolamine utilization protein eutj from2 carboxydotherrnus hydrogenoformans |
| 19 | d1nu0a | Alignment |  | 95.5 | 15 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX |
| 20 | c5m1oA | Alignment |  | 95.4 | 17 | PDB header: viral protein Chain: A: PDB Molecule: phage terminase large subunit; PDBTitle: crystal structure of the large terminase nuclease from thermophilic2 phage g20c with bound cobalt |
| 21 | d1vhxa | Alignment | not modelled | 95.3 | 14 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX |
| 22 | c4ehtA | Alignment | not modelled | 95.1 | 20 | PDB header: electron transport Chain: A: PDB Molecule: activator of 2-hydroxyisocaproyl-coa dehydratase; PDBTitle: activator of the 2-hydroxyisocaproyl-coa dehydratase from clostridium2 difficile with bound adp |
| 23 | d1rrqa1 | Alignment | not modelled | 95.0 | 12 | Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase |
| 24 | c2ap1A | Alignment | not modelled | 94.8 | 18 | PDB header: transferase Chain: A: PDB Molecule: putative regulator protein; PDBTitle: crystal structure of the putative regulatory protein |
| 25 | c3id5E | Alignment | not modelled | 94.6 | 13 | PDB header: transferase/ribosomal protein/rna Chain: E: PDB Molecule: pre mrna splicing protein; PDBTitle: crystal structure of sulfolobus solfataricus c/d rnp assembled with2 nop5, fibrillarln, l7ae and a split half c/d rna |
| 26 | c4db3A | Alignment | not modelled | 94.6 | 16 | PDB header: transferase Chain: A: PDB Molecule: n-acetyl-d-glucosamine kinase; PDBTitle: 1.95 angstrom resolution crystal structure of n-acetyl-d-glucosamine2 kinase from vibrio vulnificus. |
| 27 | d1huxa | Alignment | not modelled | 94.6 | 11 | Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like |
| 28 | d2gupa1 | Alignment | not modelled | 94.6 | 11 | Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK |
| | | | | | | PDB header: transferase |

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|----|-------------------------|-----------|--------------|------|----|---|
| 29 | c3hz6A_ | Alignment | not modelled | 94.5 | 9 | Chain: A: PDB Molecule: xylulokinase; PDBTitle: crystal structure of xylulokinase from chromobacterium violaceum |
| 30 | c2ch5D_ | Alignment | not modelled | 94.5 | 17 | PDB header: transferase Chain: D: PDB Molecule: nagk protein; PDBTitle: crystal structure of human n-acetylglucosamine kinase in2 complex with n-acetylglucosamine |
| 31 | d1keaa_ | Alignment | not modelled | 94.2 | 13 | Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase |
| 32 | c2aa4B_ | Alignment | not modelled | 94.2 | 7 | PDB header: transferase Chain: B: PDB Molecule: putative n-acetylmannosamine kinase; PDBTitle: crystal structure of human n-acetylglucosamine kinase, new york structural genomics3 consortium |
| 33 | c2gupA_ | Alignment | not modelled | 94.1 | 8 | PDB header: transferase Chain: A: PDB Molecule: rok family protein; PDBTitle: structural genomics, the crystal structure of a rok family protein2 from streptococcus pneumoniae tigr4 in complex with sucrose |
| 34 | c3vovC_ | Alignment | not modelled | 94.0 | 24 | PDB header: transferase Chain: C: PDB Molecule: glucokinase; PDBTitle: crystal structure of rok hexokinase from thermus thermophilus |
| 35 | c1zc6A_ | Alignment | not modelled | 94.0 | 16 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: probable n-acetylglucosamine kinase; PDBTitle: crystal structure of putative n-acetylglucosamine kinase from2 chromobacterium violaceum. northeast structural genomics target3 cvr23. |
| 36 | c3n0uB_ | Alignment | not modelled | 93.8 | 18 | PDB header: hydrolase, lyase Chain: B: PDB Molecule: probable n-glycosylase/dna lyase; PDBTitle: crystal structure of tm1821, the 8-oxoguanine dna glycosylase of2 thermotoga maritima |
| 37 | c3icxB_ | Alignment | not modelled | 93.5 | 14 | PDB header: rna binding protein Chain: B: PDB Molecule: pre mrna splicing protein; PDBTitle: crystal structure of sulfolobus solfataricus nop5 (135-380) |
| 38 | c6nd4a_ | Alignment | not modelled | 93.4 | 16 | PDB header: ribosome Chain: A: PDB Molecule: mpp10; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit |
| 39 | d2aq0a1 | Alignment | not modelled | 93.4 | 13 | Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like |
| 40 | d2aa4a1 | Alignment | not modelled | 93.3 | 7 | Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK |
| 41 | c1kftA_ | Alignment | not modelled | 93.3 | 15 | PDB header: dna binding protein Chain: A: PDB Molecule: excinuclease abc subunit c; PDBTitle: solution structure of the c-terminal domain of uvrc from e-2 coli |
| 42 | d1kfta_ | Alignment | not modelled | 93.3 | 15 | Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Excinuclease UvrC C-terminal domain |
| 43 | d1nt2b_ | Alignment | not modelled | 93.1 | 16 | Fold: Nop domain Superfamily: Nop domain Family: Nop domain |
| 44 | c6nd4b_ | Alignment | not modelled | 93.0 | 19 | PDB header: ribosome Chain: B: PDB Molecule: PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit |
| 45 | c3gbtA_ | Alignment | not modelled | 92.8 | 12 | PDB header: transferase Chain: A: PDB Molecule: gluconate kinase; PDBTitle: crystal structure of gluconate kinase from lactobacillus acidophilus |
| 46 | c2mutA_ | Alignment | not modelled | 92.6 | 11 | PDB header: hydrolase Chain: A: PDB Molecule: dna excision repair protein ercc-1; PDBTitle: solution structure of the f231l mutant ercc1-xpf dimerization region |
| 47 | d2bgwa1 | Alignment | not modelled | 92.6 | 20 | Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like |
| 48 | d2p3ra1 | Alignment | not modelled | 92.3 | 16 | Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase |
| 49 | c3htvA_ | Alignment | not modelled | 92.3 | 18 | PDB header: transferase Chain: A: PDB Molecule: d-allose kinase; PDBTitle: crystal structure of d-allose kinase (np_418508.1) from escherichia2 coli k12 at 1.95 a resolution |
| 50 | c1rrqA_ | Alignment | not modelled | 92.2 | 15 | PDB header: hydrolase/dna Chain: A: PDB Molecule: muty; PDBTitle: muty adenine glycosylase in complex with dna containing an2 a:oxog pair |
| 51 | d1cuka2 | Alignment | not modelled | 92.2 | 21 | Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain |
| 52 | c3g25B_ | Alignment | not modelled | 92.2 | 13 | PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: 1.9 angstrom crystal structure of glycerol kinase (glpk) from2 staphylococcus aureus in complex with glycerol. |
| 53 | c2h5xA_ | Alignment | not modelled | 92.1 | 19 | PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction atp-dependent dna helicase ruva; PDBTitle: ruva from mycobacterium tuberculosis |
| 54 | d2a1jb1 | Alignment | not modelled | 92.0 | 11 | Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like |

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|----|-------------------------|-----------|--------------|------|----|---|
| 55 | c2nrzB | Alignment | not modelled | 92.0 | 21 | PDB header: hydrolase Chain: B: PDB Molecule: uvrabc system protein c; PDBTitle: crystal structure of the c-terminal half of uvrbc bound to its2 catalytic divalent cation |
| 56 | d1ixra1 | Alignment | not modelled | 91.9 | 22 | Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain |
| 57 | c5hv7A | Alignment | not modelled | 91.8 | 19 | PDB header: transferase Chain: A: PDB Molecule: probable sugar kinase; PDBTitle: putative sugar kinases from synechococcus elongatus pcc7942 in complex2 with d-ribose |
| 58 | c5f7rA | Alignment | not modelled | 91.8 | 16 | PDB header: transcription Chain: A: PDB Molecule: lmo0178 protein; PDBTitle: rok repressor lmo0178 from listeria monocytogenes bound to inducer |
| 59 | c4ijaA | Alignment | not modelled | 91.8 | 7 | PDB header: protein binding Chain: A: PDB Molecule: xylr protein; PDBTitle: structure of s. aureus methicillin resistance factor mecR2 |
| 60 | c6gmhM | Alignment | not modelled | 91.7 | 13 | PDB header: transcription Chain: M: PDB Molecule: transcription elongation factor spt6,transcription PDBTitle: structure of activated transcription complex pol ii-dsif-paf-spt6 |
| 61 | d1bvsa2 | Alignment | not modelled | 91.7 | 28 | Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain |
| 62 | c4htIA | Alignment | not modelled | 91.7 | 7 | PDB header: transferase Chain: A: PDB Molecule: beta-glucoside kinase; PDBTitle: lmo2764 protein, a putative n-acetylmannosamine kinase, from listeria2 monocytogenes |
| 63 | d1kg2a | Alignment | not modelled | 91.7 | 12 | Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase |
| 64 | d1z6ra2 | Alignment | not modelled | 91.5 | 10 | Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK |
| 65 | c5ya2A | Alignment | not modelled | 91.4 | 20 | PDB header: structural protein Chain: A: PDB Molecule: autoinducer-2 kinase; PDBTitle: crystal structure of lsrk-hpr complex with adp |
| 66 | d1x2ia1 | Alignment | not modelled | 91.3 | 15 | Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like |
| 67 | c2d4wA | Alignment | not modelled | 91.2 | 16 | PDB header: transferase Chain: A: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of glycerol kinase from cellulomonas sp.2 nt3060 |
| 68 | c3fhgA | Alignment | not modelled | 91.2 | 10 | PDB header: dna repair, hydrolase, lyase Chain: A: PDB Molecule: n-glycosylase/dna lyase; PDBTitle: crystal structure of sulfolobus solfataricus 8-oxoguanine dna2 glycosylase (ssogg) |
| 69 | d1q18a1 | Alignment | not modelled | 91.0 | 8 | Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glucokinase |
| 70 | c1z05A | Alignment | not modelled | 91.0 | 7 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, rok family; PDBTitle: crystal structure of the rok family transcriptional regulator, homolog2 of e.coli mlc protein. |
| 71 | c2lyhA | Alignment | not modelled | 90.9 | 14 | PDB header: dna binding protein Chain: A: PDB Molecule: fanconi anemia-associated protein of 24 kda; PDBTitle: structure of faap24 residues 141-215 |
| 72 | c1z6rC | Alignment | not modelled | 90.9 | 8 | PDB header: transcription Chain: C: PDB Molecule: mlc protein; PDBTitle: crystal structure of mlc from escherichia coli |
| 73 | c2nlxA | Alignment | not modelled | 90.9 | 22 | PDB header: transferase Chain: A: PDB Molecule: xylulose kinase; PDBTitle: crystal structure of the apo e. coli xylulose kinase |
| 74 | c1ixrA | Alignment | not modelled | 90.8 | 22 | PDB header: hydrolase Chain: A: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex |
| 75 | c5htxA | Alignment | not modelled | 90.8 | 19 | PDB header: transferase Chain: A: PDB Molecule: putative xylulose kinase; PDBTitle: putative sugar kinases from arabidopsis thaliana in complex with adp |
| 76 | c4e1jA | Alignment | not modelled | 90.7 | 13 | PDB header: transferase Chain: A: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of glycerol kinase in complex with glycerol from2 sinorhizobium meliloti 1021 |
| 77 | d1ul1x1 | Alignment | not modelled | 90.7 | 13 | Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain |
| 78 | c3flcX | Alignment | not modelled | 90.5 | 19 | PDB header: transferase Chain: X: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of the his-tagged h232r mutant of glycerol kinase2 from enterococcus casseliflavus with glycerol |
| 79 | c4itqA | Alignment | not modelled | 90.5 | 23 | PDB header: gene regulation, structural protein/dna Chain: A: PDB Molecule: putative uncharacterized protein sco1480; PDBTitle: crystal structure of hypothetical protein sco1480 bound to dna |
| 80 | d1orna | Alignment | not modelled | 90.5 | 20 | Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III |
| | | | | | | PDB header: gene regulation Chain: A: PDB Molecule: protein (holliday junction dna helicase |

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|-----|-------------------------|-----------|--------------|------|----|--|
| 81 | c1d8A_ | Alignment | not modelled | 90.5 | 25 | ruva); PDBTitle: e. coli holliday junction binding protein ruva nh2 region lacking2 domain iii |
| 82 | d2ch5a2 | Alignment | not modelled | 90.4 | 18 | Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like |
| 83 | d1rxwa1 | Alignment | not modelled | 90.4 | 13 | Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain |
| 84 | c3ifrB_ | Alignment | not modelled | 90.3 | 16 | PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase, fggy; PDBTitle: the crystal structure of xylulose kinase from rhodospirillum rubrum |
| 85 | c1glbG_ | Alignment | not modelled | 90.3 | 16 | PDB header: phosphotransferase Chain: G: PDB Molecule: glycerol kinase; PDBTitle: structure of the regulatory complex of escherichia coli iiglc with2 glycerol kinase |
| 86 | c1ixrB_ | Alignment | not modelled | 90.3 | 22 | PDB header: hydrolase Chain: B: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex |
| 87 | d2noha1 | Alignment | not modelled | 90.2 | 17 | Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: DNA repair glycosylase, 2 C-terminal domains |
| 88 | c3ezwD_ | Alignment | not modelled | 89.9 | 16 | PDB header: transferase Chain: D: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of a hyperactive escherichia coli glycerol kinase2 mutant gly230 --> asp obtained using microfluidic crystallization3 devices |
| 89 | c4bxoA_ | Alignment | not modelled | 89.8 | 18 | PDB header: hydrolase/dna Chain: A: PDB Molecule: fanconi anemia group m protein; PDBTitle: architecture and dna recognition elements of the fanconi anemia fancm-2 faap24 complex |
| 90 | c6fpeG_ | Alignment | not modelled | 89.7 | 18 | PDB header: rna binding protein Chain: G: PDB Molecule: trna n6-adenosine threonylcarbamoyltransferase; PDBTitle: bacterial protein complex |
| 91 | c2dpnB_ | Alignment | not modelled | 89.6 | 20 | PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of the glycerol kinase from thermus2 thermophilus hb8 |
| 92 | c3gg4B_ | Alignment | not modelled | 89.5 | 25 | PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis |
| 93 | c5f7pA_ | Alignment | not modelled | 89.4 | 18 | PDB header: transcription Chain: A: PDB Molecule: lmo0178 protein; PDBTitle: rok repressor lmo0178 from listeria monocytogenes |
| 94 | c3wxiB_ | Alignment | not modelled | 89.1 | 28 | PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of trypanosoma brucei gambiense glycerol kinase2 (ligand-free form) |
| 95 | c5vm1A_ | Alignment | not modelled | 89.1 | 16 | PDB header: transferase Chain: A: PDB Molecule: xylulokinase; PDBTitle: crystal structure of a xylolose kinase from brucella ovis |
| 96 | c3psiA_ | Alignment | not modelled | 89.0 | 14 | PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt6; PDBTitle: crystal structure of the spt6 core domain from saccharomyces2 cerevisiae, form spt6(239-1451) |
| 97 | c2w40C_ | Alignment | not modelled | 88.9 | 16 | PDB header: transferase Chain: C: PDB Molecule: glycerol kinase, putative; PDBTitle: crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol |
| 98 | c2qm1D_ | Alignment | not modelled | 88.8 | 13 | PDB header: transferase Chain: D: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase from enterococcus faecalis |
| 99 | c3ezkB_ | Alignment | not modelled | 88.6 | 14 | PDB header: hydrolase Chain: B: PDB Molecule: dna packaging protein gp17; PDBTitle: bacteriophage t4 gp17 motor assembly based on crystal structures and2 cryo-em reconstructions |
| 100 | d3bzka1 | Alignment | not modelled | 88.4 | 18 | Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Tex HhH-containing domain-like |
| 101 | d2edua1 | Alignment | not modelled | 88.2 | 12 | Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like |
| 102 | c2zf5O_ | Alignment | not modelled | 88.2 | 16 | PDB header: transferase Chain: O: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of highly thermostable glycerol kinase from a2 hyperthermophilic archaeon |
| 103 | d2ilqa1 | Alignment | not modelled | 88.2 | 18 | Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain |
| 104 | d2axtu1 | Alignment | not modelled | 88.2 | 15 | Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: PsbU-like |
| 105 | d1a77a1 | Alignment | not modelled | 87.9 | 14 | Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain |
| 106 | c4bc2A_ | Alignment | not modelled | 87.8 | 23 | PDB header: transferase Chain: A: PDB Molecule: xylulose kinase; PDBTitle: crystal structure of human d-xylulokinase in complex with d-2 xylulose and adenosine diphosphate PDB header: hydrolase, lyase/dna Chain: C: PDB Molecule: n-glycosylase/dna lyase; |

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|-----|-------------------------|-----------|--------------|------|----|---|
| 107 | c3kntC_ | Alignment | not modelled | 87.7 | 7 | PDBTitle: crystal structure of methanocaldococcus jannaschii 8-oxoguanine2 glycosylase/lyase in complex with 15mer dna containing 8-oxoguanine |
| 108 | c3n5nX_ | Alignment | not modelled | 87.7 | 18 | PDB header: hydrolase Chain: X: PDB Molecule: a/g-specific adenine dna glycosylase; PDBTitle: crystal structure analysis of the catalytic domain and interdomain2 connector of human muty homologue |
| 109 | d2abka_ | Alignment | not modelled | 87.4 | 23 | Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III |
| 110 | d1b43a1 | Alignment | not modelled | 87.3 | 24 | Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain |
| 111 | c3jvpA_ | Alignment | not modelled | 87.3 | 18 | PDB header: transferase Chain: A: PDB Molecule: ribulokinase; PDBTitle: crystal structure of ribulokinase from bacillus halodurans |
| 112 | d2hoea3 | Alignment | not modelled | 87.0 | 14 | Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK |
| 113 | c3r8eA_ | Alignment | not modelled | 86.9 | 12 | PDB header: transferase Chain: A: PDB Molecule: hypothetical sugar kinase; PDBTitle: crystal structure of a putative sugar kinase (chu_1875) from cytophaga2 hutchinsonii atcc 33406 at 1.65 a resolution |
| 114 | d1mc8a1 | Alignment | not modelled | 86.9 | 19 | Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain |
| 115 | c1yqmA_ | Alignment | not modelled | 86.4 | 19 | PDB header: hydrolase/dna Chain: A: PDB Molecule: n-glycosylase/dna lyase; PDBTitle: catalytically inactive human 8-oxoguanine glycosylase2 crosslinked to 7-deazaguanine containing dna |
| 116 | d1xo1a1 | Alignment | not modelled | 86.2 | 12 | Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain |
| 117 | c3vgkB_ | Alignment | not modelled | 86.2 | 16 | PDB header: transferase Chain: B: PDB Molecule: glucokinase; PDBTitle: crystal structure of a rok family glucokinase from streptomyces2 griseus |
| 118 | c4bxoB_ | Alignment | not modelled | 85.9 | 13 | PDB header: hydrolase/dna Chain: B: PDB Molecule: fanconi anemia-associated protein of 24 kda; PDBTitle: architecture and dna recognition elements of the fanconi anemia fancm-2 faap24 complex |
| 119 | d1pzna1 | Alignment | not modelled | 85.8 | 17 | Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain |
| 120 | d1ngna_ | Alignment | not modelled | 85.8 | 6 | Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase |