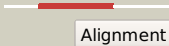

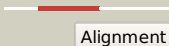

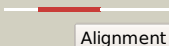




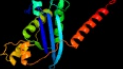















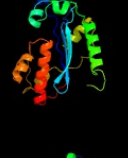




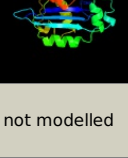


Phyre2

| | |
|---------------|----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD2191 (-) _2453827_2455764 |
| Date | Mon Aug 5 13:25:31 BST 2019 |
| Unique Job ID | 3af73f575de2ccb5 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c5fkvD_ |  Alignment |  | 100.0 | 25 | PDB header: transferase Chain: D: PDB Molecule: dna polymerase iii epsilon; PDBTitle: cryo-em structure of the e. coli replicative dna polymerase complex2 bound to dna (dna polymerase iii alpha, beta, epsilon, tau complex) |
| 2 | c1zbhA_ |  Alignment |  | 100.0 | 17 | PDB header: hydrolase/rna Chain: A: PDB Molecule: 3'-5' exonuclease eri1; PDBTitle: 3'-end specific recognition of histone mrna stem-loop by 3'-2 exonuclease |
| 3 | d1y97a1 |  Alignment |  | 100.0 | 25 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease |
| 4 | d2qxfa1 |  Alignment |  | 100.0 | 24 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease |
| 5 | c2p1jB_ |  Alignment |  | 100.0 | 39 | PDB header: transferase Chain: B: PDB Molecule: dna polymerase iii polc-type; PDBTitle: crystal structure of a polc-type dna polymerase iii exonuclease domain2 from thermotoga maritima |
| 6 | c3cm6A_ |  Alignment |  | 100.0 | 16 | PDB header: hydrolase, apoptosis Chain: A: PDB Molecule: cell death-related nuclease 4; PDBTitle: crystal structure of cell-death related nuclease 4 (crn-4)2 bound with er |
| 7 | c1zbuB_ |  Alignment |  | 100.0 | 18 | PDB header: hydrolase Chain: B: PDB Molecule: 3'-5' exonuclease eri1; PDBTitle: crystal structure of full-length 3'-exonuclease |
| 8 | c5I80B_ |  Alignment |  | 100.0 | 17 | PDB header: rna binding protein Chain: B: PDB Molecule: maternal protein exuperantia,maternal protein exuperantia; PDBTitle: structure of exuperantia exo-like and sam-like domains |
| 9 | c3u6fA_ |  Alignment |  | 100.0 | 19 | PDB header: hydrolase/dna Chain: A: PDB Molecule: three prime repair exonuclease 1; PDBTitle: mouse trex1 d200n mutant |
| 10 | d2guia1 |  Alignment |  | 100.0 | 28 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease |
| 11 | c4rg8A_ |  Alignment |  | 100.0 | 23 | PDB header: hydrolase Chain: A: PDB Molecule: exonuclease i; PDBTitle: structural and biochemical studies of a moderately thermophilic2 exonuclease i from methylocaldum szegediense |

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|----|-------------------------|-----------|---|-------|----|--|
| 12 | d2f96a1 | Alignment |  | 100.0 | 27 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease |
| 13 | d3b60a1 | Alignment |  | 100.0 | 17 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease |
| 14 | d1w0ha_ | Alignment |  | 100.0 | 16 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease |
| 15 | c2xriA_ | Alignment |  | 100.0 | 22 | PDB header: hydrolase Chain: A: PDB Molecule: eri1 exoribonuclease 3; PDBTitle: crystal structure of human eri1 exoribonuclease 3 |
| 16 | c5z9xA_ | Alignment |  | 100.0 | 22 | PDB header: plant protein/rna Chain: A: PDB Molecule: small rna degrading nuclease 1; PDBTitle: arabidopsis small rna degrading nuclease 1 in complex with an rna2 substrate |
| 17 | c3tr8A_ | Alignment |  | 100.0 | 22 | PDB header: hydrolase Chain: A: PDB Molecule: oligoribonuclease; PDBTitle: structure of an oligoribonuclease (orn) from coxiella burnetii |
| 18 | c4fzxC_ | Alignment |  | 100.0 | 32 | PDB header: hydrolase/dna Chain: C: PDB Molecule: exodeoxyribonuclease 10; PDBTitle: exonuclease x in complex with 3' overhanging duplex dna |
| 19 | c2is3B_ | Alignment |  | 100.0 | 23 | PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease t; PDBTitle: crystal structure of escherichia coli rnase t |
| 20 | c6n6jB_ | Alignment |  | 100.0 | 20 | PDB header: rna binding protein/rna Chain: B: PDB Molecule: rna exonuclease 2 homolog,small fragment nuclease; PDBTitle: human rexo2 bound to paa |
| 21 | d1j9aa_ | Alignment | not modelled | 100.0 | 19 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease |
| 22 | c6n6dA_ | Alignment | not modelled | 100.0 | 20 | PDB header: rna binding protein/rna Chain: A: PDB Molecule: oligoribonuclease; PDBTitle: vibrio cholerae oligoribonuclease bound to pag |
| 23 | c4wbqA_ | Alignment | not modelled | 100.0 | 18 | PDB header: rna binding protein Chain: A: PDB Molecule: qde-2-interacting protein; PDBTitle: crystal structure of the exonuclease domain of qip (qde-2 interacting2 protein) solved by native-sad phasing. |
| 24 | d2igia1 | Alignment | not modelled | 100.0 | 21 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease |
| 25 | c6a4dA_ | Alignment | not modelled | 100.0 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: oligoribonuclease; PDBTitle: pnp-tmp bound oligoribonuclease (orn) from colwellia psychrerythraea2 strain 34h |
| 26 | c2gbzA_ | Alignment | not modelled | 100.0 | 22 | PDB header: hydrolase Chain: A: PDB Molecule: oligoribonuclease; PDBTitle: the crystal structure of xc847 from xanthomonas campestris: a 3-52 oligoribonuclease of dnaq fold family with a novel opposingly-shifted3 helix |
| 27 | d1wlja_ | Alignment | not modelled | 100.0 | 21 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease |
| 28 | c5cy4C_ | Alignment | not modelled | 100.0 | 21 | PDB header: oxidoreductase Chain: C: PDB Molecule: oligoribonuclease; PDBTitle: crystal structure of an oligoribonuclease from acinetobacter baumannii |

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|----|-------------------------|-----------|--------------|------|----|--|
| 29 | c2wshC | Alignment | not modelled | 99.9 | 17 | PDB header: hydrolase Chain: C: PDB Molecule: endonuclease ii; PDBTitle: structure of bacteriophage t4 endoi e118a mutant |
| 30 | c1yd2A | Alignment | not modelled | 99.9 | 26 | PDB header: dna binding protein Chain: A: PDB Molecule: uvrabc system protein c; PDBTitle: crystal structure of the gij-yig n-terminal endonuclease domain of2 uvr from thermotoga maritima: point mutant y19f bound to the3 catalytic divalent cation |
| 31 | c1yd6A | Alignment | not modelled | 99.9 | 30 | PDB header: dna binding protein Chain: A: PDB Molecule: uvrc; PDBTitle: crystal structure of the gij-yig n-terminal endonuclease2 domain of uvr from bacillus caldotenax |
| 32 | d1uoca | Alignment | not modelled | 99.7 | 13 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: CAF1-like ribonuclease |
| 33 | c2p51A | Alignment | not modelled | 99.6 | 20 | PDB header: hydrolase, gene regulation Chain: A: PDB Molecule: spcc18.06c protein; PDBTitle: crystal structure of the s. pombe pop2p deadenylation subunit |
| 34 | d2d5ra1 | Alignment | not modelled | 99.6 | 15 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: CAF1-like ribonuclease |
| 35 | c4czwA | Alignment | not modelled | 99.5 | 18 | PDB header: gene regulation Chain: A: PDB Molecule: pab-dependent poly(a)-specific ribonuclease subunit pan2; PDBTitle: structure of the neurospora crassa pan2 catalytic unit (protease and2 nuclease domain) |
| 36 | c4gmjB | Alignment | not modelled | 99.5 | 16 | PDB header: rna binding protein Chain: B: PDB Molecule: ccr4-not transcription complex subunit 7; PDBTitle: structure of human not1 mif4g domain co-crystallized with caf1 |
| 37 | c4hecB | Alignment | not modelled | 99.4 | 18 | PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from2 mycobacterium tuberculosis |
| 38 | d1kfsa1 | Alignment | not modelled | 99.3 | 18 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease |
| 39 | d1x9ma1 | Alignment | not modelled | 99.3 | 17 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease |
| 40 | c2kzza | Alignment | not modelled | 99.3 | 19 | PDB header: transferase/dna Chain: A: PDB Molecule: protein (dna polymerase i); PDBTitle: klenow fragment with normal substrate and zinc only |
| 41 | c5dkuB | Alignment | not modelled | 99.2 | 13 | PDB header: transferase Chain: B: PDB Molecule: prex dna polymerase; PDBTitle: c-terminal his tagged appol exonuclease mutant |
| 42 | c3d45B | Alignment | not modelled | 99.2 | 18 | PDB header: hydrolase Chain: B: PDB Molecule: poly(a)-specific ribonuclease parn; PDBTitle: crystal structure of mouse parn in complex with m7gpppg |
| 43 | c4q8jA | Alignment | not modelled | 99.2 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: pab-dependent poly(a)-specific ribonuclease subunit pan2; PDBTitle: structure of the saccharomyces cerevisiae pan2-pan3 core complex |
| 44 | c2a1sC | Alignment | not modelled | 99.1 | 23 | PDB header: hydrolase Chain: C: PDB Molecule: poly(a)-specific ribonuclease parn; PDBTitle: crystal structure of native parn nuclease domain |
| 45 | c1tk0A | Alignment | not modelled | 99.0 | 20 | PDB header: transferase/electron transport/dna Chain: A: PDB Molecule: dna polymerase; PDBTitle: t7 dna polymerase ternary complex with 8 oxo guanosine and ddctp at2 the insertion site |
| 46 | c1njzA | Alignment | not modelled | 99.0 | 16 | PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase i; PDBTitle: cytosine-thymine mismatch at the polymerase active site |
| 47 | c4x0pB | Alignment | not modelled | 99.0 | 13 | PDB header: transferase/dna Chain: B: PDB Molecule: dna polymerase theta; PDBTitle: ternary complex of human dna polymerase theta c-terminal domain2 binding ddatp opposite a tetrahydrofuran ap site analog |
| 48 | d1qhta1 | Alignment | not modelled | 98.9 | 19 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease |
| 49 | d2hhva1 | Alignment | not modelled | 98.9 | 18 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease |
| 50 | d1wn7a1 | Alignment | not modelled | 98.9 | 21 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease |
| 51 | d1tgoa1 | Alignment | not modelled | 98.9 | 19 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease |
| 52 | d1mk0a | Alignment | not modelled | 98.8 | 14 | Fold: GIY-YIG endonuclease Superfamily: GIY-YIG endonuclease Family: GIY-YIG endonuclease |
| 53 | c4m8oA | Alignment | not modelled | 98.8 | 16 | PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase epsilon catalytic subunit a; PDBTitle: ternary complex of dna polymerase epsilon with an incoming datp |
| 54 | d1d5aa1 | Alignment | not modelled | 98.8 | 19 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease |

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|----|-------------------------|-----------|--------------|------|----|---|
| 55 | c5zo4B_ | Alignment | not modelled | 98.8 | 20 | PDB header: hydrolase Chain: B: PDB Molecule: putative 3'-5' exonuclease family protein; PDBTitle: inactive state of the nuclease |
| 56 | c5okiA_ | Alignment | not modelled | 98.7 | 18 | PDB header: replication Chain: A: PDB Molecule: dna polymerase epsilon catalytic subunit a; PDBTitle: crystal structure of the ctf18-1-8 module from ctf18-rfc in complex2 with a 63 kda fragment of dna polymerase epsilon |
| 57 | d1e52a_ | Alignment | not modelled | 98.7 | 17 | Fold: Long alpha-hairpin Superfamily: C-terminal UvrC-binding domain of UvrB Family: C-terminal UvrC-binding domain of UvrB |
| 58 | c2gv9B_ | Alignment | not modelled | 98.7 | 18 | PDB header: transferase Chain: B: PDB Molecule: dna polymerase; PDBTitle: crystal structure of the herpes simplex virus type 1 dna polymerase |
| 59 | c5mdnB_ | Alignment | not modelled | 98.7 | 22 | PDB header: transferase Chain: B: PDB Molecule: dna polymerase; PDBTitle: structure of the family b dna polymerase from the hyperthermophilic2 archaeon pyrobaculum calidifontis |
| 60 | c2vwkA_ | Alignment | not modelled | 98.6 | 19 | PDB header: dna replication Chain: A: PDB Molecule: dna polymerase; PDBTitle: uracil recognition in archaeal dna polymerases captured by2 x-ray crystallography. v93q polymerase variant |
| 61 | c2gv9A_ | Alignment | not modelled | 98.6 | 17 | PDB header: transferase Chain: A: PDB Molecule: dna polymerase; PDBTitle: crystal structure of the herpes simplex virus type 1 dna polymerase |
| 62 | c6fwkB_ | Alignment | not modelled | 98.6 | 16 | PDB header: dna binding protein Chain: B: PDB Molecule: dna polymerase epsilon catalytic subunit a; PDBTitle: the crystal structure of pol2core-m644g in complex with dna and an2 incoming nucleotide |
| 63 | c3iayA_ | Alignment | not modelled | 98.6 | 22 | PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase delta catalytic subunit; PDBTitle: ternary complex of dna polymerase delta |
| 64 | d1ih7a1 | Alignment | not modelled | 98.6 | 17 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease |
| 65 | c1d5aA_ | Alignment | not modelled | 98.5 | 19 | PDB header: transferase Chain: A: PDB Molecule: protein (dna polymerase); PDBTitle: crystal structure of an archaeobacterial dna polymerase2 d.tok. deposition of second native structure at 2.43 angstrom |
| 66 | c4q5vA_ | Alignment | not modelled | 98.5 | 16 | PDB header: transferase/dna/rna Chain: A: PDB Molecule: dna polymerase alpha catalytic subunit; PDBTitle: crystal structure of the catalytic core of human dna polymerase alpha2 in ternary complex with an rna-primed dna template and aphidicolin |
| 67 | c5exrG_ | Alignment | not modelled | 98.4 | 17 | PDB header: replication Chain: G: PDB Molecule: dna polymerase alpha catalytic subunit; PDBTitle: crystal structure of human primosome |
| 68 | c6r5kA_ | Alignment | not modelled | 98.4 | 16 | PDB header: rna binding protein Chain: A: PDB Molecule: pan2-pan3 deadenylation complex catalytic subunit pan2; PDBTitle: cryo-em structure of a poly(a) rnp bound to the pan2-pan3 deadenylase |
| 69 | c2dtuA_ | Alignment | not modelled | 98.4 | 16 | PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase; PDBTitle: crystal structure of the beta hairpin loop deletion variant of rb692 gp43 in complex with dna containing an abasic site analog |
| 70 | d1noya_ | Alignment | not modelled | 98.4 | 14 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease |
| 71 | d1q8ia1 | Alignment | not modelled | 98.4 | 18 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease |
| 72 | c4xviA_ | Alignment | not modelled | 98.3 | 14 | PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase nu; PDBTitle: binary complex of human polymerase nu and dna with the finger domain2 ajar |
| 73 | c5c0xK_ | Alignment | not modelled | 98.3 | 23 | PDB header: hydrolase/rna Chain: K: PDB Molecule: exosome complex exonuclease rrp6; PDBTitle: structure of a 12-subunit nuclear exosome complex bound to structured2 rna |
| 74 | c2nrrA_ | Alignment | not modelled | 98.3 | 11 | PDB header: hydrolase Chain: A: PDB Molecule: uvrabc system protein c; PDBTitle: crystal structure of the c-terminal rnaseh endonuclease domain of uvrC |
| 75 | d1s5ja1 | Alignment | not modelled | 98.3 | 20 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease |
| 76 | c1yt3A_ | Alignment | not modelled | 98.3 | 21 | PDB header: hydrolase,translation Chain: A: PDB Molecule: ribonuclease d; PDBTitle: crystal structure of escherichia coli rnase d, an2 exoribonuclease involved in structured rna processing |
| 77 | c4fydA_ | Alignment | not modelled | 98.2 | 13 | PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase alpha catalytic subunit a; PDBTitle: crystal structure of yeast dna polymerase alpha bound to dna/rna and2 dgtp |
| 78 | c4ktqA_ | Alignment | not modelled | 98.2 | 19 | PDB header: transferase/dna Chain: A: PDB Molecule: protein (large fragment of dna polymerase i); PDBTitle: binary complex of the large fragment of dna polymerase i2 from t. aquaticus bound to a primer/template dna |
| 79 | c5n2hA_ | Alignment | not modelled | 98.2 | 12 | PDB header: transferase Chain: A: PDB Molecule: dna polymerase; PDBTitle: structure of the e9 dna polymerase exonuclease deficient mutant2 (d166a+e168a) from vaccinia virus |

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|-----|-------------------------|-----------|--------------|------|----|--|
| 80 | c4oo1J | Alignment | not modelled | 98.2 | 23 | PDB header: hydrolase/rna Chain: J: PDB Molecule: exosome complex exonuclease rrp6; PDBTitle: structure of an rrp6-rna exosome complex bound to poly(a) rna |
| 81 | c1q8iA | Alignment | not modelled | 98.0 | 19 | PDB header: transferase Chain: A: PDB Molecule: dna polymerase ii; PDBTitle: crystal structure of escherichia coli dna polymerase ii |
| 82 | c2e6mA | Alignment | not modelled | 97.9 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: werner syndrome atp-dependent helicase homolog; PDBTitle: structure of mouse werner exonuclease domain |
| 83 | c3cymA | Alignment | not modelled | 97.9 | 20 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bad_0989; PDBTitle: crystal structure of protein bad_0989 from bifidobacterium2 adolescentis |
| 84 | d1yt3a3 | Alignment | not modelled | 97.9 | 18 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease |
| 85 | c1s5jA | Alignment | not modelled | 97.9 | 17 | PDB header: transferase Chain: A: PDB Molecule: dna polymerase i; PDBTitle: insight in dna replication: the crystal structure of dna2 polymerase b1 from the archaeon sulfobolus solfataricus |
| 86 | d2hbka2 | Alignment | not modelled | 97.8 | 21 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease |
| 87 | c6k1dB | Alignment | not modelled | 97.6 | 17 | PDB header: hydrolase Chain: B: PDB Molecule: exonuclease 3'-5' domain-containing protein 2; PDBTitle: crystal structure of exd2 exonuclease domain soaked in mn and gmp |
| 88 | c2lwfA | Alignment | not modelled | 97.4 | 26 | PDB header: hydrolase Chain: A: PDB Molecule: monothiol glutaredoxin-s16, chloroplastic; PDBTitle: structure of n-terminal domain of a plant grx |
| 89 | c2d7dB | Alignment | not modelled | 97.4 | 26 | PDB header: hydrolase/dna Chain: B: PDB Molecule: 40-mer from uvrabc system protein b; PDBTitle: structural insights into the cryptic dna dependent atp-ase2 activity of uvrB |
| 90 | c4ztuA | Alignment | not modelled | 97.3 | 34 | PDB header: dna binding protein/dna Chain: A: PDB Molecule: dna polymerase subunit gamma-1; PDBTitle: structural basis for processivity and antiviral drug toxicity in human2 mitochondrial dna replicase |
| 91 | c4ybgA | Alignment | not modelled | 97.3 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: protein maelstrom; PDBTitle: crystal structure of the mael domain of drosophila melanogaster2 maelstrom |
| 92 | c2hbka | Alignment | not modelled | 97.1 | 23 | PDB header: hydrolase, gene regulation Chain: A: PDB Molecule: exosome complex exonuclease rrp6; PDBTitle: structure of the yeast nuclear exosome component, rrp6p, reveals an2 interplay between the active site and the hrdc domain; protein in3 complex with mn |
| 93 | d1qoja | Alignment | not modelled | 97.1 | 24 | Fold: Long alpha-hairpin Superfamily: C-terminal UvrC-binding domain of UvrB Family: C-terminal UvrC-binding domain of UvrB |
| 94 | c5c0wK | Alignment | not modelled | 97.0 | 22 | PDB header: hydrolase/rna Chain: K: PDB Molecule: exosome complex exonuclease rrp6; PDBTitle: structure of a 12-subunit nuclear exosome complex bound to single-2 stranded rna substrates |
| 95 | c3ikmD | Alignment | not modelled | 97.0 | 30 | PDB header: transferase Chain: D: PDB Molecule: dna polymerase subunit gamma-1; PDBTitle: crystal structure of human mitochondrial dna polymerase holoenzyme |
| 96 | c4nlbA | Alignment | not modelled | 96.6 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: ribosomal rna processing protein 6; PDBTitle: crystal structure of the catalytic core of rrp6 from trypanosoma2 brucei |
| 97 | c3sahA | Alignment | not modelled | 96.5 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: exosome component 10; PDBTitle: crystal structure of the human rrp6 catalytic domain with y436a2 mutation in the catalytic site |
| 98 | d1vk0a | Alignment | not modelled | 96.2 | 17 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease |
| 99 | c3nicA | Alignment | not modelled | 95.7 | 23 | PDB header: hydrolase/dna Chain: A: PDB Molecule: eco29kir; PDBTitle: dna binding and cleavage by the giy-yig endonuclease r.eco29ki2 inactive variant y49f |
| 100 | c5af0B | Alignment | not modelled | 95.4 | 11 | PDB header: unknown protein Chain: B: PDB Molecule: maelstrom; PDBTitle: mael domain from bombyx mori maelstrom |
| 101 | c1ywlA | Alignment | not modelled | 95.3 | 18 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical upf0213 protein ef2693; PDBTitle: solution nmr structure of the protein ef2693 from e.2 faecalis: northeast structural genomics consortium target3 efr36 |
| 102 | c1zg2A | Alignment | not modelled | 95.1 | 20 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical upf0213 protein bh0048; PDBTitle: solution nmr structure of the upf0213 protein bh0048 from2 bacillus halodurans. northeast structural genomics target3 bhr2. |
| 103 | c1cmwA | Alignment | not modelled | 94.7 | 22 | PDB header: transferase Chain: A: PDB Molecule: protein (dna polymerase i); PDBTitle: crystal structure of taq dna-polymerase shows a new orientation for2 the structure-specific nuclease domain |
| 104 | c5v5fA | Alignment | not modelled | 93.3 | 15 | PDB header: transferase Chain: A: PDB Molecule: at3g11770; PDBTitle: crystal structure of rice1 (pnt2) |
| 105 | d2py5a1 | Alignment | not modelled | 93.0 | 24 | Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like |

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|-----|-------------------------|-----------|--------------|------|----|---|
| | | | | | | Family: DnaQ-like 3'-5' exonuclease |
| 106 | c2d7dA | Alignment | not modelled | 91.5 | 30 | PDB header: hydrolase/dna Chain: A: PDB Molecule: uvrabc system protein b; PDBTitle: structural insights into the cryptic dna dependent atp-ase2 activity of uvrbc |
| 107 | c2ex3I | Alignment | not modelled | 85.3 | 22 | PDB header: transferase/replication Chain: I: PDB Molecule: dna polymerase; PDBTitle: bacteriophage phi29 dna polymerase bound to terminal protein |
| 108 | c4xlgA | Alignment | not modelled | 84.2 | 29 | PDB header: hydrolase Chain: A: PDB Molecule: structure-specific endonuclease subunit slx1; PDBTitle: c. glabrata slx1 in complex with slx4ccd. |
| 109 | d1pd0a4 | Alignment | not modelled | 64.1 | 30 | Fold: Gelsolin-like Superfamily: C-terminal, gelsolin-like domain of Sec23/24 Family: C-terminal, gelsolin-like domain of Sec23/24 |
| 110 | c3opyE | Alignment | not modelled | 57.4 | 17 | PDB header: transferase Chain: E: PDB Molecule: 6-phosphofructo-1-kinase alpha-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state |
| 111 | c2p4vA | Alignment | not modelled | 57.1 | 11 | PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor greb; PDBTitle: crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution |
| 112 | c3opyG | Alignment | not modelled | 53.7 | 17 | PDB header: transferase Chain: G: PDB Molecule: 6-phosphofructo-1-kinase alpha-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state |
| 113 | d1utaa | Alignment | not modelled | 48.6 | 31 | Fold: Ferredoxin-like Superfamily: Sporulation related repeat Family: Sporulation related repeat |
| 114 | d2ga9d1 | Alignment | not modelled | 48.0 | 14 | Fold: Poly(A) polymerase catalytic subunit-like Superfamily: Poly(A) polymerase catalytic subunit-like Family: Poxvirus poly(A) polymerase catalytic subunit-like |
| 115 | c1f0cB | Alignment | not modelled | 41.2 | 35 | PDB header: viral protein Chain: B: PDB Molecule: ice inhibitor; PDBTitle: structure of the viral serpin crma |
| 116 | c3o8oC | Alignment | not modelled | 35.1 | 15 | PDB header: transferase Chain: C: PDB Molecule: 6-phosphofructokinase subunit alpha; PDBTitle: structure of phosphofructokinase from saccharomyces cerevisiae |
| 117 | d1xdpa4 | Alignment | not modelled | 35.0 | 25 | Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Polyphosphate kinase C-terminal domain |
| 118 | c3auoB | Alignment | not modelled | 34.6 | 14 | PDB header: transferase/dna Chain: B: PDB Molecule: dna polymerase beta family (x family); PDBTitle: dna polymerase x from thermus thermophilus hb8 ternary complex with 1-2 nt gapped dna and ddgtp |
| 119 | d2o8ra4 | Alignment | not modelled | 33.0 | 21 | Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Polyphosphate kinase C-terminal domain |
| 120 | c4hndB | Alignment | not modelled | 32.4 | 23 | PDB header: transferase Chain: B: PDB Molecule: phosphatidylinositol 4-kinase type 2-alpha; PDBTitle: crystal structure of the catalytic domain of selenomethionine2 substituted human pi4kialpha in complex with adp |