











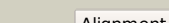











Phyre2

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|---------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD1253_(deaD)_1399976_1401667 |
| Date | Wed Jul 31 22:05:34 BST 2019 |
| Unique Job ID | 754eeacca034581c |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c4cdgA_ |  Alignment |  | 100.0 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: bloom syndrome protein; PDBTitle: crystal structure of the bloom's syndrome helicase blm in complex with2 nanobody |
| 2 | c4ljyA_ |  Alignment |  | 100.0 | 31 | PDB header: hydrolase Chain: A: PDB Molecule: pre-mrna-processing atp-dependent rna helicase prp5; PDBTitle: crystal structure of rna splicing effector prp5 in complex with adp |
| 3 | c2v1xB_ |  Alignment |  | 100.0 | 18 | PDB header: hydrolase Chain: B: PDB Molecule: atp-dependent dna helicase q1; PDBTitle: crystal structure of human recq-like dna helicase |
| 4 | c5lstA_ |  Alignment |  | 100.0 | 24 | PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent dna helicase q4; PDBTitle: crystal structure of the human recq4 helicase. |
| 5 | c1oywA_ |  Alignment |  | 100.0 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent dna helicase; PDBTitle: structure of the recq catalytic core |
| 6 | c4q47A_ |  Alignment |  | 100.0 | 19 | PDB header: dna binding protein Chain: A: PDB Molecule: dna helicase recq; PDBTitle: structure of the drrecq catalytic core in complex with adp |
| 7 | c5v9xA_ |  Alignment |  | 100.0 | 20 | PDB header: hydrolase/dna Chain: A: PDB Molecule: atp-dependent dna helicase; PDBTitle: structure of mycobacterium smegmatis helicase lhr bound to ssdna and2 amp-pnp |
| 8 | c4w7sA_ |  Alignment |  | 100.0 | 35 | PDB header: hydrolase Chain: A: PDB Molecule: pre-mrna-splicing atp-dependent rna helicase prp28; PDBTitle: crystal structure of the yeast dead-box splicing factor prp28 at 2.542 angstroms resolution |
| 9 | c1s2mA_ |  Alignment |  | 100.0 | 32 | PDB header: rna binding protein Chain: A: PDB Molecule: putative atp-dependent rna helicase dhh1; PDBTitle: crystal structure of the dead box protein dhh1p |
| 10 | c3ewsA_ |  Alignment |  | 100.0 | 32 | PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase ddx19b; PDBTitle: human dead-box rna-helicase ddx19 in complex with adp |
| 11 | c2db3D_ |  Alignment |  | 100.0 | 34 | PDB header: hydrolase/rna Chain: D: PDB Molecule: atp-dependent rna helicase vasa; PDBTitle: structural basis for rna unwinding by the dead-box protein2 drosophila vasa |

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|----|-------------------------|-----------|--------------|-------|----|---|
| 12 | c4ct4B_ | Alignment | | 100.0 | 31 | PDB header: rna binding protein Chain: B: PDB Molecule: probable atp-dependent rna helicase ddx6; PDBTitle: cnot1 mif4g domain - ddx6 complex |
| 13 | c5supB_ | Alignment | | 100.0 | 33 | PDB header: hydrolase/rna Chain: B: PDB Molecule: atp-dependent rna helicase sub2; PDBTitle: structure of mrna export factors |
| 14 | c3fhtA_ | Alignment | | 100.0 | 33 | PDB header: hydrolase/rna Chain: A: PDB Molecule: atp-dependent rna helicase ddx19b; PDBTitle: crystal structure of human dbp5 in complex with amppnp and rna |
| 15 | c1xtkA_ | Alignment | | 100.0 | 34 | PDB header: gene regulation Chain: A: PDB Molecule: probable atp-dependent rna helicase p47; PDBTitle: structure of decd to dead mutation of human uap56 |
| 16 | c4pxaA_ | Alignment | | 100.0 | 37 | PDB header: translation, rna binding protein Chain: A: PDB Molecule: atp-dependent rna helicase ddx3x; PDBTitle: dead-box rna helicase ddx3x cancer-associated mutant d354v |
| 17 | c4d25A_ | Alignment | | 100.0 | 36 | PDB header: hydrolase Chain: A: PDB Molecule: bmvlg protein; PDBTitle: crystal structure of the bombyx mori vasa helicase (e339q)2 in complex with rna and amppnp |
| 18 | c6c0fp_ | Alignment | | 100.0 | 27 | PDB header: ribosome Chain: P: PDB Molecule: 60s ribosomal protein l17-a; PDBTitle: yeast nucleolar pre-60s ribosomal subunit (state 2) |
| 19 | c5dtuA_ | Alignment | | 100.0 | 37 | PDB header: hydrolase Chain: A: PDB Molecule: prp28; PDBTitle: crystal structure of the rna-helicase prp28 from chaetomium2 thermophilum bound to adp |
| 20 | c1hv8B_ | Alignment | | 100.0 | 40 | PDB header: rna binding protein Chain: B: PDB Molecule: putative atp-dependent rna helicase mj0669; PDBTitle: crystal structure of a dead box protein from the2 hyperthermophile methanococcus jannaschii |
| 21 | c2hxyC_ | Alignment | not modelled | 100.0 | 36 | PDB header: hydrolase Chain: C: PDB Molecule: probable atp-dependent rna helicase ddx48; PDBTitle: crystal structure of human apo-eif4aiii |
| 22 | c5ivlA_ | Alignment | not modelled | 100.0 | 46 | PDB header: hydrolase Chain: A: PDB Molecule: dead-box atp-dependent rna helicase csha; PDBTitle: csha helicase |
| 23 | c4kbfA_ | Alignment | not modelled | 100.0 | 44 | PDB header: hydrolase Chain: A: PDB Molecule: heat resistant rna dependent atpase; PDBTitle: two different open conformations of the helicase core of the rna2 helicase hera |
| 24 | c6iehB_ | Alignment | not modelled | 100.0 | 19 | PDB header: rna binding protein Chain: B: PDB Molecule: exosome rna helicase mtr4; PDBTitle: crystal structures of the hmtr4-nrde2 complex |
| 25 | c3pexA_ | Alignment | not modelled | 100.0 | 34 | PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase dbp5; PDBTitle: s. cerevisiae dbp5 l327v bound to gle1 h337r and ip6 |
| 26 | c3i5yA_ | Alignment | not modelled | 100.0 | 26 | PDB header: hydrolase/rna Chain: A: PDB Molecule: atp-dependent rna helicase mss116; PDBTitle: structure of mss116p bound to ssrna containing a single 5-bru and amp-2 pnp |
| 27 | c2xgjA_ | Alignment | not modelled | 100.0 | 18 | PDB header: hydrolase/rna Chain: A: PDB Molecule: atp-dependent rna helicase dob1; PDBTitle: structure of mtr4, a dexh helicase involved in nuclear rna2 processing and surveillance |
| 28 | c4nhoA_ | Alignment | not modelled | 100.0 | 40 | PDB header: hydrolase Chain: A: PDB Molecule: probable atp-dependent rna helicase ddx23; PDBTitle: structure of the spliceosomal dead-box protein prp28 PDB header: topoisomerase |

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|----|-------------------------|-----------|--------------|-------|----|--|
| 29 | c1ql9B_ | Alignment | not modelled | 100.0 | 22 | Chain: B; PDB Molecule: reverse gyrase; PDBTitle: archaeoglobus fulgidus reverse gyrase complexed with adpnp |
| 30 | c5agaA_ | Alignment | not modelled | 100.0 | 19 | PDB header: transferase Chain: A; PDB Molecule: dna polymerase theta; PDBTitle: crystal structure of the helicase domain of human dna2 polymerase theta in complex with amppnp |
| 31 | c4bgdA_ | Alignment | not modelled | 100.0 | 18 | PDB header: transcription Chain: A; PDB Molecule: pre-mrna-splicing helicase brr2; PDBTitle: crystal structure of brr2 in complex with the jab1/mpn domain of prp8 |
| 32 | c3eiqD_ | Alignment | not modelled | 100.0 | 37 | PDB header: hydrolase/antitumor protein Chain: D; PDB Molecule: eukaryotic initiation factor 4a-i; PDBTitle: crystal structure of pdcd4-eif4a |
| 33 | c5lqwC_ | Alignment | not modelled | 100.0 | 20 | PDB header: splicing Chain: C; PDB Molecule: pre-mrna-splicing helicase brr2; PDBTitle: yeast activated spliceosome |
| 34 | c2vsxA_ | Alignment | not modelled | 100.0 | 37 | PDB header: translation/hydrolase Chain: A; PDB Molecule: atp-dependent rna helicase eif4a; PDBTitle: crystal structure of a translation initiation complex |
| 35 | c5lb5C_ | Alignment | not modelled | 100.0 | 22 | PDB header: hydrolase Chain: C; PDB Molecule: atp-dependent dna helicase q5; PDBTitle: crystal structure of human recq15 helicase in complex with adp/mg2 (tricilinc form). |
| 36 | c4xgtA_ | Alignment | not modelled | 100.0 | 20 | PDB header: hydrolase Chain: A; PDB Molecule: frq-interacting rna helicase; PDBTitle: structure of rna helicase frh a critical component of the neurospora2 crassa circadian clock |
| 37 | c3l9oA_ | Alignment | not modelled | 100.0 | 19 | PDB header: hydrolase Chain: A; PDB Molecule: atp-dependent rna helicase dob1; PDBTitle: crystal structure of mtr4, a co-factor of the nuclear exosome |
| 38 | c6iegA_ | Alignment | not modelled | 100.0 | 21 | PDB header: rna binding protein Chain: A; PDB Molecule: exosome rna helicase mtr4; PDBTitle: crystal structure of human mtr4 |
| 39 | c6c90A_ | Alignment | not modelled | 100.0 | 19 | PDB header: hydrolase/rna binding protein Chain: A; PDB Molecule: exosome rna helicase mtr4,exosome rna helicase mtr4; PDBTitle: human mtr4 helicase in complex with zcchc8-ctd |
| 40 | c2i4iA_ | Alignment | not modelled | 100.0 | 33 | PDB header: hydrolase Chain: A; PDB Molecule: atp-dependent rna helicase ddx3x; PDBTitle: crystal structure of human dead-box rna helicase ddx3x |
| 41 | c5dcaA_ | Alignment | not modelled | 100.0 | 18 | PDB header: hydrolase Chain: A; PDB Molecule: pre-mrna-splicing helicase brr2; PDBTitle: crystal structure of yeast full length brr2 in complex with prp8 jab12 domain |
| 42 | c2va8A_ | Alignment | not modelled | 100.0 | 20 | PDB header: hydrolase Chain: A; PDB Molecule: ski2-type helicase; PDBTitle: dna repair helicase hel308 |
| 43 | c2zj8A_ | Alignment | not modelled | 100.0 | 18 | PDB header: hydrolase Chain: A; PDB Molecule: putative ski2-type helicase; PDBTitle: archaeal dna helicase hjm apo state in form 2 |
| 44 | c5m52B_ | Alignment | not modelled | 100.0 | 17 | PDB header: hydrolase Chain: B; PDB Molecule: pre-mrna-splicing helicase brr2; PDBTitle: crystal structure of yeast brr2 full-lenght in complex with prp8 jab12 domain |
| 45 | c2z0mA_ | Alignment | not modelled | 100.0 | 39 | PDB header: rna binding protein Chain: A; PDB Molecule: 337aa long hypothetical atp-dependent rna PDBTitle: crystal structure of hypothetical atp-dependent rna2 helicase from sulfolobus tokodaii |
| 46 | c1gm5A_ | Alignment | not modelled | 100.0 | 18 | PDB header: helicase Chain: A; PDB Molecule: recg; PDBTitle: structure of recg bound to three-way dna junction |
| 47 | c2zj2A_ | Alignment | not modelled | 100.0 | 18 | PDB header: hydrolase Chain: A; PDB Molecule: putative ski2-type helicase; PDBTitle: archaeal dna helicase hjm apo state in form 1 |
| 48 | c4ddvA_ | Alignment | not modelled | 100.0 | 18 | PDB header: hydrolase Chain: A; PDB Molecule: reverse gyrase; PDBTitle: thermotoga maritima reverse gyrase, triclinic form |
| 49 | c6ah0D_ | Alignment | not modelled | 100.0 | 19 | PDB header: splicing Chain: D; PDB Molecule: u5 small nuclear ribonucleoprotein 200 kda helicase; PDBTitle: the cryo-em structure of the precursor of human pre-catalytic2 spliceosome (pre-b complex) |
| 50 | c5m59C_ | Alignment | not modelled | 100.0 | 19 | PDB header: splicing Chain: C; PDB Molecule: pre-mrna splicing helicase-like protein; PDBTitle: crystal structure of chaetomium thermophilum brr2 helicase core in2 complex with prp8 jab1 domain |
| 51 | c2eyqA_ | Alignment | not modelled | 100.0 | 18 | PDB header: hydrolase Chain: A; PDB Molecule: transcription-repair coupling factor; PDBTitle: crystal structure of escherichia coli transcription-repair2 coupling factor |
| 52 | c4a4zA_ | Alignment | not modelled | 100.0 | 22 | PDB header: hydrolase Chain: A; PDB Molecule: antiviral helicase ski2; PDBTitle: crystal structure of the s. cerevisiae dexh helicase ski2 bound to2 amppnp |
| 53 | c4f92B_ | Alignment | not modelled | 100.0 | 14 | PDB header: hydrolase Chain: B; PDB Molecule: u5 small nuclear ribonucleoprotein 200 kda helicase; PDBTitle: brr2 helicase region s10871 |
| 54 | c3bxzA_ | Alignment | not modelled | 100.0 | 19 | PDB header: transport protein Chain: A; PDB Molecule: preprotein translocase subunit seca; PDBTitle: crystal structure of the isolated dead motor domains from escherichia2 coli seca PDB header: splicing |

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|----|-------------------------|-----------|--------------|-------|----|---|
| 55 | c3jcrC_ | Alignment | not modelled | 100.0 | 19 | Chain: C; PDB Molecule: hbrr2; PDBTitle: 3d structure determination of the human* <u>u4/u6.u5*</u> tri-snrrp complex |
| 56 | c4bujA_ | Alignment | not modelled | 100.0 | 23 | PDB header: hydrolase Chain: A; PDB Molecule: antiviral helicase ski2; PDBTitle: crystal structure of the s. cerevisiae ski2-3-8 complex |
| 57 | c2p6uA_ | Alignment | not modelled | 100.0 | 21 | PDB header: dna binding protein Chain: A; PDB Molecule: afuhel308 helicase; PDBTitle: apo structure of the hel308 superfamily 2 helicase |
| 58 | c5jb2A_ | Alignment | not modelled | 100.0 | 20 | PDB header: immune system Chain: A; PDB Molecule: lgp2; PDBTitle: crystal structure of chicken lgp2 with 5'ppp 10-mer dsrna and adp-2 alf4-mg2+ at 2.2 a resolution. |
| 59 | c5jcfB_ | Alignment | not modelled | 100.0 | 18 | PDB header: immune system Chain: B; PDB Molecule: melanoma differentiation associated protein-5; PDBTitle: crystal structure of chicken mda5 with 5'p 10-mer dsrna and adp-mg2+2 at 2.6 a resolution (orthorhombic form). |
| 60 | c3kx2A_ | Alignment | not modelled | 100.0 | 19 | PDB header: hydrolase Chain: A; PDB Molecule: pre-mrna-splicing factor atp-dependent rna helicase prp43; PDBTitle: crystal structure of prp43p in complex with adp |
| 61 | c3tmiA_ | Alignment | not modelled | 100.0 | 18 | PDB header: hydrolase/rna Chain: A; PDB Molecule: atp-dependent rna helicase ddx58; PDBTitle: structural basis for rna recognition and activation of rig-i |
| 62 | c4gl2A_ | Alignment | not modelled | 100.0 | 20 | PDB header: rna binding protein/rna Chain: A; PDB Molecule: interferon-induced helicase c domain-containing protein 1; PDBTitle: structural basis for dsrna duplex backbone recognition by mda5 |
| 63 | c6iczy_ | Alignment | not modelled | 100.0 | 18 | PDB header: splicing Chain: Y; PDB Molecule: atp-dependent rna helicase dhx8; PDBTitle: cryo-em structure of a human post-catalytic spliceosome (p complex) at2 3.0 angstrom |
| 64 | c2fsgA_ | Alignment | not modelled | 100.0 | 17 | PDB header: protein transport Chain: A; PDB Molecule: preprotein translocase seca subunit; PDBTitle: complex seca:atp from escherichia coli |
| 65 | c3rc8A_ | Alignment | not modelled | 100.0 | 19 | PDB header: hydrolase/rna Chain: A; PDB Molecule: atp-dependent rna helicase supv3l1, mitochondrial; PDBTitle: human mitochondrial helicase suv3 in complex with short rna fragment |
| 66 | c1wp9D_ | Alignment | not modelled | 100.0 | 22 | PDB header: hydrolase Chain: D; PDB Molecule: atp-dependent rna helicase, putative; PDBTitle: crystal structure of pyrococcus furiosus hef helicase domain |
| 67 | c5wsge_ | Alignment | not modelled | 100.0 | 19 | PDB header: rna binding protein/rna Chain: E; PDB Molecule: saccharomyces cerevisiae s288c snr6 snrna; PDBTitle: cryo-em structure of the catalytic step ii spliceosome (c* complex) at2 4.0 angstrom resolution |
| 68 | c3fhoB_ | Alignment | not modelled | 100.0 | 34 | PDB header: hydrolase Chain: B; PDB Molecule: atp-dependent rna helicase dbp5; PDBTitle: structure of s. pombe dbp5 |
| 69 | c5ylzW_ | Alignment | not modelled | 100.0 | 19 | PDB header: splicing Chain: W; PDB Molecule: pre-mrna-splicing factor atp-dependent rna helicase prp22; PDBTitle: cryo-em structure of the post-catalytic spliceosome from saccharomyces2 cerevisiae at 3.6 angstrom |
| 70 | c5xdrA_ | Alignment | not modelled | 100.0 | 18 | PDB header: hydrolase Chain: A; PDB Molecule: pre-mrna-splicing factor atp-dependent rna helicase dhx15; PDBTitle: crystal structure of human deah-box rna helicase dhx15 in complex with2 adp |
| 71 | c5mqfq_ | Alignment | not modelled | 100.0 | 19 | PDB header: splicing Chain: Q; PDB Molecule: protein bud31 homolog; PDBTitle: cryo-em structure of a human spliceosome activated for step 2 of2 splicing (c* complex) |
| 72 | c5mq0V_ | Alignment | not modelled | 100.0 | 19 | PDB header: splicing Chain: V; PDB Molecule: pre-mrna-splicing factor atp-dependent rna helicase prp22; PDBTitle: structure of a spliceosome remodeled for exon ligation |
| 73 | c2fsgB_ | Alignment | not modelled | 100.0 | 20 | PDB header: protein transport Chain: B; PDB Molecule: preprotein translocase seca subunit; PDBTitle: complex seca:atp from escherichia coli |
| 74 | c5z58x_ | Alignment | not modelled | 100.0 | 20 | PDB header: splicing Chain: X; PDB Molecule: smad nuclear-interacting protein 1; PDBTitle: cryo-em structure of a human activated spliceosome (early bact) at 4.92 angstrom. |
| 75 | c5vheA_ | Alignment | not modelled | 100.0 | 20 | PDB header: hydrolase Chain: A; PDB Molecule: deah (asp-glu-ala-his) box polypeptide 36; PDBTitle: dhx36 in complex with the c-myc g-quadruplex |
| 76 | c5n8zA_ | Alignment | not modelled | 100.0 | 17 | PDB header: hydrolase Chain: A; PDB Molecule: cg9323, isoform a; PDBTitle: crystal structure of drosophila dhx36 helicase in complex with2 ctctccctt |
| 77 | c3oiyB_ | Alignment | not modelled | 100.0 | 18 | PDB header: isomerase Chain: B; PDB Molecule: reverse gyrase helicase domain; PDBTitle: helicase domain of reverse gyrase from thermotoga maritima |
| 78 | c6fa5A_ | Alignment | not modelled | 100.0 | 17 | PDB header: hydrolase Chain: A; PDB Molecule: putative mrna splicing factor; PDBTitle: crystal structure of the deah-box helicase prp2 in complex with adp |
| 79 | c6hegA_ | Alignment | not modelled | 100.0 | 20 | PDB header: hydrolase Chain: A; PDB Molecule: atp-dependent rna helicase hrpb; PDBTitle: crystal structure of escherichia coli deah/rna helicase hrpb |

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|-----|-------------------------|-----------|--------------|-------|----|---|
| 80 | c6f4aB_ | Alignment | not modelled | 100.0 | 19 | PDB header: hydrolase Chain: B: PDB Molecule: suv3 helicase; PDBTitle: yeast mitochondrial rna degradosome complex mtexo |
| 81 | c5zamA_ | Alignment | not modelled | 100.0 | 18 | PDB header: hydrolase/protein binding/rna Chain: A: PDB Molecule: endoribonuclease dicer; PDBTitle: cryo-em structure of human dicer and its complexes with a pre-mirna2 substrate |
| 82 | c5lqwO_ | Alignment | not modelled | 100.0 | 18 | PDB header: splicing Chain: O: PDB Molecule: pre-mrna-splicing factor atp-dependent rna helicase-like PDBTitle: yeast activated spliceosome |
| 83 | c5lj5Q_ | Alignment | not modelled | 100.0 | 19 | PDB header: splicing Chain: Q: PDB Molecule: pre-mrna-splicing factor atp-dependent rna helicase prp16; PDBTitle: overall structure of the yeast spliceosome immediately after2 branching. |
| 84 | c6jdeB_ | Alignment | not modelled | 100.0 | 20 | PDB header: hydrolase Chain: B: PDB Molecule: putative dna repair helicase radd; PDBTitle: crystal structure of a dna repair protein |
| 85 | c2jlrA_ | Alignment | not modelled | 100.0 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: serine protease subunit ns3; PDBTitle: dengue virus 4 ns3 helicase in complex with amppnp |
| 86 | c2ocaA_ | Alignment | not modelled | 100.0 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent dna helicase uvsw; PDBTitle: the crystal structure of t4 uvsw |
| 87 | c1tf2A_ | Alignment | not modelled | 100.0 | 20 | PDB header: protein transport Chain: A: PDB Molecule: preprotein translocase seca subunit; PDBTitle: crystal structure of seca:adp in an open conformation from2 bacillus subtilis |
| 88 | c6h57A_ | Alignment | not modelled | 100.0 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: probable atp-dependent rna helicase dhr1; PDBTitle: crystal structure of s. cerevisiae deah-box rna helicase dhr1,2 essential for small ribosomal subunit biogenesis |
| 89 | c2z83A_ | Alignment | not modelled | 100.0 | 22 | PDB header: viral protein Chain: A: PDB Molecule: helicase/nucleoside triphosphatase; PDBTitle: crystal structure of catalytic domain of japanese2 encephalitis virus ns3 helicase/nucleoside triphosphatase3 at a resolution 1.8 |
| 90 | c1c4oA_ | Alignment | not modelled | 100.0 | 29 | PDB header: replication Chain: A: PDB Molecule: dna nucleotide excision repair enzyme uvrb; PDBTitle: crystal structure of the dna nucleotide excision repair enzyme uvrb2 from thermus thermophilus |
| 91 | c3fe2B_ | Alignment | not modelled | 100.0 | 37 | PDB header: hydrolase Chain: B: PDB Molecule: probable atp-dependent rna helicase ddx5; PDBTitle: human dead-box rna helicase ddx5 (p68), conserved domain i in complex2 with adp |
| 92 | c2v6jA_ | Alignment | not modelled | 100.0 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: rna helicase; PDBTitle: kokobera virus helicase: mutant met47thr |
| 93 | c3dl8B_ | Alignment | not modelled | 100.0 | 20 | PDB header: protein transport Chain: B: PDB Molecule: protein translocase subunit seca; PDBTitle: structure of the complex of aquifex aeolicus secyeg and bacillus2 subtilis seca |
| 94 | c4px9C_ | Alignment | not modelled | 100.0 | 36 | PDB header: translation, rna binding protein Chain: C: PDB Molecule: atp-dependent rna helicase ddx3x; PDBTitle: dead-box rna helicase ddx3x domain 1 with n-terminal atp-binding loop |
| 95 | c6o16A_ | Alignment | not modelled | 100.0 | 16 | PDB header: hydrolase/rna Chain: A: PDB Molecule: deah (asp-glu-ala-his) box polypeptide 37; PDBTitle: crystal structure of murine dhx37 in complex with rna |
| 96 | c4nl4H_ | Alignment | not modelled | 100.0 | 21 | PDB header: dna binding protein Chain: H: PDB Molecule: primosome assembly protein pria; PDBTitle: pria helicase bound to adp |
| 97 | c1ymfA_ | Alignment | not modelled | 100.0 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: genome polyprotein [contains: flavivirin protease ns3 PDBTitle: crystal structure of yellow fever virus ns3 helicase complexed with2 adp |
| 98 | c5gvrA_ | Alignment | not modelled | 100.0 | 33 | PDB header: hydrolase Chain: A: PDB Molecule: probable atp-dependent rna helicase ddx41; PDBTitle: crystal structure of the ddx41 dead domain in an apo closed form |
| 99 | c2wv9A_ | Alignment | not modelled | 100.0 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: flavivirin protease ns2b regulatory subunit, flavivirin PDBTitle: crystal structure of the ns3 protease-helicase from murray2 valley encephalitis virus |
| 100 | c5aorA_ | Alignment | not modelled | 100.0 | 22 | PDB header: hydrolase/rna Chain: A: PDB Molecule: dosage compensation regulator; PDBTitle: structure of mle rna adp alf4 complex |
| 101 | c2vbcA_ | Alignment | not modelled | 100.0 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: dengue 4 ns3 full-length protein; PDBTitle: crystal structure of the ns3 protease-helicase from dengue2 virus |
| 102 | c4xqkB_ | Alignment | not modelled | 100.0 | 16 | PDB header: hydrolase/dna Chain: B: PDB Molecule: llabiii; PDBTitle: atp-dependent type isp restriction-modification enzyme llabiii bound2 to dna |
| 103 | c5fmf1_ | Alignment | not modelled | 100.0 | 18 | PDB header: transcription Chain: 1: PDB Molecule: dna repair helicase rad25, ssl2; PDBTitle: the p-lobe of rna polymerase ii pre-initiation complex |
| 104 | d2j0sa1 | Alignment | not modelled | 100.0 | 37 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain |

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|-----|-------------------------|-----------|--------------|-------|----|---|
| 105 | c5ivwV_ | Alignment | not modelled | 100.0 | 16 | PDB header: transcription/dna Chain: V: PDB Molecule: tffih basal transcription factor complex helicase xpb PDBTitle: human core tffih bound to dna within the pic |
| 106 | c6i3oA_ | Alignment | not modelled | 100.0 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: putative pre-mrna splicing factor; PDBTitle: crystal structure of deah-box atpase prp22 |
| 107 | c3tbkA_ | Alignment | not modelled | 100.0 | 21 | PDB header: hydrolase Chain: A: PDB Molecule: rig-i helicase domain; PDBTitle: mouse rig-i atpase domain |
| 108 | c2d7dA_ | Alignment | not modelled | 100.0 | 26 | 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 |
| 109 | c6nmiA_ | Alignment | not modelled | 100.0 | 15 | PDB header: transcription Chain: A: PDB Molecule: general transcription and dna repair factor iih helicase PDBTitle: cryo-em structure of the human tffih core complex |
| 110 | c2fwrA_ | Alignment | not modelled | 100.0 | 21 | PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad25; PDBTitle: structure of archaeoglobus fulgidis xpb |
| 111 | d1s2ma1 | Alignment | not modelled | 100.0 | 38 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain |
| 112 | c4qqxA_ | Alignment | not modelled | 100.0 | 21 | PDB header: hydrolase/dna Chain: A: PDB Molecule: crispr-associated helicase, cas3 family; PDBTitle: crystal structure of t. fusca cas3-atp |
| 113 | d1q0ua_ | Alignment | not modelled | 100.0 | 34 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain |
| 114 | c1a1vA_ | Alignment | not modelled | 100.0 | 20 | PDB header: hydrolase/dna Chain: A: PDB Molecule: protein (ns3 protein); PDBTitle: hepatitis c virus ns3 helicase domain complexed with single2 stranded sdna |
| 115 | c2pl3A_ | Alignment | not modelled | 100.0 | 33 | PDB header: hydrolase Chain: A: PDB Molecule: probable atp-dependent rna helicase ddx10; PDBTitle: human dead-box rna helicase ddx10, dead domain in complex with adp |
| 116 | c2kbeA_ | Alignment | not modelled | 100.0 | 34 | PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase dbp5; PDBTitle: solution structure of amino-terminal domain of dbp5p |
| 117 | c3dkpA_ | Alignment | not modelled | 100.0 | 30 | PDB header: hydrolase Chain: A: PDB Molecule: probable atp-dependent rna helicase ddx52; PDBTitle: human dead-box rna-helicase ddx52, conserved domain i in complex with2 adp |
| 118 | d1veca_ | Alignment | not modelled | 100.0 | 34 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain |
| 119 | c3ly5A_ | Alignment | not modelled | 100.0 | 33 | PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase ddx18; PDBTitle: ddx18 dead-domain |
| 120 | c2oxcA_ | Alignment | not modelled | 100.0 | 31 | PDB header: hydrolase Chain: A: PDB Molecule: probable atp-dependent rna helicase ddx20; PDBTitle: human dead-box rna helicase ddx20, dead domain in complex with adp |