Phyre2

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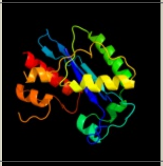
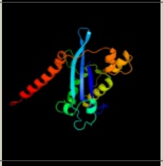
| Description | P30014 |
| Date | Thu Jan 5 11:45:43 GMT 2012 |
| Unique Job ID | c46ebb33e2691318 |

## Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d2f96a1 | Alignment |  | 100.0 | 62 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**DnaQ-like 3'-5' exonuclease |
| 2 | c2is3B_ | Alignment |  | 100.0 | 90 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**ribonuclease t;<br>**PDBTitle:** crystal structure of escherichia coli rnase t |
| 3 | d2qxfa1 | Alignment |  | 100.0 | 20 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**DnaQ-like 3'-5' exonuclease |
| 4 | c1zbuB_ | Alignment |  | 100.0 | 20 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**3'-5' exonuclease eri1;<br>**PDBTitle:** crystal structure of full-length 3'-exonuclease |
| 5 | c1zbhA_ | Alignment |  | 100.0 | 21 | **PDB header:**hydrolase/rna<br>**Chain:** A: **PDB Molecule:**3'-5' exonuclease eri1;<br>**PDBTitle:** 3'-end specific recognition of histone mrna stem-loop by 3'-2 exonuclease |
| 6 | c3cm6A_ | Alignment |  | 100.0 | 15 | **PDB header:**hydrolase, apoptosis<br>**Chain:** A: **PDB Molecule:**cell death-related nuclease 4;<br>**PDBTitle:** crystal structure of cell-death related nuclease 4 (crn-4)2 bound with er |
| 7 | d1y97a1 | Alignment |  | 100.0 | 13 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**DnaQ-like 3'-5' exonuclease |
| 8 | c2xriA_ | Alignment |  | 100.0 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**eri1 exoribonuclease 3;<br>**PDBTitle:** crystal structure of human eri1 exoribonuclease 3 |
| 9 | c2p1jB_ | Alignment |  | 100.0 | 27 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**dna polymerase iii polc-type;<br>**PDBTitle:** crystal structure of a polc-type dna polymerase iii2 exonuclease domain from thermotoga maritima |
| 10 | d2guia1 | Alignment |  | 100.0 | 23 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**DnaQ-like 3'-5' exonuclease |
| 11 | d1w0ha_ | Alignment |  | 100.0 | 17 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**DnaQ-like 3'-5' exonuclease |

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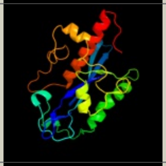
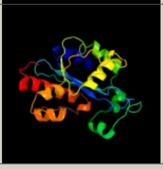
| 12 | d3b6oa1 | Alignment |  | 100.0 | 11 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**DnaQ-like 3'-5' exonuclease |
| 13 | c3u6fA_ | Alignment |  | 100.0 | 12 | **PDB header:**hydrolase/dna<br>**Chain:** A: **PDB Molecule:**three prime repair exonuclease 1;<br>**PDBTitle:** mouse trex1 d200n mutant |
| 14 | d1j9aa_ | Alignment |  | 100.0 | 14 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**DnaQ-like 3'-5' exonuclease |
| 15 | c3tr8A_ | Alignment |  | 100.0 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**oligoribonuclease;<br>**PDBTitle:** structure of an oligoribonuclease (orn) from coxiella burnetii |
| 16 | d2igia1 | Alignment |  | 100.0 | 13 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**DnaQ-like 3'-5' exonuclease |
| 17 | c2gbzA_ | Alignment |  | 99.9 | 19 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**oligoribonuclease;<br>**PDBTitle:** the crystal structure of xc847 from xanthomonas campestris: a 3-52 oligoribonuclease of dnaq fold family with a novel opposingly-shifted3 helix |
| 18 | d1wlja_ | Alignment |  | 99.9 | 15 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**DnaQ-like 3'-5' exonuclease |
| 19 | d1uoca_ | Alignment |  | 99.8 | 12 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**CAF1-like ribonuclease |
| 20 | d2d5ra1 | Alignment |  | 99.7 | 13 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**CAF1-like ribonuclease |
| 21 | c2p51A_ | Alignment | not modelled | 99.7 | 15 | **PDB header:**hydrolase, gene regulation<br>**Chain:** A: **PDB Molecule:**spcc18.06c protein;<br>**PDBTitle:** crystal structure of the s. pombe pop2p deadenylation2 subunit |
| 22 | c3d45B_ | Alignment | not modelled | 99.4 | 19 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**poly(a)-specific ribonuclease parn;<br>**PDBTitle:** crystal structure of mouse parn in complex with m7gpppg |
| 23 | c2a1sC_ | Alignment | not modelled | 99.4 | 24 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**poly(a)-specific ribonuclease parn;<br>**PDBTitle:** crystal structure of native parn nuclease domain |
| 24 | d1kfsa1 | Alignment | not modelled | 99.3 | 18 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**DnaQ-like 3'-5' exonuclease |
| 25 | d1x9ma1 | Alignment | not modelled | 99.1 | 19 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**DnaQ-like 3'-5' exonuclease |
| 26 | c2kzzA_ | Alignment | not modelled | 99.1 | 16 | **PDB header:**transferase/dna<br>**Chain:** A: **PDB Molecule:**protein (dna polymerase i);<br>**PDBTitle:** klenow fragment with normal substrate and zinc only |
| 27 | c1njzA_ | Alignment | not modelled | 98.9 | 17 | **PDB header:**transferase/dna<br>**Chain:** A: **PDB Molecule:**dna polymerase i;<br>**PDBTitle:** cytosine-thymine mismatch at the polymerase active site |
| 28 | d2hhva1 | Alignment | not modelled | 98.8 | 13 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**DnaQ-like 3'-5' exonuclease |
| 29 | c1tk0A_ | Alignment | not modelled | 98.7 | 20 | **PDB header:**transferase/electron transport/dna<br>**Chain:** A: **PDB Molecule:**dna polymerase; |

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|---|---|---|---|---|---|---|
| 29 | c1tk0A_ | Alignment | not modelled | 98.7 | 20 | **PDBTitle:** t7 dna polymerase ternary complex with 8 oxo guanosine and2 ddctp at the insertion site |
| 30 | c1yt3A_ | Alignment | not modelled | 98.4 | 19 | **PDB header:**hydrolase,translation<br>**Chain:** A: **PDB Molecule:**ribonuclease d;<br>**PDBTitle:** crystal structure of escherichia coli rnase d, an2 exoribonuclease involved in structured rna processing |
| 31 | d1wn7a1 | Alignment | not modelled | 98.4 | 17 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**DnaQ-like 3'-5' exonuclease |
| 32 | d1qhta1 | Alignment | not modelled | 98.4 | 18 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**DnaQ-like 3'-5' exonuclease |
| 33 | d1tgoa1 | Alignment | not modelled | 98.3 | 21 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**DnaQ-like 3'-5' exonuclease |
| 34 | d1yt3a3 | Alignment | not modelled | 98.3 | 16 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**DnaQ-like 3'-5' exonuclease |
| 35 | d1d5aa1 | Alignment | not modelled | 98.2 | 19 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**DnaQ-like 3'-5' exonuclease |
| 36 | c3iayA_ | Alignment | not modelled | 98.0 | 19 | **PDB header:**transferase/dna<br>**Chain:** A: **PDB Molecule:**dna polymerase delta catalytic subunit;<br>**PDBTitle:** ternary complex of dna polymerase delta |
| 37 | c2gv9B_ | Alignment | not modelled | 98.0 | 18 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**dna polymerase;<br>**PDBTitle:** crystal structure of the herpes simplex virus type 1 dna polymerase |
| 38 | c2e6mA_ | Alignment | not modelled | 97.9 | 12 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**werner syndrome atp-dependent helicase homolog;<br>**PDBTitle:** structure of mouse werner exonuclease domain |
| 39 | c4ktqA_ | Alignment | not modelled | 97.8 | 19 | **PDB header:**transferase/dna<br>**Chain:** A: **PDB Molecule:**protein (large fragment of dna polymerase i);<br>**PDBTitle:** binary complex of the large fragment of dna polymerase i2 from t. aquaticus bound to a primer/template dna |
| 40 | c3cymA_ | Alignment | not modelled | 97.8 | 23 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein bad_0989;<br>**PDBTitle:** crystal structure of protein bad_0989 from bifidobacterium2 adolescentis |
| 41 | d1s5ja1 | Alignment | not modelled | 97.5 | 14 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**DnaQ-like 3'-5' exonuclease |
| 42 | c1d5aA_ | Alignment | not modelled | 97.3 | 21 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**protein (dna polymerase);<br>**PDBTitle:** crystal structure of an archaebacterial dna polymerase2 d.tok. deposition of second native structure at 2.43 angstrom |
| 43 | d1ih7a1 | Alignment | not modelled | 97.2 | 13 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**DnaQ-like 3'-5' exonuclease |
| 44 | c2hbkA_ | Alignment | not modelled | 97.2 | 15 | **PDB header:**hydrolase, gene regulation<br>**Chain:** A: **PDB Molecule:**exosome complex exonuclease rrp6;<br>**PDBTitle:** structure of the yeast nuclear exosome component, rrp6p,2 reveals an interplay between the active site and the hrdc3 domain; protein in complex with mn |
| 45 | c3sahA_ | Alignment | not modelled | 97.1 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**exosome component 10;<br>**PDBTitle:** crystal structure of the human rrp6 catalytic domain with y436a2 mutation in the catalytic site |
| 46 | d2hbka2 | Alignment | not modelled | 97.1 | 16 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**DnaQ-like 3'-5' exonuclease |
| 47 | d1q8ia1 | Alignment | not modelled | 96.9 | 18 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**DnaQ-like 3'-5' exonuclease |
| 48 | c2vwkA_ | Alignment | not modelled | 96.8 | 18 | **PDB header:**dna replication<br>**Chain:** A: **PDB Molecule:**dna polymerase;<br>**PDBTitle:** uracil recognition in archaeal dna polymerases captured by2 x-ray crystallography. v93q polymerase variant |
| 49 | d1noya_ | Alignment | not modelled | 96.4 | 16 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**DnaQ-like 3'-5' exonuclease |
| 50 | c1s5jA_ | Alignment | not modelled | 92.8 | 19 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**dna polymerase i;<br>**PDBTitle:** insight in dna replication: the crystal structure of dna2 polymerase b1 from the archaeon sulfolobus solfataricus |
| 51 | c1q8iA_ | Alignment | not modelled | 91.7 | 18 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**dna polymerase ii;<br>**PDBTitle:** crystal structure of escherichia coli dna polymerase ii |
| 52 | d1vk0a_ | Alignment | not modelled | 83.6 | 11 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**DnaQ-like 3'-5' exonuclease |
| 53 | c2dtuA_ | Alignment | not modelled | 81.9 | 13 | **PDB header:**transferase/dna<br>**Chain:** A: **PDB Molecule:**dna polymerase;<br>**PDBTitle:** crystal structure of the beta hairpin loop deletion variant2 of rb69 gp43 in complex with dna containing an abasic site3 analog |
| 54 | c3ikmD_ | Alignment | not modelled | 81.5 | 17 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**dna polymerase subunit gamma-1;<br>**PDBTitle:** crystal structure of human mitochondrial dna polymerase2 holoenzyme |
| 55 | c1cmwA_ | Alignment | not modelled | 66.1 | 22 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**protein (dna polymerase i); |

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| 55 | c1cmwA_ | Alignment | not modelled | 66.1 | 22 | **PDBTitle:** crystal structure of taq dna-polymerase shows a new2 orientation for the structure-specific nuclease domain |
| 56 | c3mx2A_ | Alignment | not modelled | 56.8 | 16 | **PDB header:**nuclear protein<br>**Chain:** A: **PDB Molecule:**nucleoprotein;<br>**PDBTitle:** lassa fever virus nucleoprotein complexed with dttp |
| 57 | d2py5a1 | Alignment | not modelled | 32.0 | 33 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**DnaQ-like 3'-5' exonuclease |
| 58 | d1fnoa4 | Alignment | not modelled | 7.7 | 15 | **Fold:**Phosphorylase/hydrolase-like<br>**Superfamily:**Zn-dependent exopeptidases<br>**Family:**Bacterial dinuclear zinc exopeptidases |
| 59 | c2ex3I_ | Alignment | not modelled | 6.5 | 19 | **PDB header:**transferase/replication<br>**Chain:** I: **PDB Molecule:**dna polymerase;<br>**PDBTitle:** bacteriophage phi29 dna polymerase bound to terminal protein |