Phyre2

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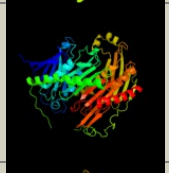
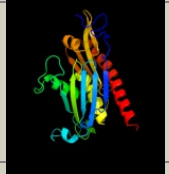
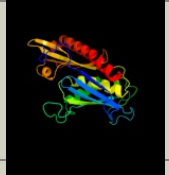
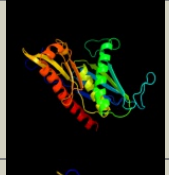
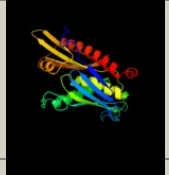
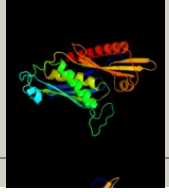
| Email | l.a.kelley@imperial.ac.uk |
| Description | P05055 |
| Date | Thu Jan 5 10:58:40 GMT 2012 |
| Unique Job ID | ca1ca738bc4b240a |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c1e3hA_ | Alignment |  | 100.0 | 45 | **PDB header:**polyribonucleotide transferase **Chain:** A: **PDB Molecule:**guanosine pentaphosphate synthetase; **PDBTitle:** semet derivative of streptomyces antibioticus pnpase/gpsi2 enzyme |
| 2 | c3cdiA_ | Alignment |  | 100.0 | 100 | **PDB header:**transferase **Chain:** A: **PDB Molecule:**polynucleotide phosphorylase; **PDBTitle:** crystal structure of e. coli pnpase |
| 3 | c3cdjA_ | Alignment |  | 100.0 | 100 | **PDB header:**transferase **Chain:** A: **PDB Molecule:**polynucleotide phosphorylase; **PDBTitle:** crystal structure of the e. coli kh/s1 domain truncated2 pnpase |
| 4 | c2po2A_ | Alignment |  | 100.0 | 28 | **PDB header:**hydrolase/hydrolase **Chain:** A: **PDB Molecule:**probable exosome complex exonuclease 1; **PDBTitle:** crystal structure of the p. abyssi exosome rnase ph ring2 complexed with cdp |
| 5 | c2wnrB_ | Alignment |  | 100.0 | 31 | **PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable exosome complex exonuclease 1; **PDBTitle:** the structure of methanothermobacter thermautotrophicus2 exosome core assembly |
| 6 | c2nn6B_ | Alignment |  | 100.0 | 22 | **PDB header:**hydrolase/transferase **Chain:** B: **PDB Molecule:**exosome complex exonuclease rrp41; **PDBTitle:** structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40 |
| 7 | c2ba1D_ | Alignment |  | 100.0 | 26 | **PDB header:**rna binding protein **Chain:** D: **PDB Molecule:**archaeal exosome complex exonuclease rrp41; **PDBTitle:** archaeal exosome core |
| 8 | c2c37L_ | Alignment |  | 100.0 | 27 | **PDB header:**hydrolase **Chain:** L: **PDB Molecule:**probable exosome complex exonuclease 1; **PDBTitle:** rnase ph core of the archaeal exosome in complex with u82 rna |
| 9 | c3dd6A_ | Alignment |  | 100.0 | 25 | **PDB header:**transferase **Chain:** A: **PDB Molecule:**ribonuclease ph; **PDBTitle:** crystal structure of rph, an exoribonuclease from bacillus2 anthracis at 1.7 a resolution |
| 10 | c2wp8B_ | Alignment |  | 100.0 | 20 | **PDB header:**hydrolase **Chain:** B: **PDB Molecule:**exosome complex component ski6; **PDBTitle:** yeast rrp44 nuclease |
| 11 | c1udsA_ | Alignment |  | 100.0 | 24 | **PDB header:**transferase **Chain:** A: **PDB Molecule:**ribonuclease ph; **PDBTitle:** crystal structure of the trna processing enzyme rnase ph r126a mutant2 from aquifex aeolicus |

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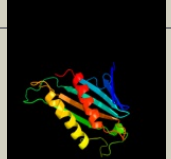
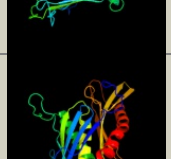
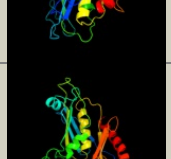
| 12 | c2pnzB_ | Alignment |  | 100.0 | 20 | **PDB header:**hydrolase/hydrolase<br>**Chain:** B: **PDB Molecule:**probable exosome complex exonuclease 2;<br>**PDBTitle:** crystal structure of the p. abyssi exosome rnase ph ring2 complexed with udp and gmp |
| 13 | c3b4tC_ | Alignment |  | 100.0 | 24 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**ribonuclease ph;<br>**PDBTitle:** crystal structure of mycobacterium tuberculosis rnase ph, the2 mycobacterium tuberculosis structural genomics consortium target3 rv1340 |
| 14 | c1r6mA_ | Alignment |  | 100.0 | 25 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**ribonuclease ph;<br>**PDBTitle:** crystal structure of the trna processing enzyme rnase ph from2 pseudomonas aeruginosa in complex with phosphate |
| 15 | d1e3ha2 | Alignment |  | 100.0 | 49 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**Ribonuclease PH domain 1-like |
| 16 | c2nn6C_ | Alignment |  | 100.0 | 18 | **PDB header:**hydrolase/transferase<br>**Chain:** C: **PDB Molecule:**exosome complex exonuclease rrp43;<br>**PDBTitle:** structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40 |
| 17 | c2wnrC_ | Alignment |  | 100.0 | 18 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**probable exosome complex exonuclease 2;<br>**PDBTitle:** the structure of methanothermobacter thermautotrophicus2 exosome core assembly |
| 18 | c3hkmB_ | Alignment |  | 100.0 | 23 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**os03g0854200 protein;<br>**PDBTitle:** crystal structure of rice(oryza sativa) rrp46 |
| 19 | c2ba0I_ | Alignment |  | 100.0 | 22 | **PDB header:**rna binding protein<br>**Chain:** I: **PDB Molecule:**archeal exosome rna binding protein rrp42;<br>**PDBTitle:** archaeal exosome core |
| 20 | c2nn6E_ | Alignment |  | 100.0 | 17 | **PDB header:**hydrolase/transferase<br>**Chain:** E: **PDB Molecule:**exosome complex exonuclease rrp42;<br>**PDBTitle:** structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40 |
| 21 | c2br2G_ | Alignment | not modelled | 100.0 | 20 | **PDB header:**hydrolase<br>**Chain:** G: **PDB Molecule:**exosome complex exonuclease 2;<br>**PDBTitle:** rnase ph core of the archaeal exosome |
| 22 | c2nn6D_ | Alignment | not modelled | 100.0 | 24 | **PDB header:**hydrolase/transferase<br>**Chain:** D: **PDB Molecule:**exosome complex exonuclease rrp46;<br>**PDBTitle:** structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40 |
| 23 | c2nn6F_ | Alignment | not modelled | 100.0 | 21 | **PDB header:**hydrolase/transferase<br>**Chain:** F: **PDB Molecule:**exosome component 6;<br>**PDBTitle:** structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40 |
| 24 | d1e3ha6 | Alignment | not modelled | 100.0 | 51 | **Fold:**Ribonuclease PH domain 2-like<br>**Superfamily:**Ribonuclease PH domain 2-like<br>**Family:**Ribonuclease PH domain 2-like |
| 25 | d1e3ha3 | Alignment | not modelled | 100.0 | 51 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**Ribonuclease PH domain 1-like |
| 26 | c2wp8A_ | Alignment | not modelled | 100.0 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**exosome complex component rrp45;<br>**PDBTitle:** yeast rrp44 nuclease |
| 27 | d2je6b1 | Alignment | not modelled | 100.0 | 30 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**Ribonuclease PH domain 1-like |
| 28 | d2ba0d1 | Alignment | not modelled | 100.0 | 29 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**Ribonuclease PH domain 1-like |
| 29 | d2nn6b1 | Alignment | not modelled | 100.0 | 23 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**Ribonuclease PH domain 1-like |

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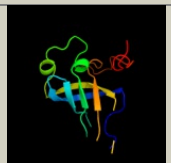
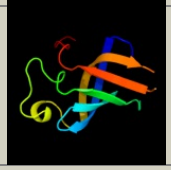
| 30 | d1r6la1 | Alignment | not modelled | 100.0 | 25 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**Ribonuclease PH domain 1-like |
| 31 | d1udsa1 | Alignment | not modelled | 100.0 | 22 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**Ribonuclease PH domain 1-like |
| 32 | d2ba0g1 | Alignment | not modelled | 100.0 | 25 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**Ribonuclease PH domain 1-like |
| 33 | d2je6a1 | Alignment | not modelled | 99.9 | 19 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**Ribonuclease PH domain 1-like |
| 34 | d2nn6e1 | Alignment | not modelled | 99.9 | 20 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**Ribonuclease PH domain 1-like |
| 35 | c3krnB_ | Alignment | not modelled | 99.9 | 18 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**protein c14a4.5, confirmed by transcript evidence;<br>**PDBTitle:** crystal structure of c. elegans cell-death-related nuclease 5(crn-5) |
| 36 | d2nn6a1 | Alignment | not modelled | 99.9 | 17 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**Ribonuclease PH domain 1-like |
| 37 | d2nn6c1 | Alignment | not modelled | 99.9 | 17 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**Ribonuclease PH domain 1-like |
| 38 | d1oysa1 | Alignment | not modelled | 99.9 | 30 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**Ribonuclease PH domain 1-like |
| 39 | d2nn6f1 | Alignment | not modelled | 99.9 | 25 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**Ribonuclease PH domain 1-like |
| 40 | d1e3ha5 | Alignment | not modelled | 99.9 | 33 | **Fold:**Ribonuclease PH domain 2-like<br>**Superfamily:**Ribonuclease PH domain 2-like<br>**Family:**Ribonuclease PH domain 2-like |
| 41 | d2nn6d1 | Alignment | not modelled | 99.9 | 31 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**Ribonuclease PH domain 1-like |
| 42 | d1udsa2 | Alignment | not modelled | 99.8 | 19 | **Fold:**Ribonuclease PH domain 2-like<br>**Superfamily:**Ribonuclease PH domain 2-like<br>**Family:**Ribonuclease PH domain 2-like |
| 43 | d1r6la2 | Alignment | not modelled | 99.7 | 19 | **Fold:**Ribonuclease PH domain 2-like<br>**Superfamily:**Ribonuclease PH domain 2-like<br>**Family:**Ribonuclease PH domain 2-like |
| 44 | d1whua_ | Alignment | not modelled | 99.7 | 24 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domain 3<br>**Family:**Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domain 3 |
| 45 | d1oysa2 | Alignment | not modelled | 99.7 | 23 | **Fold:**Ribonuclease PH domain 2-like<br>**Superfamily:**Ribonuclease PH domain 2-like<br>**Family:**Ribonuclease PH domain 2-like |
| 46 | c2cqoA_ | Alignment |  | 99.6 | 27 | **PDB header:**ribosome<br>**Chain:** A: **PDB Molecule:**nucleolar protein of 40 kda;<br>**PDBTitle:** solution structure of the s1 rna binding domain of human2 hypothetical protein flj11067 |
| 47 | c1q46A_ | Alignment |  | 99.6 | 24 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**translation initiation factor 2 alpha subunit;<br>**PDBTitle:** crystal structure of the eif2 alpha subunit from2 saccharomyces cerevisia |
| 48 | c1yz6A_ | Alignment |  | 99.6 | 42 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**probable translation initiation factor 2 alpha<br>**PDBTitle:** crystal structure of intact alpha subunit of aif2 from2 pyrococcus abyssi |
| 49 | d1e3ha1 | Alignment | not modelled | 99.5 | 35 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domain 3<br>**Family:**Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domain 3 |
| 50 | c1q8kA_ | Alignment | not modelled | 99.5 | 29 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 2<br>**PDBTitle:** solution structure of alpha subunit of human eif2 |
| 51 | d2ba0d2 | Alignment | not modelled | 99.5 | 20 | **Fold:**Ribonuclease PH domain 2-like<br>**Superfamily:**Ribonuclease PH domain 2-like<br>**Family:**Ribonuclease PH domain 2-like |

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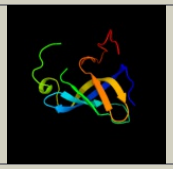
| 52 | c2k4kA_ | Alignment |  | 99.5 | 40 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**general stress protein 13;<br>**PDBTitle:** solution structure of gsp13 from bacillus subtilis |
| 53 | d1q46a2 | Alignment | not modelled | 99.5 | 26 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 54 | c2eqsA_ | Alignment |  | 99.5 | 33 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**atp-dependent rna helicase dhx8;<br>**PDBTitle:** solution structure of the s1 rna binding domain of human2 atp-dependent rna helicase dhx8 |
| 55 | d2je6b2 | Alignment | not modelled | 99.5 | 16 | **Fold:**Ribonuclease PH domain 2-like<br>**Superfamily:**Ribonuclease PH domain 2-like<br>**Family:**Ribonuclease PH domain 2-like |
| 56 | d2br2b2 | Alignment | not modelled | 99.5 | 15 | **Fold:**Ribonuclease PH domain 2-like<br>**Superfamily:**Ribonuclease PH domain 2-like<br>**Family:**Ribonuclease PH domain 2-like |
| 57 | c2khjA_ | Alignment |  | 99.4 | 35 | **PDB header:**ribosomal protein<br>**Chain:** A: **PDB Molecule:**30s ribosomal protein s1;<br>**PDBTitle:** nmr structure of the domain 6 of the e. coli ribosomal2 protein s1 |
| 58 | d2ba0a1 | Alignment | not modelled | 99.4 | 22 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 59 | d1kl9a2 | Alignment | not modelled | 99.4 | 37 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 60 | c2oceA_ | Alignment | not modelled | 99.4 | 42 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein pa5201;<br>**PDBTitle:** crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa |
| 61 | c2khiA_ | Alignment | not modelled | 99.4 | 32 | **PDB header:**ribosomal protein<br>**Chain:** A: **PDB Molecule:**30s ribosomal protein s1;<br>**PDBTitle:** nmr structure of the domain 4 of the e. coli ribosomal2 protein s1 |
| 62 | d1go3e1 | Alignment | not modelled | 99.4 | 29 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 63 | d2nn6b2 | Alignment | not modelled | 99.4 | 15 | **Fold:**Ribonuclease PH domain 2-like<br>**Superfamily:**Ribonuclease PH domain 2-like<br>**Family:**Ribonuclease PH domain 2-like |
| 64 | d1sroa_ | Alignment | not modelled | 99.4 | 100 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 65 | c2ahoB_ | Alignment | not modelled | 99.4 | 30 | **PDB header:**translation<br>**Chain:** B: **PDB Molecule:**translation initiation factor 2 alpha subunit;<br>**PDBTitle:** structure of the archaeal initiation factor eif2 alpha-2 gamma heterodimer from sulfolobus solfataricus complexed3 with gdpnp |
| 66 | c2k52A_ | Alignment | not modelled | 99.3 | 30 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein mj1198;<br>**PDBTitle:** structure of uncharacterized protein mj1198 from2 methanocaldococcus jannaschii. northeast structural3 genomics target mjr117b |
| 67 | d2z0sa1 | Alignment | not modelled | 99.3 | 16 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 68 | c1kl9A_ | Alignment | not modelled | 99.3 | 33 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 2 subunit 1;<br>**PDBTitle:** crystal structure of the n-terminal segment of human eukaryotic2 initiation factor 2alpha |
| 69 | d3bzka4 | Alignment | not modelled | 99.3 | 41 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 70 | d2nn6h1 | Alignment | not modelled | 99.3 | 20 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 71 | d2je6i1 | Alignment | not modelled | 99.3 | 21 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 72 | c3psiA_ | Alignment | not modelled | 99.3 | 15 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcription elongation factor spt6;<br>**PDBTitle:** crystal structure of the spt6 core domain from saccharomyces2 cerevisiae, form spt6(239-1451) |

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| 73 | c1hh2P_ | Alignment |  | 99.2 | 18 | **PDB header:**transcription regulation<br>**Chain:** P: **PDB Molecule:**n utilization substance protein a;<br>**PDBTitle:** crystal structure of nusa from thermotoga maritima |
| 74 | d2z0sa2 | Alignment | | 99.2 | 25 | **Fold:**Eukaryotic type KH-domain (KH-domain type I)<br>**Superfamily:**Eukaryotic type KH-domain (KH-domain type I)<br>**Family:**Eukaryotic type KH-domain (KH-domain type I) |
| 75 | d2ahob2 | Alignment | not modelled | 99.2 | 31 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 76 | d2je6a2 | Alignment | not modelled | 99.2 | 16 | **Fold:**Ribonuclease PH domain 2-like<br>**Superfamily:**Ribonuclease PH domain 2-like<br>**Family:**Ribonuclease PH domain 2-like |
| 77 | d2nn6d2 | Alignment | not modelled | 99.2 | 21 | **Fold:**Ribonuclease PH domain 2-like<br>**Superfamily:**Ribonuclease PH domain 2-like<br>**Family:**Ribonuclease PH domain 2-like |
| 78 | d1smxa_ | Alignment | not modelled | 99.1 | 31 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 79 | d1wi5a_ | Alignment | not modelled | 99.1 | 21 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 80 | c3go5A_ | Alignment | not modelled | 99.0 | 19 | **PDB header:**gene regulation<br>**Chain:** A: **PDB Molecule:**multidomain protein with s1 rna-binding domains;<br>**PDBTitle:** crystal structure of a multidomain protein with nucleic acid binding2 domains (sp_0946) from streptococcus pneumoniae tigr4 at 1.40 a3 resolution |
| 81 | c2z0sA_ | Alignment | not modelled | 99.0 | 18 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**probable exosome complex rna-binding protein 1;<br>**PDBTitle:** crystal structure of putative exosome complex rna-binding2 protein |
| 82 | d1y14b1 | Alignment | not modelled | 99.0 | 17 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 83 | c2ba0A_ | Alignment | not modelled | 99.0 | 23 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**archeal exosome rna binding protein rrp4;<br>**PDBTitle:** archaeal exosome core |
| 84 | c2bh8B_ | Alignment | not modelled | 99.0 | 36 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**1b11;<br>**PDBTitle:** combinatorial protein 1b11 |
| 85 | d2ba0a3 | Alignment | not modelled | 98.9 | 31 | **Fold:**Eukaryotic type KH-domain (KH-domain type I)<br>**Superfamily:**Eukaryotic type KH-domain (KH-domain type I)<br>**Family:**Eukaryotic type KH-domain (KH-domain type I) |
| 86 | d2nn6i1 | Alignment | not modelled | 98.9 | 23 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 87 | d2nn6f2 | Alignment | not modelled | 98.9 | 18 | **Fold:**Ribonuclease PH domain 2-like<br>**Superfamily:**Ribonuclease PH domain 2-like<br>**Family:**Ribonuclease PH domain 2-like |
| 88 | c2je6l_ | Alignment | not modelled | 98.8 | 23 | **PDB header:**hydrolase<br>**Chain:** I: **PDB Molecule:**exosome complex rna-binding protein 1;<br>**PDBTitle:** structure of a 9-subunit archaeal exosome |
| 89 | c1go3E_ | Alignment | not modelled | 98.7 | 29 | **PDB header:**transferase<br>**Chain:** E: **PDB Molecule:**dna-directed rna polymerase subunit e;<br>**PDBTitle:** structure of an archeal homolog of the eukaryotic rna2 polymerase ii rpb4/rpb7 complex |
| 90 | d1hh2p1 | Alignment | not modelled | 98.7 | 24 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 91 | c2ba1B_ | Alignment | not modelled | 98.7 | 23 | **PDB header:**rna binding protein<br>**Chain:** B: **PDB Molecule:**archaeal exosome rna binding protein csl4;<br>**PDBTitle:** archaeal exosome core |
| 92 | d2ctka1 | Alignment | not modelled | 98.6 | 20 | **Fold:**Eukaryotic type KH-domain (KH-domain type I)<br>**Superfamily:**Eukaryotic type KH-domain (KH-domain type I)<br>**Family:**Eukaryotic type KH-domain (KH-domain type I) |
| 93 | d1tuaa1 | Alignment | not modelled | 98.6 | 25 | **Fold:**Eukaryotic type KH-domain (KH-domain type I)<br>**Superfamily:**Eukaryotic type KH-domain (KH-domain type I)<br>**Family:**Eukaryotic type KH-domain (KH-domain type I) |
| 94 | c2nn6l_ | Alignment | not modelled | 98.6 | 22 | **PDB header:**hydrolase/transferase<br>**Chain:** I: **PDB Molecule:**3'-5' exoribonuclease csl4 homolog;<br>**PDBTitle:** structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40 |
| 95 | d2ba0g2 | Alignment | not modelled | 98.6 | 14 | **Fold:**Ribonuclease PH domain 2-like<br>**Superfamily:**Ribonuclease PH domain 2-like<br>**Family:**Ribonuclease PH domain 2-like |
| 96 | c1l2fA_ | Alignment | not modelled | 98.5 | 18 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**n utilization substance protein a;<br>**PDBTitle:** crystal structure of nusa from thermotoga maritima: a2 structure-based role of the n-terminal domain |
| | | | | | | **PDB header:**translation, transferase |

| | | | | | | |
|---|---|---|---|---|---|---|
| 97 | c2pmzE_ | Alignment | not modelled | 98.5 | 41 | **Chain:** E: **PDB Molecule:**dna-directed rna polymerase subunit e; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus |
| 98 | d2c35b1 | Alignment | not modelled | 98.5 | 19 | **Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like |
| 99 | c2c35F_ | Alignment | not modelled | 98.5 | 19 | **PDB header:**polymerase **Chain:** F: **PDB Molecule:**dna-directed rna polymerase ii 19 kda **PDBTitle:** subunits rpb4 and rpb7 of human rna polymerase ii |
| 100 | c2e3uA_ | Alignment | not modelled | 98.5 | 22 | **PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**hypothetical protein ph1566; **PDBTitle:** crystal structure analysis of dim2p from pyrococcus horikoshii ot3 |
| 101 | d1we8a_ | Alignment | not modelled | 98.5 | 24 | **Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I) |
| 102 | c2yqrA_ | Alignment | not modelled | 98.4 | 20 | **PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**kiaa0907 protein; **PDBTitle:** solution structure of the kh domain in kiaa0907 protein |
| 103 | d1j4wa1 | Alignment | not modelled | 98.4 | 23 | **Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I) |
| 104 | d1x4ma1 | Alignment | not modelled | 98.4 | 33 | **Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I) |
| 105 | c3h0gS_ | Alignment | not modelled | 98.4 | 21 | **PDB header:**transcription **Chain:** S: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb7; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe |
| 106 | c3n89B_ | Alignment | not modelled | 98.4 | 13 | **PDB header:**cell cycle **Chain:** B: **PDB Molecule:**defective in germ line development protein 3, isoform a; **PDBTitle:** kh domains |
| 107 | c2hh2A_ | Alignment | not modelled | 98.4 | 32 | **PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**kh-type splicing regulatory protein; **PDBTitle:** solution structure of the fourth kh domain of ksrp |
| 108 | c2b8kG_ | Alignment | not modelled | 98.4 | 16 | **PDB header:**transferase **Chain:** G: **PDB Molecule:**dna-directed rna polymerase ii 19 kda **PDBTitle:** 12-subunit rna polymerase ii |
| 109 | d1khma_ | Alignment | not modelled | 98.4 | 22 | **Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I) |
| 110 | d2ctfa1 | Alignment | not modelled | 98.4 | 17 | **Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I) |
| 111 | d1dtja_ | Alignment | not modelled | 98.4 | 24 | **Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I) |
| 112 | d1zzka1 | Alignment | not modelled | 98.3 | 22 | **Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I) |
| 113 | d1ec6a_ | Alignment | not modelled | 98.3 | 25 | **Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I) |
| 114 | c2ckzB_ | Alignment | not modelled | 98.3 | 12 | **PDB header:**transferase **Chain:** B: **PDB Molecule:**dna-directed rna polymerase iii 25 kd **PDBTitle:** x-ray structure of rna polymerase iii subcomplex c17-c25. |
| 115 | d1x4na1 | Alignment | not modelled | 98.3 | 23 | **Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I) |
| 116 | d1viga_ | Alignment | not modelled | 98.3 | 22 | **Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I) |
| 117 | c2dgrA_ | Alignment | not modelled | 98.3 | 17 | **PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**ring finger and kh domain-containing protein 1; **PDBTitle:** solution structure of the second kh domain in ring finger2 and kh domain containing protein 1 |
| 118 | d1wvna1 | Alignment | not modelled | 98.3 | 26 | **Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I) |
| 119 | d2axya1 | Alignment | not modelled | 98.3 | 19 | **Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I) |
| 120 | d2nn6a2 | Alignment | not modelled | 98.3 | 13 | **Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like |