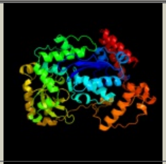
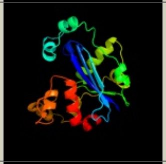
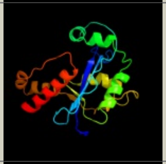
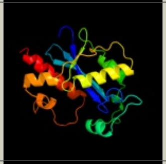
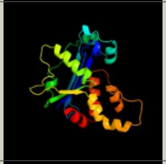
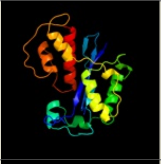
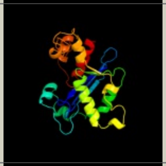
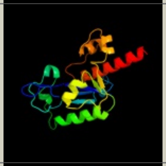
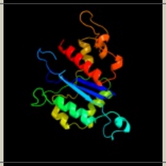
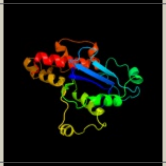
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P04995
Date	Thu Jan 5 10:58:34 GMT 2012
Unique Job ID	9e5174c606cb61ea

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2qxfa1	Alignment		100.0	100	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
2	d1y97a1	Alignment		100.0	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
3	d1j9aa_	Alignment		100.0	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
4	d2f96a1	Alignment		100.0	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
5	d3b6oa1	Alignment		100.0	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
6	c3u6fA_	Alignment		100.0	16	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**three prime repair exonuclease 1; **PDBTitle:** mouse trex1 d200n mutant
7	c3tr8A_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oligoribonuclease; **PDBTitle:** structure of an oligoribonuclease (orn) from coxiella burnetii
8	d1w0ha_	Alignment		100.0	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
9	d2igia1	Alignment		100.0	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
10	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
11	c2gbzA_	Alignment		100.0	17	**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

12	c2p1jB_	Alignment		100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna polymerase iii polc-type; **PDBTitle:** crystal structure of a polc-type dna polymerase iii2 exonuclease domain from thermotoga maritima
13	c2xriA_	Alignment		100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**eri1 exoribonuclease 3; **PDBTitle:** crystal structure of human eri1 exoribonuclease 3
14	d2guia1	Alignment		100.0	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
15	c1zbhA_	Alignment		100.0	10	**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
16	c1zbuB_	Alignment		100.0	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**3'-5' exonuclease eri1; **PDBTitle:** crystal structure of full-length 3'-exonuclease
17	d1wlja_	Alignment		99.9	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
18	c2is3B_	Alignment		99.9	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ribonuclease t; **PDBTitle:** crystal structure of escherichia coli rnase t
19	d1uoca_	Alignment		99.8	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**CAF1-like ribonuclease
20	d2d5ra1	Alignment		99.5	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**CAF1-like ribonuclease
21	c2p51A_	Alignment	not modelled	99.5	17	**PDB header:**hydrolase, gene regulation **Chain:** A: **PDB Molecule:**spcc18.06c protein; **PDBTitle:** crystal structure of the s. pombe pop2p deadenylation2 subunit
22	d1x9ma1	Alignment	not modelled	99.4	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
23	d1kfsa1	Alignment	not modelled	99.3	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
24	c2kzzA_	Alignment	not modelled	99.2	15	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**protein (dna polymerase i); **PDBTitle:** klenow fragment with normal substrate and zinc only
25	c1tk0A_	Alignment	not modelled	99.1	16	**PDB header:**transferase/electron transport/dna **Chain:** A: **PDB Molecule:**dna polymerase; **PDBTitle:** t7 dna polymerase ternary complex with 8 oxo guanosine and2 ddctp at the insertion site
26	d1qhta1	Alignment	not modelled	99.1	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
27	c2gv9B_	Alignment	not modelled	99.0	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna polymerase; **PDBTitle:** crystal structure of the herpes simplex virus type 1 dna polymerase
28	d1wn7a1	Alignment	not modelled	99.0	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
						Fold: Ribonuclease H-like motif

29	d1tgoa1	Alignment	not modelled	99.0	18	**Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
30	c2a1sC_	Alignment	not modelled	98.9	23	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**poly(a)-specific ribonuclease parn; **PDBTitle:** crystal structure of native parn nuclease domain
31	d1d5aa1	Alignment	not modelled	98.9	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
32	d2hhva1	Alignment	not modelled	98.9	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
33	c3d45B_	Alignment	not modelled	98.8	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**poly(a)-specific ribonuclease parn; **PDBTitle:** crystal structure of mouse parn in complex with m7gpppg
34	c1njzA_	Alignment	not modelled	98.8	17	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase i; **PDBTitle:** cytosine-thymine mismatch at the polymerase active site
35	c3iayA_	Alignment	not modelled	98.8	17	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase delta catalytic subunit; **PDBTitle:** ternary complex of dna polymerase delta
36	c2vwkA_	Alignment	not modelled	98.6	17	**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
37	d1s5ja1	Alignment	not modelled	98.6	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
38	d1ih7a1	Alignment	not modelled	98.6	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
39	c1d5aA_	Alignment	not modelled	98.5	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (dna polymerase); **PDBTitle:** crystal structure of an archaebacterial dna polymerase2 d.tok. deposition of second native structure at 2.43 angstrom
40	d1noya_	Alignment	not modelled	98.4	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
41	c1s5jA_	Alignment	not modelled	98.3	12	**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 sulfolobus solfataricus
42	c4ktqA_	Alignment	not modelled	98.3	17	**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
43	d1q8ia1	Alignment	not modelled	98.3	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
44	c2dtuA_	Alignment	not modelled	98.2	16	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase; **PDBTitle:** crystal structure of the beta hairpin loop deletion variant2 of rb69 gp43 in complex with dna containing an abasic site3 analog
45	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
46	c1yt3A_	Alignment	not modelled	98.0	18	**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
47	d1yt3a3	Alignment	not modelled	97.9	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
48	d2hbka2	Alignment	not modelled	97.7	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
49	c2e6mA_	Alignment	not modelled	97.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**werner syndrome atp-dependent helicase homolog; **PDBTitle:** structure of mouse werner exonuclease domain
50	c2hbkA_	Alignment	not modelled	97.4	19	**PDB header:**hydrolase, gene regulation **Chain:** A: **PDB Molecule:**exosome complex exonuclease rrp6; **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
51	c3f2cA_	Alignment	not modelled	97.2	14	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**geobacillus kaustophilus dna polc; **PDBTitle:** dna polymerase polc from geobacillus kaustophilus complex with dna,2 dgtp and mn
52	c3sahA_	Alignment	not modelled	96.0	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
53	c3cymA_	Alignment	not modelled	95.9	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein bad_0989; **PDBTitle:** crystal structure of protein bad_0989 from bifidobacterium2 adolescentis
54	c3ikmD_	Alignment	not modelled	93.9	24	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dna polymerase subunit gamma-1; **PDBTitle:** crystal structure of human mitochondrial dna polymerase2 holoenzyme
						Fold: Ribonuclease H-like motif

55	d1vk0a_	Alignment	not modelled	86.8	11	**Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
56	c1cmwA_	Alignment	not modelled	83.5	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (dna polymerase i); **PDBTitle:** crystal structure of taq dna-polymerase shows a new2 orientation for the structure-specific nuclease domain
57	d2py5a1	Alignment	not modelled	58.5	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
58	c3uo9B_	Alignment	not modelled	35.8	11	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**glutaminase kidney isoform, mitochondrial; **PDBTitle:** crystal structure of human gac in complex with glutamate and bptes
59	c2ex3I_	Alignment	not modelled	19.2	17	**PDB header:**transferase/replication **Chain:** I: **PDB Molecule:**dna polymerase; **PDBTitle:** bacteriophage phi29 dna polymerase bound to terminal protein
60	d1m0da_	Alignment	not modelled	14.2	26	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Endonuclease I (Holliday junction resolvase)
61	c2r6cG_	Alignment	not modelled	11.7	13	**PDB header:**replication **Chain:** G: **PDB Molecule:**dnag primase, helicase binding domain; **PDBTitle:** crystal form bh2
62	c2d3wB_	Alignment	not modelled	8.8	13	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**probable atp-dependent transporter sufc; **PDBTitle:** crystal structure of escherichia coli sufc, an atpase2 compenent of the suf iron-sulfur cluster assembly machinery
63	c2r6fA_	Alignment	not modelled	6.4	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**excinuclease abc subunit a; **PDBTitle:** crystal structure of bacillus stearothermophilus uvra
64	c3r03B_	Alignment	not modelled	6.3	9	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nudix hydrolase; **PDBTitle:** the crystal structure of nudix hydrolase from rhodospirillum rubrum
65	c2jo8B_	Alignment	not modelled	6.0	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase 4; **PDBTitle:** solution structure of c-terminal domain of human mammalian2 sterile 20-like kinase 1 (mst1)
66	c3ss4C_	Alignment	not modelled	6.0	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**glutaminase c; **PDBTitle:** crystal structure of mouse glutaminase c, phosphate-bound form
67	d2fmme1	Alignment	not modelled	6.0	28	**Fold:**ENT-like **Superfamily:**ENT-like **Family:**Emsy N terminal (ENT) domain-like
68	d1j6ua3	Alignment	not modelled	5.9	9	**Fold:**Ribokinase-like **Superfamily:**MurD-like peptide ligases, catalytic domain **Family:**MurCDEF
69	d1uz3a1	Alignment	not modelled	5.8	28	**Fold:**ENT-like **Superfamily:**ENT-like **Family:**Emsy N terminal (ENT) domain-like
70	c2fmmE_	Alignment	not modelled	5.8	28	**PDB header:**transcription **Chain:** E: **PDB Molecule:**protein emsy; **PDBTitle:** crystal structure of emsy-hp1 complex
71	c3e0dA_	Alignment	not modelled	5.7	9	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase iii subunit alpha; **PDBTitle:** insights into the replisome from the crystral structure of2 the ternary complex of the eubacterial dna polymerase iii3 alpha-subunit
72	c3hhjA_	Alignment	not modelled	5.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutator mutt protein; **PDBTitle:** crystal structure of mutator mutt from bartonella henselae