Email	l.a.kelley@imperial.ac.uk
Description	P09155
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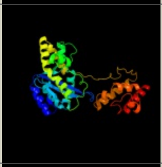
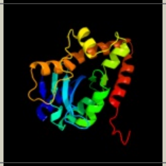
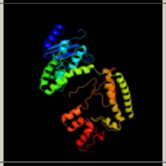
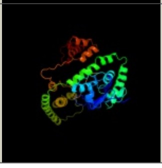
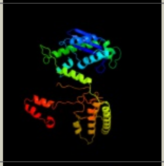
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1yt3A_	Alignment		100.0	100	**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
2	c3cymA_	Alignment		100.0	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein bad_0989; **PDBTitle:** crystal structure of protein bad_0989 from bifidobacterium2 adolescentis
3	c2hbkA_	Alignment		100.0	26	**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
4	c3sahA_	Alignment		100.0	24	**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
5	d2hbka2	Alignment		100.0	27	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
6	d1yt3a3	Alignment		100.0	100	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
7	c2kzzA_	Alignment		100.0	17	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**protein (dna polymerase i); **PDBTitle:** klenow fragment with normal substrate and zinc only
8	c1njzA_	Alignment		100.0	14	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase i; **PDBTitle:** cytosine-thymine mismatch at the polymerase active site
9	c2e6mA_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**werner syndrome atp-dependent helicase homolog; **PDBTitle:** structure of mouse werner exonuclease domain
10	d1kfsa1	Alignment		100.0	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
11	c4ktqA_	Alignment		100.0	13	**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

12	d1vk0a_	Alignment		100.0	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
13	d2hhva1	Alignment		100.0	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
14	c1cmwA_	Alignment		99.9	14	**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
15	d1yt3a1	Alignment		99.9	100	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**RNase D C-terminal domains
16	c1tk0A_	Alignment		99.8	18	**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
17	d2cpra1	Alignment		99.7	20	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**EXOSC10 HRDC domain-like
18	d2hbka1	Alignment		99.7	22	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**EXOSC10 HRDC domain-like
19	d1yt3a2	Alignment		99.7	100	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**RNase D C-terminal domains
20	d1wuda1	Alignment		99.4	21	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**HRDC domain from helicases
21	c2rrdA_	Alignment	not modelled	99.3	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**hrdc domain from bloom syndrome protein; **PDBTitle:** structure of hrdc domain from human bloom syndrome protein, blm
22	c2rhfA_	Alignment	not modelled	99.3	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna helicase recq; **PDBTitle:** d. radiodurans recq hrdc domain 3
23	d2e1fa1	Alignment	not modelled	99.2	16	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**HRDC domain from helicases
24	d1x9ma1	Alignment	not modelled	98.8	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
25	d1d8ba_	Alignment	not modelled	98.8	15	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**HRDC domain from helicases
26	d1wlja_	Alignment	not modelled	98.4	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
27	d2hhva2	Alignment	not modelled	98.3	14	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**DNA polymerase I
28	c2p1jB_	Alignment	not modelled	98.2	21	**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
						Fold:DNA/RNA polymerases

29	d1qtma2	Alignment	not modelled	98.2	11	**Superfamily:**DNA/RNA polymerases **Family:**DNA polymerase I
30	c2is3B_	Alignment	not modelled	98.0	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ribonuclease t; **PDBTitle:** crystal structure of escherichia coli rnase t
31	d2f96a1	Alignment	not modelled	98.0	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
32	d2d5ra1	Alignment	not modelled	98.0	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**CAF1-like ribonuclease
33	d1uoca_	Alignment	not modelled	97.9	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**CAF1-like ribonuclease
34	d1d5aa1	Alignment	not modelled	97.8	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
35	d1kfsa2	Alignment	not modelled	97.8	13	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**DNA polymerase I
36	d1tgoa1	Alignment	not modelled	97.8	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
37	d1qhta1	Alignment	not modelled	97.8	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
38	d2guia1	Alignment	not modelled	97.8	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
39	d1y97a1	Alignment	not modelled	97.7	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
40	d1wn7a1	Alignment	not modelled	97.6	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
41	d3b6oa1	Alignment	not modelled	97.5	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
42	c2p51A_	Alignment	not modelled	97.5	18	**PDB header:**hydrolase, gene regulation **Chain:** A: **PDB Molecule:**spcc18.06c protein; **PDBTitle:** crystal structure of the s. pombe pop2p deadenylation2 subunit
43	c3d45B_	Alignment	not modelled	97.5	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**poly(a)-specific ribonuclease parn; **PDBTitle:** crystal structure of mouse parn in complex with m7gpppg
44	c3ikmD_	Alignment	not modelled	97.5	19	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dna polymerase subunit gamma-1; **PDBTitle:** crystal structure of human mitochondrial dna polymerase2 holoenzyme
45	d2qxfa1	Alignment	not modelled	97.4	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
46	c3u6fA_	Alignment	not modelled	97.2	21	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**three prime repair exonuclease 1; **PDBTitle:** mouse trex1 d200n mutant
47	d1j9aa_	Alignment	not modelled	96.4	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
48	c2a1sC_	Alignment	not modelled	95.8	14	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**poly(a)-specific ribonuclease parn; **PDBTitle:** crystal structure of native parn nuclease domain
49	d1s5ja1	Alignment	not modelled	95.7	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
50	c2vwkA_	Alignment	not modelled	95.3	15	**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
51	c3iayA_	Alignment	not modelled	94.8	18	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase delta catalytic subunit; **PDBTitle:** ternary complex of dna polymerase delta
52	d2igia1	Alignment	not modelled	94.5	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
53	c1d5aA_	Alignment	not modelled	93.6	16	**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
54	c3cm6A_	Alignment	not modelled	93.6	18	**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
55	c3tr8A_	Alignment	not modelled	92.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oligoribonuclease; **PDBTitle:** structure of an oligoribonuclease (orn) from coxiella burnetii
56	c2gbzA_	Alignment	not modelled	92.4	15	**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
57	d1w0ha_	Alignment	not modelled	91.5	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
58	d1ih7a1	Alignment	not modelled	90.4	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
59	d1q8ia1	Alignment	not modelled	89.4	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
60	c2xriA_	Alignment	not modelled	89.4	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**eri1 exoribonuclease 3; **PDBTitle:** crystal structure of human eri1 exoribonuclease 3
61	d1x9ma2	Alignment	not modelled	88.8	15	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**DNA polymerase I
62	c1zbhA_	Alignment	not modelled	81.7	19	**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
63	c1s5jA_	Alignment	not modelled	81.5	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 sulfolobus solfataricus
64	c1q8iA_	Alignment	not modelled	79.1	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase ii; **PDBTitle:** crystal structure of escherichia coli dna polymerase ii
65	c2gv9B_	Alignment	not modelled	77.7	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna polymerase; **PDBTitle:** crystal structure of the herpes simplex virus type 1 dna polymerase
66	c2dtuA_	Alignment	not modelled	76.3	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
67	d1noya_	Alignment	not modelled	73.3	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
68	c2ex3I_	Alignment	not modelled	51.4	10	**PDB header:**transferase/replication **Chain:** I: **PDB Molecule:**dna polymerase; **PDBTitle:** bacteriophage phi29 dna polymerase bound to terminal protein
69	c1zbuB_	Alignment	not modelled	36.8	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**3'-5' exonuclease eri1; **PDBTitle:** crystal structure of full-length 3'-exonuclease
70	c2vxdA_	Alignment	not modelled	31.4	26	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**nucleophosmin; **PDBTitle:** the structure of the c-terminal domain of nucleophosmin
71	d1sgva2	Alignment	not modelled	25.0	22	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
72	d1akha_	Alignment	not modelled	23.6	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
73	d2py5a1	Alignment	not modelled	22.9	9	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
74	d1wh5a_	Alignment	not modelled	20.8	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
75	d1le8a_	Alignment	not modelled	17.3	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
76	d1mh3a1	Alignment	not modelled	16.0	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
77	c2k53A_	Alignment	not modelled	13.9	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**a3dk08 protein; **PDBTitle:** nmr solution structure of a3dk08 protein from clostridium2 thermocellum: northeast structural genomics consortium3 target cmr9
78	d1qtma1	Alignment	not modelled	13.2	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
79	d1y6ia2	Alignment	not modelled	13.2	14	**Fold:**GUN4-like **Superfamily:**GUN4-like **Family:**GUN4-like
80	c2p0tA_	Alignment	not modelled	13.2	36	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0307 protein pspto_4464; **PDBTitle:** structural genomics, the crystal structure of a conserved putative2 protein from pseudomonas syringae pv. tomato str. dc3000
81	d2p0ta1	Alignment	not modelled	13.2	36	**Fold:**PSPTO4464-like **Superfamily:**PSPTO4464-like **Family:**PSPTO4464-like
82	c2eqaA_	Alignment	not modelled	12.3	24	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**hypothetical protein st1526; **PDBTitle:** crystal structure of the hypothetical sua5 protein from2

						sulfolobus tokodaii
83	c2k5eA_	Alignment	not modelled	10.9	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of putative uncharacterized protein2 gsu1278 from methanocaldococcus jannaschii, northeast3 structural genomics consortium (nesg) target gsr195
84	c2da4A_	Alignment	not modelled	10.7	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein dkfzp686k21156; **PDBTitle:** solution structure of the homeobox domain of the2 hypothetical protein, dkfzp686k21156
85	d1f43a_	Alignment	not modelled	10.5	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
86	d1z3xa2	Alignment	not modelled	10.3	19	**Fold:**GUN4-like **Superfamily:**GUN4-like **Family:**GUN4-like
87	c1sgvA_	Alignment	not modelled	10.2	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**trna pseudouridine synthase b; **PDBTitle:** structure of trna psi55 pseudouridine synthase (trub)
88	c3narA_	Alignment	not modelled	9.7	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc fingers and homeoboxes protein 1; **PDBTitle:** crystal structure of zhx1 hd4 (zinc-fingers and homeoboxes protein 1,2 homeodomain 4)
89	c2px0D_	Alignment	not modelled	9.1	11	**PDB header:**biosynthetic protein **Chain:** D: **PDB Molecule:**flagellar biosynthesis protein flhf; **PDBTitle:** crystal structure of flhf complexed with gmppnp/mg(2+)
90	c2da1A_	Alignment	not modelled	8.8	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**alpha-fetoprotein enhancer binding protein; **PDBTitle:** solution structure of the first homeobox domain of at-2 binding transcription factor 1 (atbf1)
91	c2da5A_	Alignment	not modelled	8.8	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**zinc fingers and homeoboxes protein 3; **PDBTitle:** solution structure of the second homeobox domain of zinc2 fingers and homeoboxes protein 3 (triple homeobox 13 protein)
92	d1p7ia_	Alignment	not modelled	8.4	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
93	d2ecca1	Alignment	not modelled	8.4	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
94	d1b26a2	Alignment	not modelled	8.3	11	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
95	c3a03A_	Alignment	not modelled	8.2	17	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**t-cell leukemia homeobox protein 2; **PDBTitle:** crystal structure of hox11l1 homeodomain
96	d1s7ea1	Alignment	not modelled	8.0	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
97	c3aoeC_	Alignment	not modelled	7.8	9	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glutamate dehydrogenase; **PDBTitle:** crystal structure of hetero-hexameric glutamate dehydrogenase from2 thermus thermophilus (leu bound form)
98	c1y6iA_	Alignment	not modelled	7.1	17	**PDB header:**ligand binding protein **Chain:** A: **PDB Molecule:**mg-chelatase cofactor gun4; **PDBTitle:** synechocystis gun4
99	c2da2A_	Alignment	not modelled	7.0	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**alpha-fetoprotein enhancer binding protein; **PDBTitle:** solution structure of the second homeobox domain of at-2 binding transcription factor 1 (atbf1)