Phyre^2

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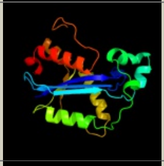
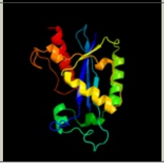
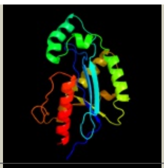
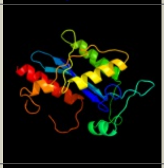
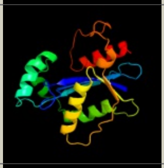
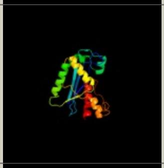
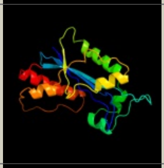
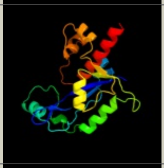
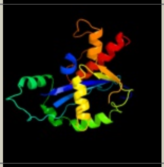
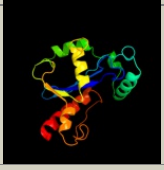
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2igia1	Alignment		100.0	100	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
2	d1j9aa_	Alignment		100.0	71	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
3	c3tr8A_	Alignment		100.0	59	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oligoribonuclease; **PDBTitle:** structure of an oligoribonuclease (orn) from coxiella burnetii
4	c2gbzA_	Alignment		100.0	58	**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
5	d2qxfa1	Alignment		100.0	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
6	d1y97a1	Alignment		100.0	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
7	d3b6oa1	Alignment		100.0	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
8	c3u6fA_	Alignment		100.0	14	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**three prime repair exonuclease 1; **PDBTitle:** mouse trex1 d200n mutant
9	c2p1jB_	Alignment		100.0	23	**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
10	d1w0ha_	Alignment		100.0	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
11	c3cm6A_	Alignment		100.0	17	**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

12	c2xriA_	Alignment		100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**eri1 exoribonuclease 3; **PDBTitle:** crystal structure of human eri1 exoribonuclease 3
13	d2f96a1	Alignment		100.0	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
14	d2guia1	Alignment		100.0	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
15	c1zbhA_	Alignment		100.0	11	**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	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**3'-5' exonuclease eri1; **PDBTitle:** crystal structure of full-length 3'-exonuclease
17	d1wlja_	Alignment		99.9	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
18	c2is3B_	Alignment		99.9	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ribonuclease t; **PDBTitle:** crystal structure of escherichia coli rnase t
19	d1uoca_	Alignment		99.2	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**CAF1-like ribonuclease
20	d2d5ra1	Alignment		99.0	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**CAF1-like ribonuclease
21	d1kfsa1	Alignment	not modelled	99.0	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
22	c2kzzA_	Alignment	not modelled	98.9	15	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**protein (dna polymerase i); **PDBTitle:** klenow fragment with normal substrate and zinc only
23	d1x9ma1	Alignment	not modelled	98.9	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
24	c2p51A_	Alignment	not modelled	98.8	17	**PDB header:**hydrolase, gene regulation **Chain:** A: **PDB Molecule:**spcc18.06c protein; **PDBTitle:** crystal structure of the s. pombe pop2p deadenylation2 subunit
25	c1tk0A_	Alignment	not modelled	98.7	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	c2gv9B_	Alignment	not modelled	98.4	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna polymerase; **PDBTitle:** crystal structure of the herpes simplex virus type 1 dna polymerase
27	c1njzA_	Alignment	not modelled	98.3	10	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase i; **PDBTitle:** cytosine-thymine mismatch at the polymerase active site
28	d1wn7a1	Alignment	not modelled	98.2	16	**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	98.2	16	**Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
30	c3iayA_	Alignment	not modelled	98.1	21	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase delta catalytic subunit; **PDBTitle:** ternary complex of dna polymerase delta
31	c3d45B_	Alignment	not modelled	98.1	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**poly(a)-specific ribonuclease parn; **PDBTitle:** crystal structure of mouse parn in complex with m7gpppg
32	c2a1sC_	Alignment	not modelled	98.1	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**poly(a)-specific ribonuclease parn; **PDBTitle:** crystal structure of native parn nuclease domain
33	d1d5aa1	Alignment	not modelled	98.0	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
34	d1qhta1	Alignment	not modelled	98.0	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
35	d2hhva1	Alignment	not modelled	98.0	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
36	c2vwkA_	Alignment	not modelled	97.9	16	**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	d1q8ia1	Alignment	not modelled	97.6	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
38	d1ih7a1	Alignment	not modelled	97.6	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
39	c1d5aA_	Alignment	not modelled	97.5	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
40	d1s5ja1	Alignment	not modelled	97.3	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
41	d1noya_	Alignment	not modelled	97.3	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
42	c1s5jA_	Alignment	not modelled	97.1	20	**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
43	c2dtuA_	Alignment	not modelled	96.8	13	**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
44	d1yt3a3	Alignment	not modelled	96.5	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
45	c1q8iA_	Alignment	not modelled	96.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase ii; **PDBTitle:** crystal structure of escherichia coli dna polymerase ii
46	c1yt3A_	Alignment	not modelled	95.5	13	**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	c2e6mA_	Alignment	not modelled	95.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**werner syndrome atp-dependent helicase homolog; **PDBTitle:** structure of mouse werner exonuclease domain
48	c4ktqA_	Alignment	not modelled	95.4	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
49	d2py5a1	Alignment	not modelled	94.7	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
50	c2ex3I_	Alignment	not modelled	93.6	13	**PDB header:**transferase/replication **Chain:** I: **PDB Molecule:**dna polymerase; **PDBTitle:** bacteriophage phi29 dna polymerase bound to terminal protein
51	d2hbka2	Alignment	not modelled	93.2	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
52	c3cymA_	Alignment	not modelled	87.9	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein bad_0989; **PDBTitle:** crystal structure of protein bad_0989 from bifidobacterium2 adolescentis
53	c3ikmD_	Alignment	not modelled	83.3	21	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dna polymerase subunit gamma-1; **PDBTitle:** crystal structure of human mitochondrial dna polymerase2 holoenzyme
54	c2hbkA_	Alignment	not modelled	79.8	17	**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
						Fold: Ribonuclease H-like motif

55	d1vk0a_	Alignment	not modelled	65.3	19	**Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
56	c3sahA_	Alignment	not modelled	61.3	18	**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
57	d2bgxa1	Alignment	not modelled	19.0	14	**Fold:**PGBD-like **Superfamily:**PGBD-like **Family:**Peptidoglycan binding domain, PGBD
58	c2d3wB_	Alignment	not modelled	10.6	35	**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
59	d1tf5a1	Alignment	not modelled	8.0	23	**Fold:**Pre-protein crosslinking domain of SecA **Superfamily:**Pre-protein crosslinking domain of SecA **Family:**Pre-protein crosslinking domain of SecA
60	c3efgA_	Alignment	not modelled	7.0	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein slyx homolog; **PDBTitle:** structure of slyx protein from xanthomonas campestris pv. campestris2 str. atcc 33913
61	c2v5iA_	Alignment	not modelled	6.7	20	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**salmonella typhimurium db7155 bacteriophage det7 **PDBTitle:** structure of the receptor-binding protein of bacteriophage2 det7: a podoviral tailspike in a myovirus
62	c3l6sA_	Alignment	not modelled	5.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aspartyl aminopeptidase; **PDBTitle:** crystal structure of human aspartyl aminopeptidase (dnpep),2 in complex with aspartic acid hydroxamate
63	c3mesB_	Alignment	not modelled	5.2	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**choline kinase; **PDBTitle:** crystal structure of choline kinase from cryptosporidium2 parvum iowa ii, cgd3_2030