Phyre2

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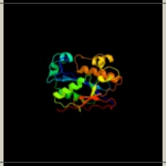
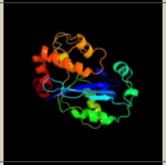
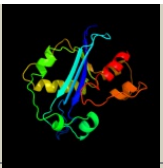
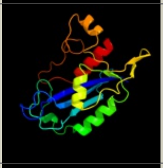
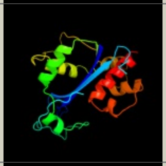
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2guia1	Alignment		100.0	100	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
2	c1zbhA_	Alignment		100.0	17	**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
3	c3cm6A_	Alignment		100.0	19	**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
4	c1zbuB_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**3'-5' exonuclease eri1; **PDBTitle:** crystal structure of full-length 3'-exonuclease
5	d1y97a1	Alignment		100.0	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
6	d2f96a1	Alignment		100.0	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
7	c2p1jB_	Alignment		100.0	29	**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
8	c2xriA_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**eri1 exoribonuclease 3; **PDBTitle:** crystal structure of human eri1 exoribonuclease 3
9	d2qxfa1	Alignment		100.0	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
10	c3u6fA_	Alignment		100.0	24	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**three prime repair exonuclease 1; **PDBTitle:** mouse trex1 d200n mutant
11	d1w0ha_	Alignment		100.0	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease

12	d3b6oa1	Alignment		100.0	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
13	c2is3B_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ribonuclease t; **PDBTitle:** crystal structure of escherichia coli rnase t
14	d1j9aa_	Alignment		100.0	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
15	d1wlja_	Alignment		100.0	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
16	c3tr8A_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oligoribonuclease; **PDBTitle:** structure of an oligoribonuclease (orn) from coxiella burnetii
17	d2igia1	Alignment		100.0	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
18	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
19	d1uoca_	Alignment		99.8	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**CAF1-like ribonuclease
20	d2d5ra1	Alignment		99.7	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**CAF1-like ribonuclease
21	c2p51A_	Alignment	not modelled	99.7	16	**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	99.5	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
23	d1kfsa1	Alignment	not modelled	99.5	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
24	c2kzzA_	Alignment	not modelled	99.5	19	**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	99.3	23	**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	c1njzA_	Alignment	not modelled	99.3	17	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase i; **PDBTitle:** cytosine-thymine mismatch at the polymerase active site
27	c3d45B_	Alignment	not modelled	99.3	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**poly(a)-specific ribonuclease parn; **PDBTitle:** crystal structure of mouse parn in complex with m7gpppg
28	c2gv9B_	Alignment	not modelled	99.2	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna polymerase; **PDBTitle:** crystal structure of the herpes simplex virus type 1 dna polymerase
						PDB header:hydrolase

29	c2a1sC_	Alignment	not modelled	99.2	25	**Chain:** C: **PDB Molecule:**poly(a)-specific ribonuclease parn; **PDBTitle:** crystal structure of native parn nuclease domain
30	c3iayA_	Alignment	not modelled	99.1	17	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase delta catalytic subunit; **PDBTitle:** ternary complex of dna polymerase delta
31	d1qhta1	Alignment	not modelled	99.1	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
32	d1tgoa1	Alignment	not modelled	99.1	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
33	d1d5aa1	Alignment	not modelled	99.0	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
34	d2hhva1	Alignment	not modelled	99.0	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
35	d1wn7a1	Alignment	not modelled	99.0	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
36	c4ktqA_	Alignment	not modelled	98.8	14	**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
37	c1d5aA_	Alignment	not modelled	98.7	17	**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
38	c2vwkA_	Alignment	not modelled	98.7	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
39	d1q8ia1	Alignment	not modelled	98.7	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
40	d1ih7a1	Alignment	not modelled	98.6	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
41	d1s5ja1	Alignment	not modelled	98.6	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
42	d1noya_	Alignment	not modelled	98.5	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
43	c1yt3A_	Alignment	not modelled	98.5	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
44	d1yt3a3	Alignment	not modelled	98.4	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
45	c2dtuA_	Alignment	not modelled	98.4	18	**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
46	c1q8iA_	Alignment	not modelled	98.4	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase ii; **PDBTitle:** crystal structure of escherichia coli dna polymerase ii
47	c2e6mA_	Alignment	not modelled	98.2	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**werner syndrome atp-dependent helicase homolog; **PDBTitle:** structure of mouse werner exonuclease domain
48	c3cymA_	Alignment	not modelled	98.2	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein bad_0989; **PDBTitle:** crystal structure of protein bad_0989 from bifidobacterium2 adolescentis
49	c1s5jA_	Alignment	not modelled	98.1	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
50	d2hbka2	Alignment	not modelled	97.7	24	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
51	c2hbkA_	Alignment	not modelled	97.5	23	**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
52	c3sahA_	Alignment	not modelled	96.8	23	**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	c1cmwA_	Alignment	not modelled	96.8	16	**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
54	d2py5a1	Alignment	not modelled	96.4	24	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
55	c3ikmD	Alignment	not modelled	95.8	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dna polymerase subunit gamma-1;

		Alignment	not modelled			**PDBTitle:** crystal structure of human mitochondrial dna polymerase2 holoenzyme
56	d1vk0a_	Alignment	not modelled	95.7	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
57	c2ex3I_	Alignment	not modelled	95.4	24	**PDB header:**transferase/replication **Chain:** I: **PDB Molecule:**dna polymerase; **PDBTitle:** bacteriophage phi29 dna polymerase bound to terminal protein
58	c3q7cA_	Alignment	not modelled	54.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nucleoprotein; **PDBTitle:** exonuclease domain of lassa virus nucleoprotein bound to manganese
59	c2x5eA_	Alignment	not modelled	26.1	36	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**upf0271 protein pa4511; **PDBTitle:** crystal structure of the hypothetical protein pa4511 from2 pseudomonas aeruginosa
60	d1xw8a_	Alignment	not modelled	22.0	18	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**LamB/YcsF-like
61	d1v6ta_	Alignment	not modelled	18.1	23	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**LamB/YcsF-like
62	c3mx2A_	Alignment	not modelled	13.6	20	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**nucleoprotein; **PDBTitle:** lassa fever virus nucleoprotein complexed with dttp
63	c2o8vA_	Alignment	not modelled	13.6	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phosphoadenosine phosphosulfate reductase; **PDBTitle:** paps reductase in a covalent complex with thioredoxin c35a
64	d1l6ra_	Alignment	not modelled	10.8	20	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
65	d2nlva1	Alignment	not modelled	10.6	16	**Fold:**XisI-like **Superfamily:**XisI-like **Family:**XisI-like
66	d1wzca1	Alignment	not modelled	10.3	42	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
67	d2nvma1	Alignment	not modelled	10.0	14	**Fold:**XisI-like **Superfamily:**XisI-like **Family:**XisI-like
68	d2rk5a1	Alignment	not modelled	8.7	21	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
69	c3m1yA_	Alignment	not modelled	8.5	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphoserine phosphatase (serb); **PDBTitle:** crystal structure of a phosphoserine phosphatase (serb) from2 helicobacter pylori
70	d2nwva1	Alignment	not modelled	8.2	19	**Fold:**XisI-like **Superfamily:**XisI-like **Family:**XisI-like
71	c2d3wB_	Alignment	not modelled	8.0	23	**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
72	d2dfaa1	Alignment	not modelled	6.1	24	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**LamB/YcsF-like
73	d1mjta_	Alignment	not modelled	6.0	14	**Fold:**Nitric oxide (NO) synthase oxygenase domain **Superfamily:**Nitric oxide (NO) synthase oxygenase domain **Family:**Nitric oxide (NO) synthase oxygenase domain
74	c3d7qB_	Alignment	not modelled	5.8	17	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**xisi protein-like; **PDBTitle:** crystal structure of a xisi-like protein (npun_ar114) from nostoc2 punctiforme pcc 73102 at 2.30 a resolution
75	c3qodB_	Alignment	not modelled	5.3	62	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**heterocyst differentiation protein; **PDBTitle:** crystal structure of heterocyst differentiation protein, hetr from2 fischerella mv11
76	d2g3ra2	Alignment	not modelled	5.2	26	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain