Phyre2

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Description	Q2A0L0
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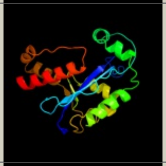
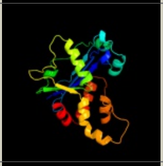
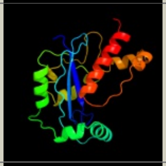
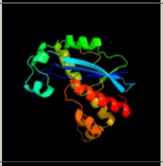
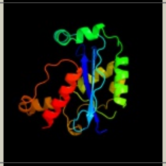
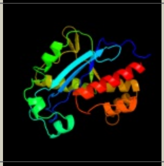
Unique Job ID	96122904a781107a

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	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
3	d1j9aa_	Alignment		100.0	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
4	d3b6oa1	Alignment		100.0	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
5	d2f96a1	Alignment		100.0	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
6	c3u6fA_	Alignment		100.0	17	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**three prime repair exonuclease 1; **PDBTitle:** mouse trex1 d200n mutant
7	c3tr8A_	Alignment		100.0	17	**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	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
10	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
11	c3cm6A_	Alignment		100.0	15	**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	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	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
15	c1zbhA_	Alignment		100.0	13	**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		99.9	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**3'-5' exonuclease eri1; **PDBTitle:** crystal structure of full-length 3'-exonuclease
17	c2is3B_	Alignment		99.9	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ribonuclease t; **PDBTitle:** crystal structure of escherichia coli rnase t
18	d1wlja_	Alignment		99.9	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
19	d1uoca_	Alignment		99.7	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**CAF1-like ribonuclease
20	d2d5ra1	Alignment		99.4	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**CAF1-like ribonuclease
21	c2p51A_	Alignment	not modelled	99.4	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	99.3	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
23	d1kfsa1	Alignment	not modelled	99.2	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
24	c2kzzA_	Alignment	not modelled	99.1	14	**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	99.0	14	**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	99.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase; **PDBTitle:** crystal structure of the herpes simplex virus type 1 dna polymerase
27	d1qhta1	Alignment	not modelled	99.0	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
28	d1wn7a1	Alignment	not modelled	98.9	17	**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	98.9	18	**Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
30	c1njzA_	Alignment	not modelled	98.8	19	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase i; **PDBTitle:** cytosine-thymine mismatch at the polymerase active site
31	d2hhva1	Alignment	not modelled	98.7	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
32	d1d5aa1	Alignment	not modelled	98.7	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
33	c3d45B_	Alignment	not modelled	98.7	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**poly(a)-specific ribonuclease parn; **PDBTitle:** crystal structure of mouse parn in complex with m7gpppg
34	c3iayA_	Alignment	not modelled	98.7	18	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase delta catalytic subunit; **PDBTitle:** ternary complex of dna polymerase delta
35	c2a1sC_	Alignment	not modelled	98.6	23	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**poly(a)-specific ribonuclease parn; **PDBTitle:** crystal structure of native parn nuclease domain
36	c2vwkA_	Alignment	not modelled	98.5	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	c1d5aA_	Alignment	not modelled	98.4	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
38	d1ih7a1	Alignment	not modelled	98.4	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
39	d1s5ja1	Alignment	not modelled	98.4	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
40	c4ktqA_	Alignment	not modelled	98.2	15	**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
41	c1s5jA_	Alignment	not modelled	98.2	13	**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	d1q8ia1	Alignment	not modelled	98.2	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
43	c2dtuA_	Alignment	not modelled	98.1	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	d1noya_	Alignment	not modelled	98.1	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
45	c1q8iA_	Alignment	not modelled	97.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase ii; **PDBTitle:** crystal structure of escherichia coli dna polymerase ii
46	c1yt3A_	Alignment	not modelled	97.7	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	97.7	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
48	d2hbka2	Alignment	not modelled	97.5	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
49	c2e6mA_	Alignment	not modelled	97.4	13	**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	97.2	18	**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	c3cymA_	Alignment	not modelled	95.6	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein bad_0989; **PDBTitle:** crystal structure of protein bad_0989 from bifidobacterium2 adolescentis
52	c3f2cA_	Alignment	not modelled	95.3	12	**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
53	c3sahA_	Alignment	not modelled	94.4	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
54	c1cmwA_	Alignment	not modelled	84.3	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
						Fold: Ribonuclease H-like motif

55	d1vk0a_	Alignment	not modelled	82.8	11	**Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
56	c3ikmD_	Alignment	not modelled	79.4	34	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dna polymerase subunit gamma-1; **PDBTitle:** crystal structure of human mitochondrial dna polymerase2 holoenzyme
57	d2py5a1	Alignment	not modelled	56.5	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
58	c3iykA_	Alignment	not modelled	32.9	24	**PDB header:**virus **Chain:** A: **PDB Molecule:**vp5; **PDBTitle:** bluetongue virus structure reveals a sialic acid binding domain,2 amphipathic helices and a central coiled coil in the outer capsid3 proteins
59	d1m0da_	Alignment	not modelled	26.8	26	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Endonuclease I (Holliday junction resolvase)
60	c2ex3l_	Alignment	not modelled	19.5	17	**PDB header:**transferase/replication **Chain:** I: **PDB Molecule:**dna polymerase; **PDBTitle:** bacteriophage phi29 dna polymerase bound to terminal protein
61	c2r6cG_	Alignment	not modelled	18.2	13	**PDB header:**replication **Chain:** G: **PDB Molecule:**dnag primase, helicase binding domain; **PDBTitle:** crystal form bh2
62	c3lp5A_	Alignment	not modelled	13.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative cell surface hydrolase; **PDBTitle:** the crystal structure of the putative cell surface hydrolase from2 lactobacillus plantarum wcfs1
63	c3hhjA_	Alignment	not modelled	10.6	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutator mutt protein; **PDBTitle:** crystal structure of mutator mutt from bartonella henselae
64	c3a7mA_	Alignment	not modelled	9.9	18	**PDB header:**gene regulation, chaperone **Chain:** A: **PDB Molecule:**flagellar protein flit; **PDBTitle:** structure of flit, the flagellar type iii chaperone for flid
65	c2d3wB_	Alignment	not modelled	9.7	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
66	c2jo8B_	Alignment	not modelled	9.5	19	**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)
67	d1f0la3	Alignment	not modelled	8.7	19	**Fold:**Toxins' membrane translocation domains **Superfamily:**Diphtheria toxin, middle domain **Family:**Diphtheria toxin, middle domain
68	d2fmme1	Alignment	not modelled	8.3	28	**Fold:**ENT-like **Superfamily:**ENT-like **Family:**Emsy N terminal (ENT) domain-like
69	d1j6ua3	Alignment	not modelled	8.2	9	**Fold:**Ribokinase-like **Superfamily:**MurD-like peptide ligases, catalytic domain **Family:**MurCDEF
70	c2fmmE_	Alignment	not modelled	8.0	28	**PDB header:**transcription **Chain:** E: **PDB Molecule:**protein emsy; **PDBTitle:** crystal structure of emsy-hp1 complex
71	d1z67a1	Alignment	not modelled	7.8	15	**Fold:**YidB-like **Superfamily:**YidB-like **Family:**YidB-like
72	c2r6fA_	Alignment	not modelled	7.6	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**excinuclease abc subunit a; **PDBTitle:** crystal structure of bacillus stearothermophilus uvra
73	c3r03B_	Alignment	not modelled	6.6	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nudix hydrolase; **PDBTitle:** the crystal structure of nudix hydrolase from rhodospirillum rubrum
74	c2fpgA_	Alignment	not modelled	6.3	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**succinyl-coa ligase [gdp-forming] alpha-chain, **PDBTitle:** crystal structure of pig gtp-specific succinyl-coa2 synthetase in complex with gdp
75	c3nrwA_	Alignment	not modelled	6.3	19	**PDB header:**recombination **Chain:** A: **PDB Molecule:**phage integrase/site-specific recombinase; **PDBTitle:** crystal structure of the n-terminal domain of phage integrase/site-2 specific recombinase (tnp) from haloarcula marismortui, northeast3 structural genomics consortium target hmr208a
76	c3fleB_	Alignment	not modelled	6.0	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**se_1780 protein; **PDBTitle:** se_1780 protein of unknown function from staphylococcus epidermidis.
77	d1bh9b_	Alignment	not modelled	5.9	14	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
78	c3tovB_	Alignment	not modelled	5.8	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycosyl transferase family 9; **PDBTitle:** the crystal structure of the glycosyl transferase family 9 from2 veillonella parvula dsm 2008
79	c3uo9B_	Alignment	not modelled	5.6	14	**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
80	c2h1fB	Alignment	not modelled	5.5	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**lipopolysaccharide heptosyltransferase-

80	c2h1fB_	Alignment	not modelled	5.5	21	1; **PDBTitle:** e. coli heptosyltransferase waac with adp
81	c3fp5A_	Alignment	not modelled	5.5	19	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**acyl-coa binding protein; **PDBTitle:** crystal structure of acbp from moniliophthora perniciosa
82	c2eqxA_	Alignment	not modelled	5.3	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**kelch repeat and btb domain-containing protein 4; **PDBTitle:** solution structure of the back domain of kelch repeat and2 btb domain-containing protein 4