







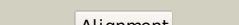

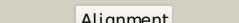
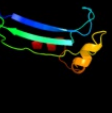
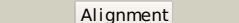

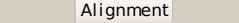

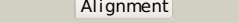

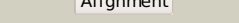

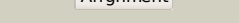
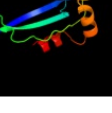
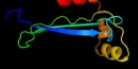

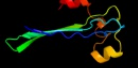
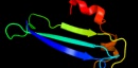
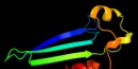



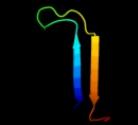


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2qxfa1</a>	 Alignment		100.0	99	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
2	<a href="#">d1y97a1</a>	 Alignment		99.8	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
3	<a href="#">d2f96a1</a>	 Alignment		99.8	24	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
4	<a href="#">c3u6fa_</a>	 Alignment		99.8	22	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> three prime repair exonuclease 1; <b>PDBTitle:</b> mouse trex1 d200n mutant
5	<a href="#">c3tr8A_</a>	 Alignment		99.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> oligoribonuclease; <b>PDBTitle:</b> structure of an oligoribonuclease (orn) from coxiella burnetii
6	<a href="#">d1j9aa_</a>	 Alignment		99.8	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
7	<a href="#">d3b6oa1</a>	 Alignment		99.8	22	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
8	<a href="#">c3cm6A_</a>	 Alignment		99.8	24	<b>PDB header:</b> hydrolase, apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> cell death-related nuclease 4; <b>PDBTitle:</b> crystal structure of cell-death related nuclease 4 (crn-4)2 bound with er
9	<a href="#">d1w0ha_</a>	 Alignment		99.8	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
10	<a href="#">c2xriA_</a>	 Alignment		99.8	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> eri1 exoribonuclease 3; <b>PDBTitle:</b> crystal structure of human eri1 exoribonuclease 3
11	<a href="#">c2gbzA_</a>	 Alignment		99.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> oligoribonuclease; <b>PDBTitle:</b> the crystal structure of xc847 from xanthomonas campestris: a 3-52 oligoribonuclease of dnaq fold family with a novel opposingly-shifted3 helix

12	<a href="#">d2igia1</a>	Alignment		99.8	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
13	<a href="#">c1zbhA</a>	Alignment		99.7	13	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> 3'-5' exonuclease eri1; <b>PDBTitle:</b> 3'-end specific recognition of histone mrna stem-loop by 3'-2 exonuclease
14	<a href="#">c1zbuB</a>	Alignment		99.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 3'-5' exonuclease eri1; <b>PDBTitle:</b> crystal structure of full-length 3'-exonuclease
15	<a href="#">d2guia1</a>	Alignment		99.7	20	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
16	<a href="#">c2p1jB</a>	Alignment		99.7	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dna polymerase iii polc-type; <b>PDBTitle:</b> crystal structure of a polc-type dna polymerase iii2 exonuclease domain from thermotoga maritima
17	<a href="#">d1wlja</a>	Alignment		99.5	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
18	<a href="#">c2is3B</a>	Alignment		98.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ribonuclease t; <b>PDBTitle:</b> crystal structure of escherichia coli rnase t
19	<a href="#">d1luoca</a>	Alignment		98.1	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> CAF1-like ribonuclease
20	<a href="#">d1x9ma1</a>	Alignment		97.4	7	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
21	<a href="#">c2p51A</a>	Alignment	not modelled	96.7	23	<b>PDB header:</b> hydrolase, gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> spcc18.06c protein; <b>PDBTitle:</b> crystal structure of the s. pombe pop2p deadenylation2 subunit
22	<a href="#">d1kfsa1</a>	Alignment	not modelled	96.4	9	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
23	<a href="#">d2d5ra1</a>	Alignment	not modelled	96.1	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> CAF1-like ribonuclease
24	<a href="#">d2hhva1</a>	Alignment	not modelled	96.1	9	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
25	<a href="#">c2kzzA</a>	Alignment	not modelled	95.7	19	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (dna polymerase i); <b>PDBTitle:</b> klenow fragment with normal substrate and zinc only
26	<a href="#">c1njzA</a>	Alignment	not modelled	93.8	8	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase i; <b>PDBTitle:</b> cytosine-thymine mismatch at the polymerase active site
27	<a href="#">c2a1sC</a>	Alignment	not modelled	93.5	25	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> poly(a)-specific ribonuclease parn; <b>PDBTitle:</b> crystal structure of native parn nuclease domain
28	<a href="#">c1tk0A</a>	Alignment	not modelled	92.8	7	<b>PDB header:</b> transferase/electron transport/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase; <b>PDBTitle:</b> t7 dna polymerase ternary complex with 8 oxo guanosine and2 ddctp at the insertion site
29	<a href="#">c3d45B</a>	Alignment	not modelled	89.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> poly(a)-specific ribonuclease parn;

					<b>PDBTitle:</b> crystal structure of mouse parn in complex with m7gpppg
30	<a href="#">d1wn7a1</a>	Alignment	not modelled	89.2	22 <b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
31	<a href="#">d1d5aa1</a>	Alignment	not modelled	83.9	15 <b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
32	<a href="#">d1tgoa1</a>	Alignment	not modelled	81.0	24 <b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
33	<a href="#">d1qhta1</a>	Alignment	not modelled	80.0	16 <b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
34	<a href="#">c2gv9B_</a>	Alignment	not modelled	74.5	12 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dna polymerase; <b>PDBTitle:</b> crystal structure of the herpes simplex virus type 1 dna polymerase
35	<a href="#">d1yt3a3</a>	Alignment	not modelled	65.2	11 <b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
36	<a href="#">c3iayA_</a>	Alignment	not modelled	64.9	18 <b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase delta catalytic subunit; <b>PDBTitle:</b> ternary complex of dna polymerase delta
37	<a href="#">c2vwkA_</a>	Alignment	not modelled	61.4	22 <b>PDB header:</b> dna replication <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase; <b>PDBTitle:</b> uracil recognition in archaeal dna polymerases captured by2 x-ray crystallography. v93q polymerase variant
38	<a href="#">c4ktqA_</a>	Alignment	not modelled	58.8	17 <b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (large fragment of dna polymerase i); <b>PDBTitle:</b> binary complex of the large fragment of dna polymerase i2 from t. aquaticus bound to a primer/template dna
39	<a href="#">c2e6mA_</a>	Alignment	not modelled	53.9	12 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> werner syndrome atp-dependent helicase homolog; <b>PDBTitle:</b> structure of mouse werner exonuclease domain
40	<a href="#">c1yt3A_</a>	Alignment	not modelled	51.0	15 <b>PDB header:</b> hydrolase,translation <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease d; <b>PDBTitle:</b> crystal structure of escherichia coli rnase d, an2 exoribonuclease involved in structured rna processing
41	<a href="#">c1d5aA_</a>	Alignment	not modelled	45.4	20 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (dna polymerase); <b>PDBTitle:</b> crystal structure of an archaeobacterial dna polymerase2 d.tok. deposition of second native structure at 2.43 angstrom
42	<a href="#">d1ih7a1</a>	Alignment	not modelled	27.7	20 <b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
43	<a href="#">c2w0iA_</a>	Alignment	not modelled	17.6	10 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> twinfilin-2; <b>PDBTitle:</b> structure of c-terminal actin depolymerizing factor2 homology (adf-h) domain of human twinfilin-2
44	<a href="#">c2kd5A_</a>	Alignment	not modelled	13.2	13 <b>PDB header:</b> hormone <b>Chain:</b> A: <b>PDB Molecule:</b> actin severing and dynamics regulatory protein; <b>PDBTitle:</b> solution structure of adf/cofilin (ldcof) from leishmania donovani
45	<a href="#">d1ak7a_</a>	Alignment	not modelled	11.0	10 <b>Fold:</b> Gelsolin-like <b>Superfamily:</b> Actin depolymerizing proteins <b>Family:</b> Cofilin-like
46	<a href="#">c3hhjA_</a>	Alignment	not modelled	10.7	11 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mutator mutt protein; <b>PDBTitle:</b> crystal structure of mutator mutt from bartonella henselae
47	<a href="#">c3cymA_</a>	Alignment	not modelled	10.6	22 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein bad_0989; <b>PDBTitle:</b> crystal structure of protein bad_0989 from bifidobacterium2 adolescentis
48	<a href="#">c2d3wB_</a>	Alignment	not modelled	10.2	18 <b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable atp-dependent transporter sufcd; <b>PDBTitle:</b> crystal structure of escherichia coli sufcd, an atpase2 component of the suf iron-sulfur cluster assembly machinery
49	<a href="#">d2dk8a1</a>	Alignment	not modelled	9.6	22 <b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> RPO3F domain-like
50	<a href="#">c2xfaA_</a>	Alignment	not modelled	9.3	10 <b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> actin depolymerization factor 2; <b>PDBTitle:</b> crystal structure of plasmodium berghei actin2 depolymerization factor 2
51	<a href="#">d2hbka2</a>	Alignment	not modelled	8.5	15 <b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
52	<a href="#">c2i2qA_</a>	Alignment	not modelled	8.4	10 <b>PDB header:</b> actin-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cofilin; <b>PDBTitle:</b> fission yeast cofilin
53	<a href="#">d1q8ga_</a>	Alignment	not modelled	8.1	10 <b>Fold:</b> Gelsolin-like <b>Superfamily:</b> Actin depolymerizing proteins <b>Family:</b> Cofilin-like
54	<a href="#">d1q8ia1</a>	Alignment	not modelled	6.5	14 <b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
55	<a href="#">c3iydB_</a>	Alignment	not modelled	6.5	24 <b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> dna-directed rna polymerase subunit alpha; <b>PDBTitle:</b> three-dimensional em structure of an intact activator-

					dependent2 transcription initiation complex
56	<a href="#">d1cnua_</a>	Alignment	not modelled	5.3	10 <b>Fold:</b> Gelsolin-like <b>Superfamily:</b> Actin depolymerizing proteins <b>Family:</b> Cofilin-like
57	<a href="#">d1s5ja1</a>	Alignment	not modelled	5.3	12 <b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
58	<a href="#">c1s5jA_</a>	Alignment	not modelled	5.2	20 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase i; <b>PDBTitle:</b> insight in dna replication: the crystal structure of dna2 polymerase b1 from the archaeon sulfolobus solfataricus