
































#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2qxfa1</a>	 Alignment		100.0	100	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
2	<a href="#">dly97a1</a>	 Alignment		100.0	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="#">dlj9aa_</a>	 Alignment		100.0	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
4	<a href="#">d2f96a1</a>	 Alignment		100.0	20	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
5	<a href="#">d3b6oa1</a>	 Alignment		100.0	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
6	<a href="#">c3u6fA_</a>	 Alignment		100.0	16	<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
7	<a href="#">c3tr8A_</a>	 Alignment		100.0	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
8	<a href="#">dlw0ha_</a>	 Alignment		100.0	11	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
9	<a href="#">d2igia1</a>	 Alignment		100.0	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
10	<a href="#">c3cm6A_</a>	 Alignment		100.0	16	<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
11	<a href="#">c2gbzA_</a>	 Alignment		100.0	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="#">c2pljB_</a>	Alignment		100.0	20	<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
13	<a href="#">c2xriA_</a>	Alignment		100.0	14	<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
14	<a href="#">d2guia1</a>	Alignment		100.0	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
15	<a href="#">c1zbhA_</a>	Alignment		100.0	10	<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
16	<a href="#">c1zbuB_</a>	Alignment		100.0	11	<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
17	<a href="#">d1wlja_</a>	Alignment		99.9	14	<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		99.9	14	<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		99.8	14	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> CAF1-like ribonuclease
20	<a href="#">d2d5ra1</a>	Alignment		99.5	14	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> CAF1-like ribonuclease
21	<a href="#">c2p51A_</a>	Alignment	not modelled	99.5	17	<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="#">d1x9ma1</a>	Alignment	not modelled	99.4	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
23	<a href="#">d1kfsa1</a>	Alignment	not modelled	99.3	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
24	<a href="#">c2kzzA_</a>	Alignment	not modelled	99.2	15	<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
25	<a href="#">c1tk0A_</a>	Alignment	not modelled	99.1	16	<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
26	<a href="#">d1qhta1</a>	Alignment	not modelled	99.1	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
27	<a href="#">c2gv9B_</a>	Alignment	not modelled	99.0	15	<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
28	<a href="#">d1wn7a1</a>	Alignment	not modelled	99.0	22	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
						<b>Fold:</b> Ribonuclease H-like motif

29	<a href="#">d1tgoa1</a>	Alignment	not modelled	99.0	18	<b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
30	<a href="#">c2a1sC</a>	Alignment	not modelled	98.9	23	<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
31	<a href="#">d1d5aa1</a>	Alignment	not modelled	98.9	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
32	<a href="#">d2hhva1</a>	Alignment	not modelled	98.9	13	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
33	<a href="#">c3d45B</a>	Alignment	not modelled	98.8	20	<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
34	<a href="#">c1njzA</a>	Alignment	not modelled	98.8	17	<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
35	<a href="#">c3iayA</a>	Alignment	not modelled	98.8	17	<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
36	<a href="#">c2vwkA</a>	Alignment	not modelled	98.6	17	<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
37	<a href="#">d1s5ja1</a>	Alignment	not modelled	98.6	13	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
38	<a href="#">d1ih7a1</a>	Alignment	not modelled	98.6	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
39	<a href="#">c1d5aA</a>	Alignment	not modelled	98.5	19	<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
40	<a href="#">d1noya</a>	Alignment	not modelled	98.4	20	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
41	<a href="#">c1s5jA</a>	Alignment	not modelled	98.3	12	<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
42	<a href="#">c4ktqA</a>	Alignment	not modelled	98.3	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
43	<a href="#">d1q8ia1</a>	Alignment	not modelled	98.3	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
44	<a href="#">c2dtuA</a>	Alignment	not modelled	98.2	16	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase; <b>PDBTitle:</b> crystal structure of the beta hairpin loop deletion variant2 of rb69 gp43 in complex with dna containing an abasic site3 analog
45	<a href="#">c1q8iA</a>	Alignment	not modelled	98.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase ii; <b>PDBTitle:</b> crystal structure of escherichia coli dna polymerase ii
46	<a href="#">c1yt3A</a>	Alignment	not modelled	98.0	18	<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
47	<a href="#">d1yt3a3</a>	Alignment	not modelled	97.9	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
48	<a href="#">d2hbka2</a>	Alignment	not modelled	97.7	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
49	<a href="#">c2e6mA</a>	Alignment	not modelled	97.5	14	<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
50	<a href="#">c2hbka</a>	Alignment	not modelled	97.4	19	<b>PDB header:</b> hydrolase, gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> exosome complex exonuclease rrp6; <b>PDBTitle:</b> 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	<a href="#">c3f2cA</a>	Alignment	not modelled	97.2	14	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> geobacillus kaustophilus dna polc; <b>PDBTitle:</b> dna polymerase polc from geobacillus kaustophilus complex with dna,2 dgtp and mn
52	<a href="#">c3sahA</a>	Alignment	not modelled	96.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> exosome component 10; <b>PDBTitle:</b> crystal structure of the human rrp6 catalytic domain with y436a2 mutation in the catalytic site
53	<a href="#">c3cymA</a>	Alignment	not modelled	95.9	25	<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
54	<a href="#">c3ikmD</a>	Alignment	not modelled	93.9	24	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> dna polymerase subunit gamma-1; <b>PDBTitle:</b> crystal structure of human mitochondrial dna polymerase2 holoenzyme
						<b>Fold:</b> Ribonuclease H-like motif

55	<a href="#">d1vk0a_</a>	Alignment	not modelled	86.8	11	<b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
56	<a href="#">c1cmwA_</a>	Alignment	not modelled	83.5	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (dna polymerase i); <b>PDBTitle:</b> crystal structure of taq dna-polymerase shows a new2 orientation for the structure-specific nuclease domain
57	<a href="#">d2py5a1</a>	Alignment	not modelled	58.5	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
58	<a href="#">c3uo9B_</a>	Alignment	not modelled	35.8	11	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> glutaminase kidney isoform, mitochondrial; <b>PDBTitle:</b> crystal structure of human gac in complex with glutamate and bptes
59	<a href="#">c2ex3l_</a>	Alignment	not modelled	19.2	17	<b>PDB header:</b> transferase/replication <b>Chain:</b> I: <b>PDB Molecule:</b> dna polymerase; <b>PDBTitle:</b> bacteriophage phi29 dna polymerase bound to terminal protein
60	<a href="#">d1m0da_</a>	Alignment	not modelled	14.2	26	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> Endonuclease I (Holliday junction resolvase)
61	<a href="#">c2r6cG_</a>	Alignment	not modelled	11.7	13	<b>PDB header:</b> replication <b>Chain:</b> G: <b>PDB Molecule:</b> dnag primase, helicase binding domain; <b>PDBTitle:</b> crystal form bh2
62	<a href="#">c2d3wB_</a>	Alignment	not modelled	8.8	13	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable atp-dependent transporter sufc; <b>PDBTitle:</b> crystal structure of escherichia coli sufc, an atpase2 compenent of the suf iron-sulfur cluster assembly machinery
63	<a href="#">c2r6fA_</a>	Alignment	not modelled	6.4	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> excinuclease abc subunit a; <b>PDBTitle:</b> crystal structure of bacillus stearothermophilus uvra
64	<a href="#">c3r03B_</a>	Alignment	not modelled	6.3	9	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> nudix hydrolase; <b>PDBTitle:</b> the crystal structure of nudix hydrolase from rhodospirillum rubrum
65	<a href="#">c2jo8B_</a>	Alignment	not modelled	6.0	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase 4; <b>PDBTitle:</b> solution structure of c-terminal domain of human mammalian2 sterile 20-like kinase 1 (mst1)
66	<a href="#">d2fmme1</a>	Alignment	not modelled	6.0	28	<b>Fold:</b> ENT-like <b>Superfamily:</b> ENT-like <b>Family:</b> Emsy N terminal (ENT) domain-like
67	<a href="#">d1j6ua3</a>	Alignment	not modelled	5.9	9	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> MurD-like peptide ligases, catalytic domain <b>Family:</b> MurCDEF
68	<a href="#">d1uz3a1</a>	Alignment	not modelled	5.8	28	<b>Fold:</b> ENT-like <b>Superfamily:</b> ENT-like <b>Family:</b> Emsy N terminal (ENT) domain-like
69	<a href="#">c2fmmE_</a>	Alignment	not modelled	5.8	28	<b>PDB header:</b> transcription <b>Chain:</b> E: <b>PDB Molecule:</b> protein emsy; <b>PDBTitle:</b> crystal structure of emsy-hp1 complex
70	<a href="#">c3e0dA_</a>	Alignment	not modelled	5.7	9	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iii subunit alpha; <b>PDBTitle:</b> insights into the replisome from the crystral structure of2 the ternary complex of the eubacterial dna polymerase iii3 alpha-subunit
71	<a href="#">c3hhjA_</a>	Alignment	not modelled	5.7	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