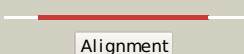
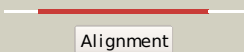
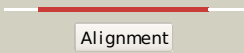
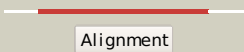
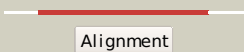
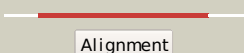
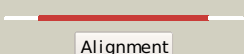
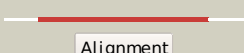
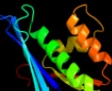


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1jl1a_	 Alignment		100.0	97	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
2	d1jl2a_	 Alignment		100.0	74	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
3	c2e4lA_	 Alignment		100.0	70	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease hi; PDBTitle: thermodynamic and structural analysis of thermolabile rnaase hi from2 shewanella oneidensis mr-1
4	d1wsib_	 Alignment		100.0	99	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
5	d1rila_	 Alignment		100.0	56	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
6	c3h08B_	 Alignment		100.0	45	PDB header: hydrolase Chain: B: PDB Molecule: rnh (ribonuclease h); PDBTitle: crystal structure of the ribonuclease h1 from chlorobium2 tepidum
7	c2qkkl_	 Alignment		100.0	35	PDB header: hydrolase/dna/rna Chain: I: PDB Molecule: ribonuclease h1; PDBTitle: human rnaase h catalytic domain mutant d210n in complex with2 14-mer rna/dna hybrid
8	c2hb5A_	 Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: reverse transcriptase/ribonuclease h; PDBTitle: crystal structure of the moloney murine leukemia virus2 rnaase h domain
9	d1eeta1	 Alignment		99.9	27	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
10	d1mu2a1	 Alignment		99.9	26	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
11	d1jl1aa1	 Alignment		99.9	26	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H

12	dlzbfa1	Alignment		99.9	21	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
13	c2kq2A_	Alignment		99.9	22	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease h-related protein; PDBTitle: solution nmr structure of the apo form of a ribonuclease h2 domain of protein dsy1790 from desulfotobacterium3 hafniense, northeast structural genomics target dhr1a
14	c2rpiA_	Alignment		99.9	63	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease h; PDBTitle: the nmr structure of the submillisecond folding2 intermediate of the thermus thermophilus ribonuclease h
15	d1o1wa_	Alignment		99.9	26	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
16	c3hstD_	Alignment		99.9	31	PDB header: hydrolase Chain: D: PDB Molecule: protein rv2228c/mt2287; PDBTitle: n-terminal rnase h domain of rv2228c from mycobacterium tuberculosis2 as a fusion protein with maltose binding protein
17	c1mu2A_	Alignment		99.9	25	PDB header: transferase Chain: A: PDB Molecule: hiv-2 rt; PDBTitle: crystal structure of hiv-2 reverse transcriptase
18	c2ehgA_	Alignment		99.8	24	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease hi; PDBTitle: crystal structure of hyperthermophilic archaeal rnase hi
19	d1s9ga1	Alignment		99.8	26	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
20	d1s1ta1	Alignment		99.8	25	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
21	c1rthA_	Alignment	not modelled	99.6	26	PDB header: nucleotidyltransferase Chain: A: PDB Molecule: hiv-1 reverse transcriptase; PDBTitle: high resolution structures of hiv-1 rt from four rt-2 inhibitor complexes
22	c2opqA_	Alignment	not modelled	99.2	27	PDB header: transferase Chain: A: PDB Molecule: reverse transcriptase/ribonuclease h; PDBTitle: crystal structure of l100i mutant hiv-1 reverse2 transcriptase in complex with gw420867x.
23	d1rw3a_	Alignment	not modelled	56.1	8	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Reverse transcriptase
24	c2hxA_	Alignment	not modelled	22.7	17	PDB header: biosynthetic protein Chain: A: PDB Molecule: diaminohydroxyphosphoribosylaminopyrimidine deaminase/ 5- PDBTitle: crystal structure of a diaminohydroxyphosphoribosylaminopyrimidine2 deaminase/ 5-amino-6-(5-phosphoribosylamino)uracil reductase (tm1828)3 from thermotoga maritima at 1.80 a resolution
25	d2b3za2	Alignment	not modelled	13.1	16	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
26	c3hl4B_	Alignment	not modelled	11.5	23	PDB header: transferase Chain: B: PDB Molecule: choline-phosphate cytidyltransferase a; PDBTitle: crystal structure of a mammalian ctp:phosphocholine2 cytidyltransferase with cdp-choline
27	d1ynja1	Alignment	not modelled	9.4	63	Fold: DCoH-like Superfamily: RBP11-like subunits of RNA polymerase Family: RNA polymerase alpha subunit dimerisation domain
						Fold: Rubredoxin-like

28	d1nuia2	Alignment	not modelled	9.4	38	Superfamily: Zinc beta-ribbon Family: DNA primase zinc finger
29	d2g84a1	Alignment	not modelled	9.2	19	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
30	d1mr4a_	Alignment	not modelled	8.2	63	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Plant defensins
31	d1cw0a_	Alignment	not modelled	8.1	36	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Very short patch repair (VSR) endonuclease
32	d1vsra_	Alignment	not modelled	7.8	36	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Very short patch repair (VSR) endonuclease
33	c2d5nB_	Alignment	not modelled	7.3	22	PDB header: hydrolase, oxidoreductase Chain: B: PDB Molecule: riboflavin biosynthesis protein ribd; PDBTitle: crystal structure of a bifunctional deaminase and reductase2 involved in riboflavin biosynthesis
34	d1smya1	Alignment	not modelled	7.3	63	Fold: DCoH-like Superfamily: RBP11-like subunits of RNA polymerase Family: RNA polymerase alpha subunit dimerisation domain