Phyre2

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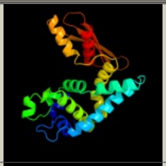
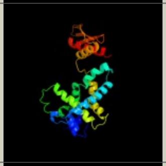
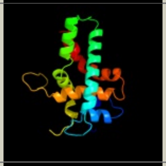
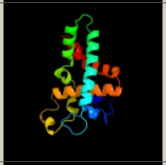
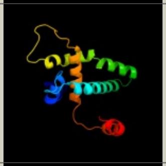
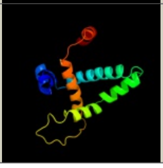
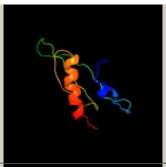
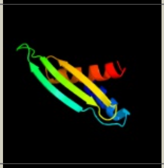
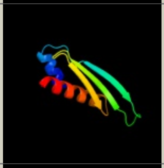
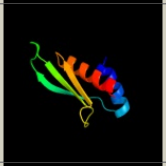
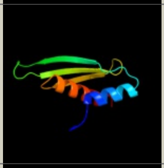
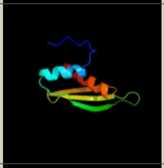
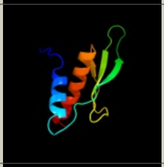
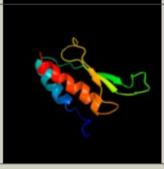
Description	P0A7Y0
Date	Thu Jan 5 11:06:26 GMT 2012
Unique Job ID	5b6a075d7128e011

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1o0wB_	Alignment		100.0	36	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ribonuclease iii; **PDBTitle:** crystal structure of ribonuclease iii (tm1102) from2 thermotoga maritima at 2.0 a resolution
2	c1yywB_	Alignment		100.0	38	**PDB header:**hydrolase/rna **Chain:** B: **PDB Molecule:**ribonuclease iii; **PDBTitle:** crystal structure of rnase iii from aquifex aeolicus2 complexed with double stranded rna at 2.8-angstrom3 resolution
3	c3c4tA_	Alignment		100.0	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoribonuclease dicer; **PDBTitle:** structure of rnaseiiib and dsrna binding domains of mouse dicer
4	d1o0wa1	Alignment		100.0	36	**Fold:**RNase III domain-like **Superfamily:**RNase III domain-like **Family:**RNase III catalytic domain-like
5	c3o2rD_	Alignment		100.0	36	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**ribonuclease iii; **PDBTitle:** structural flexibility in region involved in dimer formation of2 nuclease domain of ribonuclease iii (rnc) from campylobacter jejuni
6	c3n3wA_	Alignment		100.0	37	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease iii; **PDBTitle:** 2.2 angstrom resolution crystal structure of nuclease domain of2 ribonuclease iii (rnc) from campylobacter jejuni
7	c2eb1B_	Alignment		100.0	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endoribonuclease dicer; **PDBTitle:** crystal structure of the c-terminal rnase iii domain of human dicer
8	d2nuga1	Alignment		100.0	34	**Fold:**RNase III domain-like **Superfamily:**RNase III domain-like **Family:**RNase III catalytic domain-like
9	c2a11A_	Alignment		100.0	42	**PDB header:**transcription,translation,hydrolase **Chain:** A: **PDB Molecule:**ribonuclease iii; **PDBTitle:** crystal structure of nuclease domain of ribonuclase iii from2 mycobacterium tuberculosis
10	c3rv1B_	Alignment		100.0	26	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**k. polysporus dcr1; **PDBTitle:** crystal structure of the n-terminal and rnase iii domains of k.2 polysporus dcr1 e224q mutant
11	c3rv0C_	Alignment		100.0	27	**PDB header:**rna binding protein **Chain:** C: **PDB Molecule:**k. polysporus dcr1; **PDBTitle:** crystal structure of k. polysporus dcr1 without the c-terminal dsrbd

12	c2khxA_	Alignment		99.4	35	**PDB header:**gene regulation,nuclear protein **Chain:** A: **PDB Molecule:**ribonuclease 3; **PDBTitle:** drosha double-stranded rna binding motif
13	d1uhza_	Alignment		99.4	31	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
14	d1di2a_	Alignment		99.4	38	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
15	d1o0wa2	Alignment		99.4	35	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
16	c3adlA_	Alignment		99.4	32	**PDB header:**gene regulation/rna **Chain:** A: **PDB Molecule:**risc-loading complex subunit tarbp2; **PDBTitle:** structure of trbp2 and its molecule implications for mirna processing
17	d2cpna1	Alignment		99.4	34	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
18	c3adjA_	Alignment		99.4	25	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**f21m12.9 protein; **PDBTitle:** structure of arabidopsis hyl1 and its molecular implications for mirna2 processing
19	d1x49a1	Alignment		99.4	26	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
20	d1qu6a1	Alignment		99.4	29	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
21	d2nuga2	Alignment	not modelled	99.4	38	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
22	c2l2nA_	Alignment	not modelled	99.3	38	**PDB header:**rna binding protein, plant protein **Chain:** A: **PDB Molecule:**hyponastic leave 1; **PDBTitle:** backbone 1h, 13c, and 15n chemical shift assignments for the first2 dsrbd of protein hyl1
23	d1x47a1	Alignment	not modelled	99.3	25	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
24	d1stua_	Alignment	not modelled	99.3	27	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
25	d2dixa1	Alignment	not modelled	99.3	29	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
26	c2qvwA_	Alignment	not modelled	99.3	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glp_546_48378_50642; **PDBTitle:** structure of giardia dicer refined against twinned data
27	d1qu6a2	Alignment	not modelled	99.2	22	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
28	c3adiC_	Alignment	not modelled	99.2	40	**PDB header:**gene regulation/rna **Chain:** C: **PDB Molecule:**f21m12.9 protein; **PDBTitle:** structure of arabidopsis hyl1 and its molecular implications for mirna2 processing
29	d1uila_	Alignment	not modelled	99.2	24	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like

						Family: Double-stranded RNA-binding domain (dsRBD)
30	d1ekza_	Alignment	not modelled	99.2	26	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
31	c2yt4A_	Alignment	not modelled	99.2	27	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein dgcr8; **PDBTitle:** crystal structure of human dgcr8 core
32	d1x48a1	Alignment	not modelled	99.2	21	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
33	c1t4oA_	Alignment	not modelled	99.2	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease iii; **PDBTitle:** crystal structure of rnt1p dsrbd
34	d1t4oa_	Alignment	not modelled	99.2	21	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
35	d1whna_	Alignment	not modelled	99.2	29	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
36	c1qu6A_	Alignment	not modelled	99.2	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein kinase pkr; **PDBTitle:** structure of the double-stranded rna-binding domain of the2 protein kinase pkr reveals the molecular basis of its3 dsrna-mediated activation
37	c3llhB_	Alignment	not modelled	99.2	35	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**risc-loading complex subunit tarbp2; **PDBTitle:** crystal structure of the first dsrbd of tar rna-binding protein 2
38	d1t4na_	Alignment	not modelled	99.1	19	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
39	c2l33A_	Alignment	not modelled	99.1	29	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**interleukin enhancer-binding factor 3; **PDBTitle:** solution nmr structure of drbm 2 domain of interleukin enhancer-2 binding factor 3 from homo sapiens, northeast structural genomics3 consortium target hr4527e
40	d2dmya1	Alignment	not modelled	99.1	24	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
41	d1t4lb_	Alignment	not modelled	99.1	24	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
42	d2b7va1	Alignment	not modelled	99.1	30	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
43	d2b7ta1	Alignment	not modelled	99.0	28	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
44	c2l3jA_	Alignment	not modelled	99.0	28	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**double-stranded rna-specific editase 1; **PDBTitle:** the solution structure of the adar2 dsrbm-rna complex reveals a2 sequence-specific read out of the minor groove
45	d1u61a_	Alignment	not modelled	98.6	19	**Fold:**RNase III domain-like **Superfamily:**RNase III domain-like **Family:**RNase III catalytic domain-like
46	d1whqa_	Alignment	not modelled	98.5	22	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
47	c2gslE_	Alignment	not modelled	98.1	17	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**hypothetical protein; **PDBTitle:** x-ray crystal structure of protein fn1578 from fusobacterium2 nucleatum. northeast structural genomics consortium target nr1.
48	c3htxA_	Alignment	not modelled	95.7	25	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**hen1; **PDBTitle:** crystal structure of small rna methyltransferase hen1
49	c2db2A_	Alignment	not modelled	95.6	17	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**kiaa0890 protein; **PDBTitle:** solution structure of the double-stranded rna binding2 domain in kiaa0890 protein
50	c2kouA_	Alignment	not modelled	87.4	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dicer-like protein 4; **PDBTitle:** dicer like protein
51	d1ztda1	Alignment	not modelled	65.6	27	**Fold:**RNase III domain-like **Superfamily:**RNase III domain-like **Family:**PF0609-like
52	c3iwfA_	Alignment	not modelled	30.7	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcription regulator rpir family; **PDBTitle:** the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
53	c3f6hA_	Alignment	not modelled	29.5	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alpha-isopropylmalate synthase; **PDBTitle:** crystal structure of the regulatory domain of licms in2 complexed with isoleucine - type iii
54	c1p6gE_	Alignment	not modelled	17.3	22	**PDB header:**ribosome **Chain:** E: **PDB Molecule:**30s ribosomal protein s5; **PDBTitle:** real space refined coordinates of the 30s subunit fitted2 into the low resolution cryo-em map of the ef-g.gtp state3 of e. coli 70s ribosome
55	c1eg0B_	Alignment	not modelled	15.3	24	**PDB header:**ribosome **PDB COMPND:**

56	d1vkza1	Alignment	not modelled	14.2	26	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
57	c2qv6D_	Alignment	not modelled	14.0	26	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**gtp cyclohydrolase iii; **PDBTitle:** gtp cyclohydrolase iii from m. jannaschii (mj0145)2 complexed with gtp and metal ions
58	c3bbnE_	Alignment	not modelled	13.8	24	**PDB header:**ribosome **Chain:** E: **PDB Molecule:**ribosomal protein s5; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
59	c2ow8f_	Alignment	not modelled	13.0	16	**PDB header:**ribosome **Chain:** F: **PDB Molecule:** **PDBTitle:** crystal structure of a 70s ribosome-trna complex reveals functional2 interactions and rearrangements. this file, 2ow8, contains the 30s3 ribosome subunit, two trna, and mrna molecules. 50s ribosome subunit4 is in the file 1vsa.
60	d1gsoa1	Alignment	not modelled	12.8	18	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
61	d2qale2	Alignment	not modelled	12.7	22	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Ribosomal S5 protein, N-terminal domain
62	c2zkqe_	Alignment	not modelled	12.6	14	**PDB header:**ribosomal protein/rna **Chain:** E: **PDB Molecule:**rna expansion segment es6 part ii; **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
63	c1kjkA_	Alignment	not modelled	12.3	18	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** solution structure of the lambda integrase amino-terminal2 domain
64	d1z1ba1	Alignment	not modelled	11.6	18	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**lambda integrase N-terminal domain
65	c3kwlA_	Alignment	not modelled	11.6	21	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a hypothetical protein from helicobacter pylori
66	c2rpiA_	Alignment	not modelled	11.4	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease h; **PDBTitle:** the nmr structure of the submillisecond folding2 intermediate of the thermus thermophilus ribonuclease h
67	d1sr9a3	Alignment	not modelled	11.2	18	**Fold:**2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain **Superfamily:**2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain **Family:**2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain
68	d1pkpa2	Alignment	not modelled	10.9	24	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Ribosomal S5 protein, N-terminal domain
69	d2o3fa1	Alignment	not modelled	10.8	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**RpiR-like
70	c2o3fC_	Alignment	not modelled	10.8	7	**PDB header:**transcription **Chain:** C: **PDB Molecule:**putative hth-type transcriptional regulator ybbh; **PDBTitle:** structural genomics, the crystal structure of the n-2 terminal domain of the putative transcriptional regulator3 ybbh from bacillus subtilis subsp. subtilis str. 168.
71	d2uube2	Alignment	not modelled	9.3	16	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Ribosomal S5 protein, N-terminal domain
72	d1w5fa2	Alignment	not modelled	8.4	27	**Fold:**Bacillus chorismate mutase-like **Superfamily:**Tubulin C-terminal domain-like **Family:**Tubulin, C-terminal domain
73	c1s1hE_	Alignment	not modelled	6.8	16	**PDB header:**ribosome **Chain:** E: **PDB Molecule:**40s ribosomal protein s2; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
74	c2rqlA_	Alignment	not modelled	6.5	14	**PDB header:**translation **Chain:** A: **PDB Molecule:**probable sigma-54 modulation protein; **PDBTitle:** solution structure of the e. coli ribosome hibernation2 promoting factor hpf
75	d1w7ca3	Alignment	not modelled	6.2	32	**Fold:**Cystatin-like **Superfamily:**Amine oxidase N-terminal region **Family:**Amine oxidase N-terminal region
76	c3lhhA_	Alignment	not modelled	5.7	46	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**cbs domain protein; **PDBTitle:** the crystal structure of cbs domain protein from shewanella2 oneidensis mr-1.
77	d1kxpd2	Alignment	not modelled	5.2	13	**Fold:**Serum albumin-like **Superfamily:**Serum albumin-like **Family:**Serum albumin-like