Phyre2

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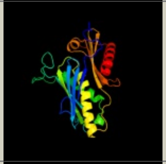
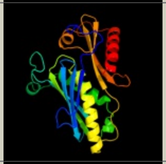
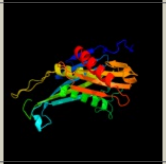
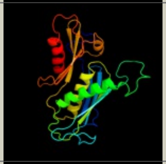
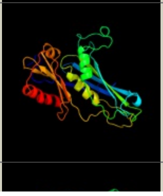
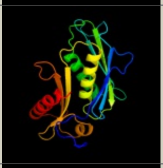
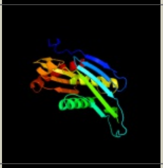
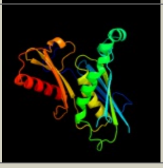
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1udsA_	Alignment		100.0	56	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribonuclease ph; **PDBTitle:** crystal structure of the trna processing enzyme rnase ph r126a mutant2 from aquifex aeolicus
2	c3dd6A_	Alignment		100.0	56	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribonuclease ph; **PDBTitle:** crystal structure of rph, an exoribonuclease from bacillus2 anthracis at 1.7 a resolution
3	c1r6mA_	Alignment		100.0	68	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribonuclease ph; **PDBTitle:** crystal structure of the trna processing enzyme rnase ph from2 pseudomonas aeruginosa in complex with phosphate
4	c3b4tC_	Alignment		100.0	56	**PDB header:**transferase **Chain:** C: **PDB Molecule:**ribonuclease ph; **PDBTitle:** crystal structure of mycobacterium tuberculosis rnase ph, the2 mycobacterium tuberculosis structural genomics consortium target3 rv1340
5	c2pnzB_	Alignment		100.0	26	**PDB header:**hydrolase/hydrolase **Chain:** B: **PDB Molecule:**probable exosome complex exonuclease 2; **PDBTitle:** crystal structure of the p. abyssi exosome rnase ph ring2 complexed with udp and gmp
6	c2wnrC_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**probable exosome complex exonuclease 2; **PDBTitle:** the structure of methanothermobacter thermautotrophicus2 exosome core assembly
7	c2ba0I_	Alignment		100.0	23	**PDB header:**rna binding protein **Chain:** I: **PDB Molecule:**archeal exosome rna binding protein rrp42; **PDBTitle:** archaeal exosome core
8	c2c37L_	Alignment		100.0	30	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**probable exosome complex exonuclease 1; **PDBTitle:** rnase ph core of the archaeal exosome in complex with u82 rna
9	c2nn6B_	Alignment		100.0	26	**PDB header:**hydrolase/transferase **Chain:** B: **PDB Molecule:**exosome complex exonuclease rrp41; **PDBTitle:** structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
10	c2wnrB_	Alignment		100.0	33	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable exosome complex exonuclease 1; **PDBTitle:** the structure of methanothermobacter thermautotrophicus2 exosome core assembly
11	c2nn6C_	Alignment		100.0	22	**PDB header:**hydrolase/transferase **Chain:** C: **PDB Molecule:**exosome complex exonuclease rrp43; **PDBTitle:** structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40

12	c2po2A_	Alignment		100.0	32	**PDB header:**hydrolase/hydrolase **Chain:** A: **PDB Molecule:**probable exosome complex exonuclease 1; **PDBTitle:** crystal structure of the p. abyssi exosome rnase ph ring2 complexed with cdp
13	c2br2G_	Alignment		100.0	26	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**exosome complex exonuclease 2; **PDBTitle:** rnase ph core of the archaeal exosome
14	c2nn6E_	Alignment		100.0	17	**PDB header:**hydrolase/transferase **Chain:** E: **PDB Molecule:**exosome complex exonuclease rrp42; **PDBTitle:** structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
15	c2ba1D_	Alignment		100.0	32	**PDB header:**rna binding protein **Chain:** D: **PDB Molecule:**archaeal exosome complex exonuclease rrp41; **PDBTitle:** archaeal exosome core
16	c3hkmB_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**os03g0854200 protein; **PDBTitle:** crystal structure of rice(oryza sativa) rrp46
17	c2wp8B_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**exosome complex component ski6; **PDBTitle:** yeast rrp44 nuclease
18	c1e3hA_	Alignment		100.0	22	**PDB header:**polyribonucleotide transferase **Chain:** A: **PDB Molecule:**guanosine pentaphosphate synthetase; **PDBTitle:** semet derivative of streptomyces antibioticus pnpase/gpsi2 enzyme
19	c2wp8A_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exosome complex component rrp45; **PDBTitle:** yeast rrp44 nuclease
20	c3cdiA_	Alignment		100.0	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polynucleotide phosphorylase; **PDBTitle:** crystal structure of e. coli pnpase
21	c3cdjA_	Alignment	not modelled	100.0	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polynucleotide phosphorylase; **PDBTitle:** crystal structure of the e. coli kh/s1 domain truncated2 pnpase
22	c2nn6F_	Alignment	not modelled	100.0	25	**PDB header:**hydrolase/transferase **Chain:** F: **PDB Molecule:**exosome component 6; **PDBTitle:** structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
23	c2nn6D_	Alignment	not modelled	100.0	22	**PDB header:**hydrolase/transferase **Chain:** D: **PDB Molecule:**exosome complex exonuclease rrp46; **PDBTitle:** structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
24	d1udsa1	Alignment	not modelled	100.0	59	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Ribonuclease PH domain 1-like
25	d1r6la1	Alignment	not modelled	100.0	70	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Ribonuclease PH domain 1-like
26	d2ba0g1	Alignment	not modelled	100.0	25	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Ribonuclease PH domain 1-like
27	d2nn6c1	Alignment	not modelled	100.0	20	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Ribonuclease PH domain 1-like
28	d2je6b1	Alignment	not modelled	100.0	30	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Ribonuclease PH domain 1-like
29	d2nn6b1	Alignment	not modelled	100.0	25	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Ribonuclease PH domain 1-like

30	d2ba0d1	Alignment	not modelled	100.0	34	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Ribonuclease PH domain 1-like
31	d2je6a1	Alignment	not modelled	100.0	29	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Ribonuclease PH domain 1-like
32	d2nn6e1	Alignment	not modelled	100.0	19	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Ribonuclease PH domain 1-like
33	d2nn6a1	Alignment	not modelled	100.0	24	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Ribonuclease PH domain 1-like
34	d1e3ha3	Alignment	not modelled	100.0	20	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Ribonuclease PH domain 1-like
35	d1oysa1	Alignment	not modelled	100.0	64	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Ribonuclease PH domain 1-like
36	d2nn6f1	Alignment	not modelled	100.0	30	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Ribonuclease PH domain 1-like
37	d1e3ha2	Alignment	not modelled	100.0	15	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Ribonuclease PH domain 1-like
38	d2nn6d1	Alignment	not modelled	100.0	24	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Ribonuclease PH domain 1-like
39	c3krnB_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein c14a4.5, confirmed by transcript evidence; **PDBTitle:** crystal structure of c. elegans cell-death-related nuclease 5(crn-5)
40	d2je6a2	Alignment	not modelled	99.7	22	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
41	d2ba0g2	Alignment	not modelled	99.7	19	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
42	d2nn6a2	Alignment	not modelled	99.6	15	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
43	d1oysa2	Alignment	not modelled	99.6	48	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
44	d2nn6e2	Alignment	not modelled	99.6	12	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
45	d2nn6c2	Alignment	not modelled	99.6	18	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
46	d1r6la2	Alignment	not modelled	99.6	60	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
47	d1udsa2	Alignment	not modelled	99.6	51	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
48	d2je6b2	Alignment	not modelled	99.4	28	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
49	d2nn6d2	Alignment	not modelled	99.4	18	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
50	d2nn6b2	Alignment	not modelled	99.4	25	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
51	d2br2b2	Alignment	not modelled	99.4	29	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
52	d2ba0d2	Alignment	not modelled	99.3	29	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
53	d2nn6f2	Alignment	not modelled	98.9	21	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
54	d1e3ha5	Alignment	not modelled	97.9	27	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
55	d1e3ha6	Alignment	not modelled	96.7	24	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
56	d1puga_	Alignment	not modelled	26.6	16	**Fold:**YbaB-like **Superfamily:**YbaB-like **Family:**YbaB-like
						Fold: YbaB-like

57	d1j8ba_	Alignment	not modelled	19.6	11	**Superfamily:**YbaB-like **Family:**YbaB-like
58	c3otbB_	Alignment	not modelled	15.6	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna(his) guanylyltransferase; **PDBTitle:** crystal structure of human trnahis guanylyltransferase (thg1) - dgtp2 complex
59	c1ybxA_	Alignment	not modelled	14.2	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** conserved hypothetical protein cth-383 from clostridium thermocellum
60	c2qm6C_	Alignment	not modelled	11.6	22	**PDB header:**transferase **Chain:** C: **PDB Molecule:**gamma-glutamyltranspeptidase; **PDBTitle:** crystal structure of helicobacter pylori gamma-glutamyltranspeptidase2 in complex with glutamate
61	c3g9kD_	Alignment	not modelled	11.6	33	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**capsule biosynthesis protein capd; **PDBTitle:** crystal structure of bacillus anthracis transpeptidase enzyme capd
62	c2v36A_	Alignment	not modelled	11.4	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gamma-glutamyltranspeptidase large chain; **PDBTitle:** crystal structure of gamma-glutamyl transferase from2 bacillus subtilis
63	c2z8jA_	Alignment	not modelled	11.3	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gamma-glutamyltranspeptidase; **PDBTitle:** crystal structure of escherichia coli gamma-2 glutamyltranspeptidase in complex with azaserine prepared3 in the dark
64	c3me8B_	Alignment	not modelled	10.1	29	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of putative electron transfer protein aq_2194 from2 aquifex aeolicus vf5
65	d2nlza1	Alignment	not modelled	8.4	33	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Gamma-glutamyltranspeptidase-like
66	d2gkpa1	Alignment	not modelled	8.3	18	**Fold:**NMB0488-like **Superfamily:**NMB0488-like **Family:**NMB0488-like
67	c2e0wA_	Alignment	not modelled	6.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gamma-glutamyltranspeptidase; **PDBTitle:** t391a precursor mutant protein of gamma-glutamyltranspeptidase from2 escherichia coli
68	d1qq2a_	Alignment	not modelled	6.7	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
69	d1pugb_	Alignment	not modelled	6.5	17	**Fold:**YbaB-like **Superfamily:**YbaB-like **Family:**YbaB-like
70	d1yexa1	Alignment	not modelled	6.2	26	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
71	d1jfua_	Alignment	not modelled	6.0	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
72	d2i3oa1	Alignment	not modelled	5.9	17	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Gamma-glutamyltranspeptidase-like
73	c3fw2A_	Alignment	not modelled	5.1	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol-disulfide oxidoreductase; **PDBTitle:** c-terminal domain of putative thiol-disulfide oxidoreductase from2 bacteroides thetaiotaomicron.
74	c2p5qA_	Alignment	not modelled	5.0	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione peroxidase 5; **PDBTitle:** crystal structure of the poplar glutathione peroxidase 5 in2 the reduced form