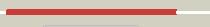
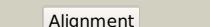
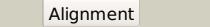
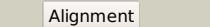
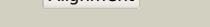
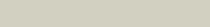
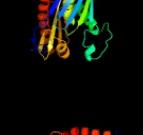
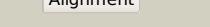
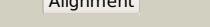
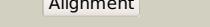
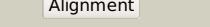
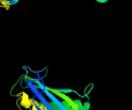


# Phyre<sup>2</sup>

Email	mdejesus@rockefeller.edu
Description	RVBD1340_(rph)_1506761_1507540
Date	Wed Jul 31 22:05:44 BST 2019
Unique Job ID	0b722a498f47549a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3b4tC_</a>			100.0	99	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> ribonuclease ph; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis rna ph, the2 mycobacterium tuberculosis structural genomics consortium target3 rv1340
2	<a href="#">c1udsA_</a>			100.0	54	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease ph; <b>PDBTitle:</b> crystal structure of the tRNA processing enzyme rna ph r126a mutant2 from aquifex aeolicus
3	<a href="#">c1r6mA_</a>			100.0	56	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease ph; <b>PDBTitle:</b> crystal structure of the tRNA processing enzyme rna ph from2 pseudomonas aeruginosa in complex with phosphate
4	<a href="#">c3dd6A_</a>			100.0	52	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease ph; <b>PDBTitle:</b> crystal structure of rph, an exoribonuclease from bacillus anthracis2 at 1.7 a resolution
5	<a href="#">c2c37L_</a>			100.0	31	<b>PDB header:</b> hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> probable exosome complex exonuclease 1; <b>PDBTitle:</b> rna ph core of the archaeal exosome in complex with u82 rna
6	<a href="#">c2pnzB_</a>			100.0	23	<b>PDB header:</b> hydrolase/hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable exosome complex exonuclease 2; <b>PDBTitle:</b> crystal structure of the p. abyssi exosome rna ph ring2 complexed with udp and gmp
7	<a href="#">c2po2A_</a>			100.0	30	<b>PDB header:</b> hydrolase/hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable exosome complex exonuclease 1; <b>PDBTitle:</b> crystal structure of the p. abyssi exosome rna ph ring2 complexed with cdp
8	<a href="#">c2wnrC_</a>			100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> probable exosome complex exonuclease 2; <b>PDBTitle:</b> the structure of methanothermobacter thermautotrophicus2 exosome core assembly
9	<a href="#">c2nn6C_</a>			100.0	20	<b>PDB header:</b> hydrolase/transferase <b>Chain:</b> C: <b>PDB Molecule:</b> exosome complex exonuclease rrp43; <b>PDBTitle:</b> structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
10	<a href="#">c2nn6A_</a>			100.0	24	<b>PDB header:</b> hydrolase/transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polymyositis/scleroderma autoantigen 1; <b>PDBTitle:</b> structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
11	<a href="#">c2nn6B_</a>			100.0	25	<b>PDB header:</b> hydrolase/transferase <b>Chain:</b> B: <b>PDB Molecule:</b> exosome complex exonuclease rrp41; <b>PDBTitle:</b> structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40

12	<a href="#">c2wnrB</a>	Alignment		100.0	33	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable exosome complex exonuclease 1; <b>PDBTitle:</b> the structure of methanothermobacter thermoautotrophicus2 exosome core assembly
13	<a href="#">c2ba1D</a>	Alignment		100.0	31	<b>PDB header:</b> rna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> archaeal exosome complex exonuclease rrp41; <b>PDBTitle:</b> archaeal exosome core
14	<a href="#">c6d6kB</a>	Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> polyribonucleotide nucleotidyltransferase; <b>PDBTitle:</b> structure of polyribonucleotide nucleotidyltransferase from2 acinetobacter baumannii
15	<a href="#">c4aidC</a>	Alignment		100.0	21	<b>PDB header:</b> transferase/peptide <b>Chain:</b> C: <b>PDB Molecule:</b> polyribonucleotide nucleotidyltransferase; <b>PDBTitle:</b> crystal structure of c. crescentus pnpase bound to rnase e2 recognition peptide
16	<a href="#">c6d6rF</a>	Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> exosome complex component mtr3; <b>PDBTitle:</b> human nuclear exosome-mtr4 rna complex - composite map after focused2 reconstruction
17	<a href="#">c2nn6E</a>	Alignment		100.0	17	<b>PDB header:</b> hydrolase/transferase <b>Chain:</b> E: <b>PDB Molecule:</b> exosome complex exonuclease rrp42; <b>PDBTitle:</b> structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
18	<a href="#">c2br2G</a>	Alignment		100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> exosome complex exonuclease 2; <b>PDBTitle:</b> rnase ph core of the archaeal exosome
19	<a href="#">c2ba0I</a>	Alignment		100.0	22	<b>PDB header:</b> rna binding protein <b>Chain:</b> I: <b>PDB Molecule:</b> archaeal exosome rna binding protein rrp42; <b>PDBTitle:</b> archaeal exosome core
20	<a href="#">c3hkmB</a>	Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> os03g0854200 protein; <b>PDBTitle:</b> crystal structure of rice(oryza sativa) rrp46
21	<a href="#">cloysA</a>	Alignment	not modelled	100.0	56	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease ph; <b>PDBTitle:</b> crystal structure of the phosphorolytic exoribonuclease2 rnase ph from bacillus subtilis <b>PDB header:</b> cytosolic protein <b>Chain:</b> E: <b>PDB Molecule:</b> polyribonucleotide nucleotidyltransferase; <b>PDBTitle:</b> crystal structure of pnpase from staphylococcus epidermidis
22	<a href="#">c5yijE</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> exosome complex component ski6; <b>PDBTitle:</b> yeast rrp44 nuclease
23	<a href="#">c2wp8B</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> polyribonucleotide nucleotidyltransferase; <b>PDBTitle:</b> crystal structure of s.aureus pnpase catalytic domain
24	<a href="#">c5xexC</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> polyribonucleotide nucleotidyltransferase; <b>PDBTitle:</b> crystal structure of c. crescentus pnpase bound to rna
25	<a href="#">c4am3A</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> polyribonucleotide transferase <b>Chain:</b> A: <b>PDB Molecule:</b> guanosine pentaphosphate synthetase; <b>PDBTitle:</b> semet derivative of streptomyces antibioticus pnpase/gpsi enzyme
26	<a href="#">c1e3hA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> exosome complex component rrp45; <b>PDBTitle:</b> yeast rrp44 nuclease
27	<a href="#">c2wp8A</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> polyribonucleotide nucleotidyltransferase 1, mitochondrial; <b>PDBTitle:</b> crystal structure of human pnpase
28	<a href="#">c3u1kB</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> polyribonucleotide transferase <b>Chain:</b> A: <b>PDB Molecule:</b> guanosine pentaphosphate synthetase; <b>PDBTitle:</b> tungstate derivative of streptomyces antibioticus
29	<a href="#">c1e3pA</a>	Alignment	not modelled	100.0	19	

						pnpase/2 gpsi enzyme
30	<a href="#">c3cdiA</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polynucleotide phosphorylase; <b>PDBTitle:</b> crystal structure of e. coli npnase
31	<a href="#">c4aimA</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase/peptide <b>Chain:</b> A: <b>PDB Molecule:</b> polyribonucleotide nucleotidyltransferase; <b>PDBTitle:</b> crystal structure of c. crescentus pnpase bound to rnas e2 recognition peptide
32	<a href="#">c4ifdE</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> E: <b>PDB Molecule:</b> exosome complex component rrp42; <b>PDBTitle:</b> crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna
33	<a href="#">c4nbqB</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> polyribonucleotide nucleotidyltransferase; <b>PDBTitle:</b> structure of the polynucleotide phosphorylase (cbu_0852) from coxiella2 burnetii
34	<a href="#">c2nn6D</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase/transferase <b>Chain:</b> D: <b>PDB Molecule:</b> exosome complex exonuclease rrp46; <b>PDBTitle:</b> structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
35	<a href="#">c3cdjA</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polynucleotide phosphorylase; <b>PDBTitle:</b> crystal structure of the e. coli kh/s1 domain truncated2 pnpase
36	<a href="#">c2nn6F</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> hydrolase/transferase <b>Chain:</b> F: <b>PDB Molecule:</b> exosome component 6; <b>PDBTitle:</b> structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
37	<a href="#">c4ifdC</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> C: <b>PDB Molecule:</b> exosome complex component rrp43; <b>PDBTitle:</b> crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna
38	<a href="#">c4ifdD</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> D: <b>PDB Molecule:</b> exosome complex component rrp46; <b>PDBTitle:</b> crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna
39	<a href="#">c4ifdF</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> F: <b>PDB Molecule:</b> exosome complex component mtr3; <b>PDBTitle:</b> crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna
40	<a href="#">d1uds1</a>	Alignment	not modelled	100.0	62	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Ribonuclease PH domain 1-like
41	<a href="#">d1r6la1</a>	Alignment	not modelled	100.0	61	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Ribonuclease PH domain 1-like
42	<a href="#">d2je6b1</a>	Alignment	not modelled	100.0	32	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Ribonuclease PH domain 1-like
43	<a href="#">d2ba0d1</a>	Alignment	not modelled	100.0	34	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Ribonuclease PH domain 1-like
44	<a href="#">d2nn6b1</a>	Alignment	not modelled	100.0	29	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Ribonuclease PH domain 1-like
45	<a href="#">d2ba0g1</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Ribonuclease PH domain 1-like
46	<a href="#">d2nn6c1</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Ribonuclease PH domain 1-like
47	<a href="#">d2je6a1</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Ribonuclease PH domain 1-like
48	<a href="#">d1e3ha3</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Ribonuclease PH domain 1-like
49	<a href="#">d2nn6e1</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Ribonuclease PH domain 1-like
50	<a href="#">d2nn6a1</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Ribonuclease PH domain 1-like
51	<a href="#">d1oysa1</a>	Alignment	not modelled	100.0	63	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Ribonuclease PH domain 1-like
52	<a href="#">c3krnB</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protein c14a4.5, confirmed by transcript evidence; <b>PDBTitle:</b> crystal structure of c. elegans cell-death-related nuclease 5(crn-5)
53	<a href="#">d2nn6f1</a>	Alignment	not modelled	100.0	28	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Ribonuclease PH domain 1-like
54	<a href="#">d1e3ha2</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Ribonuclease PH domain 1-like
55	<a href="#">d2nn6d1</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Ribonuclease PH domain 1-like
						<b>Fold:</b> Ribonuclease PH domain 2-like

56	d2je6a2	Alignment	not modelled	99.8	23	<b>Superfamily:</b> Ribonuclease PH domain 2-like <b>Family:</b> Ribonuclease PH domain 2-like
57	d2nn6a2	Alignment	not modelled	99.7	14	<b>Fold:</b> Ribonuclease PH domain 2-like <b>Superfamily:</b> Ribonuclease PH domain 2-like <b>Family:</b> Ribonuclease PH domain 2-like
58	d2nn6e2	Alignment	not modelled	99.7	13	<b>Fold:</b> Ribonuclease PH domain 2-like <b>Superfamily:</b> Ribonuclease PH domain 2-like <b>Family:</b> Ribonuclease PH domain 2-like
59	d2ba0g2	Alignment	not modelled	99.7	22	<b>Fold:</b> Ribonuclease PH domain 2-like <b>Superfamily:</b> Ribonuclease PH domain 2-like <b>Family:</b> Ribonuclease PH domain 2-like
60	d1oysa2	Alignment	not modelled	99.7	49	<b>Fold:</b> Ribonuclease PH domain 2-like <b>Superfamily:</b> Ribonuclease PH domain 2-like <b>Family:</b> Ribonuclease PH domain 2-like
61	d2nn6c2	Alignment	not modelled	99.7	19	<b>Fold:</b> Ribonuclease PH domain 2-like <b>Superfamily:</b> Ribonuclease PH domain 2-like <b>Family:</b> Ribonuclease PH domain 2-like
62	d2je6b2	Alignment	not modelled	99.7	25	<b>Fold:</b> Ribonuclease PH domain 2-like <b>Superfamily:</b> Ribonuclease PH domain 2-like <b>Family:</b> Ribonuclease PH domain 2-like
63	d1udsa2	Alignment	not modelled	99.7	38	<b>Fold:</b> Ribonuclease PH domain 2-like <b>Superfamily:</b> Ribonuclease PH domain 2-like <b>Family:</b> Ribonuclease PH domain 2-like
64	d1r6la2	Alignment	not modelled	99.7	48	<b>Fold:</b> Ribonuclease PH domain 2-like <b>Superfamily:</b> Ribonuclease PH domain 2-like <b>Family:</b> Ribonuclease PH domain 2-like
65	d2br2b2	Alignment	not modelled	99.7	25	<b>Fold:</b> Ribonuclease PH domain 2-like <b>Superfamily:</b> Ribonuclease PH domain 2-like <b>Family:</b> Ribonuclease PH domain 2-like
66	d2nn6d2	Alignment	not modelled	99.7	19	<b>Fold:</b> Ribonuclease PH domain 2-like <b>Superfamily:</b> Ribonuclease PH domain 2-like <b>Family:</b> Ribonuclease PH domain 2-like
67	d2nn6b2	Alignment	not modelled	99.6	17	<b>Fold:</b> Ribonuclease PH domain 2-like <b>Superfamily:</b> Ribonuclease PH domain 2-like <b>Family:</b> Ribonuclease PH domain 2-like
68	d2ba0d2	Alignment	not modelled	99.6	25	<b>Fold:</b> Ribonuclease PH domain 2-like <b>Superfamily:</b> Ribonuclease PH domain 2-like <b>Family:</b> Ribonuclease PH domain 2-like
69	d2nn6f2	Alignment	not modelled	99.3	17	<b>Fold:</b> Ribonuclease PH domain 2-like <b>Superfamily:</b> Ribonuclease PH domain 2-like <b>Family:</b> Ribonuclease PH domain 2-like
70	d1e3ha5	Alignment	not modelled	98.4	20	<b>Fold:</b> Ribonuclease PH domain 2-like <b>Superfamily:</b> Ribonuclease PH domain 2-like <b>Family:</b> Ribonuclease PH domain 2-like
71	d1e3ha6	Alignment	not modelled	96.2	21	<b>Fold:</b> Ribonuclease PH domain 2-like <b>Superfamily:</b> Ribonuclease PH domain 2-like <b>Family:</b> Ribonuclease PH domain 2-like
72	c4akvB_	Alignment	not modelled	58.2	23	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> sorting nexin-33; <b>PDBTitle:</b> crystal structure of human sorting nexin 33 (snx33)
73	c3dyuB_	Alignment	not modelled	40.9	23	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> sorting nexin-9; <b>PDBTitle:</b> crystal structure of snx9px-bar (230-595), h32
74	d1puga_	Alignment	not modelled	38.0	7	<b>Fold:</b> YbaB-like <b>Superfamily:</b> YbaB-like <b>Family:</b> YbaB-like
75	c2rajA_	Alignment	not modelled	33.6	21	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> sorting nexin-9; <b>PDBTitle:</b> so4 bound px-bar membrane remodeling unit of sorting nexin 9
76	c4ds1C_	Alignment	not modelled	21.8	15	<b>PDB header:</b> structural protein/transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> dynein light chain 1, cytoplasmic; <b>PDBTitle:</b> the structure of a yeast dyn2-nup159 complex and the molecular basis2 for the dynein light chain - nuclear pore interaction
77	d1pwka_	Alignment	not modelled	21.5	15	<b>Fold:</b> DLC <b>Superfamily:</b> DLC <b>Family:</b> DLC
78	d1cmia_	Alignment	not modelled	20.9	12	<b>Fold:</b> DLC <b>Superfamily:</b> DLC <b>Family:</b> DLC
79	d3e2ba1	Alignment	not modelled	19.0	15	<b>Fold:</b> DLC <b>Superfamily:</b> DLC <b>Family:</b> DLC
80	c5fx0A_	Alignment	not modelled	16.3	10	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> calcium binding protein; <b>PDBTitle:</b> fasciola hepatica calcium binding protein fhcbp2: structure of the2 dynein light chain-like domain. p6422 native.
81	c5gw1G_	Alignment	not modelled	14.2	31	<b>PDB header:</b> protein transport <b>Chain:</b> G: <b>PDB Molecule:</b> sorting nexin-16; <b>PDBTitle:</b> crystal structure of snx16 px-coiled coil in space group p212121
82	d1j8ba_	Alignment	not modelled	13.2	6	<b>Fold:</b> YbaB-like <b>Superfamily:</b> YbaB-like <b>Family:</b> YbaB-like
83	c4gdxA_	Alignment	not modelled	12.7	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gamma-glutamyltranspeptidase 1 heavy chain;

						<b>PDBTitle:</b> crystal structure of human gamma-glutamyl transpeptidase--glutamate2 complex <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> gamma-glutamyltranspeptidase large chain; <b>PDBTitle:</b> crystal structure of gamma-glutamyl transferase from bacillus subtilis
84	<a href="#">c2v36A</a>	Alignment	not modelled	12.2	28	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> gamma-glutamyltranspeptidase; <b>PDBTitle:</b> crystal structure of helicobacter pylori gamma-glutamyltranspeptidase2 in complex with glutamate
85	<a href="#">c2qm6C</a>	Alignment	not modelled	12.1	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> gamma-glutamyltranspeptidase; <b>PDBTitle:</b> crystal structure of escherichia coli gamma-glutamyltranspeptidase in2 complex with azaserine prepared in the dark
86	<a href="#">c2z8jA</a>	Alignment	not modelled	11.7	28	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> nischarin; <b>PDBTitle:</b> nischarin px-domain
87	<a href="#">c3p0cA</a>	Alignment	not modelled	11.5	22	<b>PDB header:</b> hydrolyase <b>Chain:</b> D: <b>PDB Molecule:</b> capsule biosynthesis protein capd; <b>PDBTitle:</b> crystal structure of bacillus anthracis transpeptidase enzyme capd
88	<a href="#">c3g9kD</a>	Alignment	not modelled	11.3	44	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> gamma-glutamyltransferase 1 threonine peptidase. merops <b>PDBTitle:</b> gamma-glutamyltranspeptidase from pseudomonas nitroreducens complexed2 with gly-gly
89	<a href="#">c5zjgC</a>	Alignment	not modelled	11.2	28	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> cdii immunity protein; <b>PDBTitle:</b> cdii immunity protein from yersinia kristensenii
90	<a href="#">c4zqvA</a>	Alignment	not modelled	10.5	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> gamma glutamyl transpeptidase,gamma-glutamyltranspeptidase; <b>PDBTitle:</b> crystal structure of t399a precursor mutant protein of gamma-glutamyl2 transpeptidase from bacillus licheniformis
91	<a href="#">c4y23A</a>	Alignment	not modelled	9.5	39	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> trna(his) guanylyltransferase; <b>PDBTitle:</b> crystal structure of trna(his) guanylyltransferase from saccharomyces2 cerevisiae
92	<a href="#">c5xoxD</a>	Alignment	not modelled	8.1	50	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Gamma-glutamyltranspeptidase-like
93	<a href="#">d2nlza1</a>	Alignment	not modelled	8.0	39	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> trna(his) guanylyltransferase; <b>PDBTitle:</b> crystal structure of human trnahs guanylyltransferase (thg1) - dgtp2 complex
94	<a href="#">c3otbB</a>	Alignment	not modelled	7.9	50	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> gamma-glutamyltranspeptidase; <b>PDBTitle:</b> t391a precursor mutant protein of gamma-glutamyltranspeptidase from2 escherichia coli
95	<a href="#">c2e0wA</a>	Alignment	not modelled	7.5	28	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thg1-like uncharacterized protein; <b>PDBTitle:</b> bacterial trna(his) guanylyltransferase (thg1)-like protein in complex2 with gtp
96	<a href="#">c4kgkB</a>	Alignment	not modelled	7.5	40	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> trna(his)-5'-guanylyltransferase (thg1) like protein; <b>PDBTitle:</b> crystal structure of thg1 like protein (tlp) with gtp
97	<a href="#">c5axIB</a>	Alignment	not modelled	7.3	40	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> cdia-ct/cdii toxin and immunity complex from yersinia2 pseudotuberculosis
98	<a href="#">c4zquB</a>	Alignment	not modelled	7.3	10	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase family protein; <b>PDBTitle:</b> crystal structure of a putative enoyl-coa hydratase/isomerase family2 protein from hyphomonas neptunium
99	<a href="#">c4olqD</a>	Alignment	not modelled	7.2	15	