Phyre^2

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Description	P76231
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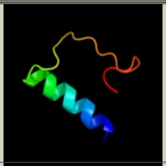
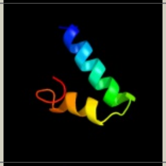
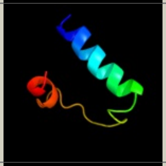
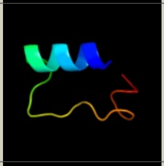
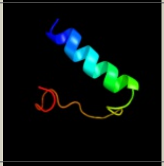
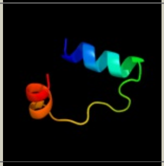
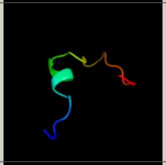
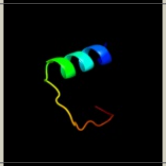
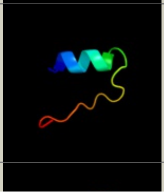
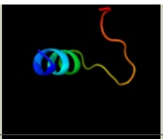
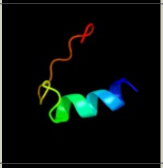
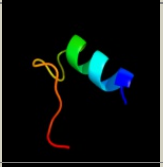
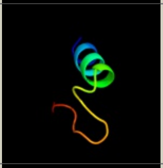
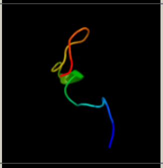
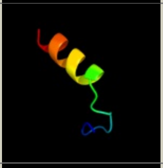
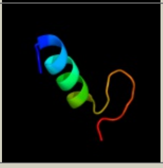
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ihuA_	Alignment		87.3	26	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, gntr family; **PDBTitle:** crystal structure of dna binding protein (yp_298823.1) from ralstonia2 eutropha jmp134 at 1.92 a resolution
2	c3fmsA_	Alignment		83.0	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, gntr family; **PDBTitle:** crystal structure of tm0439, a gntr transcriptional2 regulator
3	d2hs5a1	Alignment		82.5	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**GntR-like transcriptional regulators
4	c3c7jA_	Alignment		82.1	32	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, gntr family; **PDBTitle:** crystal structure of transcriptional regulator (gntr family member)2 from pseudomonas syringae pv. tomato str. dc3000
5	c2hs5A_	Alignment		77.9	29	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative transcriptional regulator gntr; **PDBTitle:** structural genomics, the crystal structure of a putative2 transcriptional regulator gntr from rhodococcus sp. rha1
6	c3tqnC_	Alignment		74.6	10	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcriptional regulator, gntr family; **PDBTitle:** structure of the transcriptional regulator of the gntr family, from2 coxiella burnetii.
7	d3bwga1	Alignment		67.3	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**GntR-like transcriptional regulators
8	c3by6C_	Alignment		64.5	10	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**predicted transcriptional regulator; **PDBTitle:** crystal structure of a transcriptional regulator from oenococcus oeni
9	d1hw1a1	Alignment		57.2	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**GntR-like transcriptional regulators
10	c3neuA_	Alignment		56.9	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin1836 protein; **PDBTitle:** the crystal structure of a functionally-unknown protein lin1836 from2 listeria innocua clip11262
11	c2du9A_	Alignment		56.4	4	**PDB header:**transcription **Chain:** A: **PDB Molecule:**predicted transcriptional regulators; **PDBTitle:** crystal structure of the transcriptional factor from c.glutamicum

12	c3bwgA_	Alignment		53.7	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**uncharacterized hth-type transcriptional regulator yydk; **PDBTitle:** the crystal structure of possible transcriptional regulator yydk from2 bacillus subtilis subsp. subtilis str. 168
13	d1v4ra1	Alignment		52.3	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**GntR-like transcriptional regulators
14	c1e2xA_	Alignment		51.7	18	**PDB header:**transcriptional regulation **Chain:** A: **PDB Molecule:**fatty acid metabolism regulator protein; **PDBTitle:** fadr, fatty acid responsive transcription factor from e.2 coli
15	c2di3A_	Alignment		51.4	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**bacterial regulatory proteins, gntr family; **PDBTitle:** crystal structure of the transcriptional factor cgl29152 from corynebacterium glutamicum
16	c2je2A_	Alignment		48.0	30	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**cytochrome p460; **PDBTitle:** cytochrome p460 from nitrosomonas europaea - probable2 nonphysiological oxidized form
17	c3eetA_	Alignment		42.3	21	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative gntr-family transcriptional regulator; **PDBTitle:** crystal structure of putative gntr-family transcriptional2 regulator
18	c3ic7A_	Alignment		41.0	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator of gntr family2 from bacteroides thetaiotaomicron
19	d1zlqa1	Alignment		38.7	19	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
20	d2d3qa1	Alignment		38.3	16	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Dyp-type peroxidase-like
21	c3edhA_	Alignment	not modelled	33.3	40	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**bone morphogenetic protein 1; **PDBTitle:** crystal structure of bone morphogenetic protein 1 protease2 domain in complex with partially bound dmso
22	c2wv0H_	Alignment	not modelled	32.5	20	**PDB header:**transcription **Chain:** H: **PDB Molecule:**hth-type transcriptional repressor yvoa; **PDBTitle:** crystal structure of the gntr-hutc family member yvoa from2 bacillus subtilis
23	c3t66A_	Alignment	not modelled	31.0	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**nickel abc transporter (nickel-binding protein); **PDBTitle:** crystal structure of nickel abc transporter from bacillus halodurans
24	c3edpB_	Alignment	not modelled	30.3	4	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**lin2111 protein; **PDBTitle:** the crystal structure of the protein lin2111 (functionally unknown)2 from listeria innocua clip11262
25	d3bvua3	Alignment	not modelled	29.7	8	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**alpha-mannosidase
26	d1uqwa_	Alignment	not modelled	28.9	19	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
27	d1jeta_	Alignment	not modelled	28.1	29	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
28	c3lf9A_	Alignment	not modelled	25.0	28	**PDB header:**immune system **Chain:** A: **PDB Molecule:**4e10_d0_1is1a_001_c (t161); **PDBTitle:** crystal structure of hiv epitope-scaffold 4e10_d0_1is1a_001_c
						Fold:FYSH domain

29	d1nyna_	Alignment	not modelled	22.4	30	**Superfamily:**FYSH domain **Family:**Hypothetical protein Yhr087W
30	c3rqtA_	Alignment	not modelled	21.6	27	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** 1.5 angstrom crystal structure of the complex of ligand binding2 component of abc-type import system from staphylococcus aureus with3 nickel and two histidines
31	c3o9pA_	Alignment	not modelled	21.2	29	**PDB header:**peptide binding protein/peptide **Chain:** A: **PDB Molecule:**periplasmic murein peptide-binding protein; **PDBTitle:** the structure of the escherichia coli murein tripeptide binding2 protein mppa
32	d1lbua1	Alignment	not modelled	20.9	10	**Fold:**PGBD-like **Superfamily:**PGBD-like **Family:**Peptidoglycan binding domain, PGBD
33	c3ry3B_	Alignment	not modelled	20.1	24	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**putative solute-binding protein; **PDBTitle:** putative solute-binding protein from yersinia pestis.
34	c2wokA_	Alignment	not modelled	19.2	24	**PDB header:**peptide binding protein/peptide **Chain:** A: **PDB Molecule:**clavulanic acid biosynthesis oligopeptide **PDBTitle:** clavulanic acid biosynthesis oligopeptide2 binding protein 2 complexed with bradykinin
35	c1ztyA_	Alignment	not modelled	19.2	32	**PDB header:**sugar binding protein, signaling protein **Chain:** A: **PDB Molecule:**chitin oligosaccharide binding protein; **PDBTitle:** crystal structure of the chitin oligasaccharide binding2 protein
36	d1asta_	Alignment	not modelled	18.9	16	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Astacin
37	c3ftoA_	Alignment	not modelled	17.0	29	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**oligopeptide-binding protein oppa; **PDBTitle:** crystal structure of oppa in a open conformation
38	c2grvC_	Alignment	not modelled	16.9	9	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**lpqw; **PDBTitle:** crystal structure of lpqw
39	d1xoca1	Alignment	not modelled	16.5	24	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
40	d1vr5a1	Alignment	not modelled	16.5	29	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
41	c2o7jA_	Alignment	not modelled	16.2	30	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**oligopeptide abc transporter, periplasmic **PDBTitle:** the x-ray crystal structure of a thermophilic cellobiose2 binding protein bound with cellopentaose
42	c3fxeA_	Alignment	not modelled	15.9	46	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein icmq; **PDBTitle:** crystal structure of interacting domains of icmr and icmq (seleno-2 derivative)
43	c1o7dA_	Alignment	not modelled	15.8	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysosomal alpha-mannosidase; **PDBTitle:** the structure of the bovine lysosomal a-mannosidase2 suggests a novel mechanism for low ph activation
44	c2ztbB_	Alignment	not modelled	14.9	33	**PDB header:**toxin **Chain:** B: **PDB Molecule:**crystal protein; **PDBTitle:** crystal structure of the parasporin-2 bacillus thuringiensis toxin2 that recognizes cancer cells
45	c3fiqA_	Alignment	not modelled	14.9	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**odorant-binding protein 1f; **PDBTitle:** odorant binding protein obp1
46	c3itfA_	Alignment	not modelled	14.7	50	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**periplasmic adaptor protein cpxp; **PDBTitle:** structural basis for the inhibitory function of the cpxp adaptor2 protein
47	d1qh4a1	Alignment	not modelled	13.2	14	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
48	d1cola_	Alignment	not modelled	13.2	27	**Fold:**Toxins' membrane translocation domains **Superfamily:**Colicin **Family:**Colicin
49	c3oeoD_	Alignment	not modelled	12.9	63	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**spheroplast protein y; **PDBTitle:** the crystal structure e. coli spy
50	c3o39A_	Alignment	not modelled	12.5	63	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**periplasmic protein related to spheroblast formation; **PDBTitle:** crystal structure of spy
51	c3lqbA_	Alignment	not modelled	12.4	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**loc792177 protein; **PDBTitle:** crystal structure of the hatching enzyme zhe1 from the zebrafish danio2 rerio
52	d1qk1a1	Alignment	not modelled	12.1	36	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
53	d1rh1a2	Alignment	not modelled	11.9	13	**Fold:**Toxins' membrane translocation domains **Superfamily:**Colicin **Family:**Colicin
54	c2da4A_	Alignment	not modelled	11.8	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein dkfzp686k21156; **PDBTitle:** solution structure of the homeobox domain of the2 hypothetical protein, dkfzp686k21156

55	d1g0wa1	Alignment	not modelled	11.6	29	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
56	c3qzcA_	Alignment	not modelled	11.5	50	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**periplasmic protein cpxp; **PDBTitle:** structure of the periplasmic stress response protein cpxp
57	c1wnmA_	Alignment	not modelled	11.3	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fibroin-modulator binding-protein-1; **PDBTitle:** nmr structure of fmbp-1 tandem repeat 2 in 30%(v/v) tfe2 solution
58	c2i88A_	Alignment	not modelled	11.1	20	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**colicin-e1; **PDBTitle:** crystal structure of the channel-forming domain of colicin2 e1
59	d1ciia1	Alignment	not modelled	11.0	20	**Fold:**Toxins' membrane translocation domains **Superfamily:**Colicin **Family:**Colicin
60	c2k0mA_	Alignment	not modelled	11.0	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of the uncharacterized protein from2 rhodospirillum rubrum gene locus rru_a0810. northeast3 structural genomics target rrr43
61	d1hq1a_	Alignment	not modelled	10.9	45	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
62	c1wnkA_	Alignment	not modelled	10.5	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fibroin-modulator-binding-protein-1; **PDBTitle:** nmr structure of fmbp-1 tandem repeat 3 in 30%(v/v) tfe2 solution
63	d1uoua1	Alignment	not modelled	10.4	26	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
64	c3rnvA_	Alignment	not modelled	10.4	100	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**helper component proteinase; **PDBTitle:** structure of the autocatalytic cysteine protease domain of potyvirus2 helper-component proteinase
65	d2qqsa2	Alignment	not modelled	10.4	50	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
66	c3h01A_	Alignment	not modelled	10.1	17	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**envelope glycoprotein gp160; **PDBTitle:** structure of the c-terminal domain of a putative hiv-1 gp412 fusion intermediate
67	d1a87a_	Alignment	not modelled	10.0	13	**Fold:**Toxins' membrane translocation domains **Superfamily:**Colicin **Family:**Colicin
68	c1a87A_	Alignment	not modelled	10.0	13	**PDB header:**bacteriocin **Chain:** A: **PDB Molecule:**colicin n; **PDBTitle:** colicin n
69	d1m15a1	Alignment	not modelled	10.0	7	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
70	c2d5wA_	Alignment	not modelled	10.0	29	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**peptide abc transporter, peptide-binding protein; **PDBTitle:** the crystal structure of oligopeptide binding protein from thermus2 thermophilus hb8 complexed with pentapeptide
71	d1dula_	Alignment	not modelled	9.9	36	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
72	d1crka1	Alignment	not modelled	9.9	21	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
73	d2c42a2	Alignment	not modelled	9.8	60	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**PFOR PP module
74	d1i0ea1	Alignment	not modelled	9.8	21	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
75	d1k1xa3	Alignment	not modelled	9.7	20	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**4-alpha-glucanotransferase, N-terminal domain
76	d1vrpa1	Alignment	not modelled	9.5	14	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
77	c2wyhA_	Alignment	not modelled	9.3	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-mannosidase; **PDBTitle:** structure of the streptococcus pyogenes family gh38 alpha-2 mannosidase
78	d1u6ra1	Alignment	not modelled	9.3	21	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
79	c3cyoA_	Alignment	not modelled	9.2	19	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**transmembrane protein; **PDBTitle:** structure of a longer thermalstable core domain of hiv-12 gp41 containing the enfuvirtide resistance mutation n43d3 and complementary mutation e137k
80	c2ba0I_	Alignment	not modelled	8.9	21	**PDB header:**rna binding protein **Chain:** I: **PDB Molecule:**archeal exosome rna binding protein rrp42; **PDBTitle:** archaeal exosome core

81	d1lv3a_	Alignment	not modelled	8.8	25	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Hypothetical zinc finger protein YacG
82	d2tpta1	Alignment	not modelled	8.7	28	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
83	c3qiiA_	Alignment	not modelled	8.2	38	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**phd finger protein 20; **PDBTitle:** crystal structure of tudor domain 2 of human phd finger protein 20
84	c2ow7A_	Alignment	not modelled	8.0	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-mannosidase 2; **PDBTitle:** golgi alpha-mannosidase ii complex with (1r,6s,7r,8s)-1-2 thioniabicyclo[4.3.0]nonan-7,8-diol chloride
85	d1chka_	Alignment	not modelled	7.8	25	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Chitosanase
86	d2qqra2	Alignment	not modelled	7.8	50	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
87	c3fewX_	Alignment	not modelled	7.7	27	**PDB header:**immune system **Chain:** X: **PDB Molecule:**colicin s4; **PDBTitle:** structure and function of colicin s4, a colicin with a2 duplicated receptor binding domain
88	c2ex3I_	Alignment	not modelled	7.7	25	**PDB header:**transferase/replication **Chain:** I: **PDB Molecule:**dna polymerase; **PDBTitle:** bacteriophage phi29 dna polymerase bound to terminal protein
89	c1i5xA_	Alignment	not modelled	7.7	19	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**transmembrane glycoprotein (gp41); **PDBTitle:** hiv-1 gp41 core
90	d1z9ha1	Alignment	not modelled	7.7	24	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
91	d1stfi_	Alignment	not modelled	7.4	17	**Fold:**Cystatin-like **Superfamily:**Cystatin/monellin **Family:**Cystatins
92	c2o61A_	Alignment	not modelled	7.2	50	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**transcription factor p65/interferon regulatory factor **PDBTitle:** crystal structure of nfkb, irf7, irf3 bound to the interferon-b2 enhancer
93	d1o17a1	Alignment	not modelled	7.0	11	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
94	c3letB_	Alignment	not modelled	7.0	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**adenosine monophosphate-protein transferase vops; **PDBTitle:** crystal structure of fic domain containing ampylator, vops
95	d2ffha2	Alignment	not modelled	7.0	55	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
96	d1zela2	Alignment	not modelled	6.7	25	**Fold:**Rv2827c C-terminal domain-like **Superfamily:**Rv2827c C-terminal domain-like **Family:**Rv2827c C-terminal domain-like
97	c2nn6E_	Alignment	not modelled	6.7	11	**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
98	c3epvB_	Alignment	not modelled	6.5	25	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**nickel and cobalt resistance protein cnrr; **PDBTitle:** x-ray structure of the metal-sensor cnrx in both the apo-and copper-2 bound forms
99	d1f46a_	Alignment	not modelled	6.5	4	**Fold:**TBP-like **Superfamily:**Cell-division protein ZipA, C-terminal domain **Family:**Cell-division protein ZipA, C-terminal domain