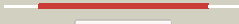



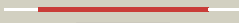














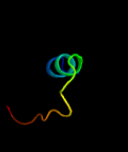


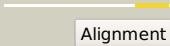
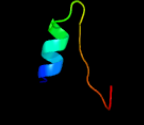
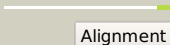

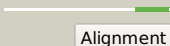
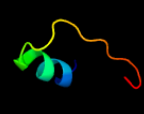
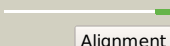


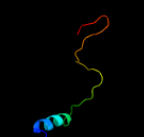
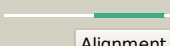

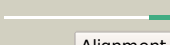
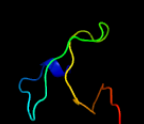

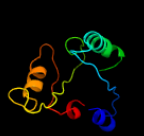



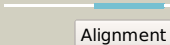
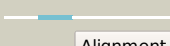



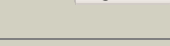


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2540c_(aroF)_2863217_2864422
Date	Wed Aug 7 12:50:17 BST 2019
Unique Job ID	a44a5184e6516579

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1ztbA_</a>	 Alignment		100.0	99	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> chorismate synthase; <b>PDBTitle:</b> crystal structure of chorismate synthase from mycobacterium2 tuberculosis
2	<a href="#">d1qxoA_</a>	 Alignment		100.0	44	<b>Fold:</b> Chorismate synthase, AroC <b>Superfamily:</b> Chorismate synthase, AroC <b>Family:</b> Chorismate synthase, AroC
3	<a href="#">d1um0a_</a>	 Alignment		100.0	34	<b>Fold:</b> Chorismate synthase, AroC <b>Superfamily:</b> Chorismate synthase, AroC <b>Family:</b> Chorismate synthase, AroC
4	<a href="#">d1q1la_</a>	 Alignment		100.0	47	<b>Fold:</b> Chorismate synthase, AroC <b>Superfamily:</b> Chorismate synthase, AroC <b>Family:</b> Chorismate synthase, AroC
5	<a href="#">c4lj2A_</a>	 Alignment		100.0	37	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> chorismate synthase; <b>PDBTitle:</b> crystal structure of chorismate synthase from acinetobacter baumannii2 at 3.15a resolution
6	<a href="#">d1sq1a_</a>	 Alignment		100.0	37	<b>Fold:</b> Chorismate synthase, AroC <b>Superfamily:</b> Chorismate synthase, AroC <b>Family:</b> Chorismate synthase, AroC
7	<a href="#">d1r53a_</a>	 Alignment		100.0	40	<b>Fold:</b> Chorismate synthase, AroC <b>Superfamily:</b> Chorismate synthase, AroC <b>Family:</b> Chorismate synthase, AroC
8	<a href="#">c4ecdB_</a>	 Alignment		100.0	62	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> chorismate synthase; <b>PDBTitle:</b> 2.5 angstrom resolution crystal structure of bifidobacterium longum2 chorismate synthase
9	<a href="#">c5z9aB_</a>	 Alignment		100.0	41	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> chorismate synthase; <b>PDBTitle:</b> crystal structure of chorismate synthase from pseudomonas aeruginosa
10	<a href="#">c2k1bA_</a>	 Alignment		78.6	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ser13; <b>PDBTitle:</b> solution nmr structure of ser13 from staphylococcus epidermidis.2 northeast structural genomics consortium target ser13
11	<a href="#">d2ffma1</a>	 Alignment		75.6	9	<b>Fold:</b> Hypothetical protein SAV1430 <b>Superfamily:</b> Hypothetical protein SAV1430 <b>Family:</b> Hypothetical protein SAV1430

12	<a href="#">c2ltmA_</a>			72.6	30	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> nfu1 iron-sulfur cluster scaffold homolog, mitochondrial; <b>PDBTitle:</b> solution nmr structure of nfu1 iron-sulfur cluster scaffold homolog2 from homo sapiens, northeast structural genomics consortium (nesg)3 target hr2876b
13	<a href="#">d1ciya1</a>			62.9	13	<b>Fold:</b> Galactose-binding domain-like <b>Superfamily:</b> Galactose-binding domain-like <b>Family:</b> delta-Endotoxin, C-terminal domain
14	<a href="#">c2ltlA_</a>			56.2	30	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> nifu-like protein, mitochondrial; <b>PDBTitle:</b> solution nmr structure of nifu-like protein from saccharomyces2 cerevisiae, northeast structural genomics consortium (nesg) target3 yr313a
15	<a href="#">d1ji6a1</a>			53.1	10	<b>Fold:</b> Galactose-binding domain-like <b>Superfamily:</b> Galactose-binding domain-like <b>Family:</b> delta-Endotoxin, C-terminal domain
16	<a href="#">c1m1gB_</a>			52.9	19	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription antitermination protein nusg; <b>PDBTitle:</b> crystal structure of aquifex aeolicus n-utilization2 substance g (nusg), space group p2(1)
17	<a href="#">c4grdA_</a>			46.9	29	<b>PDB header:</b> lyase, isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase catalytic subunit; <b>PDBTitle:</b> crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from burkholderia cenocepacia j2315
18	<a href="#">d1dlca1</a>			43.1	10	<b>Fold:</b> Galactose-binding domain-like <b>Superfamily:</b> Galactose-binding domain-like <b>Family:</b> delta-Endotoxin, C-terminal domain
19	<a href="#">d1o4va_</a>			38.5	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) <b>Family:</b> N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
20	<a href="#">c2lhuA_</a>			37.2	27	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> mybpc3 protein; <b>PDBTitle:</b> structural insight into the unique cardiac myosin binding protein-c2 motif: a partially folded domain
21	<a href="#">c2c9kA_</a>		not modelled	36.3	14	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> pesticidal crystal protein cry4aa; <b>PDBTitle:</b> structure of the functional form of the mosquito-larvicidal2 cry4aa toxin from bacillus thuringiensis at 2.8 a3 resolution
22	<a href="#">c3lp6D_</a>		not modelled	36.0	24	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase catalytic subunit; <b>PDBTitle:</b> crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution
23	<a href="#">c2xznF_</a>		not modelled	33.3	13	<b>PDB header:</b> ribosome <b>Chain:</b> F: <b>PDB Molecule:</b> eif1; <b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
24	<a href="#">d1qcza_</a>		not modelled	33.2	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) <b>Family:</b> N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
25	<a href="#">c5mqfB_</a>		not modelled	30.1	25	<b>PDB header:</b> splicing <b>Chain:</b> B: <b>PDB Molecule:</b> 116 kda u5 small nuclear ribonucleoprotein component; <b>PDBTitle:</b> cryo-em structure of a human spliceosome activated for step 2 of2 splicing (c* complex)
26	<a href="#">c5z58C_</a>		not modelled	27.5	25	<b>PDB header:</b> splicing <b>Chain:</b> C: <b>PDB Molecule:</b> 116 kda u5 small nuclear ribonucleoprotein component; <b>PDBTitle:</b> cryo-em structure of a human activated spliceosome (early bact) at 4.92 angstrom.
27	<a href="#">c5ganC_</a>		not modelled	27.0	22	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> pre-mrna-splicing factor snu114;

27	<a href="#">c3ganC</a>	Alignment	not modelled	27.0	22	<b>PDBTitle:</b> the overall structure of the yeast spliceosomal u4/u6.u5 tri-snrnp at 2.37 angstrom <b>PDB header:</b> isomerase
28	<a href="#">c4b4kK</a>	Alignment	not modelled	26.9	21	<b>Chain:</b> K: <b>PDB Molecule:</b> n5-carboxyaminoimidazole ribonucleotide mutase; <b>PDBTitle:</b> crystal structure of bacillus anthracis pure
29	<a href="#">c3r3sD</a>	Alignment	not modelled	26.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> structure of the ygha oxidoreductase from salmonella enterica
30	<a href="#">c2kw0A</a>	Alignment	not modelled	26.8	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ccmh protein; <b>PDBTitle:</b> solution structure of n-terminal domain of ccmh from escherichia.coli
31	<a href="#">c1ciyA</a>	Alignment	not modelled	26.7	13	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> cryia(a); <b>PDBTitle:</b> insecticidal toxin: structure and channel formation
32	<a href="#">c2a73B</a>	Alignment	not modelled	26.6	9	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> complement c3; <b>PDBTitle:</b> human complement component c3
33	<a href="#">c1dlcA</a>	Alignment	not modelled	26.6	9	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> delta-endotoxin cryiiia; <b>PDBTitle:</b> crystal structure of insecticidal delta-endotoxin from2 bacillus thuringiensis at 2.5 angstroms resolution
34	<a href="#">c2hl7A</a>	Alignment	not modelled	26.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c-type biogenesis protein ccmh; <b>PDBTitle:</b> crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa
35	<a href="#">d1xmpa</a>	Alignment	not modelled	24.8	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) <b>Family:</b> N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
36	<a href="#">c2b39B</a>	Alignment	not modelled	24.1	5	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> c3; <b>PDBTitle:</b> structure of mammalian c3 with an intact thioester at 3a resolution
37	<a href="#">c2ymyB</a>	Alignment	not modelled	23.6	19	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> ras association domain-containing protein 5; <b>PDBTitle:</b> structure of the murine nore1-sarah domain
38	<a href="#">c5lj3C</a>	Alignment	not modelled	23.0	22	<b>PDB header:</b> splicing <b>Chain:</b> C: <b>PDB Molecule:</b> pre-mrna-splicing factor snu114; <b>PDBTitle:</b> structure of the core of the yeast spliceosome immediately after2 branching
39	<a href="#">c6g2iK</a>	Alignment	not modelled	22.6	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> K: <b>PDB Molecule:</b> nadh-ubiquinone oxidoreductase chain 4l; <b>PDBTitle:</b> mouse mitochondrial complex i in the active state
40	<a href="#">c3jb9B</a>	Alignment	not modelled	21.4	25	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> B: <b>PDB Molecule:</b> pre-mrna-splicing factor cwf10; <b>PDBTitle:</b> cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution
41	<a href="#">c1w99A</a>	Alignment	not modelled	20.3	17	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> pesticidal crystal protein cry4ba; <b>PDBTitle:</b> mosquito-larvicidal toxin cry4ba from bacillus thuringiensis ssp.2 israelensis
42	<a href="#">c5hcdD</a>	Alignment	not modelled	19.5	29	<b>PDB header:</b> immune system <b>Chain:</b> D: <b>PDB Molecule:</b> rhipicephalus microplus raci2; <b>PDBTitle:</b> ternary complex of human complement c5 with ornithodoros moubata omci2 and rhipicephalus microplus raci2
43	<a href="#">c2yadA</a>	Alignment	not modelled	19.3	33	<b>PDB header:</b> surfactant protein <b>Chain:</b> A: <b>PDB Molecule:</b> surfactant protein c brichos domain; <b>PDBTitle:</b> brichos domain of surfactant protein c precursor protein
44	<a href="#">c3jcrB</a>	Alignment	not modelled	18.0	25	<b>PDB header:</b> splicing <b>Chain:</b> B: <b>PDB Molecule:</b> hsnu114; <b>PDBTitle:</b> 3d structure determination of the human*u4/u6.u5* tri-snrnp complex
45	<a href="#">c6ovbA</a>	Alignment	not modelled	17.7	16	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> active core crystal toxin protein 1d; <b>PDBTitle:</b> crystal structure of a bacillus thuringiensis cry1da tryptic core2 variant
46	<a href="#">c3trhl</a>	Alignment	not modelled	17.3	23	<b>PDB header:</b> lyase <b>Chain:</b> I: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase <b>PDBTitle:</b> structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
47	<a href="#">c3zf7Z</a>	Alignment	not modelled	17.1	22	<b>PDB header:</b> ribosome <b>Chain:</b> Z: <b>PDB Molecule:</b> 60s ribosomal protein l26, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
48	<a href="#">c6dj6B</a>	Alignment	not modelled	16.4	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid kinase (fak) b2 protein (spr1019); <b>PDBTitle:</b> the x-ray crystal structure of the streptococcus pneumoniae fatty acid2 kinase (fak) b2 protein loaded with cis-oleic acid to 1.9 angstrom3 resolution
49	<a href="#">c3w66A</a>	Alignment	not modelled	16.4	20	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> magnetosome protein mamm; <b>PDBTitle:</b> mamm-ctd d249a and h285a
50	<a href="#">c3ieeA</a>	Alignment	not modelled	15.8	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative exported protein; <b>PDBTitle:</b> crystal structure of an alpha helical protein (bf3319) from2 bacteroides fragilis nctc 9343 at 1.70 a resolution
51	<a href="#">c5lc5K</a>	Alignment	not modelled	15.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> K: <b>PDB Molecule:</b> nadh-ubiquinone oxidoreductase chain 4l; <b>PDBTitle:</b> structure of mammalian respiratory complex i, class2
52	<a href="#">c5ldwK</a>	Alignment	not modelled	15.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> K: <b>PDB Molecule:</b> nadh-ubiquinone oxidoreductase chain 4l;

						<b>PDBTitle:</b> structure of mammalian respiratory complex i, class1
53	<a href="#">d1g9pa_</a>	Alignment	not modelled	15.0	57	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> omega toxin-like <b>Family:</b> Spider toxins
54	<a href="#">c1g9pA_</a>	Alignment	not modelled	15.0	57	<b>PDB header:</b> toxin <b>Chain:</b> A; <b>PDB Molecule:</b> omega-atracotoxin-hv2a; <b>PDBTitle:</b> solution structure of the insecticidal calcium channel2 blocker omega-atracotoxin-hv2a
55	<a href="#">c2ejeA_</a>	Alignment	not modelled	14.8	50	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> general transcription factor ii-i; <b>PDBTitle:</b> solution structure of rsgi ruh-071, a gtf2i domain in human2 cdna
56	<a href="#">c5iecA_</a>	Alignment	not modelled	14.1	29	<b>PDB header:</b> blood clotting <b>Chain:</b> A; <b>PDB Molecule:</b> raci2; <b>PDBTitle:</b> structural basis for therapeutic inhibition of complement c5
57	<a href="#">c2k19A_</a>	Alignment	not modelled	14.0	10	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A; <b>PDB Molecule:</b> putative piscicolin 126 immunity protein; <b>PDBTitle:</b> nmr solution structure of pisi
58	<a href="#">c2dn5A_</a>	Alignment	not modelled	13.5	17	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> general transcription factor ii-i repeat domain- <b>PDBTitle:</b> solution structure of rsgi ruh-057, a gtf2i domain in human2 cdna
59	<a href="#">c6owkA_</a>	Alignment	not modelled	13.2	10	<b>PDB header:</b> toxin <b>Chain:</b> A; <b>PDB Molecule:</b> pesticidal crystal protein cry1be, cry1k-like protein <b>PDBTitle:</b> crystal structure of a bacillus thuringiensis cry1b.867 tryptic core2 variant
60	<a href="#">c2dzrA_</a>	Alignment	not modelled	12.8	25	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> general transcription factor ii-i repeat domain- <b>PDBTitle:</b> solution structure of rsgi ruh-067, a gtf2i domain in human2 cdna
61	<a href="#">c4uysA_</a>	Alignment	not modelled	12.7	31	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> flocculation protein flo11; <b>PDBTitle:</b> x-ray structure of the n-terminal domain of the flocculin2 flo11 from saccharomyces cerevisiae
62	<a href="#">c4hhuA_</a>	Alignment	not modelled	12.6	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> or280; <b>PDBTitle:</b> crystal structure of engineered protein. northeast structural genomics2 consortium target or280.
63	<a href="#">d1q60a_</a>	Alignment	not modelled	12.4	42	<b>Fold:</b> GTF2I-like repeat <b>Superfamily:</b> GTF2I-like repeat <b>Family:</b> GTF2I-like repeat
64	<a href="#">c4moaA_</a>	Alignment	not modelled	12.2	17	<b>PDB header:</b> toxin <b>Chain:</b> A; <b>PDB Molecule:</b> pesticidal crystal protein cry4ba; <b>PDBTitle:</b> crystal structure of cry4ba-r203q toxin
65	<a href="#">c6r5kA_</a>	Alignment	not modelled	12.1	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> pan2-pan3 deadenylation complex catalytic subunit pan2; <b>PDBTitle:</b> cryo-em structure of a poly(a) rnp bound to the pan2-pan3 deadenylase
66	<a href="#">c2d99A_</a>	Alignment	not modelled	12.1	25	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> general transcription factor ii-i repeat domain- <b>PDBTitle:</b> solution structure of rsgi ruh-048, a gtf2i domain in human2 cdna
67	<a href="#">c2yadE_</a>	Alignment	not modelled	11.9	40	<b>PDB header:</b> surfactant protein <b>Chain:</b> E; <b>PDB Molecule:</b> surfactant protein c brichos domain; <b>PDBTitle:</b> brichos domain of surfactant protein c precursor protein
68	<a href="#">c2dn4A_</a>	Alignment	not modelled	11.8	33	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> general transcription factor ii-i; <b>PDBTitle:</b> solution structure of rsgi ruh-060, a gtf2i domain in human2 cdna
69	<a href="#">c2diuA_</a>	Alignment	not modelled	11.8	20	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> kiaa0430 protein; <b>PDBTitle:</b> solution structure of the rrm domain of kiaa0430 protein
70	<a href="#">d1kkma_</a>	Alignment	not modelled	11.3	16	<b>Fold:</b> PEP carboxykinase-like <b>Superfamily:</b> PEP carboxykinase-like <b>Family:</b> HPr kinase HPrK C-terminal domain
71	<a href="#">c5zi1A_</a>	Alignment	not modelled	10.9	25	<b>PDB header:</b> toxin <b>Chain:</b> A; <b>PDB Molecule:</b> insecticidal crystal protein cry7ca1; <b>PDBTitle:</b> crystal structure of bacillus thuringiensis insecticidal crystal2 protein cry7ca1 (wild type)
72	<a href="#">c2e3lA_</a>	Alignment	not modelled	10.8	42	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> transcription factor gtf2ird2 beta; <b>PDBTitle:</b> solution structure of rsgi ruh-068, a gtf2i domain in human2 cdna
73	<a href="#">c2ed2A_</a>	Alignment	not modelled	10.7	25	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> general transcription factor ii-i; <b>PDBTitle:</b> solution structure of rsgi ruh-069, a gtf2i domain in human2 cdna
74	<a href="#">c3b8hA_</a>	Alignment	not modelled	10.7	40	<b>PDB header:</b> biosynthetic protein/transferase <b>Chain:</b> A; <b>PDB Molecule:</b> elongation factor 2; <b>PDBTitle:</b> structure of the eef2-exoa(e546a)-nad+ complex
75	<a href="#">c4qjty_</a>	Alignment	not modelled	10.7	20	<b>PDB header:</b> ribosome <b>Chain:</b> Y; <b>PDB Molecule:</b> <b>PDBTitle:</b> crystal structure of elongation factor 4 (ef4/lepa) bound to the2 thermus thermophilus 70s ribosome, 30s subunit of the 70s ribosome
76	<a href="#">c2dzqA_</a>	Alignment	not modelled	10.5	25	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> general transcription factor ii-i repeat domain- <b>PDBTitle:</b> solution structure of rsgi ruh-066, a gtf2i domain in human2 cdna
						<b>PDB header:</b> translation regulation/hydrolase

77	<a href="#">c3mcaB_</a>	Alignment	not modelled	9.9	22	<b>Chain:</b> B: <b>PDB Molecule:</b> protein dom34; <b>PDBTitle:</b> structure of the dom34-hbs1 complex and implications for its role in2 no-go decay
78	<a href="#">c1ji6A_</a>	Alignment	not modelled	9.6	10	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> pesticidal crystal protein cry3bb; <b>PDBTitle:</b> crystal structure of the insecticidal bacterial del endotoxin cry3bb12 bacillus thuringiensis
79	<a href="#">c4wsbC_</a>	Alignment	not modelled	9.5	22	<b>PDB header:</b> transferase/rna <b>Chain:</b> C: <b>PDB Molecule:</b> polymerase pb2; <b>PDBTitle:</b> bat influenza a polymerase with bound vrna promoter
80	<a href="#">c4rmxC_</a>	Alignment	not modelled	9.4	25	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> phi92_gp150; <b>PDBTitle:</b> apo crystal structure of the colanidase tailspike protein gp150 of2 phage phi92
81	<a href="#">c5fn2B_</a>	Alignment	not modelled	9.3	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> presenilin-1; <b>PDBTitle:</b> cryo-em structure of gamma secretase in complex with a drug dapt
82	<a href="#">c2ywxA_</a>	Alignment	not modelled	9.3	26	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase catalytic subunit; <b>PDBTitle:</b> crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from methanocaldococcus jannaschii
83	<a href="#">c4yjwA_</a>	Alignment	not modelled	9.0	21	<b>PDB header:</b> structural genomics unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> duf3829 family protein; <b>PDBTitle:</b> crystal structure of a duf3829 family protein (bvu_3067) from2 bacteroides vulgatus atcc 8482 at 1.80 a resolution
84	<a href="#">c6o55B_</a>	Alignment	not modelled	8.8	23	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> n5-carboxyaminoimidazole ribonucleotide mutase; <b>PDBTitle:</b> crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 (pure) from legionella pneumophila
85	<a href="#">c4hb9A_</a>	Alignment	not modelled	8.7	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> similarities with probable monooxygenase; <b>PDBTitle:</b> crystal structure of a putative fad containing monooxygenase from2 photorhabdus luminescens subsp. laumondii tto1 (target psi-012791)
86	<a href="#">d2do3a1</a>	Alignment	not modelled	8.7	35	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> SPT5 KOW domain-like
87	<a href="#">d1pzxa_</a>	Alignment	not modelled	8.4	10	<b>Fold:</b> DAK1/DegV-like <b>Superfamily:</b> DAK1/DegV-like <b>Family:</b> DegV-like
88	<a href="#">c4x9xA_</a>	Alignment	not modelled	8.4	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> degv domain-containing protein mw1315; <b>PDBTitle:</b> biochemical roles for conserved residues in the bacterial fatty acid2 binding protein family
89	<a href="#">c2e85B_</a>	Alignment	not modelled	8.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hydrogenase 3 maturation protease; <b>PDBTitle:</b> crystal structure of the hydrogenase 3 maturation protease
90	<a href="#">d1nz9a_</a>	Alignment	not modelled	8.2	41	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> N-utilization substance G protein NusG, C-terminal domain
91	<a href="#">c2qmhK_</a>	Alignment	not modelled	8.0	16	<b>PDB header:</b> transferase <b>Chain:</b> K: <b>PDB Molecule:</b> hpr kinase/phosphorylase; <b>PDBTitle:</b> structure of v267f mutant hprk/p
92	<a href="#">c3izq1_</a>	Alignment	not modelled	7.9	33	<b>PDB header:</b> ribosomal protein,hydrolase <b>Chain:</b> 1: <b>PDB Molecule:</b> elongation factor 1 alpha-like protein; <b>PDBTitle:</b> structure of the dom34-hbs1-gdnpn complex bound to a translating2 ribosome
93	<a href="#">c3j38z_</a>	Alignment	not modelled	7.9	40	<b>PDB header:</b> ribosome <b>Chain:</b> Z: <b>PDB Molecule:</b> 40s ribosomal protein s25; <b>PDBTitle:</b> structure of the d. melanogaster 40s ribosomal proteins
94	<a href="#">c2dt8A_</a>	Alignment	not modelled	7.8	10	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> degv family protein; <b>PDBTitle:</b> fatty acid binding of a degv family protein from thermus thermophilus
95	<a href="#">c4kd6A_</a>	Alignment	not modelled	7.8	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of a enoyl-coa hydratase/isomerase from burkholderia2 graminis c4d1m
96	<a href="#">c5ttxB_</a>	Alignment	not modelled	7.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hydrogenase 2 maturation peptidase; <b>PDBTitle:</b> crystal structure of hydrogenase 2 maturation peptidase from2 thaumarchaeota archaeon scgc_ab-539-e09
97	<a href="#">c3qxiA_</a>	Alignment	not modelled	7.8	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase echa1; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase echa1 from mycobacterium2 marinum
98	<a href="#">c4ytiB_</a>	Alignment	not modelled	7.7	35	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription elongation factor spt5; <b>PDBTitle:</b> structure of the kow2-kow3 domain of transcription elongation factor2 spt5.
99	<a href="#">c3pl5A_</a>	Alignment	not modelled	7.7	10	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> fatty acid binding protein