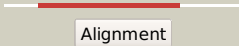

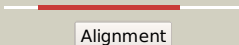





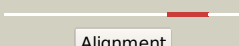

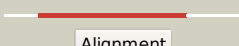

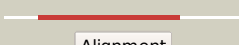







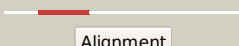
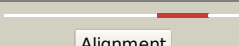
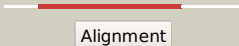

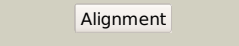



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2793c_(truB)_3102374_3103270
Date	Wed Aug 7 12:50:45 BST 2019
Unique Job ID	7f8b027743952654

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1k8wA_</a>	Alignment		100.0	34	<b>PDB header:</b> lyase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> trna pseudouridine synthase b; <b>PDBTitle:</b> crystal structure of the e. coli pseudouridine synthase2 trub bound to a t stem-loop rna
2	<a href="#">c1sgvA_</a>	Alignment		100.0	93	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> trna pseudouridine synthase b; <b>PDBTitle:</b> structure of trna psi55 pseudouridine synthase (trub)
3	<a href="#">d1k8wa5</a>	Alignment		100.0	40	<b>Fold:</b> Pseudouridine synthase <b>Superfamily:</b> Pseudouridine synthase <b>Family:</b> Pseudouridine synthase II TruB
4	<a href="#">d1r3ea2</a>	Alignment		100.0	38	<b>Fold:</b> Pseudouridine synthase <b>Superfamily:</b> Pseudouridine synthase <b>Family:</b> Pseudouridine synthase II TruB
5	<a href="#">c2ey4A_</a>	Alignment		100.0	31	<b>PDB header:</b> isomerase/biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable trna pseudouridine synthase b; <b>PDBTitle:</b> crystal structure of a cbf5-nop10-gar1 complex
6	<a href="#">c3uiaiA_</a>	Alignment		100.0	32	<b>PDB header:</b> isomerase/chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> h/aca ribonucleoprotein complex subunit 4; <b>PDBTitle:</b> structure of the shq1-cbf5-nop10-gar1 complex from saccharomyces2 cerevisiae
7	<a href="#">c2apoA_</a>	Alignment		100.0	35	<b>PDB header:</b> isomerase/rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable trna pseudouridine synthase b; <b>PDBTitle:</b> crystal structure of the methanococcus jannaschii cbf52 nop10 complex
8	<a href="#">d1sgva2</a>	Alignment		100.0	92	<b>Fold:</b> Pseudouridine synthase <b>Superfamily:</b> Pseudouridine synthase <b>Family:</b> Pseudouridine synthase II TruB
9	<a href="#">d2ey4a2</a>	Alignment		100.0	38	<b>Fold:</b> Pseudouridine synthase <b>Superfamily:</b> Pseudouridine synthase <b>Family:</b> Pseudouridine synthase II TruB
10	<a href="#">c1ze2B_</a>	Alignment		100.0	38	<b>PDB header:</b> lyase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> trna pseudouridine synthase b; <b>PDBTitle:</b> conformational change of pseudouridine 55 synthase upon its2 association with rna substrate
11	<a href="#">d2apoa2</a>	Alignment		100.0	41	<b>Fold:</b> Pseudouridine synthase <b>Superfamily:</b> Pseudouridine synthase <b>Family:</b> Pseudouridine synthase II TruB

12	<a href="#">c2omIA</a>	 Alignment		99.2	16	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> ribosomal large subunit pseudouridine synthase e; <b>PDBTitle:</b> crystal structure of e. coli pseudouridine synthase rlue
13	<a href="#">c2olwB</a>	 Alignment		98.6	17	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> ribosomal large subunit pseudouridine synthase e; <b>PDBTitle:</b> crystal structure of e. coli pseudouridine synthase rlue
14	<a href="#">d1sgva1</a>	 Alignment		97.9	100	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> PUA domain
15	<a href="#">d1kska4</a>	 Alignment		97.9	24	<b>Fold:</b> Pseudouridine synthase <b>Superfamily:</b> Pseudouridine synthase <b>Family:</b> Pseudouridine synthase RsuA/RLuD
16	<a href="#">d1k8wa3</a>	 Alignment		97.9	16	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> PUA domain
17	<a href="#">d1vioa1</a>	 Alignment		97.9	18	<b>Fold:</b> Pseudouridine synthase <b>Superfamily:</b> Pseudouridine synthase <b>Family:</b> Pseudouridine synthase RsuA/RLuD
18	<a href="#">c3dh3C</a>	 Alignment		97.8	25	<b>PDB header:</b> isomerase/rna <b>Chain:</b> C; <b>PDB Molecule:</b> ribosomal large subunit pseudouridine synthase f; <b>PDBTitle:</b> crystal structure of rluf in complex with a 22 nucleotide rna2 substrate
19	<a href="#">c2v9ka</a>	 Alignment		97.7	23	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein flj32312; <b>PDBTitle:</b> crystal structure of human pus10, a novel pseudouridine2 synthase.
20	<a href="#">c2gmIA</a>	 Alignment		97.7	25	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> ribosomal large subunit pseudouridine synthase f; <b>PDBTitle:</b> crystal structure of catalytic domain of e.coli rluf
21	<a href="#">c4lgtA</a>	 Alignment	not modelled	97.6	28	<b>PDB header:</b> isomerase/rna <b>Chain:</b> A; <b>PDB Molecule:</b> ribosomal large subunit pseudouridine synthase b; <b>PDBTitle:</b> crystal structure of the catalytic domain of rlub in complex with a2 21-nucleotide rna substrate
22	<a href="#">d1v9ka</a>	 Alignment	not modelled	97.3	25	<b>Fold:</b> Pseudouridine synthase <b>Superfamily:</b> Pseudouridine synthase <b>Family:</b> Pseudouridine synthase RsuA/RLuD
23	<a href="#">c1qyuA</a>	 Alignment	not modelled	97.2	24	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> ribosomal large subunit pseudouridine synthase d; <b>PDBTitle:</b> structure of the catalytic domain of 23s rrna pseudouridine2 synthase rlud
24	<a href="#">c3zv0D</a>	 Alignment	not modelled	97.2	21	<b>PDB header:</b> cell cycle <b>Chain:</b> D; <b>PDB Molecule:</b> h/aca ribonucleoprotein complex subunit 4; <b>PDBTitle:</b> structure of the shq1p-cbf5p complex
25	<a href="#">c1vioA</a>	 Alignment	not modelled	97.2	21	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> ribosomal small subunit pseudouridine synthase a; <b>PDBTitle:</b> crystal structure of pseudouridylylase synthase
26	<a href="#">c1kska</a>	 Alignment	not modelled	97.1	23	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> ribosomal small subunit pseudouridine synthase a; <b>PDBTitle:</b> structure of rsua
27	<a href="#">c5ubaA</a>	 Alignment	not modelled	97.1	26	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> rna pseudouridylylase domain-containing protein 4; <b>PDBTitle:</b> human rna pseudouridylylase synthase domain containing 4
28	<a href="#">c2ista</a>	 Alignment	not modelled	97.1	23	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> ribosomal large subunit pseudouridine synthase d;

						<b>PDBTitle:</b> crystal structure of rlud from e. coli
29	<a href="#">d1v9fa_</a>	Alignment	not modelled	97.0	24	<b>Fold:</b> Pseudouridine synthase <b>Superfamily:</b> Pseudouridine synthase <b>Family:</b> Pseudouridine synthase RsuA/RluD
30	<a href="#">c1v9fA_</a>	Alignment	not modelled	97.0	24	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal large subunit pseudouridine synthase d; <b>PDBTitle:</b> crystal structure of catalytic domain of pseudouridine2 synthase rlud from escherichia coli
31	<a href="#">c2i82D_</a>	Alignment	not modelled	97.0	26	<b>PDB header:</b> lyase/rna <b>Chain:</b> D: <b>PDB Molecule:</b> ribosomal large subunit pseudouridine synthase a; <b>PDBTitle:</b> crystal structure of pseudouridine synthase rlua: indirect2 sequence readout through protein-induced rna structure
32	<a href="#">c5vbbA_</a>	Alignment	not modelled	97.0	17	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna pseudouridylyate synthase domain-containing protein 1; <b>PDBTitle:</b> human rna pseudouridylyate synthase domain containing 1
33	<a href="#">d2apoa1</a>	Alignment	not modelled	96.2	17	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> PUA domain
34	<a href="#">d2ey4a1</a>	Alignment	not modelled	95.5	21	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> PUA domain
35	<a href="#">d1r3ea1</a>	Alignment	not modelled	93.9	17	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> PUA domain
36	<a href="#">d1szwa_</a>	Alignment	not modelled	89.1	16	<b>Fold:</b> Pseudouridine synthase <b>Superfamily:</b> Pseudouridine synthase <b>Family:</b> tRNA pseudouridine synthase TruD
37	<a href="#">c1sb7A_</a>	Alignment	not modelled	88.9	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> trna pseudouridine synthase d; <b>PDBTitle:</b> crystal structure of the e.coli pseudouridine synthase trud
38	<a href="#">c3m4xA_</a>	Alignment	not modelled	84.8	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> no11/nop2/sun family protein; <b>PDBTitle:</b> structure of a ribosomal methyltransferase
39	<a href="#">c1z2zB_</a>	Alignment	not modelled	82.9	31	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> probable trna pseudouridine synthase d; <b>PDBTitle:</b> crystal structure of the putative trna pseudouridine synthase d (trud)2 from methanosarcina mazei, northeast structural genomics target mar1
40	<a href="#">c5kkpA_</a>	Alignment	not modelled	81.3	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> pseudouridylyate synthase 7; <b>PDBTitle:</b> crystal structure of human pseudouridylyate synthase 7
41	<a href="#">d1iq8a3</a>	Alignment	not modelled	76.2	17	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> PUA domain
42	<a href="#">c1q7hA_</a>	Alignment	not modelled	73.8	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> structure of a conserved pua domain protein from thermoplasma2 acidophilum
43	<a href="#">d2a2pa1</a>	Alignment	not modelled	63.2	26	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Selenoprotein W-related
44	<a href="#">d1q7ha1</a>	Alignment	not modelled	59.9	24	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> PUA domain
45	<a href="#">c2b78A_</a>	Alignment	not modelled	59.3	7	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein smu.776; <b>PDBTitle:</b> a putative sam-dependent methyltransferase from streptococcus mutans
46	<a href="#">c2frxD_</a>	Alignment	not modelled	59.3	22	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical protein yebu; <b>PDBTitle:</b> crystal structure of yebu, a m5c rna methyltransferase from e.coli
47	<a href="#">c3d79A_</a>	Alignment	not modelled	59.2	23	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein ph0734; <b>PDBTitle:</b> crystal structure of hypothetical protein ph0734.1 from2 hyperthermophilic archaea pyrococcus horikoshii ot3
48	<a href="#">c3m6wA_</a>	Alignment	not modelled	58.6	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rrna methylase; <b>PDBTitle:</b> multi-site-specific 16s rna methyltransferase rsmf from thermus2 thermophilus in space group p21212 in complex with s-adenosyl-l-3 methionine
49	<a href="#">d2as0a1</a>	Alignment	not modelled	55.2	15	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> Hypothetical RNA methyltransferase domain (HRMD)
50	<a href="#">d2b78a1</a>	Alignment	not modelled	52.8	10	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> Hypothetical RNA methyltransferase domain (HRMD)
51	<a href="#">c6em5l_</a>	Alignment	not modelled	47.1	5	<b>PDB header:</b> ribosome <b>Chain:</b> L: <b>PDB Molecule:</b> 60s ribosomal protein l13-a; <b>PDBTitle:</b> state d architectural model (nsa1-tap flag-ytm1) - visualizing the2 assembly pathway of nucleolar pre-60s ribosomes
52	<a href="#">c1iq8B_</a>	Alignment	not modelled	45.9	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> archaeosine trna-guanine transglycosylase; <b>PDBTitle:</b> crystal structure of archaeosine trna-guanine transglycosylase from2 pyrococcus horikoshii
53	<a href="#">c1zs7A_</a>	Alignment	not modelled	23.5	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ape0525; <b>PDBTitle:</b> the structure of gene product ape0525 from aeropyrum pernix
						<b>PDB header:</b> transcription

54	<a href="#">c5ey0A_</a>	Alignment	not modelled	23.0	57	<b>Chain:</b> A: <b>PDB Molecule:</b> gtp-sensing transcriptional pleiotropic repressor cody; <b>PDBTitle:</b> crystal structure of cody from staphylococcus aureus with gtp and ile
55	<a href="#">d1lzia_</a>	Alignment	not modelled	22.8	26	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> alpha-1,3-galactosyltransferase-like
56	<a href="#">d1k7ia2</a>	Alignment	not modelled	22.3	39	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Serralysin-like metalloprotease, catalytic (N-terminal) domain
57	<a href="#">d1r9ha_</a>	Alignment	not modelled	21.5	18	<b>Fold:</b> FKBP-like <b>Superfamily:</b> FKBP-like <b>Family:</b> FKBP immunophilin/proline isomerase
58	<a href="#">c4ayjA_</a>	Alignment	not modelled	21.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bogt - metal-independent glycosyltransferase; <b>PDBTitle:</b> molecular structure of a metal-independent bacterial2 glycosyltransferase that catalyzes the synthesis of histo-blood group3 a antigen
59	<a href="#">d1g9ka2</a>	Alignment	not modelled	20.4	39	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Serralysin-like metalloprotease, catalytic (N-terminal) domain
60	<a href="#">c3r90E_</a>	Alignment	not modelled	18.4	11	<b>PDB header:</b> rna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> malignant t cell-amplified sequence 1; <b>PDBTitle:</b> crystal structure of malignant t cell-amplified sequence 1 protein
61	<a href="#">c3lfaA_</a>	Alignment	not modelled	18.4	40	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein fto; <b>PDBTitle:</b> crystal structure of the fat mass and obesity associated (fto) protein2 reveals basis for its substrate specificity
62	<a href="#">d2gx8a1</a>	Alignment	not modelled	17.8	17	<b>Fold:</b> NIF3 (NGG1p interacting factor 3)-like <b>Superfamily:</b> NIF3 (NGG1p interacting factor 3)-like <b>Family:</b> NIF3 (NGG1p interacting factor 3)-like
63	<a href="#">c2vg2C_</a>	Alignment	not modelled	17.6	15	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> undecaprenyl pyrophosphate synthetase; <b>PDBTitle:</b> rv2361 with ipp
64	<a href="#">c3czxA_</a>	Alignment	not modelled	17.3	50	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative n-acetylmuramoyl-l-alanine amidase; <b>PDBTitle:</b> the crystal structure of the putative n-acetylmuramoyl-l-2 alanine amidase from neisseria meningitidis
65	<a href="#">d1muga_</a>	Alignment	not modelled	17.3	19	<b>Fold:</b> Uracil-DNA glycosylase-like <b>Superfamily:</b> Uracil-DNA glycosylase-like <b>Family:</b> Mug-like
66	<a href="#">d2jn9a1</a>	Alignment	not modelled	16.7	16	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> YkvR-like <b>Family:</b> YkvR-like
67	<a href="#">d1sata2</a>	Alignment	not modelled	16.6	33	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Serralysin-like metalloprotease, catalytic (N-terminal) domain
68	<a href="#">d2fug21</a>	Alignment	not modelled	16.3	11	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> NQO2-like
69	<a href="#">c2lgoA_</a>	Alignment	not modelled	16.1	20	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> fkbp; <b>PDBTitle:</b> solution nmr structure of a fkbp-type peptidyl-prolyl cis-trans2 isomerase from giardia lamblia, seattle structural genomics center3 for infectious disease target gilaa.00840.a
70	<a href="#">d3saka_</a>	Alignment	not modelled	15.5	17	<b>Fold:</b> p53 tetramerization domain <b>Superfamily:</b> p53 tetramerization domain <b>Family:</b> p53 tetramerization domain
71	<a href="#">c5n9jA_</a>	Alignment	not modelled	15.2	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> mediator of rna polymerase ii transcription subunit 14; <b>PDBTitle:</b> core mediator of transcriptional regulation
72	<a href="#">c2gx8B_</a>	Alignment	not modelled	15.0	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> nif3-related protein; <b>PDBTitle:</b> the crystal structure of bacillus cereus protein related to nif3
73	<a href="#">c4dmgA_</a>	Alignment	not modelled	14.4	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein ttha1493; <b>PDBTitle:</b> thermus thermophilus m5c1942 methyltransferase rlmo
74	<a href="#">d2cx1a1</a>	Alignment	not modelled	14.3	22	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> PUA domain
75	<a href="#">c3c7tB_</a>	Alignment	not modelled	13.3	31	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ecdysteroid-phosphate phosphatase; <b>PDBTitle:</b> crystal structure of the ecdysone phosphate phosphatase, eppase, from2 bombix mori in complex with tungstate
76	<a href="#">c1sqwA_</a>	Alignment	not modelled	12.7	8	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> saccharomyces cerevisiae nip7p homolog; <b>PDBTitle:</b> crystal structure of kd93, a novel protein expressed in the2 human pro
77	<a href="#">d1kapp2</a>	Alignment	not modelled	12.6	39	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Serralysin-like metalloprotease, catalytic (N-terminal) domain
78	<a href="#">c5u0pN_</a>	Alignment	not modelled	12.1	15	<b>PDB header:</b> transcription <b>Chain:</b> N: <b>PDB Molecule:</b> mediator complex subunit 14; <b>PDBTitle:</b> cryo-em structure of the transcriptional mediator
79	<a href="#">d1g5ua_</a>	Alignment	not modelled	12.0	14	<b>Fold:</b> Profilin-like <b>Superfamily:</b> Profilin (actin-binding protein)

						<b>Family:</b> Profilin (actin-binding protein)
80	<a href="#">c1mszA_</a>	Alignment	not modelled	11.7	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding protein smubp-2; <b>PDBTitle:</b> solution structure of the r3h domain from human smubp-2
81	<a href="#">d1msza_</a>	Alignment	not modelled	11.7	14	<b>Fold:</b> IF3-like <b>Superfamily:</b> R3H domain <b>Family:</b> R3H domain
82	<a href="#">d1t8sa_</a>	Alignment	not modelled	11.7	21	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
83	<a href="#">c3vseA_</a>	Alignment	not modelled	11.7	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of methyltransferase
84	<a href="#">d3nula_</a>	Alignment	not modelled	11.3	17	<b>Fold:</b> Profilin-like <b>Superfamily:</b> Profilin (actin-binding protein) <b>Family:</b> Profilin (actin-binding protein)
85	<a href="#">c1pk1B_</a>	Alignment	not modelled	11.2	18	<b>PDB header:</b> transcription repression <b>Chain:</b> B: <b>PDB Molecule:</b> sex comb on midleg cg9495-pa; <b>PDBTitle:</b> hetero sam domain structure of ph and scm.
86	<a href="#">c4binA_</a>	Alignment	not modelled	11.2	50	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylmuramoyl-l-alanine amidase amic; <b>PDBTitle:</b> crystal structure of the e. coli n-acetylmuramoyl-l-alanine amidase2 amic
87	<a href="#">c2nydB_</a>	Alignment	not modelled	11.1	15	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> upf0135 protein sa1388; <b>PDBTitle:</b> crystal structure of staphylococcus aureus hypothetical protein sa1388
88	<a href="#">c4uwqK_</a>	Alignment	not modelled	11.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> K: <b>PDB Molecule:</b> soxy protein; <b>PDBTitle:</b> crystal structure of the disulfide-linked complex of the2 thiosulfodyrolase soxb with the carrier-protein soxyz from3 thermus thermophilus
89	<a href="#">c2xs4A_</a>	Alignment	not modelled	11.0	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> karilysin protease; <b>PDBTitle:</b> structure of karilysin catalytic mmp domain in complex with magnesium
90	<a href="#">d1bqqm_</a>	Alignment	not modelled	11.0	37	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
91	<a href="#">c3dnhB_</a>	Alignment	not modelled	10.9	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein atu2129; <b>PDBTitle:</b> the crystal structure of the protein atu2129 (unknown function) from2 agrobacterium tumefaciens str. c58
92	<a href="#">d1o7qa_</a>	Alignment	not modelled	10.8	21	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> alpha-1,3-galactosyltransferase-like
93	<a href="#">d3blhb1</a>	Alignment	not modelled	10.7	17	<b>Fold:</b> Cyclin-like <b>Superfamily:</b> Cyclin-like <b>Family:</b> Cyclin
94	<a href="#">c3ne8A_</a>	Alignment	not modelled	10.6	50	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylmuramoyl-l-alanine amidase; <b>PDBTitle:</b> the crystal structure of a domain from n-acetylmuramoyl-l-alanine2 amidase of bartonella henselae str. houston-1
95	<a href="#">d1cglA_</a>	Alignment	not modelled	10.4	28	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
96	<a href="#">d2ovxa1</a>	Alignment	not modelled	10.4	33	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
97	<a href="#">d2gy9i1</a>	Alignment	not modelled	10.1	16	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Translational machinery components
98	<a href="#">d1hv5a_</a>	Alignment	not modelled	10.1	33	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Matrix metalloproteases, catalytic domain
99	<a href="#">d2vqe11</a>	Alignment	not modelled	9.5	25	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Translational machinery components