



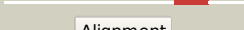


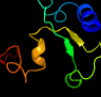








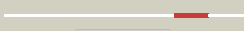

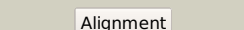


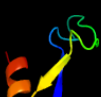


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1128c_(-)_1251622_1252977
Date	Wed Jul 31 22:05:21 BST 2019
Unique Job ID	d1434d67f1a8692c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2qgpA_</a>	 Alignment		99.2	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hnh endonuclease; <b>PDBTitle:</b> x-ray structure of the hnh endonuclease from geobacter2 metallireducens. northeast structural genomics consortium target3 gmr87.
2	<a href="#">c6ghcA_</a>	 Alignment		98.9	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-methylcytosine-specific restriction enzyme a; <b>PDBTitle:</b> modification dependent eokmcra restriction endonuclease
3	<a href="#">c5mkwA_</a>	 Alignment		98.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dna annealing helicase and endonuclease zranb3; <b>PDBTitle:</b> crystal structure of the human zranb3 hnh domain
4	<a href="#">c5x1hS_</a>	 Alignment		98.7	14	<b>PDB header:</b> protein transport <b>Chain:</b> S: <b>PDB Molecule:</b> icmj (dotn); <b>PDBTitle:</b> structure of legionella pneumophila dotn
5	<a href="#">c5h0mA_</a>	 Alignment		98.3	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hnh endonuclease; <b>PDBTitle:</b> crystal structure of deep-sea thermophilic bacteriophage gve2 hnh2 endonuclease with zinc ion
6	<a href="#">c5vgbA_</a>	 Alignment		98.2	23	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> crispr-associated endonuclease cas9; <b>PDBTitle:</b> crystal structure of nmecas9 hnh domain bound to anti-crispr acric1
7	<a href="#">c5zmmD_</a>	 Alignment		98.0	23	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein mcra; <b>PDBTitle:</b> structure of the type iv phosphorothioation-dependent restriction2 endonuclease scomcra
8	<a href="#">c4ogeA_</a>	 Alignment		97.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hnh endonuclease domain protein; <b>PDBTitle:</b> crystal structure of the type ii-c cas9 enzyme from actinomyces2 naeslundii
9	<a href="#">c5axwA_</a>	 Alignment		97.1	11	<b>PDB header:</b> hydrolase/rna/dna <b>Chain:</b> A: <b>PDB Molecule:</b> crispr-associated endonuclease cas9; <b>PDBTitle:</b> crystal structure of staphylococcus aureus cas9 in complex with sgrna2 and target dna (ttgggt pam)
10	<a href="#">c6ghsA_</a>	 Alignment		95.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tagi restriction endonuclease; <b>PDBTitle:</b> modification dependent tagi restriction endonuclease
11	<a href="#">d2gykb1</a>	 Alignment		87.2	27	<b>Fold:</b> His-Me finger endonucleases <b>Superfamily:</b> His-Me finger endonucleases <b>Family:</b> HNH-motif

12	<a href="#">c4cmqB_</a>	Alignment		85.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> crispr-associated endonuclease cas9/csn1; <b>PDBTitle:</b> crystal structure of mn-bound s.pyogenes cas9
13	<a href="#">d2jb0b1</a>	Alignment		77.9	23	<b>Fold:</b> His-Me finger endonucleases <b>Superfamily:</b> His-Me finger endonucleases <b>Family:</b> HNH-motif
14	<a href="#">c4qkoH_</a>	Alignment		59.2	19	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> H: <b>PDB Molecule:</b> pyocin-s2; <b>PDBTitle:</b> the crystal structure of the pyocin s2 nuclease domain, immunity2 protein complex at 1.8 angstroms
15	<a href="#">c4uhpA_</a>	Alignment		55.1	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> large component of pyocin ap41; <b>PDBTitle:</b> crystal structure of the pyocin ap41 dnase-immunity complex
16	<a href="#">c7ceiB_</a>	Alignment		55.0	23	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> protein (colicin e7 immunity protein); <b>PDBTitle:</b> the endonuclease domain of colicin e7 in complex with its inhibitor2 im7 protein
17	<a href="#">c5ew5C_</a>	Alignment		54.5	25	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> colicin-e9; <b>PDBTitle:</b> crystal structure of colicin e9 in complex with its immunity protein2 im9
18	<a href="#">c5g2xC_</a>	Alignment		51.9	28	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> group ii intron-encoded protein Itra; <b>PDBTitle:</b> structure a of group ii intron complexed with its reverse2 transcriptase
19	<a href="#">c3plwA_</a>	Alignment		46.7	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> recombination enhancement function protein; <b>PDBTitle:</b> ref protein from p1 bacteriophage
20	<a href="#">c3mkzU_</a>	Alignment		45.4	16	<b>PDB header:</b> dna-binding protein/dna <b>Chain:</b> U: <b>PDB Molecule:</b> protein sobp; <b>PDBTitle:</b> structure of sobp(155-272)-18mer complex, p21 form
21	<a href="#">d2dlka1</a>	Alignment	not modelled	43.9	50	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
22	<a href="#">c3mkyP_</a>	Alignment	not modelled	36.1	16	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> P: <b>PDB Molecule:</b> protein sobp; <b>PDBTitle:</b> structure of sobp(155-323)-18mer dna complex, i23 form
23	<a href="#">d1zfda_</a>	Alignment	not modelled	33.1	42	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
24	<a href="#">d1a1ga1</a>	Alignment	not modelled	32.1	21	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
25	<a href="#">c1va1A_</a>	Alignment	not modelled	32.1	38	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor sp1; <b>PDBTitle:</b> solution structure of transcription factor sp1 dna binding2 domain (zinc finger 1)
26	<a href="#">d1a1ia1</a>	Alignment	not modelled	31.4	38	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
27	<a href="#">d2glia4</a>	Alignment	not modelled	29.1	33	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
28	<a href="#">d1vz0a1</a>	Alignment	not modelled	28.9	29	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> KorB DNA-binding domain-like <b>Family:</b> KorB DNA-binding domain-like
29	<a href="#">d1nlsa_</a>	Alignment	not modelled	28.4	33	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers

						<b>Family:</b> Classic zinc finger, C2H2
30	<a href="#">d1w6ga1</a>	Alignment	not modelled	27.8	19	<b>Fold:</b> Supersandwich <b>Superfamily:</b> Amine oxidase catalytic domain <b>Family:</b> Amine oxidase catalytic domain
31	<a href="#">d2ysca1</a>	Alignment	not modelled	26.8	32	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
32	<a href="#">d1a1ha1</a>	Alignment	not modelled	25.4	38	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
33	<a href="#">d1u86a1</a>	Alignment	not modelled	24.4	50	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
34	<a href="#">c1pxeA</a>	Alignment	not modelled	23.8	55	<b>PDB header:</b> metal binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> neural zinc finger transcription factor 1; <b>PDBTitle:</b> solution structure of a cchhc domain of neural zinc finger2 factor-1
35	<a href="#">d1tf3a2</a>	Alignment	not modelled	23.5	38	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
36	<a href="#">d1bhia</a>	Alignment	not modelled	23.2	63	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
37	<a href="#">d1ubdc3</a>	Alignment	not modelled	22.6	38	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
38	<a href="#">d1aaya1</a>	Alignment	not modelled	22.5	38	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
39	<a href="#">d1ejga</a>	Alignment	not modelled	21.8	27	<b>Fold:</b> Crambin-like <b>Superfamily:</b> Crambin-like <b>Family:</b> Crambin-like
40	<a href="#">d1f2ig1</a>	Alignment	not modelled	21.8	38	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
41	<a href="#">d1ubdc4</a>	Alignment	not modelled	21.6	33	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
42	<a href="#">d2glia3</a>	Alignment	not modelled	21.3	25	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
43	<a href="#">d1sp2a</a>	Alignment	not modelled	20.9	17	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
44	<a href="#">d2dlka2</a>	Alignment	not modelled	19.8	38	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
45	<a href="#">d1jmna</a>	Alignment	not modelled	19.5	20	<b>Fold:</b> Crambin-like <b>Superfamily:</b> Crambin-like <b>Family:</b> Crambin-like
46	<a href="#">c3cwbQ</a>	Alignment	not modelled	19.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> Q; <b>PDB Molecule:</b> mitochondrial cytochrome c1, heme protein; <b>PDBTitle:</b> chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
47	<a href="#">d1w2za1</a>	Alignment	not modelled	18.9	13	<b>Fold:</b> Supersandwich <b>Superfamily:</b> Amine oxidase catalytic domain <b>Family:</b> Amine oxidase catalytic domain
48	<a href="#">c2pncB</a>	Alignment	not modelled	18.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> copper amine oxidase, liver isozyme; <b>PDBTitle:</b> crystal structure of bovine plasma copper-containing amine oxidase in2 complex with clonidine
49	<a href="#">d2glia5</a>	Alignment	not modelled	17.9	50	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
50	<a href="#">c2b8tA</a>	Alignment	not modelled	17.1	13	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> thymidine kinase; <b>PDBTitle:</b> crystal structure of thymidine kinase from u.urealyticum in complex2 with thymidine
51	<a href="#">c3ga3A</a>	Alignment	not modelled	16.6	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> interferon-induced helicase c domain-containing <b>PDBTitle:</b> crystal structure of the c-terminal domain of human mda5
52	<a href="#">d1d6za1</a>	Alignment	not modelled	16.3	9	<b>Fold:</b> Supersandwich <b>Superfamily:</b> Amine oxidase catalytic domain <b>Family:</b> Amine oxidase catalytic domain
53	<a href="#">c1orxA</a>	Alignment	not modelled	15.9	33	<b>PDB header:</b> antibiotic <b>Chain:</b> A; <b>PDB Molecule:</b> kalata b1; <b>PDBTitle:</b> solution structure of the acyclic permutant des-(24-28)-2 kalata b1.
54	<a href="#">d2ho2a1</a>	Alignment	not modelled	15.7	22	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
55	<a href="#">d2b8ta2</a>	Alignment	not modelled	15.4	30	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> Type II thymidine kinase zinc finger
						<b>Fold:</b> Supersandwich

56	<a href="#">d2oqea1</a>	Alignment	not modelled	15.3	16	<b>Superfamily:</b> Amine oxidase catalytic domain <b>Family:</b> Amine oxidase catalytic domain
57	<a href="#">c1ui7A_</a>	Alignment	not modelled	14.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phenylethylamine oxidase; <b>PDBTitle:</b> site-directed mutagenesis of his433 involved in binding of 2 copper ion in arthrobacter globiformis amine oxidase
58	<a href="#">c3higB_</a>	Alignment	not modelled	14.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> amiloride-sensitive amine oxidase; <b>PDBTitle:</b> crystal structure of human diamine oxidase in complex with the2 inhibitor berenil
59	<a href="#">c5yixB_</a>	Alignment	not modelled	14.8	27	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> cell cycle regulatory protein gcrA; <b>PDBTitle:</b> caulobacter crescentus gcrA sigma-interacting domain (sid) in complex2 with domain 2 of sigma 70
60	<a href="#">c2c10D_</a>	Alignment	not modelled	14.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> membrane copper amine oxidase; <b>PDBTitle:</b> the structure of a truncated, soluble version of semicarbazide-2 sensitive amine oxidase
61	<a href="#">d1tf3a1</a>	Alignment	not modelled	14.4	38	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
62	<a href="#">c2w4rB_</a>	Alignment	not modelled	14.2	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable atp-dependent rna helicase dhx58; <b>PDBTitle:</b> crystal structure of the regulatory domain of human lgp2
63	<a href="#">c2jydA_</a>	Alignment	not modelled	14.1	60	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> f5 domain of myelin transcription factor 1; <b>PDBTitle:</b> structure of the fifth zinc finger of myelin transcription2 factor 1
64	<a href="#">d1tf6a1</a>	Alignment	not modelled	13.7	38	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
65	<a href="#">c1nbwA_</a>	Alignment	not modelled	13.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol dehydratase reactivase alpha subunit; <b>PDBTitle:</b> glycerol dehydratase reactivase
66	<a href="#">c4ttnA_</a>	Alignment	not modelled	13.5	44	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> kalata-b1; <b>PDBTitle:</b> quasi-racemic structure of [g6a]kalata b1
67	<a href="#">c4ttoA_</a>	Alignment	not modelled	13.4	44	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> kalata-b1; <b>PDBTitle:</b> quasi-racemic structure of [v25a] kalata b1
68	<a href="#">c4ttmA_</a>	Alignment	not modelled	13.3	44	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> kalata-b1; <b>PDBTitle:</b> racemic structure of kalata b1 (kb1)
69	<a href="#">d1pt4a_</a>	Alignment	not modelled	13.3	44	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Cyclotides <b>Family:</b> Kalata B1
70	<a href="#">c1d6uB_</a>	Alignment	not modelled	13.2	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> copper amine oxidase; <b>PDBTitle:</b> crystal structure of e. coli amine oxidase anaerobically reduced with2 beta-phenylethylamine
71	<a href="#">c2jxbA_</a>	Alignment	not modelled	13.1	26	<b>PDB header:</b> signaling protein complex <b>Chain:</b> A: <b>PDB Molecule:</b> t-cell surface glycoprotein cd3 epsilon chain, <b>PDBTitle:</b> structure of cd3epsilon-nck2 first sh3 domain complex
72	<a href="#">c2khaA_</a>	Alignment	not modelled	13.1	44	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> kalata-b1; <b>PDBTitle:</b> solution structure of linear kalata b1 (loop 6)
73	<a href="#">d1nbla_</a>	Alignment	not modelled	13.1	33	<b>Fold:</b> Crambin-like <b>Superfamily:</b> Crambin-like <b>Family:</b> Crambin-like
74	<a href="#">c2mn1A_</a>	Alignment	not modelled	13.0	44	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> kalata b1[w23ww]; <b>PDBTitle:</b> solution structure of kalata b1[w23ww]
75	<a href="#">d1lorA_</a>	Alignment	not modelled	12.8	20	<b>Fold:</b> Crambin-like <b>Superfamily:</b> Crambin-like <b>Family:</b> Crambin-like
76	<a href="#">d1okha_</a>	Alignment	not modelled	12.7	30	<b>Fold:</b> Crambin-like <b>Superfamily:</b> Crambin-like <b>Family:</b> Crambin-like
77	<a href="#">c1nb1A_</a>	Alignment	not modelled	12.6	44	<b>PDB header:</b> antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> kalata b1; <b>PDBTitle:</b> high resolution solution structure of kalata b1
78	<a href="#">d1nb1a_</a>	Alignment	not modelled	12.6	44	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Cyclotides <b>Family:</b> Kalata B1
79	<a href="#">c6dhrA_</a>	Alignment	not modelled	12.3	44	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> rivi3; <b>PDBTitle:</b> nmr solution structure of rivi3
80	<a href="#">c3loyB_</a>	Alignment	not modelled	12.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> copper amine oxidase; <b>PDBTitle:</b> crystal structure of a copper-containing benzylamine oxidase from2 hansenula polymorpha
81	<a href="#">c1ekmC_</a>	Alignment	not modelled	12.2	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> copper amine oxidase; <b>PDBTitle:</b> crystal structure at 2.5 a resolution of zinc-substituted2 copper amine oxidase of hansenula polymorpha expressed in3 escherichia coli
82	<a href="#">c4esrB_</a>	Alignment	not modelled	12.0	17	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> jouberin; <b>PDBTitle:</b> molecular and structural characterization of the sh3 domain of ahi-12 in regulation of cellular resistance of bcr-abl+

						chronic myeloid leukemia cells to tyrosine kinase inhibitors <b>PDB header:</b> oxidoreductase
83	<a href="#">c6fcxA_</a>	Alignment	not modelled	11.6	12	<b>Chain:</b> A; <b>PDB Molecule:</b> methylenetetrahydrofolate reductase; <b>PDBTitle:</b> structure of human 5,10-methylenetetrahydrofolate reductase (mthfr)
84	<a href="#">c3pg6D_</a>	Alignment	not modelled	11.6	16	<b>PDB header:</b> ligase <b>Chain:</b> D; <b>PDB Molecule:</b> e3 ubiquitin-protein ligase dtx3l; <b>PDBTitle:</b> the carboxyl terminal domain of human deltex 3-like
85	<a href="#">d1jmpa_</a>	Alignment	not modelled	11.3	20	<b>Fold:</b> Crambin-like <b>Superfamily:</b> Crambin-like <b>Family:</b> Crambin-like
86	<a href="#">c2lamA_</a>	Alignment	not modelled	11.3	33	<b>PDB header:</b> antiviral protein <b>Chain:</b> A; <b>PDB Molecule:</b> cyclotide cter m; <b>PDBTitle:</b> three-dimensional structure of the cyclotide cter m
87	<a href="#">c3e4hA_</a>	Alignment	not modelled	11.0	33	<b>PDB header:</b> plant protein <b>Chain:</b> A; <b>PDB Molecule:</b> varv peptide f; <b>PDBTitle:</b> crystal structure of the cyclotide varv f
88	<a href="#">c3npgB_</a>	Alignment	not modelled	10.9	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> putative dipeptidyl-peptidase vi; <b>PDBTitle:</b> crystal structure of a putative dipeptidyl-peptidase vi (bacova_00612)2 from bacteroides ovatus at 1.72 a resolution
89	<a href="#">c1k48A_</a>	Alignment	not modelled	10.8	33	<b>PDB header:</b> plant protein <b>Chain:</b> A; <b>PDB Molecule:</b> kalata b1; <b>PDBTitle:</b> refined structure and disulfide pairing of the kalata b12 peptide
90	<a href="#">c1jzA_</a>	Alignment	not modelled	10.8	33	<b>PDB header:</b> plant protein <b>Chain:</b> A; <b>PDB Molecule:</b> kalata b1; <b>PDBTitle:</b> refined structure and disulfide pairing of the kalata b12 peptide
91	<a href="#">c3nbbC_</a>	Alignment	not modelled	10.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> peroxisomal primary amine oxidase; <b>PDBTitle:</b> crystal structure of mutant y305f expressed in e. coli in the copper2 amine oxidase from hansenula polymorpha
92	<a href="#">c2kq0A_</a>	Alignment	not modelled	10.5	23	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> e3 ubiquitin-protein ligase nedd4; <b>PDBTitle:</b> human nedd4 3rd ww domain complex with ebola zaire virus matrix2 protein vp40 derived peptide ilptappeyme
93	<a href="#">c2rf0D_</a>	Alignment	not modelled	10.2	21	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> mitogen-activated protein kinase kinase kinase 10; <b>PDBTitle:</b> crystal structure of human mixed lineage kinase map3k10 sh3 domain
94	<a href="#">c1ymzA_</a>	Alignment	not modelled	10.1	23	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> cc45; <b>PDBTitle:</b> cc45, an artificial ww domain designed using statistical2 coupling analysis
95	<a href="#">c2k7gA_</a>	Alignment	not modelled	10.1	33	<b>PDB header:</b> plant protein <b>Chain:</b> A; <b>PDB Molecule:</b> varv peptide f; <b>PDBTitle:</b> solution structure of varv f
96	<a href="#">c6bx3F_</a>	Alignment	not modelled	10.0	6	<b>PDB header:</b> gene regulation/transferase <b>Chain:</b> F; <b>PDB Molecule:</b> compass component spp1; <b>PDBTitle:</b> structure of histone h3k4 methyltransferase
97	<a href="#">c2f2iA_</a>	Alignment	not modelled	9.2	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A; <b>PDB Molecule:</b> kalata-b1; <b>PDBTitle:</b> solution structure of [p20d,v21k]-kalata b1
98	<a href="#">c1emxA_</a>	Alignment	not modelled	9.2	42	<b>PDB header:</b> toxin <b>Chain:</b> A; <b>PDB Molecule:</b> heteropodatoxin 2; <b>PDBTitle:</b> solution structure of hptx2, a toxin from heteropoda2 venatoria spider venom that blocks kv4.2 potassium channel
99	<a href="#">c1zw8A_</a>	Alignment	not modelled	9.1	27	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> zinc-responsive transcriptional regulator zap1; <b>PDBTitle:</b> solution structure of a zap1 zinc-responsive domain2 provides insights into metalloregulatory transcriptional3 repression in saccharomyces cerevisiae