






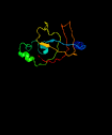



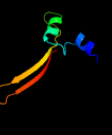



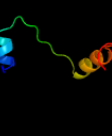





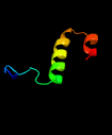


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2203 (-) _2468239_2468931
Date	Mon Aug 5 13:25:33 BST 2019
Unique Job ID	ddcbcebfe5bdf45

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5im3A_</a>	 Alignment		53.8	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonucleoside-diphosphate reductase; <b>PDBTitle:</b> crystal structure of the class i ribonucleotide reductase from2 pseudomonas aeruginosa in complex with datp
2	<a href="#">d1rra1</a>	 Alignment		48.7	10	<b>Fold:</b> R1 subunit of ribonucleotide reductase, N-terminal domain <b>Superfamily:</b> R1 subunit of ribonucleotide reductase, N-terminal domain <b>Family:</b> R1 subunit of ribonucleotide reductase, N-terminal domain
3	<a href="#">c3r1rB_</a>	 Alignment		47.5	11	<b>PDB header:</b> complex (oxidoreductase/peptide) <b>Chain:</b> B: <b>PDB Molecule:</b> ribonucleotide reductase r1 protein; <b>PDBTitle:</b> ribonucleotide reductase r1 protein with amppnp occupying2 the activity site from escherichia coli
4	<a href="#">c2wn8A_</a>	 Alignment		40.6	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adp-ribosyltransferase enzymatic component; <b>PDBTitle:</b> structural basis for substrate recognition in the enzymatic2 component of adp-ribosyltransferase toxin cdta from3 clostridium difficile
5	<a href="#">d2k54a1</a>	 Alignment		38.9	25	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Atu0742-like
6	<a href="#">c2nytB_</a>	 Alignment		37.2	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable c->u-editing enzyme apobec-2; <b>PDBTitle:</b> the apobec2 crystal structure and functional implications2 for aid
7	<a href="#">d3cu3a1</a>	 Alignment		34.1	9	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
8	<a href="#">c4hpmA_</a>	 Alignment		33.6	34	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> bcl-6 corepressor-like protein 1; <b>PDBTitle:</b> pcgf1 ub fold (rawul)/bcor1 pufd complex
9	<a href="#">c3bb9D_</a>	 Alignment		32.2	12	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> putative orphan protein; <b>PDBTitle:</b> crystal structure of a putative ketosteroid isomerase (sfri_1973) from2 shewanella frigidimarina ncimb 400 at 1.80 a resolution
10	<a href="#">c4u13B_</a>	 Alignment		31.3	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative polyketide cyclase sma1630; <b>PDBTitle:</b> crystal structure of putative polyketide cyclase (protein sma1630)2 from sinorhizobium meliloti at 2.3 a resolution
11	<a href="#">d1nwwa_</a>	 Alignment		31.2	16	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Limonene-1,2-epoxide hydrolase-like

12	<a href="#">c5h03A_</a>	Alignment		30.5	9	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> binary enterotoxin of clostridium perfringens component a; <b>PDBTitle:</b> crystal structure of an adp-ribosylating toxin beca from c.2 perfringens
13	<a href="#">d1oh0a_</a>	Alignment		30.1	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ketosteroid isomerase-like
14	<a href="#">d1vqo2l</a>	Alignment		28.8	71	<b>Fold:</b> Non-globular all-alpha subunits of globular proteins <b>Superfamily:</b> Ribosomal protein L39e <b>Family:</b> Ribosomal protein L39e
15	<a href="#">c5cxoA_</a>	Alignment		28.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxide hydrolase; <b>PDBTitle:</b> intriguing role of epoxide hydrolase/cyclase-like enzyme salbiii in2 pyran ring formation in polyether salinomycin
16	<a href="#">d1m1eb_</a>	Alignment		27.9	16	<b>Fold:</b> beta-catenin-interacting protein ICAT <b>Superfamily:</b> beta-catenin-interacting protein ICAT <b>Family:</b> beta-catenin-interacting protein ICAT
17	<a href="#">c6of9G_</a>	Alignment		27.9	12	<b>PDB header:</b> unknown function <b>Chain:</b> G: <b>PDB Molecule:</b> camkii hub; <b>PDBTitle:</b> structure of the chlamydomonas reinhardtii camkii hub homology domain
18	<a href="#">c4hplA_</a>	Alignment		26.9	37	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> bcl-6 corepressor; <b>PDBTitle:</b> pcgf1 ub fold (rawul)/bcor pufd complex
19	<a href="#">c3dukD_</a>	Alignment		26.4	18	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> ntf2-like protein of unknown function; <b>PDBTitle:</b> crystal structure of a ntf2-like protein of unknown function2 (mfla_0564) from methylobacillus flagellatus kt at 2.200 a resolution
20	<a href="#">d3en8a1</a>	Alignment		25.5	21	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rpa4348-like
21	<a href="#">d2a15a1</a>	Alignment	not modelled	24.3	20	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ketosteroid isomerase-like
22	<a href="#">d2gexa1</a>	Alignment	not modelled	22.4	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Snoal-like polyketide cyclase
23	<a href="#">c1giqA_</a>	Alignment	not modelled	22.3	12	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> iota toxin component ia; <b>PDBTitle:</b> crystal structure of the enzymatic componet of iota-toxin from2 clostridium perfringens with nadh
24	<a href="#">c4e1tA_</a>	Alignment	not modelled	22.1	23	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> invasin; <b>PDBTitle:</b> x-ray crystal structure of the transmembrane beta-domain from invasins from yersinia pseudotuberculosis
25	<a href="#">c3j2lf_</a>	Alignment	not modelled	20.7	71	<b>PDB header:</b> ribosome <b>Chain:</b> F: <b>PDB Molecule:</b> 50s ribosomal protein l6p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
26	<a href="#">c5ifeC_</a>	Alignment	not modelled	20.4	22	<b>PDB header:</b> splicing <b>Chain:</b> C: <b>PDB Molecule:</b> splicing factor 3b subunit 1; <b>PDBTitle:</b> crystal structure of the human sf3b core complex
27	<a href="#">c4e1sA_</a>	Alignment	not modelled	20.1	19	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> intimin; <b>PDBTitle:</b> x-ray crystal structure of the transmembrane beta-domain from intimin2 from ehcc strain o157:h7
28	<a href="#">c3wmdA_</a>	Alignment	not modelled	20.1	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> probable monensin biosynthesis isomerase; <b>PDBTitle:</b> crystal structure of epoxide hydrolase monbi
						<b>PDB header:</b> unknown function

29	<a href="#">c6bjuD_</a>	Alignment	not modelled	17.2	15	<b>Chain:</b> D; <b>PDB Molecule:</b> atzn; <b>PDBTitle:</b> the structure of atzh: a little known member of the atrazine breakdown2 pathway
30	<a href="#">c5ezuA_</a>	Alignment	not modelled	16.2	27	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> protein a46; <b>PDBTitle:</b> crystal structure of the n-terminal domain of vaccinia virus2 immunomodulator a46 in complex with myristic acid.
31	<a href="#">d1ohpa1</a>	Alignment	not modelled	15.9	32	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ketosteroid isomerase-like
32	<a href="#">c4kvhA_</a>	Alignment	not modelled	13.9	23	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> ketosteroid isomerase fold protein hmuk_0747; <b>PDBTitle:</b> crystal structure of ketosteroid isomerase fold protein hmuk_0747
33	<a href="#">c4i4kB_</a>	Alignment	not modelled	13.8	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein sgcj; <b>PDBTitle:</b> streptomyces globisporus c-1027 9-membered enediyne conserved protein2 sgce6
34	<a href="#">c3msoA_</a>	Alignment	not modelled	13.4	19	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> steroid delta-isomerase; <b>PDBTitle:</b> crystal structure of a steroid delta-isomerase (np_250810.1) from2 pseudomonas aeruginosa at 2.57 a resolution
35	<a href="#">c4dbgB_</a>	Alignment	not modelled	13.1	35	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> ring finger protein 31; <b>PDBTitle:</b> crystal structure of hoil-1l-ubl complexed with a hoip-uba derivative
36	<a href="#">c3robC_</a>	Alignment	not modelled	13.1	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C; <b>PDB Molecule:</b> uncharacterized conserved protein; <b>PDBTitle:</b> the crystal structure of a conserved protein from planctomyces2 limnophilus dsm 3776
37	<a href="#">d1z1sa1</a>	Alignment	not modelled	12.8	32	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> PhzA/PhzB-like
38	<a href="#">c3zf7q_</a>	Alignment	not modelled	12.7	71	<b>PDB header:</b> ribosome <b>Chain:</b> Q; <b>PDB Molecule:</b> ribosomal protein l15; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
39	<a href="#">d3dmca1</a>	Alignment	not modelled	12.4	10	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> PhzA/PhzB-like
40	<a href="#">d1m98a2</a>	Alignment	not modelled	11.9	18	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Orange carotenoid protein, C-terminal domain
41	<a href="#">c3izso_</a>	Alignment	not modelled	11.7	57	<b>PDB header:</b> ribosome <b>Chain:</b> O; <b>PDB Molecule:</b> 60s ribosomal protein rpl28 (l15p); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
42	<a href="#">c3fkaD_</a>	Alignment	not modelled	11.2	18	<b>PDB header:</b> unknown function <b>Chain:</b> D; <b>PDB Molecule:</b> uncharacterized ntf-2 like protein; <b>PDBTitle:</b> crystal structure of a ntf-2 like protein of unknown function2 (spo1084) from silicibacter pomeroyi dss-3 at 1.69 a resolution
43	<a href="#">c1kqfB_</a>	Alignment	not modelled	11.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> formate dehydrogenase, nitrate-inducible, iron-sulfur <b>PDBTitle:</b> formate dehydrogenase n from e. coli
44	<a href="#">c4a1bB_</a>	Alignment	not modelled	10.4	67	<b>PDB header:</b> ribosome <b>Chain:</b> B; <b>PDB Molecule:</b> rpl39; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rrna and3 proteins of molecule 3.
45	<a href="#">c3k13A_</a>	Alignment	not modelled	10.3	12	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> 5-methyltetrahydrofolate-homocysteine methyltransferase; <b>PDBTitle:</b> structure of the pterin-binding domain metr of 5-2 methyltetrahydrofolate-homocysteine methyltransferase from3 bacteroides thetaiotaomicron
46	<a href="#">c2zkr3_</a>	Alignment	not modelled	10.1	83	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> 3; <b>PDB Molecule:</b> 60s ribosomal protein l39e; <b>PDBTitle:</b> structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
47	<a href="#">c3sy8C_</a>	Alignment	not modelled	9.8	9	<b>PDB header:</b> transcription regulator <b>Chain:</b> C; <b>PDB Molecule:</b> rocr; <b>PDBTitle:</b> crystal structure of the response regulator rocr
48	<a href="#">c5ig0A_</a>	Alignment	not modelled	9.7	19	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> camk/camk2 protein kinase; <b>PDBTitle:</b> crystal structure of s. rosetta camkii hub
49	<a href="#">c2rbfB_</a>	Alignment	not modelled	9.5	56	<b>PDB header:</b> oxidoreductase/dna <b>Chain:</b> B; <b>PDB Molecule:</b> bifunctional protein puta; <b>PDBTitle:</b> structure of the ribbon-helix-helix domain of escherichia coli puta2 (puta52) complexed with operator dna (o2)
50	<a href="#">c1z1sa_</a>	Alignment	not modelled	9.5	32	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein pa3332; <b>PDBTitle:</b> crystal structure of putative isomerase pa3332 from2 pseudomonas aeruginosa
51	<a href="#">c5ig5E_</a>	Alignment	not modelled	9.4	12	<b>PDB header:</b> transferase <b>Chain:</b> E; <b>PDB Molecule:</b> camkii-b hub; <b>PDBTitle:</b> crystal structure of n. vectensis camkii-b hub at ph 4.2
52	<a href="#">c3c8B_</a>	Alignment	not modelled	9.3	21	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> fts-like protein of unknown function; <b>PDBTitle:</b> crystal structure of a fts-like protein of unknown function2 (npun_r1471) from nostoc punctiforme pcc 73102 at 1.22 a resolution
53	<a href="#">c3fovB_</a>	Alignment	not modelled	8.9	12	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized ntf2-like protein;

53	<a href="#">c3lgyb_</a>	Alignment	not modelled	8.9	42	<b>PDBTitle:</b> crystal structure of a ntf2-like protein (bx_e_b1094) from burkholderia2 xenovorans lb400 at 1.59 a resolution
54	<a href="#">d1z21a1</a>	Alignment	not modelled	8.9	25	<b>Fold:</b> Type III secretion system domain <b>Superfamily:</b> Type III secretion system domain <b>Family:</b> YopR Core
55	<a href="#">c2amnA_</a>	Alignment	not modelled	8.8	38	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> cathelicidin; <b>PDBTitle:</b> solution structure of fowlicidin-1, a novel cathelicidin2 antimicrobial peptide from chicken
56	<a href="#">d2np5a2</a>	Alignment	not modelled	8.6	10	<b>Fold:</b> Tetracyclin repressor-like, C-terminal domain <b>Superfamily:</b> Tetracyclin repressor-like, C-terminal domain <b>Family:</b> Tetracyclin repressor-like, C-terminal domain
57	<a href="#">d2gxfa1</a>	Alignment	not modelled	8.4	32	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> YybH-like
58	<a href="#">c5jthB_</a>	Alignment	not modelled	8.4	29	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> myosin light chain kinase, smooth muscle; <b>PDBTitle:</b> crystal structure of e67a calmodulin - cam:rm20 complex
59	<a href="#">c5jqab_</a>	Alignment	not modelled	8.4	29	<b>PDB header:</b> calcium binding protein/protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> myosin light chain kinase, smooth muscle; <b>PDBTitle:</b> cam:rm20 complex
60	<a href="#">c5aiiP_</a>	Alignment	not modelled	8.4	17	<b>PDB header:</b> hydrolase <b>Chain:</b> P: <b>PDB Molecule:</b> limonene-1,2-epoxide hydrolase; <b>PDBTitle:</b> discovery and characterization of thermophilic limonene-1,2-epoxide2 hydrolases from hot spring metagenomic libraries.3 ch55-sample-peg complex
61	<a href="#">d2bnga1</a>	Alignment	not modelled	8.3	42	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Limonene-1,2-epoxide hydrolase-like
62	<a href="#">c5k8qB_</a>	Alignment	not modelled	8.2	45	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> zgc:136689; <b>PDBTitle:</b> crystal structure of calcium-loaded calmodulin in complex with stra62 campb2-site peptide.
63	<a href="#">c3h3hA_</a>	Alignment	not modelled	8.2	19	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized snoal-like protein; <b>PDBTitle:</b> crystal structure of a snoal-like protein of unknown function2 (bth_ii0226) from burkholderia thailandensis e264 at 1.60 a3 resolution
64	<a href="#">d1giga2</a>	Alignment	not modelled	8.0	13	<b>Fold:</b> ADP-ribosylation <b>Superfamily:</b> ADP-ribosylation <b>Family:</b> ADP-ribosylating toxins
65	<a href="#">c6fejA_</a>	Alignment	not modelled	7.9	15	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> all4940 protein; <b>PDBTitle:</b> anabaena apo-c-terminal domain homolog protein
66	<a href="#">c3f8hA_</a>	Alignment	not modelled	7.9	23	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative polyketide cyclase; <b>PDBTitle:</b> crystal structure of a putative polyketide cyclase (tm1040_3560) from2 silicibacter sp. tm1040 at 2.00 a resolution
67	<a href="#">d3cx5e2</a>	Alignment	not modelled	7.8	21	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> ISP transmembrane anchor <b>Family:</b> ISP transmembrane anchor
68	<a href="#">d2ay0a1</a>	Alignment	not modelled	7.7	54	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> PutA pre-N-terminal region-like
69	<a href="#">c3vowB_</a>	Alignment	not modelled	7.7	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable dna dc->du-editing enzyme apobec-3c; <b>PDBTitle:</b> crystal structure of the human apobec3c having hiv-1 vif-binding2 interface
70	<a href="#">d1t6ua_</a>	Alignment	not modelled	7.6	15	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Nickel-containing superoxide dismutase, NiSOD <b>Family:</b> Nickel-containing superoxide dismutase, NiSOD
71	<a href="#">d1uf0a_</a>	Alignment	not modelled	7.6	24	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Doublecortin (DC) <b>Family:</b> Doublecortin (DC)
72	<a href="#">c4bj5A_</a>	Alignment	not modelled	7.4	43	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> protein rif2; <b>PDBTitle:</b> crystal structure of rif2 in complex with the c-terminal domain of2 rap1 (rap1-rct)
73	<a href="#">c5li2C_</a>	Alignment	not modelled	7.2	19	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> tail sheath protein; <b>PDBTitle:</b> bacteriophage phi812k1-420 tail sheath and tail tube protein in native2 tail
74	<a href="#">d1gr0a2</a>	Alignment	not modelled	7.1	29	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> Dihydrodipicolinate reductase-like
75	<a href="#">c5wqhE_</a>	Alignment	not modelled	6.9	5	<b>PDB header:</b> isomerase <b>Chain:</b> E: <b>PDB Molecule:</b> isomerase trt14; <b>PDBTitle:</b> structure of fungal meroterpenoid isomerase trt14 complexed with2 substrate analog and endo-terretonin d
76	<a href="#">c3f7sA_</a>	Alignment	not modelled	6.9	13	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized ntf2-like protein; <b>PDBTitle:</b> crystal structure of a ntf2-like protein of unknown function (pp_4556)2 from pseudomonas putida kt2440 at 2.11 a resolution
77	<a href="#">c6s2pN_</a>	Alignment	not modelled	6.8	26	<b>PDB header:</b> plant protein <b>Chain:</b> N: <b>PDB Molecule:</b> nrc1; <b>PDBTitle:</b> structure of the nb-arc domain from the tomato immune receptor nrc1
78	<a href="#">c1qsuC_</a>	Alignment	not modelled	6.7	56	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> protein ((pro-hyp-gly)4- glu-lys-gly(pro-hyp-gly)5); <b>PDBTitle:</b> crystal structure of the triple-helical collagen-like peptide, (pro-2 hyp-gly)4-glu-lys-gly(pro-hyp-gly)5

79	<a href="#">d3blza1</a>	Alignment	not modelled	6.7	9	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Sbal0622-like
80	<a href="#">d2oz4a1</a>	Alignment	not modelled	6.4	35	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C2 set domains
81	<a href="#">c5ir2A_</a>	Alignment	not modelled	6.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulase; <b>PDBTitle:</b> crystal structure of novel cellulases from microbes associated with2 the gut ecosystem
82	<a href="#">c1qsuA_</a>	Alignment	not modelled	6.2	56	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein ((pro-hyp-gly)4- glu-lys-gly((pro-hyp-gly)5); <b>PDBTitle:</b> crystal structure of the triple-helical collagen-like peptide, (pro-2 hyp-gly)4-glu-lys-gly((pro-hyp-gly)5
83	<a href="#">c1qsuB_</a>	Alignment	not modelled	6.2	56	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein ((pro-hyp-gly)4- glu-lys-gly((pro-hyp-gly)5); <b>PDBTitle:</b> crystal structure of the triple-helical collagen-like peptide, (pro-2 hyp-gly)4-glu-lys-gly((pro-hyp-gly)5
84	<a href="#">c5x9jB_</a>	Alignment	not modelled	6.2	4	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> prhc; <b>PDBTitle:</b> strcutre of prhc from penicillium brasilianum nbrc 6234
85	<a href="#">c6b4aB_</a>	Alignment	not modelled	6.1	20	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> doublecortin; <b>PDBTitle:</b> crystal structure of the c-terminal domain of doublecortin (tgdcx)2 from toxoplasma gondii me49
86	<a href="#">d2f86b1</a>	Alignment	not modelled	6.0	12	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
87	<a href="#">c5tkmA_</a>	Alignment	not modelled	5.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dna dc->du-editing enzyme apobec-3b; <b>PDBTitle:</b> crystal structure of human apobec3b n-terminal domain
88	<a href="#">c5evhA_</a>	Alignment	not modelled	5.9	30	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of known function protein from kribbella flavida dsm2 17836
89	<a href="#">c4yptA_</a>	Alignment	not modelled	5.7	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> replicase polyprotein 1ab; <b>PDBTitle:</b> x-ray structural of three tandemly linked domains of nsp3 from murine2 hepatitis virus at 2.60 angstroms resolution
90	<a href="#">c3f40A_</a>	Alignment	not modelled	5.6	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized ntf2-like protein; <b>PDBTitle:</b> crystal structure of ntf2-like protein of unknown function2 (yp_677363.1) from cytophaga hutchinsonii atcc 33406 at 1.27 a3 resolution
91	<a href="#">c4atuL_</a>	Alignment	not modelled	5.6	30	<b>PDB header:</b> hydrolase <b>Chain:</b> I: <b>PDB Molecule:</b> neuronal migration protein doublecortin; <b>PDBTitle:</b> human doublecortin n-dc repeat plus linker, and tubulin (2xrp) docked2 into an 8a cryo-em map of doublecortin-stabilised microtubules3 reconstructed in absence of kinesin
92	<a href="#">c6iyaD_</a>	Alignment	not modelled	5.6	31	<b>PDB header:</b> antitoxin <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator copg family; <b>PDBTitle:</b> structure of the dna binding domain of antitoxin copaso
93	<a href="#">d3b7ca1</a>	Alignment	not modelled	5.5	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SO0125-like
94	<a href="#">c3tu6A_</a>	Alignment	not modelled	5.4	26	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> pseudoazurin (blue copper protein); <b>PDBTitle:</b> the structure of a pseudoazurin from sinorhizobium meliloti
95	<a href="#">c6fc1D_</a>	Alignment	not modelled	5.4	60	<b>PDB header:</b> translation <b>Chain:</b> D: <b>PDB Molecule:</b> protein eap1; <b>PDBTitle:</b> crystal structure of the eif4e-eap1p complex from saccharomyces2 cerevisiae in the cap-bound state
96	<a href="#">d2rcda1</a>	Alignment	not modelled	5.3	24	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BxeB1374-like
97	<a href="#">c3fniA_</a>	Alignment	not modelled	5.3	43	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative diflavin flavoprotein a 3; <b>PDBTitle:</b> crystal structure of a diflavin flavoprotein a3 (all3895) from nostoc2 sp., northeast structural genomics consortium target nsr431a
98	<a href="#">c4fc9B_</a>	Alignment	not modelled	5.3	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> structure of the c-terminal domain of the type iii effector xcv32202 (xopl)
99	<a href="#">c3pawD_</a>	Alignment	not modelled	5.3	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> ribonucleoside-diphosphate reductase large chain 1; <b>PDBTitle:</b> low resolution x-ray crystal structure of yeast rnr1p with datp bound2 in the a-site