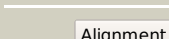

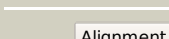

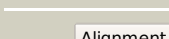

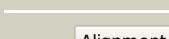

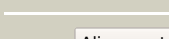
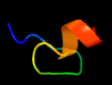







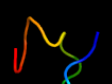





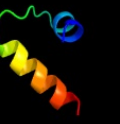




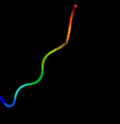
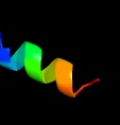



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1944c (-) _2195351_2195941
Date	Mon Aug 5 13:25:04 BST 2019
Unique Job ID	4bdafc4d6af4277b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2i9wA_</a>	 Alignment		98.1	40	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a sec-c motif containing protein (psyc_2064) from2 psychrobacter arcticus at 1.75 a resolution
2	<a href="#">c1ozbl_</a>	 Alignment		97.9	60	<b>PDB header:</b> protein transport <b>Chain:</b> I: <b>PDB Molecule:</b> preprotein translocase seca subunit; <b>PDBTitle:</b> crystal structure of secb complexed with seca c-terminus
3	<a href="#">d1ozbi_</a>	 Alignment		97.9	60	<b>Fold:</b> Sec-C motif <b>Superfamily:</b> Sec-C motif <b>Family:</b> Sec-C motif
4	<a href="#">c1ozbj_</a>	 Alignment		97.9	60	<b>PDB header:</b> protein transport <b>Chain:</b> J: <b>PDB Molecule:</b> preprotein translocase seca subunit; <b>PDBTitle:</b> crystal structure of secb complexed with seca c-terminus
5	<a href="#">d1tm6a_</a>	 Alignment		97.8	67	<b>Fold:</b> Sec-C motif <b>Superfamily:</b> Sec-C motif <b>Family:</b> Sec-C motif
6	<a href="#">c1tm6A_</a>	 Alignment		97.8	67	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> preprotein translocase seca subunit; <b>PDBTitle:</b> nmr structure of the free zinc binding c-terminal domain of2 seca
7	<a href="#">c1sx1A_</a>	 Alignment		97.6	67	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> seca; <b>PDBTitle:</b> solution nmr structure and x-ray absorption analysis of the2 c-terminal zinc-binding domain of the seca atpase
8	<a href="#">c1sx0A_</a>	 Alignment		97.5	67	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> seca; <b>PDBTitle:</b> solution nmr structure and x-ray absorption analysis of the2 c-terminal zinc-binding domain of the seca atpase
9	<a href="#">d2i9wa3</a>	 Alignment		93.5	59	<b>Fold:</b> Sec-C motif <b>Superfamily:</b> Sec-C motif <b>Family:</b> Sec-C motif
10	<a href="#">d1tpna_</a>	 Alignment		50.1	63	<b>Fold:</b> Fnl-like domain <b>Superfamily:</b> Fnl-like domain <b>Family:</b> Fibronectin type I module
11	<a href="#">c2e1xA_</a>	 Alignment		42.7	63	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> gag-pol polyprotein (pr160gag-pol); <b>PDBTitle:</b> nmr structure of the hiv-2 nucleocapsid protein

12	<a href="#">c2iwjA</a>	Alignment		40.9	63	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> gag-pol polyprotein; <b>PDBTitle:</b> solution structure of the zn complex of hiv-2 ncp(23-49)2 peptide, encompassing protein cchc-linker, distal cchc zn-3 binding motif and c-terminal tail.
13	<a href="#">d1f44a1</a>	Alignment		34.7	41	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> lambda integrase-like, N-terminal domain <b>Family:</b> lambda integrase-like, N-terminal domain
14	<a href="#">c4e82B</a>	Alignment		25.8	55	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> defensin-5; <b>PDBTitle:</b> crystal structure of monomeric variant of human alpha-defensin 5, hd52 (glu21eme mutant)
15	<a href="#">c4e82A</a>	Alignment		25.8	55	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> defensin-5; <b>PDBTitle:</b> crystal structure of monomeric variant of human alpha-defensin 5, hd52 (glu21eme mutant)
16	<a href="#">d1mkya3</a>	Alignment		25.2	14	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Probable GTPase Der, C-terminal domain <b>Family:</b> Probable GTPase Der, C-terminal domain
17	<a href="#">d2ca5a1</a>	Alignment		14.4	40	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> MxiH-like <b>Family:</b> MxiH-like
18	<a href="#">c1zmpD</a>	Alignment		13.8	56	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> D: <b>PDB Molecule:</b> defensin 5; <b>PDBTitle:</b> crystal structure of human defensin-5
19	<a href="#">c4ng2E</a>	Alignment		12.8	42	<b>PDB header:</b> transcription regulator <b>Chain:</b> E: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of lasr lbd-qla complex from pseudomonas aeruginosa
20	<a href="#">c3i5wA</a>	Alignment		11.2	56	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> defensin-5; <b>PDBTitle:</b> crystal structure of human alpha-defensin 5 (mutant r13h)
21	<a href="#">c3i5wB</a>	Alignment	not modelled	11.2	56	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> defensin-5; <b>PDBTitle:</b> crystal structure of human alpha-defensin 5 (mutant r13h)
22	<a href="#">c5ezdB</a>	Alignment	not modelled	11.0	38	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> kunitz-type protease inhibitor 1; <b>PDBTitle:</b> crystal structure of a hepatocyte growth factor activator inhibitor-12 (hai-1) fragment covering the pkd-like 'internal' domain and kunitz3 domain 1
23	<a href="#">c5n9mA</a>	Alignment	not modelled	10.9	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cobyrinic acid synthase; <b>PDBTitle:</b> crystal structure of gatd - a glutamine amidotransferase from staphylococcus aureus involved in peptidoglycan amidation
24	<a href="#">c2lxzA</a>	Alignment	not modelled	10.8	56	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> defensin-5; <b>PDBTitle:</b> solution structure of the antimicrobial peptide human defensin 5
25	<a href="#">c1zmpA</a>	Alignment	not modelled	10.8	56	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> defensin 5; <b>PDBTitle:</b> crystal structure of human defensin-5
26	<a href="#">c2mitA</a>	Alignment	not modelled	10.8	56	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> defensin-5; <b>PDBTitle:</b> solution structure of oxidized dimeric form of human defensin 5
27	<a href="#">c1zmpB</a>	Alignment	not modelled	10.8	56	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> defensin 5; <b>PDBTitle:</b> crystal structure of human defensin-5
28	<a href="#">c2mitB</a>	Alignment	not modelled	10.8	56	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> defensin-5; <b>PDBTitle:</b> solution structure of oxidized dimeric form of human defensin 5
						<b>PDB header:</b> antimicrobial protein

29	<a href="#">c1zmpC_</a>	Alignment	not modelled	10.8	56	<b>Chain:</b> C: <b>PDB Molecule:</b> defensin 5; <b>PDBTitle:</b> crystal structure of human defensin-5
30	<a href="#">c5ol7A_</a>	Alignment	not modelled	10.7	29	<b>PDB header:</b> splicing <b>Chain:</b> A: <b>PDB Molecule:</b> dna-directed dna polymerase,dna-directed dna polymerase; <b>PDBTitle:</b> crystal structure of an inactivated npu siclopps intein with cfahpg2 extein
31	<a href="#">c4rbxA_</a>	Alignment	not modelled	10.4	56	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> defensin-5; <b>PDBTitle:</b> crystal structure of human alpha-defensin 5, hd5 (glu21arg mutant)
32	<a href="#">c3n70F_</a>	Alignment	not modelled	10.4	54	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> transport activator; <b>PDBTitle:</b> the crystal structure of the p-loop ntpase domain of the sigma-542 transport activator from e. coli to 2.8a
33	<a href="#">c2v6ll_</a>	Alignment	not modelled	10.3	40	<b>PDB header:</b> protein transport <b>Chain:</b> I: <b>PDB Molecule:</b> mxih; <b>PDBTitle:</b> molecular model of a type iii secretion system needle
34	<a href="#">c5znhA_</a>	Alignment	not modelled	10.2	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> catechol 2,3-dioxygenase, extradiol protein; <b>PDBTitle:</b> catechol 2,3-dioxygenase with 4-methyl catechol from diaphorobacter sp2 ds2
35	<a href="#">c2vbcA_</a>	Alignment	not modelled	9.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dengue 4 ns3 full-length protein; <b>PDBTitle:</b> crystal structure of the ns3 protease-helicase from dengue2 virus
36	<a href="#">c2leyA_</a>	Alignment	not modelled	9.4	71	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-defensin 4; <b>PDBTitle:</b> solution structure of (r7g)-crp4
37	<a href="#">c5laaB_</a>	Alignment	not modelled	9.4	28	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> tetrahydromethanopterin s-methyltransferase subunit a; <b>PDBTitle:</b> x-ray structure of the methyltransferase subunit a from methanothermus2 fervidus in complex with cobalamin
38	<a href="#">d1t3ta2</a>	Alignment	not modelled	9.1	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
39	<a href="#">c3d87A_</a>	Alignment	not modelled	9.1	48	<b>PDB header:</b> cytokine <b>Chain:</b> A: <b>PDB Molecule:</b> interleukin-23 subunit p19; <b>PDBTitle:</b> crystal structure of interleukin-23
40	<a href="#">c5j0jC_</a>	Alignment	not modelled	8.9	27	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> designed protein 2l6hc3_6; <b>PDBTitle:</b> de novo design of protein homo-oligomers with modular hydrogen bond2 network-mediated specificity
41	<a href="#">c1vryA_</a>	Alignment	not modelled	8.8	46	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycine receptor alpha-1 chain; <b>PDBTitle:</b> second and third transmembrane domains of the alpha-12 subunit of human glycine receptor
42	<a href="#">d2g0ua1</a>	Alignment	not modelled	8.4	33	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> MxiH-like <b>Family:</b> MxiH-like
43	<a href="#">d1hyua4</a>	Alignment	not modelled	8.4	24	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> PDI-like
44	<a href="#">c2jowA_</a>	Alignment	not modelled	8.3	33	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein prgi; <b>PDBTitle:</b> differences in the electrostatic surfaces of the type iii2 secretion needle proteins
45	<a href="#">c2n3pA_</a>	Alignment	not modelled	8.0	63	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> asteropsin_g; <b>PDBTitle:</b> solution nmr structure of asteropsin g from marine sponge asteropus
46	<a href="#">d1k28d1</a>	Alignment	not modelled	7.7	33	<b>Fold:</b> Phage tail proteins <b>Superfamily:</b> Phage tail proteins <b>Family:</b> Baseplate protein-like
47	<a href="#">c4ecnA_</a>	Alignment	not modelled	7.7	64	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> leucine-rich repeat protein; <b>PDBTitle:</b> crystal structure of a leucine-rich repeat protein (bt_0210) from2 bacteroides thetaiotaomicron vpi-5482 at 2.80 a resolution
48	<a href="#">c5l8xA_</a>	Alignment	not modelled	7.6	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tetrahydromethanopterin s-methyltransferase subunit a; <b>PDBTitle:</b> x-ray structure of apo methanocaldococcus jannaschii methyltransferase2 subunit a at 1.85 angstrom
49	<a href="#">c3l4eA_</a>	Alignment	not modelled	7.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized peptidase lmo0363; <b>PDBTitle:</b> 1.5a crystal structure of a putative peptidase e protein from listeria2 monocytogenes egd-e
50	<a href="#">c2jrtA_</a>	Alignment	not modelled	7.5	58	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> nmr solution structure of the protein coded by gene2 rhos4_12090 of rhodobacter sphaeroides. northeast3 structural genomics target rhr5
51	<a href="#">c4dt1B_</a>	Alignment	not modelled	7.5	50	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> platinum sensitivity protein 3; <b>PDBTitle:</b> crystal structure of the psy3-csm2 complex
52	<a href="#">d1en2a2</a>	Alignment	not modelled	7.5	63	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Plant lectins/antimicrobial peptides <b>Family:</b> Hevein-like agglutinin (lectin) domain
53	<a href="#">c4rbwD_</a>	Alignment	not modelled	7.4	56	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> D: <b>PDB Molecule:</b> defensin-5; <b>PDBTitle:</b> crystal structure of human alpha-defensin 5, hd5 (thr7arg glu21arg2 mutant)
54	<a href="#">c4rbwB_</a>	Alignment	not modelled	7.4	56	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> defensin-5;

54	<a href="#">c4rbwB</a>	Alignment	not modelled	7.4	50	<b>PDBTitle:</b> crystal structure of human alpha-defensin 5, hd5 (thr7arg glu21arg2 mutant) <b>PDB header:</b> antimicrobial protein
55	<a href="#">c4rbwA</a>	Alignment	not modelled	7.4	56	<b>Chain:</b> A: <b>PDB Molecule:</b> defensin-5; <b>PDBTitle:</b> crystal structure of human alpha-defensin 5, hd5 (thr7arg glu21arg2 mutant)
56	<a href="#">c4rbwC</a>	Alignment	not modelled	7.4	56	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> C: <b>PDB Molecule:</b> defensin-5; <b>PDBTitle:</b> crystal structure of human alpha-defensin 5, hd5 (thr7arg glu21arg2 mutant)
57	<a href="#">c2cwbA</a>	Alignment	not modelled	7.2	18	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> chimera of immunoglobulin g binding protein g <b>PDBTitle:</b> solution structure of the ubiquitin-associated domain of2 human bmsc-ubp and its complex with ubiquitin
58	<a href="#">d1ehda2</a>	Alignment	not modelled	7.1	63	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Plant lectins/antimicrobial peptides <b>Family:</b> Hevein-like agglutinin (lectin) domain
59	<a href="#">c4f82A</a>	Alignment	not modelled	7.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> x-ray crystal structure of a putative thioredoxin reductase from2 burkholderia cenocepacia
60	<a href="#">d1sgva1</a>	Alignment	not modelled	7.0	23	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> PUA domain
61	<a href="#">c3nadB</a>	Alignment	not modelled	6.9	27	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> ferulate decarboxylase; <b>PDBTitle:</b> crystal structure of phenolic acid decarboxylase from bacillus pumilus2 ui-670
62	<a href="#">c2fqcA</a>	Alignment	not modelled	6.8	53	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> conotoxin pl14a; <b>PDBTitle:</b> solution structure of conotoxin pl14a
63	<a href="#">d2oa4a1</a>	Alignment	not modelled	6.8	50	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> SPO1678-like
64	<a href="#">c3ecjC</a>	Alignment	not modelled	6.8	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> protein (homoprotocatechuate 2,3-dioxygenase); <b>PDBTitle:</b> structure of e323l mutant of homoprotocatechuate 2,3-dioxygenase from2 brevibacterium fuscum at 1.65a resolution
65	<a href="#">c4v1aa</a>	Alignment	not modelled	6.7	30	<b>PDB header:</b> ribosome <b>Chain:</b> A: <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 22 of 2
66	<a href="#">d1v58a1</a>	Alignment	not modelled	6.7	19	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> DsbC/DsbG C-terminal domain-like
67	<a href="#">c1t3bA</a>	Alignment	not modelled	6.6	28	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsbc; <b>PDBTitle:</b> x-ray structure of dsbc from haemophilus influenzae
68	<a href="#">c1mkyA</a>	Alignment	not modelled	6.5	14	<b>PDB header:</b> ligand binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable gtp-binding protein enga; <b>PDBTitle:</b> structural analysis of the domain interactions in der, a switch2 protein containing two gtpase domains
69	<a href="#">c4ntxC</a>	Alignment	not modelled	6.3	31	<b>PDB header:</b> transport protein/toxin <b>Chain:</b> C: <b>PDB Molecule:</b> basic phospholipase a2 homolog tx-beta; <b>PDBTitle:</b> structure of acid-sensing ion channel in complex with snake toxin and2 amiloride
70	<a href="#">c2n2hB</a>	Alignment	not modelled	6.2	35	<b>PDB header:</b> transcription, protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> paired amphipathic helix protein sin3a; <b>PDBTitle:</b> solution structure of sds3 in complex with sin3a
71	<a href="#">c3umaC</a>	Alignment	not modelled	6.1	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> hypothetical peroxiredoxin protein; <b>PDBTitle:</b> crystal structure of a hypothetical peroxiredoxin protein frm2 sinorhizobium melloti
72	<a href="#">c2lssF</a>	Alignment	not modelled	6.0	25	<b>PDB header:</b> lyase, transferase <b>Chain:</b> F: <b>PDB Molecule:</b> glutamine amidotransferase subunit pdxt; <b>PDBTitle:</b> structure of the plp synthase holoenzyme from thermotoga maritima
73	<a href="#">d1e9ya1</a>	Alignment	not modelled	5.9	24	<b>Fold:</b> beta-clip <b>Superfamily:</b> Urease, beta-subunit <b>Family:</b> Urease, beta-subunit
74	<a href="#">d2nv0a1</a>	Alignment	not modelled	5.9	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
75	<a href="#">c1zpzA</a>	Alignment	not modelled	5.8	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> proto-oncogene tyrosine-protein kinase abl1; <b>PDBTitle:</b> solution structure of the f-actin binding domain of bcr-2 abl/c-abl
76	<a href="#">c1mpyD</a>	Alignment	not modelled	5.6	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> catechol 2,3-dioxygenase; <b>PDBTitle:</b> structure of catechol 2,3-dioxygenase (metapyrocatechase)2 from pseudomonas putida mt-2
77	<a href="#">c4incA</a>	Alignment	not modelled	5.5	67	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> histidine triad nucleotide-binding protein 2, <b>PDBTitle:</b> human histidine triad nucleotide binding protein 2
78	<a href="#">c4e86B</a>	Alignment	not modelled	5.5	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> defensin-5; <b>PDBTitle:</b> crystal structure of human alpha-defensin 5, hd5 (leu29aba mutant)
79	<a href="#">c4e83A</a>	Alignment	not modelled	5.5	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> defensin-5; <b>PDBTitle:</b> crystal structure of human alpha-defensin 5, hd5 (leu29nle mutant)
						<b>PDB header:</b> antimicrobial protein

80	<a href="#">c4e86C</a>	Alignment	not modelled	5.5	33	<b>Chain:</b> C; <b>PDB Molecule:</b> defensin-5; <b>PDBTitle:</b> crystal structure of human alpha-defensin 5, hd5 (leu29aba mutant)
81	<a href="#">c4e86G</a>	Alignment	not modelled	5.5	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> G; <b>PDB Molecule:</b> defensin-5; <b>PDBTitle:</b> crystal structure of human alpha-defensin 5, hd5 (leu29aba mutant)
82	<a href="#">c4e86E</a>	Alignment	not modelled	5.5	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> E; <b>PDB Molecule:</b> defensin-5; <b>PDBTitle:</b> crystal structure of human alpha-defensin 5, hd5 (leu29aba mutant)
83	<a href="#">c4e86F</a>	Alignment	not modelled	5.5	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> F; <b>PDB Molecule:</b> defensin-5; <b>PDBTitle:</b> crystal structure of human alpha-defensin 5, hd5 (leu29aba mutant)
84	<a href="#">c4e86A</a>	Alignment	not modelled	5.5	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A; <b>PDB Molecule:</b> defensin-5; <b>PDBTitle:</b> crystal structure of human alpha-defensin 5, hd5 (leu29aba mutant)
85	<a href="#">c4e83B</a>	Alignment	not modelled	5.5	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> B; <b>PDB Molecule:</b> defensin-5; <b>PDBTitle:</b> crystal structure of human alpha-defensin 5, hd5 (leu29nle mutant)
86	<a href="#">c2n8hA</a>	Alignment	not modelled	5.4	50	<b>PDB header:</b> toxin <b>Chain:</b> A; <b>PDB Molecule:</b> conotoxin-muoxi-gvijj; <b>PDBTitle:</b> structural basis for the inhibition of voltage-gated sodium channels2 with conotoxin-muoxi-gvijj
87	<a href="#">d1owsb</a>	Alignment	not modelled	5.3	71	<b>Fold:</b> Phospholipase A2, PLA2 <b>Superfamily:</b> Phospholipase A2, PLA2 <b>Family:</b> Vertebrate phospholipase A2
88	<a href="#">c5cuiA</a>	Alignment	not modelled	5.3	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A; <b>PDB Molecule:</b> defensin-5; <b>PDBTitle:</b> crystal structure of human defensin-5 r28a mutant.
89	<a href="#">c5cuiD</a>	Alignment	not modelled	5.3	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> D; <b>PDB Molecule:</b> defensin-5; <b>PDBTitle:</b> crystal structure of human defensin-5 r28a mutant.
90	<a href="#">c5cuiE</a>	Alignment	not modelled	5.3	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> E; <b>PDB Molecule:</b> defensin-5; <b>PDBTitle:</b> crystal structure of human defensin-5 r28a mutant.
91	<a href="#">c5cuiC</a>	Alignment	not modelled	5.3	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> C; <b>PDB Molecule:</b> defensin-5; <b>PDBTitle:</b> crystal structure of human defensin-5 r28a mutant.
92	<a href="#">c5cuiF</a>	Alignment	not modelled	5.3	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> F; <b>PDB Molecule:</b> defensin-5; <b>PDBTitle:</b> crystal structure of human defensin-5 r28a mutant.
93	<a href="#">c5cuiB</a>	Alignment	not modelled	5.3	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> B; <b>PDB Molecule:</b> defensin-5; <b>PDBTitle:</b> crystal structure of human defensin-5 r28a mutant.
94	<a href="#">c4f4mA</a>	Alignment	not modelled	5.2	100	<b>PDB header:</b> hydrolase regulator <b>Chain:</b> A; <b>PDB Molecule:</b> papain peptidoglycan amidase effector tse1; <b>PDBTitle:</b> structure of the type vi peptidoglycan amidase effector tse1 (c30a)2 from pseudomonas aeruginosa
95	<a href="#">c5cujC</a>	Alignment	not modelled	5.2	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> C; <b>PDB Molecule:</b> defensin-5; <b>PDBTitle:</b> crystal structure of human defensin-5 y27a mutant crystal form 2.
96	<a href="#">c5cumC</a>	Alignment	not modelled	5.2	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> C; <b>PDB Molecule:</b> defensin-5; <b>PDBTitle:</b> crystal structure of human defensin-5 y27a mutant crystal form 1.
97	<a href="#">c5cumB</a>	Alignment	not modelled	5.2	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> B; <b>PDB Molecule:</b> defensin-5; <b>PDBTitle:</b> crystal structure of human defensin-5 y27a mutant crystal form 1.
98	<a href="#">c5cujE</a>	Alignment	not modelled	5.2	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> E; <b>PDB Molecule:</b> defensin-5; <b>PDBTitle:</b> crystal structure of human defensin-5 y27a mutant crystal form 2.
99	<a href="#">c5cujF</a>	Alignment	not modelled	5.2	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> F; <b>PDB Molecule:</b> defensin-5; <b>PDBTitle:</b> crystal structure of human defensin-5 y27a mutant crystal form 2.