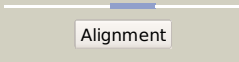
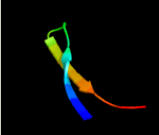
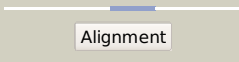
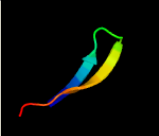
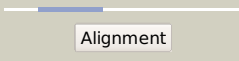
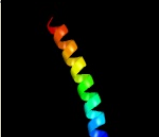
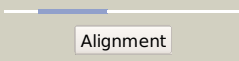

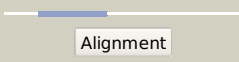

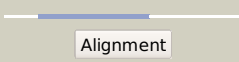
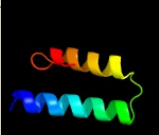
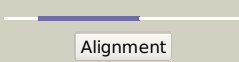
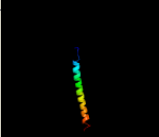
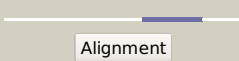
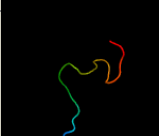
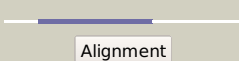
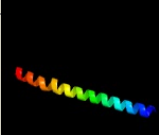
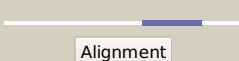
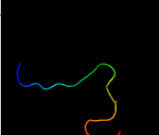
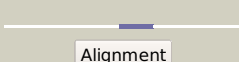

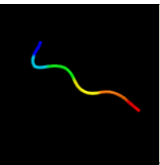
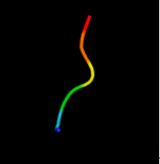
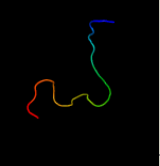
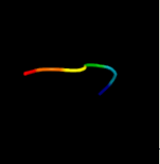
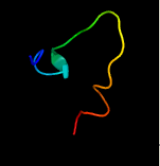
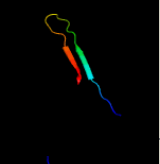
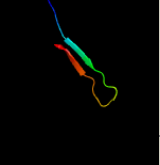
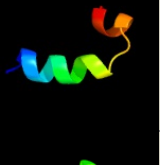
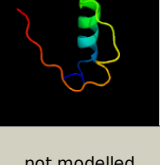


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0590A (- )_688811_689065
Date	Fri Jul 26 01:50:14 BST 2019
Unique Job ID	613126204f6c40dd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3zfnA_</a>			28.6	41	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n-terminal protease npro; <b>PDBTitle:</b> crystal structure of product-like, processed n-terminal protease npro
2	<a href="#">c4h9kA_</a>			27.2	41	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hog cholera virus; <b>PDBTitle:</b> crystal structure of cleavage site mutant of npro of classical swine2 fever virus.
3	<a href="#">c2akfB_</a>			22.2	26	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> coronin-1a; <b>PDBTitle:</b> crystal structure of the coiled-coil domain of coronin 1
4	<a href="#">c2akfC_</a>			20.7	25	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> coronin-1a; <b>PDBTitle:</b> crystal structure of the coiled-coil domain of coronin 1
5	<a href="#">c2akfA_</a>			20.7	25	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> coronin-1a; <b>PDBTitle:</b> crystal structure of the coiled-coil domain of coronin 1
6	<a href="#">c6bs9A_</a>			20.5	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> stage iii sporulation protein ab; <b>PDBTitle:</b> stage iii sporulation protein ab (spoiiaab)
7	<a href="#">c2fxpA_</a>			16.1	15	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> spike glycoprotein; <b>PDBTitle:</b> solution structure of the sars-coronavirus hr2 domain
8	<a href="#">d1qqp1_</a>			15.6	27	<b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins) <b>Superfamily:</b> Positive stranded ssRNA viruses <b>Family:</b> Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
9	<a href="#">c3h01A_</a>			15.3	12	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelope glycoprotein gp160; <b>PDBTitle:</b> structure of the c-terminal domain of a putative hiv-1 gp41 fusion2 intermediate
10	<a href="#">c1qgc1_</a>			14.6	27	<b>PDB header:</b> virus/immune system <b>Chain:</b> 1: <b>PDB Molecule:</b> protein (virus capsid protein vp1); <b>PDB Fragment:</b> residues 133-156 <b>PDBTitle:</b> structure of the complex of a fab fragment of a neutralizing antibody2 with foot and mouth disease virus
11	<a href="#">d1ubea2</a>			14.1	33	<b>Fold:</b> Anti-LPS factor/recA domain <b>Superfamily:</b> RecA protein, C-terminal domain <b>Family:</b> RecA protein, C-terminal domain

12	<a href="#">d1xp8a2</a>	Alignment		13.8	33	<b>Fold:</b> Anti-LPS factor/recA domain <b>Superfamily:</b> RecA protein, C-terminal domain <b>Family:</b> RecA protein, C-terminal domain
13	<a href="#">d1u94a2</a>	Alignment		13.7	17	<b>Fold:</b> Anti-LPS factor/recA domain <b>Superfamily:</b> RecA protein, C-terminal domain <b>Family:</b> RecA protein, C-terminal domain
14	<a href="#">d1fmd1</a>	Alignment		12.9	27	<b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins) <b>Superfamily:</b> Positive stranded ssRNA viruses <b>Family:</b> Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
15	<a href="#">d1mo6a2</a>	Alignment		12.7	33	<b>Fold:</b> Anti-LPS factor/recA domain <b>Superfamily:</b> RecA protein, C-terminal domain <b>Family:</b> RecA protein, C-terminal domain
16	<a href="#">c6irwA</a>	Alignment		12.2	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphorylated ctd-interacting factor 1; <b>PDBTitle:</b> crystal structure of the human cap-specific adenosine2 methyltransferase bound to sah
17	<a href="#">d1txna</a>	Alignment		10.2	21	<b>Fold:</b> Coproporphyrinogen III oxidase <b>Superfamily:</b> Coproporphyrinogen III oxidase <b>Family:</b> Coproporphyrinogen III oxidase
18	<a href="#">d1tkla</a>	Alignment		9.4	21	<b>Fold:</b> Coproporphyrinogen III oxidase <b>Superfamily:</b> Coproporphyrinogen III oxidase <b>Family:</b> Coproporphyrinogen III oxidase
19	<a href="#">c3vepA</a>	Alignment		8.4	30	<b>PDB header:</b> membrane protein/transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable rna polymerase sigma-d factor; <b>PDBTitle:</b> crystal structure of sigd4 in complex with its negative regulator rsda
20	<a href="#">c3k8hA</a>	Alignment		8.4	21	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> 30klp; <b>PDBTitle:</b> structure of crystal form i of tp0453
21	<a href="#">c2ld3A</a>	Alignment	not modelled	8.4	14	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> myosin vi; <b>PDBTitle:</b> solution structure of myosin vi lever arm extension
22	<a href="#">c2aexA</a>	Alignment	not modelled	7.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> coproporphyrinogen iii oxidase, mitochondrial; <b>PDBTitle:</b> the 1.58a crystal structure of human coproporphyrinogen oxidase2 reveals the structural basis of hereditary coproporphria
23	<a href="#">c1zbe1</a>	Alignment	not modelled	7.8	27	<b>PDB header:</b> virus <b>Chain:</b> 1: <b>PDB Molecule:</b> coat protein vp1; <b>PDBTitle:</b> foot-and mouth disease virus serotype a1061
24	<a href="#">c4udeA</a>	Alignment	not modelled	7.8	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> ginlfy protein; <b>PDBTitle:</b> an oligomerization domain confers pioneer properties to the2 leafy master floral regulator
25	<a href="#">d1qtma2</a>	Alignment	not modelled	7.4	17	<b>Fold:</b> DNA/RNA polymerases <b>Superfamily:</b> DNA/RNA polymerases <b>Family:</b> DNA polymerase I
26	<a href="#">c1bqfA</a>	Alignment	not modelled	6.3	71	<b>PDB header:</b> hormone/growth factor <b>Chain:</b> A: <b>PDB Molecule:</b> protein (growth-blocking peptide); <b>PDBTitle:</b> growth-blocking peptide (gpb) from pseudaletia separata
27	<a href="#">c4e86L</a>	Alignment	not modelled	6.3	50	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> L: <b>PDB Molecule:</b> defensin-5; <b>PDBTitle:</b> crystal structure of human alpha-defensin 5, hd5 (leu29aba mutant)
28	<a href="#">c4e86H</a>	Alignment	not modelled	6.2	50	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> H: <b>PDB Molecule:</b> defensin-5; <b>PDBTitle:</b> crystal structure of human alpha-defensin 5, hd5 (leu29aba mutant)

29	<a href="#">c4e86D</a>	Alignment	not modelled	6.2	50	<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 (leu29aba mutant)
30	<a href="#">d1vmha</a>	Alignment	not modelled	6.2	18	<b>Fold:</b> YjbQ-like <b>Superfamily:</b> YjbQ-like <b>Family:</b> YjbQ-like
31	<a href="#">d2cmua1</a>	Alignment	not modelled	6.2	27	<b>Fold:</b> Pentain, beta/alpha-propeller <b>Superfamily:</b> Pentain <b>Family:</b> Porphyromonas-type peptidylarginine deiminase
32	<a href="#">d1vjua</a>	Alignment	not modelled	6.2	24	<b>Fold:</b> Coproporphyrinogen III oxidase <b>Superfamily:</b> Coproporphyrinogen III oxidase <b>Family:</b> Coproporphyrinogen III oxidase
33	<a href="#">d1vmja</a>	Alignment	not modelled	6.1	9	<b>Fold:</b> YjbQ-like <b>Superfamily:</b> YjbQ-like <b>Family:</b> YjbQ-like
34	<a href="#">c4e83B</a>	Alignment	not modelled	6.1	50	<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)
35	<a href="#">c4e86B</a>	Alignment	not modelled	6.1	50	<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)
36	<a href="#">c4e86C</a>	Alignment	not modelled	6.1	50	<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 (leu29aba mutant)
37	<a href="#">c4e86A</a>	Alignment	not modelled	6.1	50	<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)
38	<a href="#">c4e86E</a>	Alignment	not modelled	6.0	50	<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)
39	<a href="#">c4e86G</a>	Alignment	not modelled	6.0	50	<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)
40	<a href="#">c4e83A</a>	Alignment	not modelled	6.0	50	<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)
41	<a href="#">c4e86F</a>	Alignment	not modelled	6.0	50	<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)
42	<a href="#">c4qr1B</a>	Alignment	not modelled	5.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> crispr-associated endoribonuclease cas2; <b>PDBTitle:</b> crystal structure of streptococcus pyogenes cas2 at ph 6.5
43	<a href="#">c5mszA</a>	Alignment	not modelled	5.9	50	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thermobia domestica domestica aa15; <b>PDBTitle:</b> lytic polysaccharide monooxygenase aa15 from thermobia domestica in2 the cu(i) state
44	<a href="#">d2ewoa1</a>	Alignment	not modelled	5.9	18	<b>Fold:</b> Pentain, beta/alpha-propeller <b>Superfamily:</b> Pentain <b>Family:</b> Porphyromonas-type peptidylarginine deiminase
45	<a href="#">c5x0wH</a>	Alignment	not modelled	5.8	30	<b>PDB header:</b> ligase/protein binding <b>Chain:</b> H: <b>PDB Molecule:</b> sharpin; <b>PDBTitle:</b> molecular mechanism for the binding between sharpin and hoip
46	<a href="#">d1q44a</a>	Alignment	not modelled	5.8	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> PAPS sulfotransferase
47	<a href="#">c2p6cB</a>	Alignment	not modelled	5.7	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> aq_2013 protein; <b>PDBTitle:</b> crystal structure of hypothetical protein aq_2013 from aquifex2 aeolicus vf5.
48	<a href="#">c5fqmA</a>	Alignment	not modelled	5.7	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ecf rna polymerase sigma factor sigr; <b>PDBTitle:</b> streptomyces coelicolor sigr region 4
49	<a href="#">c5eo6A</a>	Alignment	not modelled	5.6	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> coproporphyrinogen oxidase; <b>PDBTitle:</b> coproporphyrinogen iii oxidase (hemf) from acinetobacter baumannii
50	<a href="#">c5cuiD</a>	Alignment	not modelled	5.6	50	<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.
51	<a href="#">c5cuiB</a>	Alignment	not modelled	5.6	50	<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.
52	<a href="#">c5cuiE</a>	Alignment	not modelled	5.6	50	<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.
53	<a href="#">c5cuiC</a>	Alignment	not modelled	5.6	50	<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.
54	<a href="#">c5cuiA</a>	Alignment	not modelled	5.6	50	<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.
55	<a href="#">c5cuiF</a>	Alianment	not modelled	5.6	50	<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.
56	<a href="#">c2veqA_</a>	Alignment	not modelled	5.6	12	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> centromere dna-binding protein complex cbf3 subunit b; <b>PDBTitle:</b> insights into kinetochore-dna interactions from the structure of cep3p
57	<a href="#">c4e82B_</a>	Alignment	not modelled	5.5	50	<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)
58	<a href="#">c4e82A_</a>	Alignment	not modelled	5.5	50	<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)
59	<a href="#">c2mitB_</a>	Alignment	not modelled	5.5	50	<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
60	<a href="#">d1w0ba_</a>	Alignment	not modelled	5.4	24	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> Alpha-hemoglobin stabilizing protein AHSP <b>Family:</b> Alpha-hemoglobin stabilizing protein AHSP
61	<a href="#">c1zmpC_</a>	Alignment	not modelled	5.4	50	<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
62	<a href="#">c2lxzA_</a>	Alignment	not modelled	5.4	50	<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
63	<a href="#">c1zmpB_</a>	Alignment	not modelled	5.4	50	<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
64	<a href="#">c1zmpA_</a>	Alignment	not modelled	5.4	50	<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
65	<a href="#">c3excX_</a>	Alignment	not modelled	5.4	8	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> structure of the rna'se sso8090 from sulfolobus solfataricus
66	<a href="#">c4merD_</a>	Alignment	not modelled	5.4	20	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> streptococcal histidine-rich glycoprotein interacting <b>PDBTitle:</b> crystal structure of the novel protein and virulence factor ship2 (q99xu0) from streptococcus pyogenes
67	<a href="#">c2mitA_</a>	Alignment	not modelled	5.4	50	<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
68	<a href="#">d1z8ua1</a>	Alignment	not modelled	5.3	24	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> Alpha-hemoglobin stabilizing protein AHSP <b>Family:</b> Alpha-hemoglobin stabilizing protein AHSP
69	<a href="#">d2p12a1</a>	Alignment	not modelled	5.3	14	<b>Fold:</b> FomD barre-like <b>Superfamily:</b> FomD-like <b>Family:</b> FomD-like
70	<a href="#">c5cujF_</a>	Alignment	not modelled	5.3	50	<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.
71	<a href="#">c5cumA_</a>	Alignment	not modelled	5.3	50	<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 y27a mutant crystal form 1.
72	<a href="#">c5cujB_</a>	Alignment	not modelled	5.3	50	<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 2.
73	<a href="#">c5cujE_</a>	Alignment	not modelled	5.3	50	<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.
74	<a href="#">c5cumB_</a>	Alignment	not modelled	5.3	50	<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.
75	<a href="#">c5cujC_</a>	Alignment	not modelled	5.3	50	<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.
76	<a href="#">c5cumC_</a>	Alignment	not modelled	5.3	50	<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.
77	<a href="#">c5cujA_</a>	Alignment	not modelled	5.3	50	<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 y27a mutant crystal form 2.
78	<a href="#">c5cujD_</a>	Alignment	not modelled	5.3	50	<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 y27a mutant crystal form 2.
79	<a href="#">c1ve0A_</a>	Alignment	not modelled	5.3	18	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein (st2072); <b>PDBTitle:</b> crystal structure of uncharacterized protein st2072 from sulfolobus2 tokodaii
80	<a href="#">c2cu5C_</a>	Alignment	not modelled	5.2	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> conserved hypothetical protein tt1486; <b>PDBTitle:</b> crystal structure of the conserved hypothetical protein tt1486 from2 thermus thermophilus hb8
						<b>Fold:</b> Common fold of diphtheria toxin/transcription

81	<a href="#">d1p5vb_</a>	Alignment	not modelled	5.2	39	factors/cytochrome f <b>Superfamily:</b> Bacterial adhesins <b>Family:</b> Pilus subunits
82	<a href="#">c2p6hB_</a>	Alignment	not modelled	5.2	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of hypothetical protein ape1520 from aeropyrum2 pernix k1
83	<a href="#">c4rbxA_</a>	Alignment	not modelled	5.1	50	<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)
84	<a href="#">c2vziB_</a>	Alignment	not modelled	5.1	22	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-parvin; <b>PDBTitle:</b> crystal structure of the c-terminal calponin homology domain of alpha-2 parvin in complex with paxillin Id4 motif
85	<a href="#">c2o8xA_</a>	Alignment	not modelled	5.1	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable rna polymerase sigma-c factor; <b>PDBTitle:</b> crystal structure of the "-35 element" promoter recognition domain of f2 mycobacterium tuberculosis sigc