

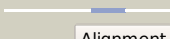
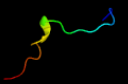

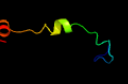
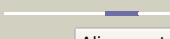








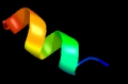



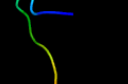

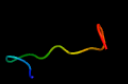











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0249c_(-)_300834_301655
Date	Tue Jul 23 14:50:31 BST 2019
Unique Job ID	1dda95bced74854d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6odmW_</a>	 Alignment		27.5	44	<b>PDB header:</b> viral protein <b>Chain:</b> W: <b>PDB Molecule:</b> major capsid protein; <b>PDBTitle:</b> herpes simplex virus type 1 (hsv-1) portal vertex-adjacent2 capsid/catc, asymmetric unit
2	<a href="#">d1t61c2</a>	 Alignment		20.0	56	<b>Fold:</b> C-type lectin-like <b>Superfamily:</b> C-type lectin-like <b>Family:</b> Noncollagenous (NC1) domain of collagen IV
3	<a href="#">c3izbE_</a>	 Alignment		18.2	32	<b>PDB header:</b> ribosome <b>Chain:</b> E: <b>PDB Molecule:</b> 40s ribosomal protein rps2 (s5p); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
4	<a href="#">c3loeA_</a>	 Alignment		14.8	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (f28a mutant)
5	<a href="#">c3gnyA_</a>	 Alignment		14.7	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (hnp1)
6	<a href="#">c3lo1A_</a>	 Alignment		14.6	36	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (y16a mutant)
7	<a href="#">c3hj2B_</a>	 Alignment		13.3	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> human neutrophil peptide 1; <b>PDBTitle:</b> crystal structure of covalent dimer of hnp1
8	<a href="#">c3ixzB_</a>	 Alignment		13.2	36	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> potassium-transporting atpase subunit beta; <b>PDBTitle:</b> pig gastric h+/k+/-atpase complexed with aluminium fluoride
9	<a href="#">c4lb7A_</a>	 Alignment		12.4	43	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (hnp1) y16a/i20a/i25a/f28a2 mutant.
10	<a href="#">c4lb7E_</a>	 Alignment		12.4	43	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> E: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (hnp1) y16a/i20a/i25a/f28a2 mutant.
11	<a href="#">c4lb7D_</a>	 Alignment		12.4	43	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> D: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (hnp1) y16a/i20a/i25a/f28a2 mutant.

12	<a href="#">c4lb7B_</a>	Alignment		12.4	43	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (hnp1) y16a/i20a/i25a/f28a2 mutant.
13	<a href="#">c4lb1B_</a>	Alignment		12.2	36	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (hnp1) y16a/f28a mutant
14	<a href="#">c4lb1E_</a>	Alignment		12.2	36	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> E: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (hnp1) y16a/f28a mutant
15	<a href="#">c4lb1A_</a>	Alignment		12.2	36	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (hnp1) y16a/f28a mutant
16	<a href="#">c4lb1D_</a>	Alignment		12.2	36	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> D: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (hnp1) y16a/f28a mutant
17	<a href="#">c1zmiB_</a>	Alignment		11.8	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> neutrophil defensin 2; <b>PDBTitle:</b> crystal structure of human alpha_defensin-2 (variant gly16->d-ala), p2 32 2 1 space group )
18	<a href="#">c1zmkB_</a>	Alignment		11.8	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> neutrophil defensin 2; <b>PDBTitle:</b> crystal structure of human alpha-defensin-2 (variant gly16-> d-ala), p2 42 21 2 space group
19	<a href="#">c1zmhB_</a>	Alignment		11.8	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> neutrophil defensin 2; <b>PDBTitle:</b> crystal structure of human neutrophil peptide 2, hnp-2 (variant gly16-2 > d-ala)
20	<a href="#">c1zmkA_</a>	Alignment		11.8	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> neutrophil defensin 2; <b>PDBTitle:</b> crystal structure of human alpha-defensin-2 (variant gly16-> d-ala), p2 42 21 2 space group
21	<a href="#">c1zmhD_</a>	Alignment	not modelled	11.8	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> D: <b>PDB Molecule:</b> neutrophil defensin 2; <b>PDBTitle:</b> crystal structure of human neutrophil peptide 2, hnp-2 (variant gly16-2 > d-ala)
22	<a href="#">c1zmiC_</a>	Alignment	not modelled	11.8	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> C: <b>PDB Molecule:</b> neutrophil defensin 2; <b>PDBTitle:</b> crystal structure of human alpha_defensin-2 (variant gly16->d-ala), p2 32 2 1 space group )
23	<a href="#">c1zmhA_</a>	Alignment	not modelled	11.8	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> neutrophil defensin 2; <b>PDBTitle:</b> crystal structure of human neutrophil peptide 2, hnp-2 (variant gly16-2 > d-ala)
24	<a href="#">c1zmhC_</a>	Alignment	not modelled	11.8	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> C: <b>PDB Molecule:</b> neutrophil defensin 2; <b>PDBTitle:</b> crystal structure of human neutrophil peptide 2, hnp-2 (variant gly16-2 > d-ala)
25	<a href="#">c1zmiA_</a>	Alignment	not modelled	11.8	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> neutrophil defensin 2; <b>PDBTitle:</b> crystal structure of human alpha_defensin-2 (variant gly16->d-ala), p2 32 2 1 space group )
26	<a href="#">c1zmiD_</a>	Alignment	not modelled	11.8	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> D: <b>PDB Molecule:</b> neutrophil defensin 2; <b>PDBTitle:</b> crystal structure of human alpha_defensin-2 (variant gly16->d-ala), p2 32 2 1 space group )
27	<a href="#">c3lo6A_</a>	Alignment	not modelled	11.6	28	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (w26aba mutant)
28	<a href="#">c3lo9A_</a>	Alignment	not modelled	11.4	28	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (w26ahp mutant)

29	<a href="#">c3lo9B_</a>	Alignment	not modelled	11.4	28	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (w26ahp mutant)
30	<a href="#">c3lo6B_</a>	Alignment	not modelled	11.4	28	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (w26aba mutant)
31	<a href="#">c4lbfE_</a>	Alignment	not modelled	11.2	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> E: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (hnp1) i20a/i25a mutant
32	<a href="#">c1dfnA_</a>	Alignment	not modelled	11.0	33	<b>PDB header:</b> defensin <b>Chain:</b> A: <b>PDB Molecule:</b> defensin hnp-3; <b>PDBTitle:</b> crystal structure of defensin hnp-3, an amphiphilic dimer: mechanisms2 of membrane permeabilization
33	<a href="#">d1dfna_</a>	Alignment	not modelled	11.0	33	<b>Fold:</b> Defensin-like <b>Superfamily:</b> Defensin-like <b>Family:</b> Defensin
34	<a href="#">c1dfnB_</a>	Alignment	not modelled	11.0	33	<b>PDB header:</b> defensin <b>Chain:</b> B: <b>PDB Molecule:</b> defensin hnp-3; <b>PDBTitle:</b> crystal structure of defensin hnp-3, an amphiphilic dimer: mechanisms2 of membrane permeabilization
35	<a href="#">c4lbfH_</a>	Alignment	not modelled	10.9	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> H: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (hnp1) i20a/i25a mutant
36	<a href="#">c4lbfD_</a>	Alignment	not modelled	10.9	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> D: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (hnp1) i20a/i25a mutant
37	<a href="#">c3hjdB_</a>	Alignment	not modelled	10.9	36	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> human neutrophil peptide 1; <b>PDBTitle:</b> x-ray structure of monomeric variant of hnp1
38	<a href="#">c3hjdA_</a>	Alignment	not modelled	10.9	36	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> human neutrophil peptide 1; <b>PDBTitle:</b> x-ray structure of monomeric variant of hnp1
39	<a href="#">d5crxb2</a>	Alignment	not modelled	10.9	50	<b>Fold:</b> DNA breaking-rejoining enzymes <b>Superfamily:</b> DNA breaking-rejoining enzymes <b>Family:</b> Lambda integrase-like, catalytic core
40	<a href="#">c4lbfF_</a>	Alignment	not modelled	10.9	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> F: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (hnp1) i20a/i25a mutant
41	<a href="#">c4lbfA_</a>	Alignment	not modelled	10.9	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (hnp1) i20a/i25a mutant
42	<a href="#">c4lbfC_</a>	Alignment	not modelled	10.9	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> C: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (hnp1) i20a/i25a mutant
43	<a href="#">c4lbfG_</a>	Alignment	not modelled	10.9	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> G: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (hnp1) i20a/i25a mutant
44	<a href="#">c4lbfB_</a>	Alignment	not modelled	10.9	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (hnp1) i20a/i25a mutant
45	<a href="#">c2khtA_</a>	Alignment	not modelled	10.7	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> nmr structure of human alpha defensin hnp-1
46	<a href="#">c3gnyB_</a>	Alignment	not modelled	10.6	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (hnp1)
47	<a href="#">c3lo4B_</a>	Alignment	not modelled	10.6	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (r24a mutant)
48	<a href="#">c3lo4A_</a>	Alignment	not modelled	10.6	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (r24a mutant)
49	<a href="#">c4du0A_</a>	Alignment	not modelled	10.5	33	<b>PDB header:</b> antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1, hnp1 (g17a mutant)
50	<a href="#">c4du0C_</a>	Alignment	not modelled	10.5	33	<b>PDB header:</b> antibiotic <b>Chain:</b> C: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1, hnp1 (g17a mutant)
51	<a href="#">c4du0D_</a>	Alignment	not modelled	10.4	33	<b>PDB header:</b> antibiotic <b>Chain:</b> D: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1, hnp1 (g17a mutant)
52	<a href="#">c4du0B_</a>	Alignment	not modelled	10.4	33	<b>PDB header:</b> antibiotic <b>Chain:</b> B: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1, hnp1 (g17a mutant)
53	<a href="#">c3lvxA_</a>	Alignment	not modelled	10.4	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (i6a mutant)
54	<a href="#">c4lbbA_</a>	Alignment	not modelled	10.3	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (hnp1) i20a mutant
						<b>PDB header:</b> antimicrobial protein

55	<a href="#">c4lbbB_</a>	Alignment	not modelled	10.3	33	<b>Chain:</b> B: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (hnp1) i20a mutant
56	<a href="#">c3lvxB_</a>	Alignment	not modelled	10.3	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (i6a mutant)
57	<a href="#">c3h6cA_</a>	Alignment	not modelled	10.3	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (mutant gln22ala)
58	<a href="#">c3h6cB_</a>	Alignment	not modelled	10.3	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (mutant gln22ala)
59	<a href="#">c5b2gG_</a>	Alignment	not modelled	10.3	44	<b>PDB header:</b> membrane protein <b>Chain:</b> G: <b>PDB Molecule:</b> endolysin,claudin-4; <b>PDBTitle:</b> crystal structure of human claudin-4 in complex with c-terminal2 fragment of clostridium perfringens enterotoxin
60	<a href="#">c4iapB_</a>	Alignment	not modelled	10.2	44	<b>PDB header:</b> lipid binding protein/ hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> oxysterol-binding protein homolog 3,endolysin,oxysterol- <b>PDBTitle:</b> crystal structure of ph domain of osh3 from saccharomyces cerevisiae
61	<a href="#">c3lo2A_</a>	Alignment	not modelled	10.2	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (y21a mutant)
62	<a href="#">c3lo2B_</a>	Alignment	not modelled	10.2	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> neutrophil defensin 1; <b>PDBTitle:</b> crystal structure of human alpha-defensin 1 (y21a mutant)
63	<a href="#">d1t61a2</a>	Alignment	not modelled	10.1	63	<b>Fold:</b> C-type lectin-like <b>Superfamily:</b> C-type lectin-like <b>Family:</b> Noncollagenous (NC1) domain of collagen IV
64	<a href="#">c5kw2A_</a>	Alignment	not modelled	9.9	44	<b>PDB header:</b> fatty acid binding protein/hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> free fatty acid receptor 1,lysozyme,free fatty acid <b>PDBTitle:</b> the extra-helical binding site of gpr40 and the structural basis for2 allosteric agonism and incretin stimulation
65	<a href="#">c2lr5A_</a>	Alignment	not modelled	9.8	27	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> micasin; <b>PDBTitle:</b> 1h chemical shift assignments for micasin
66	<a href="#">d2bosa_</a>	Alignment	not modelled	9.5	41	<b>Fold:</b> OB-fold <b>Superfamily:</b> Bacterial enterotoxins <b>Family:</b> Bacterial AB5 toxins, B-subunits
67	<a href="#">c4n9nA_</a>	Alignment	not modelled	9.4	44	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> sterol uptake control protein 2, lysozyme; <b>PDBTitle:</b> crystal structure of saccharomyces cerevisiae upc2 transcription2 factor fused with t4 lysozyme
68	<a href="#">c5lr6B_</a>	Alignment	not modelled	9.1	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> bd-type quinol oxidase subunit ii; <b>PDBTitle:</b> the structure of bd oxidase from geobacillus thermodenitrificans
69	<a href="#">c6a9eA_</a>	Alignment	not modelled	8.8	44	<b>PDB header:</b> lipid transport <b>Chain:</b> A: <b>PDB Molecule:</b> endolysin,autophagy-related protein 2; <b>PDBTitle:</b> crystal structure of the n-terminal domain of atg2
70	<a href="#">c5mqcA_</a>	Alignment	not modelled	8.7	43	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> vp1; <b>PDBTitle:</b> structure of black queen cell virus
71	<a href="#">c4xsjA_</a>	Alignment	not modelled	8.4	44	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> lysozyme,calcium uniporter protein, mitochondrial; <b>PDBTitle:</b> crystal structure of the n-terminal domain of the human mitochondrial2 calcium uniporter fused with t4 lysozyme
72	<a href="#">d1r4pb_</a>	Alignment	not modelled	8.0	35	<b>Fold:</b> OB-fold <b>Superfamily:</b> Bacterial enterotoxins <b>Family:</b> Bacterial AB5 toxins, B-subunits
73	<a href="#">c2voyE_</a>	Alignment	not modelled	7.9	31	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> sarcoplasmic/endoplasmic reticulum calcium atpase 1; <b>PDBTitle:</b> cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
74	<a href="#">c3sn6R_</a>	Alignment	not modelled	7.9	26	<b>PDB header:</b> signaling protein/hydrolase <b>Chain:</b> R: <b>PDB Molecule:</b> endolysin,beta-2 adrenergic receptor; <b>PDBTitle:</b> crystal structure of the beta2 adrenergic receptor-gs protein complex
75	<a href="#">c2pm4A_</a>	Alignment	not modelled	7.6	22	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> neutrophil defensin 1 (hnp-1) (hp-1) (hp1) (defensin, alpha <b>PDBTitle:</b> human alpha-defensin 1 (multiple arg->lys mutant)
76	<a href="#">c2pm4B_</a>	Alignment	not modelled	7.6	22	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> neutrophil defensin 1 (hnp-1) (hp-1) (hp1) (defensin, alpha <b>PDBTitle:</b> human alpha-defensin 1 (multiple arg->lys mutant)
77	<a href="#">c5vl1D_</a>	Alignment	not modelled	7.4	25	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> lysine--trna ligase; <b>PDBTitle:</b> crystal structure of lysyl-trna synthetase from mycobacterium ulcerans2 complexed with l-lysine
78	<a href="#">c4ex5A_</a>	Alignment	not modelled	7.3	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lysine--trna ligase; <b>PDBTitle:</b> crystal structure of lysyl-trna synthetase lysrs from burkholderia2 thailandensis bound to lysine
79	<a href="#">c6od8A_</a>	Alignment	not modelled	7.3	44	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> putative aspartyl-trna synthetase; <b>PDBTitle:</b> crystal structure of a putative aspartyl-trna synthetase from2 leishmania major friedlin
						<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> bmkdfsin3;

80	<a href="#">c5xa6A</a>	Alignment	not modelled	7.1	40	<b>PDBTitle:</b> ion channel modulation by scorpion haemolymph and its defensin2 ingredients uncovers origin of neurotoxins in telson formed in3 paleozoic scorpion
81	<a href="#">c5hggD</a>	Alignment	not modelled	7.0	25	<b>PDB header:</b> ligase/ligase inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> lysine--trna ligase; <b>PDBTitle:</b> loa loa lysyl-trna synthetase in complex with cladosporin.
82	<a href="#">c5elnC</a>	Alignment	not modelled	6.9	31	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> lysine--trna ligase; <b>PDBTitle:</b> crystal structure of lysyl-trna synthetase from cryptosporidium parvum2 complexed with l-lysine
83	<a href="#">d1ftb2</a>	Alignment	not modelled	6.9	14	<b>Fold:</b> Transmembrane helix hairpin <b>Superfamily:</b> Cytochrome c oxidase subunit II-like, transmembrane region <b>Family:</b> Cytochrome c oxidase subunit II-like, transmembrane region
84	<a href="#">c5yqrA</a>	Alignment	not modelled	6.8	44	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> endolysin/membrane-anchored lipid-binding protein lam6 <b>PDBTitle:</b> crystal structure of the ph-like domain of lam6
85	<a href="#">d1nmla1</a>	Alignment	not modelled	6.7	26	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Di-heme cytochrome c peroxidase
86	<a href="#">c4h02B</a>	Alignment	not modelled	6.7	25	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> lysyl-trna synthetase; <b>PDBTitle:</b> crystal structure of p. falciparum lysyl-trna synthetase
87	<a href="#">d1ql1i</a>	Alignment	not modelled	6.6	50	<b>Fold:</b> PMP inhibitors <b>Superfamily:</b> PMP inhibitors <b>Family:</b> PMP inhibitors
88	<a href="#">d1c4qa</a>	Alignment	not modelled	6.5	29	<b>Fold:</b> OB-fold <b>Superfamily:</b> Bacterial enterotoxins <b>Family:</b> Bacterial AB5 toxins, B-subunits
89	<a href="#">c1efwA</a>	Alignment	not modelled	6.2	19	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> aspartyl-trna synthetase; <b>PDBTitle:</b> crystal structure of aspartyl-trna synthetase from thermus2 thermophilus complexed to trnaasp from escherichia coli
90	<a href="#">c4a8eA</a>	Alignment	not modelled	6.0	38	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> probable tyrosine recombinase xerc-like; <b>PDBTitle:</b> the structure of a dimeric xer recombinase from archaea
91	<a href="#">c3mdoB</a>	Alignment	not modelled	5.9	23	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> putative phosphoribosylformylglycinamide cyclo-ligase; <b>PDBTitle:</b> crystal structure of a putative phosphoribosylformylglycinamide2 cyclo-ligase (bdi_2101) from parabacteroides distasonis atcc 8503 at3 1.91 a resolution
92	<a href="#">c6ns0A</a>	Alignment	not modelled	5.7	31	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> lysine--trna ligase; <b>PDBTitle:</b> crystal structure of lysyl-trna synthetase from chlamydia trachomatis2 complexed with l-lysine and cladosporin
93	<a href="#">d1clia2</a>	Alignment	not modelled	5.7	32	<b>Fold:</b> PurM C-terminal domain-like <b>Superfamily:</b> PurM C-terminal domain-like <b>Family:</b> PurM C-terminal domain-like
94	<a href="#">d1f44a2</a>	Alignment	not modelled	5.6	50	<b>Fold:</b> DNA breaking-rejoining enzymes <b>Superfamily:</b> DNA breaking-rejoining enzymes <b>Family:</b> Lambda integrase-like, catalytic core
95	<a href="#">c2a3vA</a>	Alignment	not modelled	5.6	50	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> site-specific recombinase inti4; <b>PDBTitle:</b> structural basis for broad dna-specificity in integron recombination
96	<a href="#">c3bjuB</a>	Alignment	not modelled	5.5	31	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> lysyl-trna synthetase; <b>PDBTitle:</b> crystal structure of tetrameric form of human lysyl-trna synthetase
97	<a href="#">d1iyb1</a>	Alignment	not modelled	5.5	32	<b>Fold:</b> BRCA2 helical domain <b>Superfamily:</b> BRCA2 helical domain <b>Family:</b> BRCA2 helical domain
98	<a href="#">c5ndzA</a>	Alignment	not modelled	5.5	44	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> lysozyme,proteinase-activated receptor 2,soluble cytochrome <b>PDBTitle:</b> crystal structure of a thermostabilised human protease-activated2 receptor-2 (par2) in complex with az3451 at 3.6 angstrom resolution
99	<a href="#">c4j15A</a>	Alignment	not modelled	5.4	38	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate--trna ligase, cytoplasmic; <b>PDBTitle:</b> crystal structure of human cytosolic aspartyl-trna synthetase, a2 component of multi-trna synthetase complex