

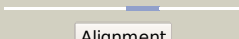
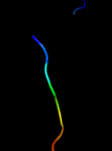
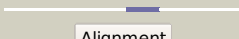


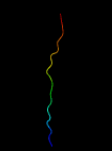

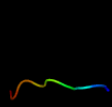

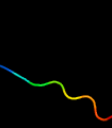
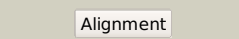
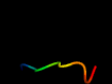










# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2369c_(-)_2649956_2650258
Date	Mon Aug 5 13:25:52 BST 2019
Unique Job ID	b172c954529c95d7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3a10C_</a>	 Alignment		28.8	47	<b>PDB header:</b> ligase/rna <b>Chain:</b> C: <b>PDB Molecule:</b> glutamyl-trna (gln) amidotransferase subunit c,linker, <b>PDBTitle:</b> crystal structure of the glutamine transamidosome from thermotoga2 maritima in the glutamylation state.
2	<a href="#">c2o5rA_</a>	 Alignment		21.9	56	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase 1; <b>PDBTitle:</b> crystal structure of glutamyl-trna synthetase 1 (ec 6.1.1.17)2 (glutamate-trna ligase 1) (glurs 1) (tm1351) from thermotoga maritima3 at 2.5 a resolution
3	<a href="#">c3afhA_</a>	 Alignment		19.4	56	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase 2; <b>PDBTitle:</b> crystal structure of thermotoga maritima nondiscriminating glutamyl-2 trna synthetase in complex with a glutamyl-amp analog
4	<a href="#">c5o60S_</a>	 Alignment		19.3	37	<b>PDB header:</b> ribosome <b>Chain:</b> S: <b>PDB Molecule:</b> 50s ribosomal protein l21; <b>PDBTitle:</b> structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
5	<a href="#">c5tgtA_</a>	 Alignment		18.9	44	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate--trna ligase; <b>PDBTitle:</b> crystal structure of glytamyl-trna synthetase glurs from pseudomonas2 aeruginosa
6	<a href="#">c1g59A_</a>	 Alignment		17.5	56	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase; <b>PDBTitle:</b> glutamyl-trna synthetase complexed with trna(glu).
7	<a href="#">c2cfoA_</a>	 Alignment		16.7	56	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase; <b>PDBTitle:</b> non-discriminating glutamyl-trna synthetase from2 thermosynechococcus elongatus in complex with glu
8	<a href="#">d2goma1</a>	 Alignment		14.2	58	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> Efb C-domain-like <b>Family:</b> Efb C-domain-like
9	<a href="#">d2nojb1</a>	 Alignment		13.8	67	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> Efb C-domain-like <b>Family:</b> Efb C-domain-like
10	<a href="#">c2nojD_</a>	 Alignment		13.8	67	<b>PDB header:</b> immune system <b>Chain:</b> D: <b>PDB Molecule:</b> efb homologous protein; <b>PDBTitle:</b> crystal structure of ehp / c3d complex
11	<a href="#">c2ja2A_</a>	 Alignment		13.1	44	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase; <b>PDBTitle:</b> mycobacterium tuberculosis glutamyl-trna synthetase

12	<a href="#">c4griB</a>	Alignment			12.8	63	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> glutamate--trna ligase; <b>PDBTitle:</b> crystal structure of a glutamyl-trna synthetase glurs from borrelia2 burgdorferi bound to glutamic acid and zinc
13	<a href="#">c1vw4N</a>	Alignment			12.8	22	<b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> 54s ribosomal protein l49, mitochondrial; <b>PDBTitle:</b> structure of the yeast mitochondrial large ribosomal subunit
14	<a href="#">c5mlcT</a>	Alignment			12.7	44	<b>PDB header:</b> ribosome <b>Chain:</b> T: <b>PDB Molecule:</b> 50s ribosomal protein l21, chloroplastic; <b>PDBTitle:</b> cryo-em structure of the spinach chloroplast ribosome reveals the2 location of plastid-specific ribosomal proteins and extensions
15	<a href="#">c3j3vR</a>	Alignment			12.3	26	<b>PDB header:</b> ribosome <b>Chain:</b> R: <b>PDB Molecule:</b> 50s ribosomal protein l21; <b>PDBTitle:</b> atomic model of the immature 50s subunit from bacillus subtilis (state2 i-a)
16	<a href="#">c4ce4V</a>	Alignment			11.8	6	<b>PDB header:</b> ribosome <b>Chain:</b> V: <b>PDB Molecule:</b> mrpl21; <b>PDBTitle:</b> 39s large subunit of the porcine mitochondrial ribosome
17	<a href="#">c3bboT</a>	Alignment			10.6	44	<b>PDB header:</b> ribosome <b>Chain:</b> T: <b>PDB Molecule:</b> ribosomal protein l21; <b>PDBTitle:</b> homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
18	<a href="#">d2zjro1</a>	Alignment			10.6	47	<b>Fold:</b> L21p-like <b>Superfamily:</b> L21p-like <b>Family:</b> Ribosomal protein L21p
19	<a href="#">c2c60A</a>	Alignment			9.9	36	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> human mitogen-activated protein kinase kinase kinase 3 <b>PDBTitle:</b> crystal structure of human mitogen-activated protein kinase kinase2 kinase 3 isoform 2 phox domain at 1.25 a resolution
20	<a href="#">c5mmiS</a>	Alignment			9.6	42	<b>PDB header:</b> ribosome <b>Chain:</b> S: <b>PDB Molecule:</b> 50s ribosomal protein l21, chloroplastic; <b>PDBTitle:</b> structure of the large subunit of the chloroplast ribosome
21	<a href="#">d2j01v1</a>	Alignment		not modelled	8.9	26	<b>Fold:</b> L21p-like <b>Superfamily:</b> L21p-like <b>Family:</b> Ribosomal protein L21p
22	<a href="#">c6b1zA</a>	Alignment		not modelled	8.6	56	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate--trna ligase; <b>PDBTitle:</b> crystal structure of glutamate-trna synthetase from elizabethkingia2 anophelis
23	<a href="#">c6jxaA</a>	Alignment		not modelled	8.5	60	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase tel1; <b>PDBTitle:</b> tel1 kinase compact monomer
24	<a href="#">d2qamr1</a>	Alignment		not modelled	8.4	28	<b>Fold:</b> L21p-like <b>Superfamily:</b> L21p-like <b>Family:</b> Ribosomal protein L21p
25	<a href="#">d1v5sa</a>	Alignment		not modelled	7.7	64	<b>Fold:</b> TBP-like <b>Superfamily:</b> KA1-like <b>Family:</b> Kinase associated domain 1, KA1
26	<a href="#">c5np1A</a>	Alignment		not modelled	7.3	60	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine-protein kinase atm; <b>PDBTitle:</b> open protomer of human atm (ataxia telangiectasia mutated)
27	<a href="#">d2zjra2</a>	Alignment		not modelled	6.5	44	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
28	<a href="#">c2mitB</a>	Alignment		not modelled	6.1	64	<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
29	<a href="#">c2mitA</a>	Alignment		not modelled	6.0	64	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> defensin-5;

29	<a href="#">c2mva_</a>	Alignment	not modelled	5.9	64	<b>PDBTitle:</b> solution structure of oxidized dimeric form of human defensin 5
30	<a href="#">c2liyA_</a>	Alignment	not modelled	5.9	50	<b>PDB header:</b> hormone <b>Chain:</b> A: <b>PDB Molecule:</b> epidermal patterning factor-like protein 9; <b>PDBTitle:</b> plant peptide hormone regulating stomatal density
31	<a href="#">c3i5wA_</a>	Alignment	not modelled	5.8	64	<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)
32	<a href="#">c3i5wB_</a>	Alignment	not modelled	5.8	64	<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)
33	<a href="#">c4e82B_</a>	Alignment	not modelled	5.6	64	<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)
34	<a href="#">c4e82A_</a>	Alignment	not modelled	5.6	64	<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)
35	<a href="#">c5np0A_</a>	Alignment	not modelled	5.6	60	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> serine-protein kinase atm; <b>PDBTitle:</b> closed dimer of human atm (ataxia telangiectasia mutated)
36	<a href="#">c5cuiE_</a>	Alignment	not modelled	5.5	64	<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.
37	<a href="#">c1zmpA_</a>	Alignment	not modelled	5.5	64	<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
38	<a href="#">c1zmpB_</a>	Alignment	not modelled	5.5	64	<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
39	<a href="#">c2lxzA_</a>	Alignment	not modelled	5.5	64	<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
40	<a href="#">c4e86D_</a>	Alignment	not modelled	5.5	64	<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)
41	<a href="#">c4e86H_</a>	Alignment	not modelled	5.5	64	<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)
42	<a href="#">c5cuiC_</a>	Alignment	not modelled	5.5	64	<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.
43	<a href="#">c5cuiD_</a>	Alignment	not modelled	5.5	64	<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.
44	<a href="#">c5cuiB_</a>	Alignment	not modelled	5.5	64	<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.
45	<a href="#">c5cuiA_</a>	Alignment	not modelled	5.5	64	<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.
46	<a href="#">c5cuiF_</a>	Alignment	not modelled	5.5	64	<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.
47	<a href="#">c1zmpC_</a>	Alignment	not modelled	5.4	64	<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
48	<a href="#">c4rbxA_</a>	Alignment	not modelled	5.4	64	<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)
49	<a href="#">c2h1zA_</a>	Alignment	not modelled	5.4	54	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> hybrid atracotoxin; <b>PDBTitle:</b> structure of a dual-target spider toxin
50	<a href="#">c4e83A_</a>	Alignment	not modelled	5.3	64	<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)
51	<a href="#">c5cujD_</a>	Alignment	not modelled	5.3	64	<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.
52	<a href="#">c5cumB_</a>	Alignment	not modelled	5.3	64	<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.
53	<a href="#">c5cujB_</a>	Alignment	not modelled	5.3	64	<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.
54	<a href="#">c5cujE_</a>	Alignment	not modelled	5.3	64	<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.
55	<a href="#">c5cumC_</a>	Alignment	not modelled	5.3	64	<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.

56	<a href="#">c5cujC_</a>	Alignment	not modelled	5.3	64	<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.
57	<a href="#">c5cujF_</a>	Alignment	not modelled	5.3	64	<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.
58	<a href="#">c5cumA_</a>	Alignment	not modelled	5.3	64	<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.
59	<a href="#">c5cujA_</a>	Alignment	not modelled	5.3	64	<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.
60	<a href="#">c4e86G_</a>	Alignment	not modelled	5.3	64	<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)
61	<a href="#">c4e86E_</a>	Alignment	not modelled	5.3	64	<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)
62	<a href="#">c4e86F_</a>	Alignment	not modelled	5.3	64	<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)
63	<a href="#">d2j01d2</a>	Alignment	not modelled	5.3	56	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
64	<a href="#">c4e86L_</a>	Alignment	not modelled	5.2	64	<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)
65	<a href="#">c4e86A_</a>	Alignment	not modelled	5.1	64	<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)
66	<a href="#">c4e83B_</a>	Alignment	not modelled	5.1	64	<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)
67	<a href="#">c4e86C_</a>	Alignment	not modelled	5.1	64	<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)
68	<a href="#">c4e86B_</a>	Alignment	not modelled	5.1	64	<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)