


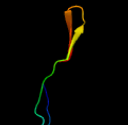


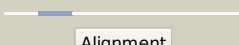

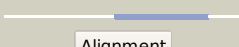

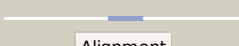
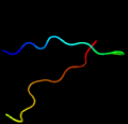
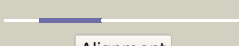
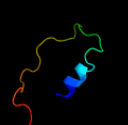



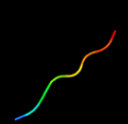

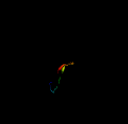




Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2341_(lppQ)_2619607_2620026
 Date Mon Aug 5 13:25:49 BST 2019
 Unique Job ID 522bcefd831c135d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1c5ea_	 Alignment		35.0	18	Fold: beta-clip Superfamily: Head decoration protein D (gpD, major capsid protein D) Family: Head decoration protein D (gpD, major capsid protein D)
2	d2h62d1	 Alignment		33.3	18	Fold: Snake toxin-like Superfamily: Snake toxin-like Family: Extracellular domain of cell surface receptors
3	c1djbB_	 Alignment		26.1	33	PDB header: lipid degradation Chain: B: PDB Molecule: phosphoinositide-specific phospholipase c, PDBTitle: phosphoinositide-specific phospholipase c-delta1 from rat2 complexed with inositol-2,4,5-trisphosphate
4	c5x3IA_	 Alignment		25.7	56	PDB header: antimicrobial protein Chain: A: PDB Molecule: pilosulin-1; PDBTitle: solution structure of a novel antimicrobial peptide, p1, from jumper2 ant myrmecia pilosula
5	c4pewB_	 Alignment		23.3	27	PDB header: hydrolase Chain: B: PDB Molecule: putative secreted protein; PDBTitle: structure of sactelam55a from streptomyces sp. sirexaa-e
6	c2xfeA_	 Alignment		20.7	50	PDB header: sugar binding protein Chain: A: PDB Molecule: carbohydrate binding module; PDBTitle: vcbm60 in complex with galactobiose
7	c5gzxD_	 Alignment		18.9	26	PDB header: hydrolase Chain: D: PDB Molecule: (r)-2-haloacid dehalogenase; PDBTitle: the complex structure of d-2-haloacid dehalogenase mutant with d-2-cpa
8	d1td4a_	 Alignment		17.5	45	Fold: beta-clip Superfamily: Head decoration protein D (gpD, major capsid protein D) Family: Head decoration protein D (gpD, major capsid protein D)
9	d1e8ob_	 Alignment		16.9	56	Fold: Signal recognition particle alu RNA binding heterodimer, SRP9/14 Superfamily: Signal recognition particle alu RNA binding heterodimer, SRP9/14 Family: Signal recognition particle alu RNA binding heterodimer, SRP9/14
10	c4faoL_	 Alignment		16.5	18	PDB header: signaling protein/signaling protein Chain: L: PDB Molecule: activin receptor type-2b; PDBTitle: specificity and structure of a high affinity activin-like 1 (alk1)2 signaling complex
11	c4bxtD_	 Alignment		15.6	70	PDB header: viral protein Chain: D: PDB Molecule: phosphoprotein p; PDBTitle: crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain

12	c5oixA_	Alignment		15.6	70	PDB header: viral protein Chain: A; PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 1.6 a
13	c5oixE_	Alignment		15.6	70	PDB header: viral protein Chain: E; PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 1.6 a
14	c5oixE_	Alignment		15.6	70	PDB header: viral protein Chain: E; PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 2.2 a
15	c5oixG_	Alignment		15.6	70	PDB header: viral protein Chain: G; PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 2.2 a
16	c5oixF_	Alignment		15.4	70	PDB header: viral protein Chain: F; PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 1.6 a
17	c5oixC_	Alignment		15.3	70	PDB header: viral protein Chain: C; PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 2.2 a
18	c4bxtG_	Alignment		15.2	70	PDB header: viral protein Chain: G; PDB Molecule: phosphoprotein p; PDBTitle: crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain
19	c5oixA_	Alignment		15.2	70	PDB header: viral protein Chain: A; PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 2.2 a
20	c5oixB_	Alignment		15.2	70	PDB header: viral protein Chain: B; PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 2.2 a
21	c5oixC_	Alignment	not modelled	15.0	70	PDB header: viral protein Chain: C; PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 1.6 a
22	c4bxtF_	Alignment	not modelled	14.9	70	PDB header: viral protein Chain: F; PDB Molecule: phosphoprotein p; PDBTitle: crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain
23	c5oixH_	Alignment	not modelled	14.9	70	PDB header: viral protein Chain: H; PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 2.2 a
24	c4bxtB_	Alignment	not modelled	14.9	70	PDB header: viral protein Chain: B; PDB Molecule: phosphoprotein p; PDBTitle: crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain
25	c5oixB_	Alignment	not modelled	14.9	70	PDB header: viral protein Chain: B; PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 1.6 a
26	c4bxtE_	Alignment	not modelled	14.9	70	PDB header: viral protein Chain: E; PDB Molecule: phosphoprotein p; PDBTitle: crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain
27	c5oixG_	Alignment	not modelled	14.7	70	PDB header: viral protein Chain: G; PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 1.6 a
28	c4bxtH_	Alignment	not modelled	14.5	70	PDB header: viral protein Chain: H; PDB Molecule: phosphoprotein p; PDBTitle: crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain
						PDB header: viral protein

29	c5oiyF_	Alignment	not modelled	14.5	70	Chain: F: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 2.2 a
30	c5oixH_	Alignment	not modelled	13.7	70	PDB header: viral protein Chain: H: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 1.6 a
31	c5oiyD_	Alignment	not modelled	13.7	70	PDB header: viral protein Chain: D: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 2.2 a
32	c5oixD_	Alignment	not modelled	13.7	70	PDB header: viral protein Chain: D: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 1.6 a
33	c4bxtA_	Alignment	not modelled	13.7	70	PDB header: viral protein Chain: A: PDB Molecule: phosphoprotein p; PDBTitle: crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain
34	c4bxtC_	Alignment	not modelled	13.7	70	PDB header: viral protein Chain: C: PDB Molecule: phosphoprotein p; PDBTitle: crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain
35	d1qasa2	Alignment	not modelled	13.4	33	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
36	c3ff0A_	Alignment	not modelled	13.0	19	PDB header: biosynthetic protein Chain: A: PDB Molecule: phenazine biosynthesis protein phzb 2; PDBTitle: crystal structure of a phenazine biosynthesis-related protein (phzb2)2 from pseudomonas aeruginosa at 1.90 a resolution
37	c3ghpA_	Alignment	not modelled	12.8	26	PDB header: structural protein Chain: A: PDB Molecule: cellulosomal scaffoldin adaptor protein b; PDBTitle: structure of the second type ii cohesin module from the adaptor scaa2 scaffoldin of acetivbrio cellulolyticus (including long c-terminal3 linker)
38	d1btea_	Alignment	not modelled	12.3	39	Fold: Snake toxin-like Superfamily: Snake toxin-like Family: Extracellular domain of cell surface receptors
39	c2hlqA_	Alignment	not modelled	12.1	17	PDB header: transferase Chain: A: PDB Molecule: bone morphogenetic protein receptor type-2; PDBTitle: crystal structure of the extracellular domain of the type2 ii bmp receptor
40	d1g0da4	Alignment	not modelled	11.8	33	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
41	c2i9uB_	Alignment	not modelled	11.7	44	PDB header: membrane protein Chain: B: PDB Molecule: receptor tyrosine-protein kinase erbb-3; PDBTitle: spatial structure of dimeric erbb3 transmembrane domain
42	c2i9uA_	Alignment	not modelled	11.7	44	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-3; PDBTitle: spatial structure of dimeric erbb3 transmembrane domain
43	c5lo2A_	Alignment	not modelled	11.2	54	PDB header: structural protein Chain: A: PDB Molecule: ppatyr; PDBTitle: engineering protein stability with atomic precision in a monomeric2 miniprotein
44	c5lo4A_	Alignment	not modelled	11.1	54	PDB header: structural protein Chain: A: PDB Molecule: ppa-ch3; PDBTitle: engineering protein stability with atomic precision in a monomeric2 miniprotein
45	c5lo3A_	Alignment	not modelled	11.1	54	PDB header: structural protein Chain: A: PDB Molecule: ppaome; PDBTitle: engineering protein stability with atomic precision in a monomeric2 miniprotein
46	d2bpa1_	Alignment	not modelled	10.0	32	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: ssDNA viruses Family: Microviridae-like VP
47	c1yz2A_	Alignment	not modelled	8.5	55	PDB header: toxin Chain: A: PDB Molecule: delta-conotoxin am 2766; PDBTitle: solution structure of am2766
48	d1kvpa_	Alignment	not modelled	8.3	32	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: ssDNA viruses Family: Microviridae-like VP
49	d1lmra_	Alignment	not modelled	8.3	43	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like Family: Insect toxins
50	c1lmrA_	Alignment	not modelled	8.3	43	PDB header: toxin Chain: A: PDB Molecule: toxin ado1; PDBTitle: solution of ado1, a toxin from the assassin bugs2 agriosphodrus dohrni that blocks the voltage sensitive3 calcium channel I-type
51	c3bz5A_	Alignment	not modelled	7.3	35	PDB header: cell adhesion Chain: A: PDB Molecule: internalin-j; PDBTitle: functional domain of injl from listeria monocytogenes includes a2 cysteine ladder
52	d1n1ua_	Alignment	not modelled	6.8	100	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
53	c1n1uA_	Alignment	not modelled	6.8	100	PDB header: antibiotic Chain: A: PDB Molecule: kalata b1; PDBTitle: nmr structure of [ala1,15]kalata b1
54	d1g3nc2	Alignment	not modelled	6.6	67	Fold: Cyclin-like Superfamily: Cyclin-like Family: Cyclin
						PDB header: antibiotic

55	c1orxA_	Alignment	not modelled	6.6	100	Chain: A; PDB Molecule: kalata b1; PDBTitle: solution structure of the acyclic permutant des-(24-28)-2 kalata b1.
56	c4ntqB_	Alignment	not modelled	6.4	38	PDB header: toxin Chain: B; PDB Molecule: ecl cdii; PDBTitle: cdia-ct/cdii toxin and immunity complex from enterobacter cloacae
57	c2f2IA_	Alignment	not modelled	6.3	100	PDB header: antimicrobial protein Chain: A; PDB Molecule: kalata-b1; PDBTitle: solution structure of [p20d,v21k]-kalata b1
58	c4ttnA_	Alignment	not modelled	6.3	100	PDB header: plant protein Chain: A; PDB Molecule: kalata-b1; PDBTitle: quasi-racemic structure of [g6a]kalata b1
59	c1nb1A_	Alignment	not modelled	6.3	100	PDB header: antibiotic Chain: A; PDB Molecule: kalata b1; PDBTitle: high resolution solution structure of kalata b1
60	d1nb1a_	Alignment	not modelled	6.3	100	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
61	c2mn1A_	Alignment	not modelled	6.2	100	PDB header: unknown function Chain: A; PDB Molecule: kalata b1[w23ww]; PDBTitle: solution structure of kalata b1[w23ww]
62	c1k48A_	Alignment	not modelled	6.2	100	PDB header: plant protein Chain: A; PDB Molecule: kalata b1; PDBTitle: refined structure and disulfide pairing of the kalata b12 peptide
63	c1jjzA_	Alignment	not modelled	6.2	100	PDB header: plant protein Chain: A; PDB Molecule: kalata b1; PDBTitle: refined structure and disulfide pairing of the kalata b12 peptide
64	c2f2jA_	Alignment	not modelled	6.2	100	PDB header: antimicrobial protein Chain: A; PDB Molecule: kalata-b1; PDBTitle: solution structure of [w19k, p20n, v21k]-kalata b1
65	c4ttoA_	Alignment	not modelled	6.2	100	PDB header: plant protein Chain: A; PDB Molecule: kalata-b1; PDBTitle: quasi-racemic structure of [v25a] kalata b1
66	c4ttmA_	Alignment	not modelled	6.2	100	PDB header: plant protein Chain: A; PDB Molecule: kalata-b1; PDBTitle: racemic structure of kalata b1 (kb1)
67	d1pt4a_	Alignment	not modelled	6.2	100	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
68	c4q96C_	Alignment	not modelled	6.1	75	PDB header: protein binding Chain: C; PDB Molecule: rpb1-ctd; PDBTitle: cid of human rprd1b in complex with an unmodified ctd peptide
69	c4q96F_	Alignment	not modelled	6.1	75	PDB header: protein binding Chain: F; PDB Molecule: rpb1-ctd; PDBTitle: cid of human rprd1b in complex with an unmodified ctd peptide
70	c2khaA_	Alignment	not modelled	6.1	100	PDB header: antimicrobial protein Chain: A; PDB Molecule: kalata-b1; PDBTitle: solution structure of linear kalata b1 (loop 6)
71	d1dx5i3	Alignment	not modelled	5.8	38	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: EGF/Laminin Family: EGF-type module
72	d1sqwa2	Alignment	not modelled	5.8	42	Fold: Cystatin-like Superfamily: Pre-PUA domain Family: Nip7p homolog, N-terminal domain
73	c2lvfC_	Alignment	not modelled	5.7	33	PDB header: oxidoreductase Chain: C; PDB Molecule: ethylbenzene dehydrogenase gamma-subunit; PDBTitle: ethylbenzene dehydrogenase from aromatoleum aromaticum
74	c2xu6B_	Alignment	not modelled	5.7	27	PDB header: protein binding Chain: B; PDB Molecule: mdv1 coiled coil; PDBTitle: mdv1 coiled coil domain
75	c1wz5A_	Alignment	not modelled	5.7	63	PDB header: toxin Chain: A; PDB Molecule: potassium channel blocking toxin 1; PDBTitle: solution structure of pi1-3p
76	c2rmzA_	Alignment	not modelled	5.4	43	PDB header: cell adhesion Chain: A; PDB Molecule: integrin beta-3; PDBTitle: bicelle-embedded integrin beta3 transmembrane segment
77	d1e4ta_	Alignment	not modelled	5.4	50	Fold: Defensin-like Superfamily: Defensin-like Family: Defensin
78	c1kalaA_	Alignment	not modelled	5.4	100	PDB header: plant protein Chain: A; PDB Molecule: kalata b1; PDBTitle: elucidation of the primary and three-dimensional structure2 of the uterotonic polypeptide kalata b1
79	c2lurA_	Alignment	not modelled	5.3	100	PDB header: plant protein Chain: A; PDB Molecule: kalata; PDBTitle: nmr solution structure of kb1[ghrw;23-28]
80	d1eu1a2	Alignment	not modelled	5.3	27	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
81	c4uw8F_	Alignment	not modelled	5.3	38	PDB header: viral protein Chain: F; PDB Molecule: l-shaped tail fiber protein; PDBTitle: structure of the carboxy-terminal domain of the bacteriophage t5 l-2 shaped tail fiber with its intra-molecular

						chaperone domain
82	d1gmia_	Alignment	not modelled	5.2	13	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
83	c5a52A_	Alignment	not modelled	5.1	20	PDB header: lipid binding protein Chain: A: PDB Molecule: calcium-dependent lipid-binding domain-containing protein; PDBTitle: the crystal structure of arabidopsis thaliana car1 in2 complex with one calcium ion
84	c2nq3A_	Alignment	not modelled	5.1	21	PDB header: ligase Chain: A: PDB Molecule: itchy homolog e3 ubiquitin protein ligase; PDBTitle: crystal structure of the c2 domain of human itchy homolog2 e3 ubiquitin protein ligase
85	d2nq3a1	Alignment	not modelled	5.1	21	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
86	d3ci0k3	Alignment	not modelled	5.1	27	Fold: Pili subunits Superfamily: Pili subunits Family: GspK pilin-like domain