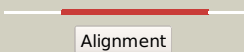

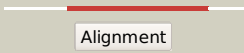

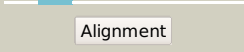
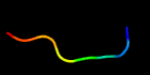

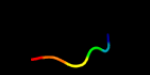


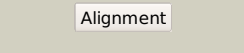
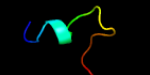
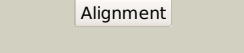


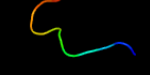
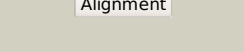

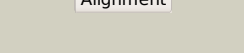
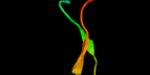
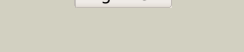
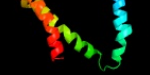
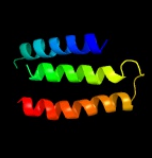
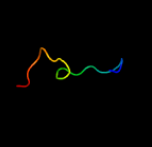
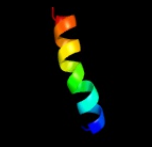

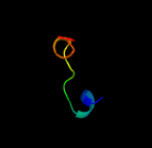

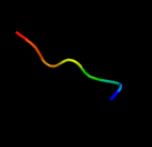
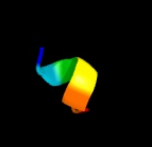
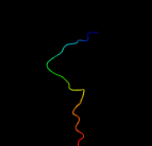


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1140_(-)_1267352_1268200
Date	Wed Jul 31 22:05:22 BST 2019
Unique Job ID	85737805d952de7e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4cadF_	 Alignment		99.7	16	PDB header: protein binding Chain: F; PDB Molecule: ras and a-factor converting enzyme 1, rce1; PDBTitle: mechanism of farnesylated caax protein processing by the integral2 membrane protease rce1
2	c4cadC_	 Alignment		99.7	14	PDB header: protein binding Chain: C; PDB Molecule: ras and a-factor converting enzyme 1, rce1; PDBTitle: mechanism of farnesylated caax protein processing by the integral2 membrane protease rce1
3	c2mx4A_	 Alignment		30.3	50	PDB header: translation,protein binding Chain: A; PDB Molecule: eukaryotic translation initiation factor 4e-binding protein PDBTitle: nmr structure of phosphorylated 4e-bp2
4	c4a1sE_	 Alignment		22.5	83	PDB header: cell cycle Chain: E; PDB Molecule: re60102p; PDBTitle: crystallographic structure of the pins:insc complex
5	c2m0qA_	 Alignment		22.1	19	PDB header: membrane protein Chain: A; PDB Molecule: potassium voltage-gated channel subfamily e member 2; PDBTitle: solution nmr analysis of intact kcne2 in detergent micelles2 demonstrate a straight transmembrane helix
6	c2l1nA_	 Alignment		18.3	38	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of the protein yp_399305.1
7	c2jpwA_	 Alignment		14.7	86	PDB header: contractile protein Chain: A; PDB Molecule: troponin i, cardiac muscle; PDBTitle: solution structure of the bisphosphorylated cardiac2 specific n-extension of cardiac troponin i
8	c4luqB_	 Alignment		13.4	50	PDB header: protein binding/toxin inhibitor Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of virulence effector tse3 in complex with2 neutralizer tsi3
9	c2l35A_	 Alignment		12.6	14	PDB header: protein binding Chain: A; PDB Molecule: dap12-nkg2c_tm; PDBTitle: structure of the dap12-nkg2C transmembrane heterotrimer
10	d2veaa2	 Alignment		11.3	32	Fold: Profilin-like Superfamily: GAF domain-like Family: Phytochrome-specific domain
11	c3dh4A_	 Alignment		10.8	18	PDB header: transport protein Chain: A; PDB Molecule: sodium/glucose cotransporter; PDBTitle: crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus

12	c4huqS_	Alignment		10.6	16	PDB header: hydrolase Chain: S: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a transporter
13	c6ht4A_	Alignment		9.5	41	PDB header: unknown function Chain: A: PDB Molecule: ns5a; PDBTitle: nmr structure of ns5a-d2 (jfh1) peptide (304-323)
14	c2k21A_	Alignment		8.3	15	PDB header: membrane protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily e PDBTitle: nmr structure of human kcne1 in Impg micelles at ph 6.0 and 2 40 degree c
15	c3tdsC_	Alignment		8.1	16	PDB header: membrane protein Chain: C: PDB Molecule: formate/nitrite transporter; PDBTitle: crystal structure of hsc f194i
16	d1cmca_	Alignment		7.3	26	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Met repressor, Metj (MetR)
17	c2xq2A_	Alignment		7.2	17	PDB header: transport protein Chain: A: PDB Molecule: sodium/glucose cotransporter; PDBTitle: structure of the k294a mutant of vsplt
18	d3c2wa2	Alignment		7.1	38	Fold: Profilin-like Superfamily: GAF domain-like Family: Phytochrome-specific domain
19	c2e6xD_	Alignment		6.8	33	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein ttha1281; PDBTitle: x-ray structure of tt1592 from thermus thermophilus hb8
20	c5zvtM_	Alignment		6.7	13	PDB header: virus Chain: M: PDB Molecule: n-terminus of outer capsid protein vp5; PDBTitle: structure of rna polymerase complex and genome within a dsrna virus2 provides insights into the mechanisms of transcription and assembly
21	c2ndjA_	Alignment	not modelled	6.3	19	PDB header: membrane protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily e member 3; PDBTitle: structural basis for kcne3 and estrogen modulation of the kcnq12 channel
22	c6hqeq_	Alignment	not modelled	6.3	43	PDB header: protein fibril Chain: Q: PDB Molecule: peptide lrv_m3delta1; PDBTitle: cryo-em of self-assembly peptide filament lrv_m3delta1
23	c6hqep_	Alignment	not modelled	6.3	43	PDB header: protein fibril Chain: P: PDB Molecule: peptide lrv_m3delta1; PDBTitle: cryo-em of self-assembly peptide filament lrv_m3delta1
24	c6hqet_	Alignment	not modelled	6.3	43	PDB header: protein fibril Chain: T: PDB Molecule: peptide lrv_m3delta1; PDBTitle: cryo-em of self-assembly peptide filament lrv_m3delta1
25	c6hqej_	Alignment	not modelled	6.3	43	PDB header: protein fibril Chain: J: PDB Molecule: peptide lrv_m3delta1; PDBTitle: cryo-em of self-assembly peptide filament lrv_m3delta1
26	c6hqeb_	Alignment	not modelled	6.3	43	PDB header: protein fibril Chain: B: PDB Molecule: peptide lrv_m3delta1; PDBTitle: cryo-em of self-assembly peptide filament lrv_m3delta1
27	c6hqeu_	Alignment	not modelled	6.3	43	PDB header: protein fibril Chain: U: PDB Molecule: peptide lrv_m3delta1; PDBTitle: cryo-em of self-assembly peptide filament lrv_m3delta1
28	c6hqep_	Alignment	not modelled	6.3	43	PDB header: protein fibril Chain: P: PDB Molecule: peptide lrv_m3delta1; PDBTitle: cryo-em of self-assembly peptide filament lrv_m3delta1
						PDB header: protein fibril

57	c6hqeI_	Alignment	not modelled	6.3	43	Chain: I: PDB Molecule: peptide lrv_m3delta1; PDBTitle: cryo-em of self-assembly peptide filament lrv_m3delta1
58	c6hqeC_	Alignment	not modelled	6.3	43	PDB header: protein fibril Chain: C: PDB Molecule: peptide lrv_m3delta1; PDBTitle: cryo-em of self-assembly peptide filament lrv_m3delta1
59	c6hqeN_	Alignment	not modelled	6.3	43	PDB header: protein fibril Chain: N: PDB Molecule: peptide lrv_m3delta1; PDBTitle: cryo-em of self-assembly peptide filament lrv_m3delta1
60	c6hqeF_	Alignment	not modelled	6.3	43	PDB header: protein fibril Chain: F: PDB Molecule: peptide lrv_m3delta1; PDBTitle: cryo-em of self-assembly peptide filament lrv_m3delta1
61	c6hqeA_	Alignment	not modelled	6.3	43	PDB header: protein fibril Chain: A: PDB Molecule: peptide lrv_m3delta1; PDBTitle: cryo-em of self-assembly peptide filament lrv_m3delta1
62	c6hqeD_	Alignment	not modelled	6.3	43	PDB header: protein fibril Chain: D: PDB Molecule: peptide lrv_m3delta1; PDBTitle: cryo-em of self-assembly peptide filament lrv_m3delta1
63	c6hqeK_	Alignment	not modelled	6.3	43	PDB header: protein fibril Chain: K: PDB Molecule: peptide lrv_m3delta1; PDBTitle: cryo-em of self-assembly peptide filament lrv_m3delta1
64	c6hqeY_	Alignment	not modelled	6.3	43	PDB header: protein fibril Chain: Y: PDB Molecule: PDBTitle: cryo-em of self-assembly peptide filament lrv_m3delta1
65	c6hqem_	Alignment	not modelled	6.3	43	PDB header: protein fibril Chain: M: PDB Molecule: peptide lrv_m3delta1; PDBTitle: cryo-em of self-assembly peptide filament lrv_m3delta1
66	c6hqeS_	Alignment	not modelled	6.3	43	PDB header: protein fibril Chain: S: PDB Molecule: peptide lrv_m3delta1; PDBTitle: cryo-em of self-assembly peptide filament lrv_m3delta1
67	c6hqeC_	Alignment	not modelled	6.3	43	PDB header: protein fibril Chain: C: PDB Molecule: peptide lrv_m3delta1; PDBTitle: cryo-em of self-assembly peptide filament lrv_m3delta1
68	c6hqeV_	Alignment	not modelled	6.3	43	PDB header: protein fibril Chain: V: PDB Molecule: PDBTitle: cryo-em of self-assembly peptide filament lrv_m3delta1
69	c6hqeE_	Alignment	not modelled	6.3	43	PDB header: protein fibril Chain: E: PDB Molecule: peptide lrv_m3delta1; PDBTitle: cryo-em of self-assembly peptide filament lrv_m3delta1
70	c6hqeT_	Alignment	not modelled	6.3	43	PDB header: protein fibril Chain: T: PDB Molecule: peptide lrv_m3delta1; PDBTitle: cryo-em of self-assembly peptide filament lrv_m3delta1
71	c6hqeI_	Alignment	not modelled	6.3	43	PDB header: protein fibril Chain: L: PDB Molecule: peptide lrv_m3delta1; PDBTitle: cryo-em of self-assembly peptide filament lrv_m3delta1
72	c6hqeW_	Alignment	not modelled	6.3	43	PDB header: protein fibril Chain: W: PDB Molecule: PDBTitle: cryo-em of self-assembly peptide filament lrv_m3delta1
73	c6hqeF_	Alignment	not modelled	6.3	43	PDB header: protein fibril Chain: F: PDB Molecule: peptide lrv_m3delta1; PDBTitle: cryo-em of self-assembly peptide filament lrv_m3delta1
74	c4b1vM_	Alignment	not modelled	6.3	56	PDB header: structural protein Chain: M: PDB Molecule: phosphatase and actin regulator 1; PDBTitle: structure of the phactr1 rpe1-n domain bound to g-actin
75	c4b1vN_	Alignment	not modelled	6.3	56	PDB header: structural protein Chain: N: PDB Molecule: phosphatase and actin regulator 1; PDBTitle: structure of the phactr1 rpe1-n domain bound to g-actin
76	c4z7fD_	Alignment	not modelled	6.2	9	PDB header: transport protein Chain: D: PDB Molecule: folate ecf transporter; PDBTitle: crystal structure of folt bound with folic acid
77	c5d7tC_	Alignment	not modelled	6.2	10	PDB header: transport protein Chain: C: PDB Molecule: s-component for folate; PDBTitle: folate ecf transporter: apo state
78	c3q1jA_	Alignment	not modelled	6.1	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: integron cassette protein; PDBTitle: structure from the mobile metagenome of vibrio cholerae.2 integron cassette protein vch_cass4.
79	c3shpA_	Alignment	not modelled	6.0	33	PDB header: transferase Chain: A: PDB Molecule: putative acetyltransferase sthe_0691; PDBTitle: crystal structure of putative acetyltransferase from sphaerobacter2 thermophilus dsm 20745
80	c4b1uM_	Alignment	not modelled	5.9	56	PDB header: structural protein Chain: M: PDB Molecule: phosphatase and actin regulator 1; PDBTitle: structure of the phactr1 rpe1 domain and rpe1 motif directed2 assemblies with g-actin reveal the molecular basis for actin binding3 cooperativity.
81	c3o0rC_	Alignment	not modelled	5.9	12	PDB header: immune system/oxidoreductase Chain: C: PDB Molecule: nitric oxide reductase subunit c; PDBTitle: crystal structure of nitric oxide reductase from pseudomonas2 aeruginosa in complex with antibody fragment
82	c2i9uB_	Alignment	not modelled	5.6	21	PDB header: membrane protein Chain: B: PDB Molecule: receptor tyrosine-protein kinase erbB-3; PDBTitle: spatial structure of dimeric erbB3 transmembrane domain
83	c2i9uA_	Alignment	not modelled	5.6	21	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbB-3; PDBTitle: spatial structure of dimeric erbB3 transmembrane domain
						PDB header: transport protein

84	c3jqoF_	Alignment	not modelled	5.6	45	Chain: F: PDB Molecule: tran protein; PDBTitle: crystal structure of the outer membrane complex of a type iv secretion2 system
85	c3jqom_	Alignment	not modelled	5.6	45	PDB header: transport protein Chain: M: PDB Molecule: traf protein; PDBTitle: crystal structure of the outer membrane complex of a type iv secretion2 system
86	c3jqog_	Alignment	not modelled	5.6	45	PDB header: transport protein Chain: G: PDB Molecule: traf protein; PDBTitle: crystal structure of the outer membrane complex of a type iv secretion2 system
87	c3jqoj_	Alignment	not modelled	5.6	45	PDB header: transport protein Chain: J: PDB Molecule: traf protein; PDBTitle: crystal structure of the outer membrane complex of a type iv secretion2 system
88	c3jqol_	Alignment	not modelled	5.6	45	PDB header: transport protein Chain: I: PDB Molecule: traf protein; PDBTitle: crystal structure of the outer membrane complex of a type iv secretion2 system
89	c3jqoR_	Alignment	not modelled	5.6	45	PDB header: transport protein Chain: R: PDB Molecule: tran protein; PDBTitle: crystal structure of the outer membrane complex of a type iv secretion2 system
90	c3jqoX_	Alignment	not modelled	5.6	45	PDB header: transport protein Chain: X: PDB Molecule: tran protein; PDBTitle: crystal structure of the outer membrane complex of a type iv secretion2 system
91	c3jqoO_	Alignment	not modelled	5.6	45	PDB header: transport protein Chain: O: PDB Molecule: tran protein; PDBTitle: crystal structure of the outer membrane complex of a type iv secretion2 system
92	c3jqoa_	Alignment	not modelled	5.6	45	PDB header: transport protein Chain: A: PDB Molecule: traf protein; PDBTitle: crystal structure of the outer membrane complex of a type iv secretion2 system
93	c3jqod_	Alignment	not modelled	5.6	45	PDB header: transport protein Chain: D: PDB Molecule: traf protein; PDBTitle: crystal structure of the outer membrane complex of a type iv secretion2 system
94	c2ofqB_	Alignment	not modelled	5.6	45	PDB header: protein transport/protein transport Chain: B: PDB Molecule: tran; PDBTitle: nmr solution structure of a complex between the virb9/virb72 interaction domains of the pkm101 type iv secretion system
95	c3jqoC_	Alignment	not modelled	5.6	45	PDB header: transport protein Chain: C: PDB Molecule: tran protein; PDBTitle: crystal structure of the outer membrane complex of a type iv secretion2 system
96	c3jqop_	Alignment	not modelled	5.5	45	PDB header: transport protein Chain: P: PDB Molecule: traf protein; PDBTitle: crystal structure of the outer membrane complex of a type iv secretion2 system
97	d1vpa1	Alignment	not modelled	5.5	25	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: Monomeric nicotinate phosphoribosyltransferase N-terminal domain-like
98	c3jqoU_	Alignment	not modelled	5.4	45	PDB header: transport protein Chain: U: PDB Molecule: tran protein; PDBTitle: crystal structure of the outer membrane complex of a type iv secretion2 system
99	c4k0dB_	Alignment	not modelled	5.4	58	PDB header: signaling protein Chain: B: PDB Molecule: periplasmic sensor hybrid histidine kinase; PDBTitle: periplasmic sensor domain of sensor histidine kinase, adeh_2942