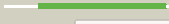

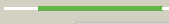

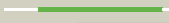


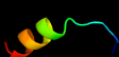


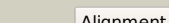

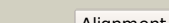
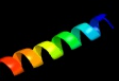
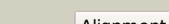
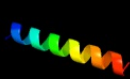








Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3697A_(RVBD3697A)_4140417_4140641
Date	Fri Aug 9 18:20:39 BST 2019
Unique Job ID	a8230c2da973eca8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2k5jB_	 Alignment		56.0	17	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: uncharacterized protein yiif; PDBTitle: solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
2	d2bsqe1	 Alignment		54.9	16	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Trafficking protein A-like
3	c2h1oH_	 Alignment		52.6	16	PDB header: gene regulation/dna complex Chain: H; PDB Molecule: trafficking protein a; PDBTitle: structure of fitab bound to ir36 dna fragment
4	c6a7vU_	 Alignment		37.2	47	PDB header: toxin/antitoxin Chain: U; PDB Molecule: antitoxin vapb11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
5	c6ochB_	 Alignment		26.7	45	PDB header: hydrolase/hydrolase inhibitor Chain: B; PDB Molecule: small vasohibin-binding protein; PDBTitle: crystal structure of vash1-svbp complex bound with parthenolide
6	c6nvqB_	 Alignment		25.4	45	PDB header: hydrolase Chain: B; PDB Molecule: small vasohibin-binding protein; PDBTitle: crystal structure of the vash1-svbp complex
7	c6qbyB_	 Alignment		25.4	45	PDB header: cytosolic protein Chain: B; PDB Molecule: small vasohibin-binding protein; PDBTitle: crystal structure of vash 2 in complex with svbp
8	c6qbyD_	 Alignment		25.3	42	PDB header: cytosolic protein Chain: D; PDB Molecule: small vasohibin-binding protein; PDBTitle: crystal structure of vash 2 in complex with svbp
9	c6j4qK_	 Alignment		25.1	42	PDB header: hydrolase Chain: K; PDB Molecule: small vasohibin-binding protein; PDBTitle: structural basis of tubulin detyrosination by vasohibins-svbp enzyme2 complex and functional implications
10	c3kk4B_	 Alignment		23.2	16	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: uncharacterized protein bp1543; PDBTitle: uncharacterized protein bp1543 from bordetella pertussis tohama i
11	c6j4oB_	 Alignment		22.9	42	PDB header: hydrolase Chain: B; PDB Molecule: small vasohibin-binding protein; PDBTitle: structural basis of tubulin detyrosination by vasohibins-svbp enzyme2 complex and functional implications

12	c6j4qG_	Alignment		22.3	42	PDB header: hydrolase Chain: G: PDB Molecule: small vasohibin-binding protein; PDBTitle: structural basis of tubulin detyrosination by vasohibinsvbp enzyme2 complex and functional implications
13	d2g9ha2	Alignment		22.1	42	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
14	c6j8nA_	Alignment		21.3	47	PDB header: peptide binding protein/hydrolase Chain: A: PDB Molecule: small vasohibin-binding protein; PDBTitle: crystal structure of svbp-vash1 complex, mutation c169a of vash1
15	c6j8nC_	Alignment		21.3	47	PDB header: peptide binding protein/hydrolase Chain: C: PDB Molecule: small vasohibin-binding protein; PDBTitle: crystal structure of svbp-vash1 complex, mutation c169a of vash1
16	c6j4qB_	Alignment		21.3	42	PDB header: hydrolase Chain: B: PDB Molecule: small vasohibin-binding protein; PDBTitle: structural basis of tubulin detyrosination by vasohibinsvbp enzyme2 complex and functional implications
17	c6j4qD_	Alignment		21.0	42	PDB header: hydrolase Chain: D: PDB Molecule: small vasohibin-binding protein; PDBTitle: structural basis of tubulin detyrosination by vasohibinsvbp enzyme2 complex and functional implications
18	c6ocqB_	Alignment		20.8	47	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: small vasohibin-binding protein; PDBTitle: crystal structure of vash1-svbp complex bound with epoxy
19	c6j7bB_	Alignment		20.4	45	PDB header: hydrolase Chain: B: PDB Molecule: small vasohibin-binding protein; PDBTitle: crystal structure of vash1-svbp in complex with epoxy
20	c6j4sB_	Alignment		20.2	42	PDB header: hydrolase Chain: B: PDB Molecule: small vasohibin-binding protein; PDBTitle: structural basis of tubulin detyrosination by vasohibinsvbp enzyme2 complex and functional implications
21	c6jzcD_	Alignment	not modelled	19.8	42	PDB header: cytosolic protein Chain: D: PDB Molecule: small vasohibin-binding protein; PDBTitle: structural basis of tubulin detyrosination
22	d1iaka2	Alignment	not modelled	19.8	58	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
23	c6ochD_	Alignment	not modelled	19.6	47	PDB header: hydrolase/hydrolase inhibitor Chain: D: PDB Molecule: small vasohibin-binding protein; PDBTitle: crystal structure of vash1-svbp complex bound with parthenolide
24	d1klua2	Alignment	not modelled	19.5	42	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
25	d2p24a2	Alignment	not modelled	19.4	50	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
26	d1s9va2	Alignment	not modelled	19.3	50	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
27	c6j9hC_	Alignment	not modelled	19.1	47	PDB header: peptide binding protein/hydrolase Chain: C: PDB Molecule: small vasohibin-binding protein; PDBTitle: crystal structure of svbp-vash1 complex
28	c6jzcC_	Alignment	not modelled	19.0	42	PDB header: cytosolic protein Chain: C: PDB Molecule: small vasohibin-binding protein; PDBTitle: structural basis of tubulin detyrosination
29	c6jzdB_	Alignment	not modelled	19.0	42	PDB header: cytosolic protein Chain: B: PDB Molecule: small vasohibin-binding protein;

						PDBTitle: crystal structure of peptide-bound vash2-svbp complex
30	c6j91A_	Alignment	not modelled	18.8	47	PDB header: peptide binding protein/hydrolase Chain: A: PDB Molecule: small vasohibin-binding protein; PDBTitle: structure of a hypothetical protease
31	d1jk8a2	Alignment	not modelled	18.7	50	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
32	d1es0a2	Alignment	not modelled	18.5	58	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
33	d1muja2	Alignment	not modelled	18.4	58	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
34	c6j4vB_	Alignment	not modelled	17.9	42	PDB header: hydrolase Chain: B: PDB Molecule: small vasohibin-binding protein; PDBTitle: structural basis of tubulin detyrosination by vasohibins-svbp enzyme2 complex and functional implications
35	d1uvqa2	Alignment	not modelled	16.9	42	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
36	c6j4uB_	Alignment	not modelled	16.7	47	PDB header: hydrolase Chain: B: PDB Molecule: small vasohibin-binding protein; PDBTitle: structural basis of tubulin detyrosination by vasohibins-svbp enzyme2 complex and functional implications
37	c5x3tA_	Alignment	not modelled	16.5	30	PDB header: antitoxin/toxin Chain: A: PDB Molecule: antitoxin vapp26; PDBTitle: vapbc from mycobacterium tuberculosis
38	d1fnga2	Alignment	not modelled	16.3	25	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
39	c6j9hA_	Alignment	not modelled	15.8	47	PDB header: peptide binding protein/hydrolase Chain: A: PDB Molecule: small vasohibin-binding protein; PDBTitle: crystal structure of svbp-vash1 complex
40	c5f5uB_	Alignment	not modelled	15.7	39	PDB header: splicing Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the snu23-prp38-mfap1(217-258) complex of2 chaetomium thermophilum
41	c6j4pB_	Alignment	not modelled	12.8	42	PDB header: hydrolase Chain: B: PDB Molecule: small vasohibin-binding protein; PDBTitle: structural basis of tubulin detyrosination by vasohibins-svbp enzyme2 complex and functional implications
42	d1q9ja2	Alignment	not modelled	12.3	20	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
43	d2b5ua2	Alignment	not modelled	10.1	50	Fold: Cloacin translocation domain Superfamily: Cloacin translocation domain Family: Cloacin translocation domain
44	c2yy0D_	Alignment	not modelled	10.0	37	PDB header: transcription Chain: D: PDB Molecule: c-myc-binding protein; PDBTitle: crystal structure of ms0802, c-myc-1 binding protein domain2 from homo sapiens
45	c1qjjA_	Alignment	not modelled	9.5	35	PDB header: membrane protein Chain: A: PDB Molecule: lap2; PDBTitle: n-terminal constant region of the nuclear envelope protein2 lap2
46	c6mbeB_	Alignment	not modelled	8.8	60	PDB header: apoptosis Chain: B: PDB Molecule: dm7; PDBTitle: human mcl-1 in complex with the designed peptide dm7
47	c3fmtF_	Alignment	not modelled	8.7	29	PDB header: replication inhibitor/dna Chain: F: PDB Molecule: protein seqa; PDBTitle: crystal structure of seqa bound to dna
48	c3ugsB_	Alignment	not modelled	8.7	33	PDB header: transferase Chain: B: PDB Molecule: undecaprenyl pyrophosphate synthase; PDBTitle: crystal structure of a probable undecaprenyl diphosphate synthase2 (upps) from campylobacter jejuni
49	c3tbxB_	Alignment	not modelled	7.8	38	PDB header: immune system/agonist Chain: B: PDB Molecule: beta-2-microglobulin; PDBTitle: crystal structure of the murine class i major histocompatibility2 complex h-2db in complex with lcmv-derived gp33 altered peptide3 ligand v3p
50	c5f5uH_	Alignment	not modelled	7.7	35	PDB header: splicing Chain: H: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the snu23-prp38-mfap1(217-258) complex of2 chaetomium thermophilum
51	c4bl6A_	Alignment	not modelled	6.9	40	PDB header: protein transport Chain: A: PDB Molecule: protein bicaudal d; PDBTitle: bicaudal-d uses a parallel, homodimeric coiled coil with heterotypic2 registry to co-ordinate recruitment of cargos to dynein
52	d2joka1	Alignment	not modelled	6.2	43	Fold: SopE-like GEF domain Superfamily: SopE-like GEF domain Family: SopE-like GEF domain
53	d1ueha_	Alignment	not modelled	5.8	23	Fold: Undecaprenyl diphosphate synthase Superfamily: Undecaprenyl diphosphate synthase Family: Undecaprenyl diphosphate synthase
54	c2vfwB_	Alignment	not modelled	5.8	23	PDB header: transferase Chain: B: PDB Molecule: short-chain z-isoprenyl diphosphate synthetase; PDBTitle: rv1086 native
55	c2axcA_	Alignment	not modelled	5.6	50	PDB header: hydrolase Chain: A: PDB Molecule: colicin e7; PDBTitle: crystal structure of cole7 translocation domain
						PDB header: transferase/transferase inhibitor

