
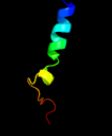


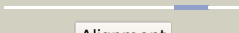




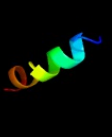





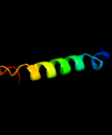





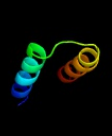




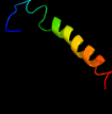






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1332_(-)_1500932_1501588
Date	Wed Jul 31 22:05:43 BST 2019
Unique Job ID	ef0df10d3c73980b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kduB_	 Alignment		62.3	27	PDB header: metal binding protein/exocytosis Chain: B: PDB Molecule: protein unc-13 homolog a; PDBTitle: structural basis of the munc13-1/ca2+-calmodulin2 interaction: a novel 1-26 calmodulin binding motif with a3 bipartite binding mode
2	c6hqaF_	 Alignment		23.0	31	PDB header: transcription Chain: F: PDB Molecule: subunit (17 kda) of tfiid and saga complexes, involved in PDBTitle: molecular structure of promoter-bound yeast tfiid
3	c2ebkA_	 Alignment		23.0	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: rwd domain-containing protein 3; PDBTitle: solution structure of the rwd domain of human rwd domain2 containing protein 3
4	d1wgqa_	 Alignment		20.9	18	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Pleckstrin-homology domain (PH domain)
5	d2dawa1	 Alignment		20.1	18	Fold: UBC-like Superfamily: UBC-like Family: RWD domain
6	d1qqga1	 Alignment		18.0	27	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Phosphotyrosine-binding domain (PTB)
7	d2elba2	 Alignment		16.5	27	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Pleckstrin-homology domain (PH domain)
8	c5j1hB_	 Alignment		15.6	24	PDB header: structural protein Chain: B: PDB Molecule: plectin,plectin; PDBTitle: structure of the spectrin repeats 5 and 6 of the plakin domain of2 plectin
9	c5todD_	 Alignment		13.3	44	PDB header: lipid transport Chain: D: PDB Molecule: transmembrane protein 24; PDBTitle: transmembrane protein 24 smp domain
10	d2daxa1	 Alignment		13.1	8	Fold: UBC-like Superfamily: UBC-like Family: RWD domain
11	c2jo7A_	 Alignment		12.3	38	PDB header: surface active protein Chain: A: PDB Molecule: glycosylphosphatidylinositol-anchored merozoite PDBTitle: solution structure of the adhesion protein bd37 from2 babesia divergens

12	c5hwiA_	Alignment		11.5	38	PDB header: transferase Chain: A; PDB Molecule: glutathione-specific gamma-glutamylcyclotransferase; PDBTitle: crystal structure of selenomethionine labelled gama glutamyl2 cyclotransferease specific to glutathione from yeast
13	d1x1ga1	Alignment		10.9	27	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Pleckstrin-homology domain (PH domain)
14	d1u5fa1	Alignment		10.7	23	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Pleckstrin-homology domain (PH domain)
15	d1ddfa_	Alignment		10.5	11	Fold: DEATH domain Superfamily: DEATH domain Family: DEATH domain, DD
16	c2wsc1_	Alignment		10.0	22	PDB header: photosynthesis Chain: 1; PDB Molecule: at3g54890; PDBTitle: improved model of plant photosystem i
17	c3nsuA_	Alignment		9.6	13	PDB header: signaling protein Chain: A; PDB Molecule: phosphatidylinositol 4,5-bisphosphate-binding protein slm1; PDBTitle: a systematic screen for protein-lipid interactions in saccharomyces2 cerevisiae
18	c3cqcA_	Alignment		9.4	19	PDB header: protein transport Chain: A; PDB Molecule: nuclear pore complex protein nup107; PDBTitle: nucleoporin nup107/nup133 interaction complex
19	c2ws94_	Alignment		9.4	60	PDB header: virus Chain: 4; PDB Molecule: p1; PDB Fragment: capsid protein vp4, residues 1-80 PDBTitle: equine rhinitis a virus at low ph
20	c3fybA_	Alignment		9.4	30	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: protein of unknown function (duf1244); PDBTitle: crystal structure of a protein of unknown function (duf1244) from2 alcanivorax borkumensis
21	c4cwlv_	Alignment	not modelled	9.2	60	PDB header: virus Chain: V; PDB Molecule: PDBTitle: the limits of structural plasticity in a picornavirus2 capsid revealed by a massively expanded equine rhinitis a3 virus particle
22	c4cwlx_	Alignment	not modelled	9.2	60	PDB header: virus Chain: X; PDB Molecule: PDBTitle: the limits of structural plasticity in a picornavirus2 capsid revealed by a massively expanded equine rhinitis a3 virus particle
23	c4cwlI_	Alignment	not modelled	9.2	60	PDB header: virus Chain: I; PDB Molecule: p1; PDBTitle: the limits of structural plasticity in a picornavirus2 capsid revealed by a massively expanded equine rhinitis a3 virus particle
24	c4cwlO_	Alignment	not modelled	9.2	60	PDB header: virus Chain: O; PDB Molecule: p1; PDBTitle: the limits of structural plasticity in a picornavirus2 capsid revealed by a massively expanded equine rhinitis a3 virus particle
25	c4cwlQ_	Alignment	not modelled	9.2	60	PDB header: virus Chain: Q; PDB Molecule: p1; PDBTitle: the limits of structural plasticity in a picornavirus2 capsid revealed by a massively expanded equine rhinitis a3 virus particle
26	c4cwlG_	Alignment	not modelled	9.2	60	PDB header: virus Chain: G; PDB Molecule: p1; PDBTitle: the limits of structural plasticity in a picornavirus2 capsid revealed by a massively expanded equine rhinitis a3 virus particle
27	c4cwlK_	Alignment	not modelled	9.2	60	PDB header: virus Chain: K; PDB Molecule: p1; PDBTitle: the limits of structural plasticity in a picornavirus2 capsid revealed by a massively expanded equine rhinitis a3 virus particle
28	c4cwlB_	Alignment	not modelled	9.2	60	PDB header: virus Chain: B; PDB Molecule: p1; PDBTitle: the limits of structural plasticity in a picornavirus2 capsid revealed by a massively expanded equine rhinitis a3 virus particle
						PDB header: virus

80	c2wff4_	Alignment	not modelled	9.2	60	PDB header: virus Chain: 4; PDB Molecule: p1; PDB Fragment: capsid protein vp4, residues 1-80 PDBTitle: equine rhinitis a virus
81	c4cwij_	Alignment	not modelled	9.2	60	PDB header: virus Chain: J; PDB Molecule: p1; PDBTitle: the limits of structural plasticity in a picornavirus2 capsid revealed by a massively expanded equine rhinitis a3 virus particle
82	d2daya1	Alignment	not modelled	9.1	23	Fold: UBC-like Superfamily: UBC-like Family: RWD domain
83	d1u5da1	Alignment	not modelled	9.0	20	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Pleckstrin-homology domain (PH domain)
84	c2xbo4_	Alignment	not modelled	8.9	60	PDB header: virus Chain: 4; PDB Molecule: p1; PDB Fragment: capsid protein vp4, residues 1-80 PDBTitle: equine rhinitis a virus in complex with its sialic acid2 receptor
85	d1ukxa_	Alignment	not modelled	8.9	17	Fold: UBC-like Superfamily: UBC-like Family: RWD domain
86	c2dhiA_	Alignment	not modelled	8.2	31	PDB header: signaling protein Chain: A; PDB Molecule: pleckstrin homology domain-containing family b PDBTitle: solution structure of the ph domain of evectin-2 from mouse
87	c1wmvA_	Alignment	not modelled	8.1	15	PDB header: oxidoreductase, apoptosis Chain: A; PDB Molecule: ww domain containing oxidoreductase; PDBTitle: solution structure of the second ww domain of wwox
88	c3pp2A_	Alignment	not modelled	8.0	20	PDB header: hydrolase activator Chain: A; PDB Molecule: rho gtpase-activating protein 27; PDBTitle: crystal structure of the pleckstrin homology domain of arhgap27
89	d2i5ua1	Alignment	not modelled	7.9	19	Fold: DnaD domain-like Superfamily: DnaD domain-like Family: DnaD domain
90	d1ie6a_	Alignment	not modelled	7.7	56	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like Family: Spider toxins
91	d1u29a1	Alignment	not modelled	7.5	20	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Pleckstrin-homology domain (PH domain)
92	c1u5fA_	Alignment	not modelled	7.4	20	PDB header: signaling protein Chain: A; PDB Molecule: src-associated adaptor protein; PDBTitle: crystal structure of the ph domain of skap-hom with 8 vector-derived2 n-terminal residues
93	c3enoC_	Alignment	not modelled	7.4	16	PDB header: hydrolase/unknown function Chain: C; PDB Molecule: uncharacterized protein pf2011; PDBTitle: crystal structure of pyrococcus furiosus pcc1 in complex2 with thermoplasma acidophilum kae1
94	d1l0wa2	Alignment	not modelled	7.3	18	Fold: DCoH-like Superfamily: GAD domain-like Family: GAD domain
95	d1tafa_	Alignment	not modelled	7.2	46	Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs
96	d1unqa_	Alignment	not modelled	6.9	21	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Pleckstrin-homology domain (PH domain)
97	d1ghea_	Alignment	not modelled	6.5	27	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
98	d1fgya_	Alignment	not modelled	6.4	7	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Pleckstrin-homology domain (PH domain)
99	c2mcfA_	Alignment	not modelled	6.4	78	PDB header: unknown function Chain: A; PDB Molecule: tgam_1934; PDBTitle: nmr structure of tgam_1934