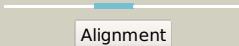
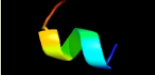



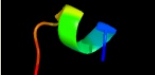
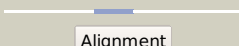

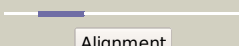
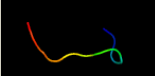
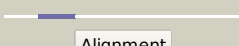
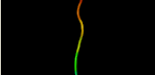
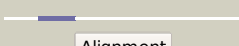




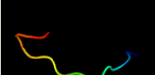




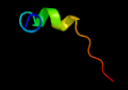

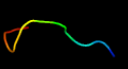

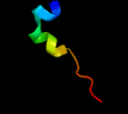
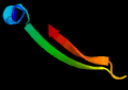





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3678A (-) _4118708_4118869
Date	Fri Aug 9 18:20:37 BST 2019
Unique Job ID	ec2fe5966edb34c2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2rqyA_	 Alignment		38.4	60	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure and dynamics of mouse armet
2	c2kveA_	 Alignment		34.0	60	PDB header: hormone Chain: A: PDB Molecule: mesencephalic astrocyte-derived neurotrophic factor; PDBTitle: c-terminal domain of mesencephalic astrocyte-derived neurotrophic2 factor (manf)
3	c4bitA_	 Alignment		31.3	60	PDB header: signaling protein Chain: A: PDB Molecule: cerebral dopamine neurotrophic factor; PDBTitle: solution structure of cerebral dopamine neurotrophic factor (cdfn)
4	c2w51A_	 Alignment		21.0	60	PDB header: hormone Chain: A: PDB Molecule: protein armet; PDBTitle: human mesencephalic astrocyte-derived neurotrophic factor (manf)
5	c2n7fA_	 Alignment		19.9	50	PDB header: toxin Chain: A: PDB Molecule: muo-conotoxin mfvia; PDBTitle: nmr solution structure of muo-conotoxin mfvia
6	c1rmkA_	 Alignment		16.8	60	PDB header: toxin Chain: A: PDB Molecule: mu-o-conotoxin mrvib; PDBTitle: solution structure of conotoxin mrvib
7	d1rmkA_	 Alignment		16.8	60	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like Family: Conotoxin
8	d1o59a2	 Alignment		13.8	57	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Allantoicase repeat
9	d1v8da_	 Alignment		11.9	50	Fold: TTHA0583/YokD-like Superfamily: TTHA0583/YokD-like Family: Hypothetical protein TT1679
10	d2b3aa1	 Alignment		11.9	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
11	c1v8dC_	 Alignment		11.1	50	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein (tt1679); PDBTitle: crystal structure of the conserved hypothetical protein2 tt1679 from thermus thermophilus

12	d1ofda1	Alignment		10.4	26	Fold: Single-stranded right-handed beta-helix Superfamily: Alpha subunit of glutamate synthase, C-terminal domain Family: Alpha subunit of glutamate synthase, C-terminal domain
13	d1ef5a_	Alignment		10.3	42	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
14	c2kywA_	Alignment		9.3	38	PDB header: cell adhesion Chain: A: PDB Molecule: adhesion exoprotein; PDBTitle: solution nmr structure of a domain of adhesion exoprotein from2 pediococcus pentosaceus, northeast structural genomics consortium3 target ptr41o
15	c4o7kA_	Alignment		8.7	28	PDB header: antitumor protein Chain: A: PDB Molecule: protein osa; PDBTitle: crystal structure of oncogenic suppression activity protein - a2 plasmid fertility inhibition factor
16	d1ea0a1	Alignment		8.4	26	Fold: Single-stranded right-handed beta-helix Superfamily: Alpha subunit of glutamate synthase, C-terminal domain Family: Alpha subunit of glutamate synthase, C-terminal domain
17	d1e0ba_	Alignment		7.5	19	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo domain
18	c2zdiA_	Alignment		7.4	38	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein tma177; PDBTitle: crystal structure of tma177, a hypothetical protein from2 thermus thermophilus phage tma
19	c6c0fs_	Alignment		7.1	21	PDB header: ribosome Chain: S: PDB Molecule: 60s ribosomal protein l20-a; PDBTitle: yeast nucleolar pre-60s ribosomal subunit (state 2)
20	c2m7cA_	Alignment		6.9	55	PDB header: de novo protein Chain: A: PDB Molecule: trp-cage mini-protein; PDBTitle: circular permutation of the trp-cage: fold rescue upon addition of a2 hydrophobic staple
21	d1lfda_	Alignment	not modelled	6.9	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
22	c3kh0A_	Alignment	not modelled	6.6	25	PDB header: signaling protein Chain: A: PDB Molecule: ral guanine nucleotide dissociation stimulator; PDBTitle: crystal structure of the ras-association (ra) domain of ralgds
23	d1d2zb_	Alignment	not modelled	6.5	25	Fold: DEATH domain Superfamily: DEATH domain Family: DEATH domain, DD
24	c2vhfB_	Alignment	not modelled	6.4	38	PDB header: hydrolase Chain: B: PDB Molecule: ubiquitin carboxyl-terminal hydrolase cyld; PDBTitle: structure of the cyld usp domain
25	c2gnxA_	Alignment	not modelled	6.3	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: x-ray structure of a hypothetical protein from mouse mm.209172
26	c1icfB_	Alignment	not modelled	6.0	33	PDB header: hydrolase Chain: B: PDB Molecule: protein (cathepsin I: light chain); PDBTitle: crystal structure of mhc class ii associated p41 ii fragment in2 complex with cathepsin I
27	c2dmxA_	Alignment	not modelled	5.7	23	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily b member 8; PDBTitle: solution structure of the j domain of dnaj homolog2 subfamily b member 8
28	d1xbla_	Alignment	not modelled	5.7	31	Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain

29	d2v4ja2	Alignment	not modelled	5.7	34	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: DsrA/DsrB N-terminal-domain-like
30	c3ov5A	Alignment	not modelled	5.6	50	PDB header: protein transport Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: atomic structure of the xanthomonas citri virb7 globular domain.
31	d1ji6a1	Alignment	not modelled	5.4	28	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: delta-Endotoxin, C-terminal domain
32	d2bjra2	Alignment	not modelled	5.4	55	Fold: MFPT repeat-like Superfamily: MFPT repeat-like Family: MFPT repeat