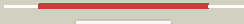



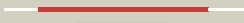










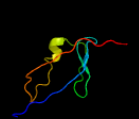

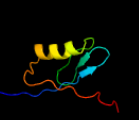




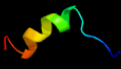





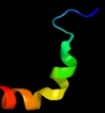
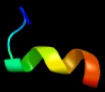
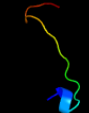


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0038 (-)_41304_41912
Date	Tue Jul 23 14:50:06 BST 2019
Unique Job ID	3a76cdc2ddcc4e92

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2gs5a1	 Alignment		100.0	42	Fold: VC0467-like Superfamily: VC0467-like Family: VC0467-like
2	c2muiA	 Alignment		100.0	26	PDB header: unknown function Chain: A: PDB Molecule: upf0301 protein algh; PDBTitle: solution structure of the algh protein from pseudomonas aeruginosa,2 pa0405, upf0301
3	d2gzoa1	 Alignment		100.0	25	Fold: VC0467-like Superfamily: VC0467-like Family: VC0467-like
4	c2aj2A	 Alignment		100.0	29	PDB header: unknown function Chain: A: PDB Molecule: hypothetical upf0301 protein vc0467; PDBTitle: x-ray crystal structure of protein vc0467 from vibrio2 cholerae. northeast structural genomics consortium target3 vcr8.
5	d2ew0a1	 Alignment		100.0	24	Fold: VC0467-like Superfamily: VC0467-like Family: VC0467-like
6	d2do8a1	 Alignment		100.0	24	Fold: VC0467-like Superfamily: VC0467-like Family: VC0467-like
7	d2hafa1	 Alignment		100.0	30	Fold: VC0467-like Superfamily: VC0467-like Family: VC0467-like
8	c6j4uA	 Alignment		51.1	17	PDB header: hydrolase Chain: A: PDB Molecule: tubuliny-tyr carboxypeptidase 1; PDBTitle: structural basis of tubulin detyrosination by vasohibins-svbp enzyme2 complex and functional implications
9	c6qbyA	 Alignment		46.4	19	PDB header: cytosolic protein Chain: A: PDB Molecule: tubuliny-tyr carboxypeptidase 2; PDBTitle: crystal structure of vash 2 in complex with svbp
10	d1vpqa	 Alignment		22.5	40	Fold: TIM beta/alpha-barrel Superfamily: TM1631-like Family: TM1631-like
11	d2b78a1	 Alignment		12.7	15	Fold: PUA domain-like Superfamily: PUA domain-like Family: Hypothetical RNA methyltransferase domain (HRMD)

12	c1byyA	Alignment		12.5	5	PDB header: membrane protein Chain: A; PDB Molecule: protein (sodium channel alpha-subunit); PDBTitle: sodium channel iia inactivation gate
13	d1sy6a1	Alignment		8.9	13	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains
14	c4lqlF	Alignment		8.8	14	PDB header: isomerase Chain: F; PDB Molecule: l-arabinose isomerase; PDBTitle: crystal structure of l-arabinose isomerase from lactobacillus2 fermentum cgmcc2921
15	c2zjtB	Alignment		8.4	10	PDB header: isomerase Chain: B; PDB Molecule: dna gyrase subunit b; PDBTitle: crystal structure of dna gyrase b' domain sheds lights on the2 mechanism for t-segment navigation
16	d1jl3a	Alignment		8.2	9	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
17	c4m7vA	Alignment		7.9	19	PDB header: oxidoreductase Chain: A; PDB Molecule: dihydrofolate reductase; PDBTitle: dihydrofolate reductase from enterococcus faecalis complexed with2 nadp(h)and rab-propyl
18	c6dy3G	Alignment		7.7	24	PDB header: hydrolase Chain: G; PDB Molecule: n-acylethanolamine-hydrolyzing acid amidase alpha-subunit; PDBTitle: caenorhabditis elegans n-acylethanolamine-hydrolyzing acid amidase2 (naaa) ortholog
19	c6dy1A	Alignment		7.1	36	PDB header: hydrolase Chain: A; PDB Molecule: n-acylethanolamine acid amidase alpha-subunit; PDBTitle: rabbit n-acylethanolamine-hydrolyzing acid amidase (naaa) with fatty2 acid (myristate), in presence of triton x-100
20	d2ajta2	Alignment		6.9	15	Fold: Fucl/AraA N-terminal and middle domains Superfamily: Fucl/AraA N-terminal and middle domains Family: AraA N-terminal and middle domain-like
21	c2eapA	Alignment	not modelled	6.6	21	PDB header: signaling protein Chain: A; PDB Molecule: lymphocyte cytosolic protein 2; PDBTitle: solution structure of the n-terminal sam-domain of human2 lymphocyte cytosolic protein 2
22	d1bjja1	Alignment	not modelled	6.3	15	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains
23	c5my7A	Alignment	not modelled	6.2	18	PDB header: cell adhesion Chain: A; PDB Molecule: adhesin; PDBTitle: adhesin complex protein from neisseria meningitidis
24	c4qxzA	Alignment	not modelled	6.2	50	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a hypothetical protein from staphylococcus aureus
25	c6cxmA	Alignment	not modelled	5.9	14	PDB header: oxidoreductase/inhibitor Chain: A; PDB Molecule: dihydrofolate reductase; PDBTitle: crystal structure of a dihydrofolate reductase from mycobacterium2 smegmatis in complex with nadp and p218
26	d1vm6a3	Alignment	not modelled	5.8	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
27	c6i52A	Alignment	not modelled	5.6	33	PDB header: dna binding protein Chain: A; PDB Molecule: replication factor a protein 3; PDBTitle: yeast rpa bound to ssdna
28	c4p37A	Alignment	not modelled	5.3	23	PDB header: transferase Chain: A; PDB Molecule: putative poly(a) polymerase catalytic subunit; PDBTitle: crystal structure of the megavirus polyadenylate synthase PDB header: rna binding protein

29	c4a4fA_	Alignment	not modelled	5.3	10 Chain: A: PDB Molecule: survival of motor neuron-related-splicing factor 30; PDBTitle: solution structure of spf30 tudor domain in complex with symmetrically2 dimethylated arginine
30	c4i5iA_	Alignment	not modelled	5.2	21 PDB header: hydrolase Chain: A: PDB Molecule: nad-dependent protein deacetylase sirtuin-1; PDBTitle: crystal structure of the sirt1 catalytic domain bound to nad and an2 ex527 analog