
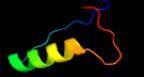

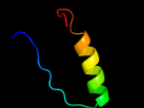

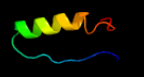



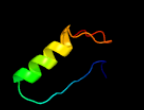

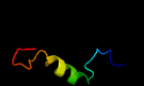



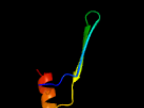

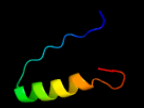

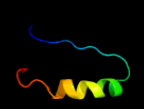




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1312_(-)_1467694_1468137
Date	Wed Jul 31 22:05:41 BST 2019
Unique Job ID	a0cdb02abf4401f0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2lxFA_	 Alignment		66.9	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of a potential acylphosphatase from giardia2 lamblia, seattle structural genomics center for infectious disease3 target glaa.01396.a
2	c2bjeA_	 Alignment		65.2	19	PDB header: hydrolase Chain: A: PDB Molecule: acylphosphatase; PDBTitle: acylphosphatase from sulfolobus solfataricus. monlinic p212 space group
3	d1w2ia_	 Alignment		64.6	19	Fold: Ferredoxin-like Superfamily: Acylphosphatase/BLUF domain-like Family: Acylphosphatase-like
4	c3br8A_	 Alignment		62.7	19	PDB header: hydrolase Chain: A: PDB Molecule: probable acylphosphatase; PDBTitle: crystal structure of acylphosphatase from bacillus subtilis
5	c4hi2B_	 Alignment		58.5	18	PDB header: hydrolase Chain: B: PDB Molecule: acylphosphatase; PDBTitle: crystal structure of an acylphosphatase protein cage
6	d1apsa_	 Alignment		57.1	13	Fold: Ferredoxin-like Superfamily: Acylphosphatase/BLUF domain-like Family: Acylphosphatase-like
7	c1uv7A_	 Alignment		43.8	9	PDB header: transport Chain: A: PDB Molecule: general secretion pathway protein m; PDBTitle: periplasmic domain of epsm from vibrio cholerae
8	d1uv7a_	 Alignment		43.8	9	Fold: RRF/tRNA synthetase additional domain-like Superfamily: General secretion pathway protein M, EpsM Family: General secretion pathway protein M, EpsM
9	d1ulra_	 Alignment		43.4	29	Fold: Ferredoxin-like Superfamily: Acylphosphatase/BLUF domain-like Family: Acylphosphatase-like
10	c2gv1A_	 Alignment		42.9	26	PDB header: hydrolase Chain: A: PDB Molecule: probable acylphosphatase; PDBTitle: nmr solution structure of the acylphosphatase from2 eschaerichia coli
11	c2kncB_	 Alignment		36.7	15	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfaib-beta3 transmembrane-cytoplasmic2 heterocomplex

12	d2acya_	Alignment		34.8	19	Fold: Ferredoxin-like Superfamily: Acylphosphatase/BLUF domain-like Family: Acylphosphatase-like
13	d1urra_	Alignment		34.5	23	Fold: Ferredoxin-like Superfamily: Acylphosphatase/BLUF domain-like Family: Acylphosphatase-like
14	c6ithA_	Alignment		29.6	28	PDB header: membrane protein Chain: A: PDB Molecule: syndecan-2; PDBTitle: structure of the transmembrane domain of syndecan 2 in micelles
15	c2pebB_	Alignment		28.4	22	PDB header: oxidoreductase Chain: B: PDB Molecule: putative dioxygenase; PDBTitle: crystal structure of a putative dioxygenase (npun_f1925) from nostoc punctiforme pcc 73102 at 1.46 a resolution
16	c5zazA_	Alignment		21.8	23	PDB header: cell adhesion Chain: A: PDB Molecule: integrin beta-2; PDBTitle: solution structure of integrin b2 monomer tranmembrane domain in2 bicelle
17	d2p8ia1	Alignment		20.2	22	Fold: Ferredoxin-like Superfamily: DOPA-like Family: DOPA dioxygenase-like
18	c2m20B_	Alignment		17.9	19	PDB header: signaling protein Chain: B: PDB Molecule: epidermal growth factor receptor; PDBTitle: egfr transmembrane - juxtamembrane (tm-jm) segment in bicelles: md2 guided nmr refined structure.
19	c6nhwC_	Alignment		16.2	41	PDB header: immune system Chain: C: PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
20	c6nhwA_	Alignment		16.2	41	PDB header: immune system Chain: A: PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
21	c6nhwB_	Alignment	not modelled	16.2	41	PDB header: immune system Chain: B: PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
22	c6nhwD_	Alignment	not modelled	16.2	41	PDB header: immune system Chain: D: PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
23	c6nhwF_	Alignment	not modelled	16.2	41	PDB header: immune system Chain: F: PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
24	c6nhwE_	Alignment	not modelled	16.2	41	PDB header: immune system Chain: E: PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
25	c2rmzA_	Alignment	not modelled	13.2	15	PDB header: cell adhesion Chain: A: PDB Molecule: integrin beta-3; PDBTitle: bicelle-embedded integrin beta3 transmembrane segment
26	c2jh3C_	Alignment	not modelled	12.2	10	PDB header: ribosomal protein Chain: C: PDB Molecule: ribosomal protein s2-related protein; PDBTitle: the crystal structure of dr2241 from deinococcus2 radiodurans at 1.9 a resolution reveals a multi-domain3 protein with structural similarity to chelatases but also4 with two additional novel domains
27	c6nf8n_	Alignment	not modelled	12.2	18	PDB header: ribosomal protein Chain: N: PDB Molecule: 28s ribosomal protein s14, mitochondrial;

27	c0ntrn_	Alignment	not modelled	12.2	10	PDBTitle: structure of human mitochondrial translation initiation factor 3 bound2 to the small ribosomal subunit -class i
28	d2j49a1	Alignment	not modelled	12.0	22	Fold: Taf5 N-terminal domain-like Superfamily: Taf5 N-terminal domain-like Family: Taf5 N-terminal domain-like
29	d1h3za_	Alignment	not modelled	10.1	19	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: PWWP domain
30	d1tdha3	Alignment	not modelled	9.1	33	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
31	c1t5qA_	Alignment	not modelled	9.0	33	PDB header: hormone/growth factor Chain: A: PDB Molecule: gastric inhibitory polypeptide; PDBTitle: solution structure of gip(1-30)amide in tfe/water
32	c5camC_	Alignment	not modelled	8.4	29	PDB header: transcription Chain: C: PDB Molecule: pupr protein; PDBTitle: crystal structure of the cytoplasmic domain of the pseudomonas putida2 anti-sigma factor pupr (semet)
33	c2yopB_	Alignment	not modelled	8.3	15	PDB header: apoptosis Chain: B: PDB Molecule: protein fam3b; PDBTitle: long wavelength s-sad structure of fam3b pander
34	c2ks1B_	Alignment	not modelled	8.3	25	PDB header: transferase Chain: B: PDB Molecule: epidermal growth factor receptor; PDBTitle: heterodimeric association of transmembrane domains of erb1 and erbb22 receptors enabling kinase activation
35	c2kakA_	Alignment	not modelled	8.1	58	PDB header: metal binding protein Chain: A: PDB Molecule: ec protein i/ii; PDBTitle: solution structure of the beta-e-domain of wheat ec-12 metallothionein
36	d1t95a2	Alignment	not modelled	7.9	19	Fold: FYSH domain Superfamily: FYSH domain Family: Hypothetical protein AF0491, N-terminal domain
37	c6gtsC_	Alignment	not modelled	7.5	20	PDB header: transcription Chain: C: PDB Molecule: duf1778 domain-containing protein; PDBTitle: structure of the atat-atar complex bound dna
38	d2nxpa1	Alignment	not modelled	7.3	13	Fold: Taf5 N-terminal domain-like Superfamily: Taf5 N-terminal domain-like Family: Taf5 N-terminal domain-like
39	c2obuA_	Alignment	not modelled	7.3	33	PDB header: hormone/growth factor Chain: A: PDB Molecule: gastric inhibitory polypeptide; PDBTitle: solution structure of gip in tfe/water
40	d2j4ba1	Alignment	not modelled	7.0	22	Fold: Taf5 N-terminal domain-like Superfamily: Taf5 N-terminal domain-like Family: Taf5 N-terminal domain-like
41	c6ge2A_	Alignment	not modelled	6.5	26	PDB header: hormone Chain: A: PDB Molecule: exendin-4; PDBTitle: exendin-4 based dual glp-1/glucagon receptor agonist
42	c6c61N_	Alignment	not modelled	6.4	19	PDB header: membrane protein Chain: N: PDB Molecule: v0 assembly protein 1; PDBTitle: yeast vacuolar atpase vo in lipid nanodisc
43	c6hqaC_	Alignment	not modelled	6.3	17	PDB header: transcription Chain: C: PDB Molecule: subunit (90 kda) of tfiid and saga complexes; PDBTitle: molecular structure of promoter-bound yeast tfiid
44	c4fu6A_	Alignment	not modelled	6.1	22	PDB header: transcription Chain: A: PDB Molecule: pc4 and sfrs1-interacting protein; PDBTitle: crystal structure of the psp1 pwwp domain
45	c3l6aA_	Alignment	not modelled	5.9	33	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 4 gamma 2; PDBTitle: crystal structure of the c-terminal region of human p97
46	c5tgnA_	Alignment	not modelled	5.9	21	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein sthe_2403 from sphaerobacter thermophilus
47	c5cwwB_	Alignment	not modelled	5.4	38	PDB header: transport protein Chain: B: PDB Molecule: nucleoporin nup82; PDBTitle: crystal structure of the chaetomium thermophilum heterotrimeric nup822 ntd-nup159 tail-nup145n apd complex