

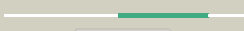


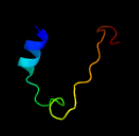

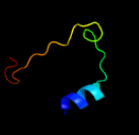








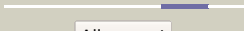
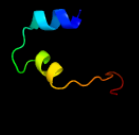

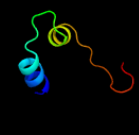

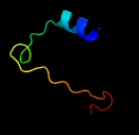


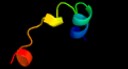




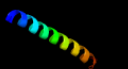



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3123 (-)_3488566_3489060
Date	Thu Aug 8 16:20:30 BST 2019
Unique Job ID	01d01794784273ae

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2f7fa1	 Alignment		62.8	18	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
2	c2f7fa_	 Alignment		42.4	18	PDB header: transferase Chain: A: PDB Molecule: nicotinate phosphoribosyltransferase, putative; PDBTitle: crystal structure of enterococcus faecalis putative nicotinate2 phosphoribosyltransferase, new york structural genomics consortium
3	c2zl5A_	 Alignment		17.8	33	PDB header: viral protein Chain: A: PDB Molecule: 58 kd capsid protein; PDBTitle: atomic resolution structural characterization of2 recognition of histo-blood group antigen by norwalk virus
4	c4p2nD_	 Alignment		16.5	30	PDB header: viral protein Chain: D: PDB Molecule: major capsid protein; PDBTitle: structure of the p domain from a gi.7 norovirus variant in complex2 with lex hbga
5	d1c7ka_	 Alignment		15.8	40	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Zinc protease
6	d1yira1	 Alignment		15.6	17	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: Monomeric nicotinate phosphoribosyltransferase C-terminal domain
7	c4yubB_	 Alignment		13.9	26	PDB header: ligase Chain: B: PDB Molecule: nicotinate phosphoribosyltransferase; PDBTitle: crystal structure of human nicotinic acid phosphoribosyltransferase
8	c5e6tA_	 Alignment		13.2	13	PDB header: viral protein Chain: A: PDB Molecule: capsid; PDBTitle: crystal structure of bovine norovirus p domain
9	c3lq6A_	 Alignment		11.6	20	PDB header: viral protein Chain: A: PDB Molecule: capsid protein; PDBTitle: crystal structure of murine norovirus protruding (p) domain
10	c4rdkB_	 Alignment		11.1	27	PDB header: viral protein Chain: B: PDB Molecule: capsid; PDBTitle: crystal structure of norovirus boxer p domain in complex with lewis b2 tetrasaccharide
11	c3assB_	 Alignment		9.1	23	PDB header: viral protein Chain: B: PDB Molecule: capsid protein; PDBTitle: crystal structure of p domain from norovirus funabashi258 stain in the2 complex with lewis-b

12	c2a7uA_	Alignment		9.0	44	PDB header: hydrolase Chain: A: PDB Molecule: atp synthase alpha chain; PDBTitle: nmr solution structure of the e.coli f-atpase delta subunit n-terminal2 domain in complex with alpha subunit n-terminal 22 residues
13	c5b02C_	Alignment		8.8	56	PDB header: transferase, dna binding protein Chain: C: PDB Molecule: moen5,dna-binding protein 7d; PDBTitle: structure of the prenyltransferase moen5 with a fusion protein tag of f2 sso7d
14	c2innA_	Alignment		8.4	21	PDB header: oxidoreductase Chain: A: PDB Molecule: phenol hydroxylase component phn; PDBTitle: structure of the phenol hydroxylase-regulatory protein complex
15	c5b0mB_	Alignment		8.4	52	PDB header: transferase, dna binding protein Chain: B: PDB Molecule: moen5,dna-binding protein 7d; PDBTitle: structure of moen5-ss07d fusion protein in complex with beta-dodecyl2 maltoside
16	c3ajaA_	Alignment		7.9	24	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of msmege_6394
17	c4ok7A_	Alignment		7.8	30	PDB header: hydrolase Chain: A: PDB Molecule: endolysin; PDBTitle: structure of bacteriophage spn1s endolysin from salmonella typhimurium
18	d1ytda1	Alignment		7.7	9	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
19	d1ppje2	Alignment		7.2	11	Fold: Single transmembrane helix Superfamily: ISP transmembrane anchor Family: ISP transmembrane anchor
20	d2inca1	Alignment		6.3	14	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like
21	c3dhiA_	Alignment	not modelled	6.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: toluene 4-monoxygenase hydroxylase alpha subunit; PDBTitle: crystal structure of reduced toluene 4-monoxygenase hydroxylase2 complexed with effector protein
22	c3os4A_	Alignment	not modelled	6.1	17	PDB header: transferase Chain: A: PDB Molecule: nicotinate phosphoribosyltransferase; PDBTitle: the crystal structure of nicotinate phosphoribosyltransferase from yersinia pestis
23	c2l0rA_	Alignment	not modelled	6.0	13	PDB header: hydrolase,toxin Chain: A: PDB Molecule: lethal factor; PDBTitle: conformational dynamics of the anthrax lethal factor catalytic center
24	c3d11A_	Alignment	not modelled	5.8	50	PDB header: hydrolase Chain: A: PDB Molecule: putative metal-dependent hydrolase; PDBTitle: crystal structure of a putative metal-dependent hydrolase2 (yp_001336084.1) from klebsiella pneumoniae subsp. pneumoniae mgh3 78578 at 2.20 a resolution
25	c2dxcG_	Alignment	not modelled	5.7	42	PDB header: hydrolase Chain: G: PDB Molecule: thiocyanate hydrolase subunit alpha; PDBTitle: recombinant thiocyanate hydrolase, fully-matured form
26	c2d11H_	Alignment	not modelled	5.7	30	PDB header: cell adhesion Chain: H: PDB Molecule: na(+)/h(+) exchange regulatory cofactor nhe-rf2; PDBTitle: crystal structure of the radixin ferm domain complexed with2 the nherf-2 c-terminal tail peptide
27	c2d11G_	Alignment	not modelled	5.7	30	PDB header: cell adhesion Chain: G: PDB Molecule: na(+)/h(+) exchange regulatory cofactor nhe-rf2; PDBTitle: crystal structure of the radixin ferm domain complexed with2 the nherf-2 c-terminal tail peptide
						PDB header: cell adhesion Chain: E: PDB Molecule: na(+)/h(+) exchange regulatory cofactor

28	c2d11E_	Alignment	not modelled	5.7	30	nhe-rf2; PDBTitle: crystal structure of the radixin ferm domain complexed with2 the nherf-2 c-terminal tail peptide
29	c2d11F_	Alignment	not modelled	5.7	30	PDB header: cell adhesion Chain: F; PDB Molecule: na(+)/h(+) exchange regulatory cofactor nhe-rf2; PDBTitle: crystal structure of the radixin ferm domain complexed with2 the nherf-2 c-terminal tail peptide
30	d1ywy1	Alignment	not modelled	5.3	58	Fold: PH domain-like barrel Superfamily: PA2021-like Family: PA2021-like
31	c5tizA_	Alignment	not modelled	5.2	19	PDB header: transferase Chain: A; PDB Molecule: sulfotransferase; PDBTitle: schistosoma japonicum (blood fluke) sulfotransferase