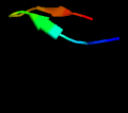





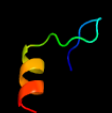




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2722_(-)_3034645_3034893
Date	Wed Aug 7 12:50:37 BST 2019
Unique Job ID	e501c5b1fa8caa73

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1xm5a_	Alignment		18.1	20	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Predicted metal-dependent hydrolase
2	c6ht4A_	Alignment		15.7	47	PDB header: unknown function Chain: A; PDB Molecule: ns5a; PDBTitle: nmr structure of ns5a-d2 (jfh1) peptide (304-323)
3	c2mfrA_	Alignment		14.0	100	PDB header: transferase Chain: A; PDB Molecule: insulin receptor; PDBTitle: solution structure of the transmembrane domain of the insulin receptor2 in micelles
4	c1xaxA_	Alignment		13.9	16	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical upf0054 protein hi0004; PDBTitle: nmr structure of hi0004, a putative essential gene product2 from haemophilus influenzae
5	d1qcsa1	Alignment		13.4	29	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
6	d1tvia_	Alignment		11.9	24	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Predicted metal-dependent hydrolase
7	c2n73B_	Alignment		11.8	32	PDB header: transferase/transferase regulator Chain: B; PDB Molecule: phosphatidylinositol 4-kinase beta; PDBTitle: solution structure of the acbd3:pi4kb complex
8	c5od4A_	Alignment		10.9	31	PDB header: unknown function Chain: A; PDB Molecule: secreted in xylem 3; PDBTitle: avr2 effector protein from the fungal plant pathogen fusarium2 oxysporum
9	c2esyA_	Alignment		9.7	42	PDB header: lipid binding protein Chain: A; PDB Molecule: lung surfactant protein c; PDBTitle: structure and influence on stability and activity of the n-2 terminal propetide part of lung surfactant protein c
10	c3k8hA_	Alignment		9.2	28	PDB header: membrane protein Chain: A; PDB Molecule: 30klp; PDBTitle: structure of crystal form i of tp0453
11	d1oz9a_	Alignment		9.2	24	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Predicted metal-dependent hydrolase

12	d1na6a1	Alignment		9.2	25	Fold: DNA-binding pseudobarrel domain Superfamily: DNA-binding pseudobarrel domain Family: Type II restriction endonuclease effector domain
13	d1x99a_	Alignment		8.5	46	Fold: Cytolysin/lectin Superfamily: Cytolysin/lectin Family: Fungal fruit body lectin
14	c3la6P_	Alignment		8.4	29	PDB header: transferase Chain: P: PDB Molecule: tyrosine-protein kinase wzc; PDBTitle: octameric kinase domain of the e. coli tyrosine kinase wzc with bound2 adp
15	d2h28a1	Alignment		8.2	37	Fold: Profilin-like Superfamily: YeeU-like Family: YagB/YeeU/YfjZ-like
16	c2eocA_	Alignment		7.8	36	PDB header: transferase Chain: A: PDB Molecule: poly [adp-ribose] polymerase 3; PDBTitle: solution structure of the wgr domain from human poly [adp-2 ribose] polymerase-3
17	c4v194_	Alignment		7.6	25	PDB header: ribosome Chain: 4: PDB Molecule: mitoribosomal protein bl31m, mrp155; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
18	c4yamA_	Alignment		7.2	33	PDB header: transferase Chain: A: PDB Molecule: beta-etherase; PDBTitle: crystal structure of lige-apo form from sphingobium sp. strain syk-6
19	c3iynR_	Alignment		7.0	60	PDB header: virus Chain: R: PDB Molecule: hexon-associated protein; PDBTitle: 3.6-angstrom cryoem structure of human adenovirus type 5
20	d1rk4a2	Alignment		6.9	25	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
21	c2m5IA_	Alignment	not modelled	6.8	40	PDB header: viral protein Chain: A: PDB Molecule: ns5a protein; PDBTitle: ns5a308
22	d1j8yf2	Alignment	not modelled	6.6	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
23	c5xcoB_	Alignment	not modelled	6.4	31	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: ace-arg-arg-arg-arg-cys-pro-leu-tyr-ile-ser-tyr-asn-pro- PDBTitle: crystal structure of human k-ras g12d mutant in complex with gdp and2 cyclic inhibitory peptide
24	c6qvfc_	Alignment	not modelled	6.0	50	PDB header: dna binding protein Chain: C: PDB Molecule: prepilin-like protein; PDBTitle: tt_c0855 competence pilin from thermus thermophilus hb27
25	d1g7oa2	Alignment	not modelled	5.9	38	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
26	c3iynQ_	Alignment	not modelled	5.5	60	PDB header: virus Chain: Q: PDB Molecule: hexon-associated protein; PDBTitle: 3.6-angstrom cryoem structure of human adenovirus type 5
27	c6j3fB_	Alignment	not modelled	5.2	38	PDB header: transferase Chain: B: PDB Molecule: glutathione s-transferase; PDBTitle: crystal structure of the glutathione s-transferase, csgst63524, of2 ceriporiopsis subvermispota in complex with glutathione
28	d1vgya4	Alignment	not modelled	5.2	38	Fold: FwdE/GAPDH domain-like Superfamily: Serine metabolism enzymes domain Family: SerA intervening domain-like

29 [c4lmwA_](#)

Alignment

not modelled

5.2

29

PDB header:transferase
Chain: A: **PDB Molecule:**glutathione transferase;
PDBTitle: crystal structure of glutathione transferase gsfua3 from2 phanerochaete chrysosporium