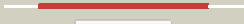



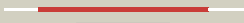
















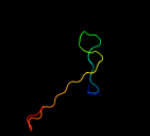


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3304 (-) _3691312_3691791
Date	Thu Aug 8 16:20:51 BST 2019
Unique Job ID	57f7fb3ccad9223a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2rbhA_</a>	 Alignment		100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> gamma-glutamyl cyclotransferase; <b>PDBTitle:</b> gamma-glutamyl cyclotransferase
2	<a href="#">c2qikA_</a>	 Alignment		100.0	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0131 protein ykqa; <b>PDBTitle:</b> crystal structure of ykqa from bacillus subtilis. northeast structural2 genomics target sr631
3	<a href="#">c5hwiA_</a>	 Alignment		99.8	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione-specific gamma-glutamylcyclotransferase; <b>PDBTitle:</b> crystal structure of selenomethionine labelled gama glutamyl2 cyclotransferase specific to glutathione from yeast
4	<a href="#">c2g0qA_</a>	 Alignment		99.7	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> at5g39720.1 protein; <b>PDBTitle:</b> solution structure of at5g39720.1 from arabidopsis thaliana
5	<a href="#">c2jqvA_</a>	 Alignment		99.7	17	<b>PDB header:</b> structural genomics <b>Chain:</b> A: <b>PDB Molecule:</b> aig2 protein-like; <b>PDBTitle:</b> solution structure at3g28950.1 from arabidopsis thaliana
6	<a href="#">d1xhsa_</a>	 Alignment		99.6	20	<b>Fold:</b> Gamma-glutamyl cyclotransferase-like <b>Superfamily:</b> Gamma-glutamyl cyclotransferase-like <b>Family:</b> Gamma-glutamyl cyclotransferase-like
7	<a href="#">c3jubA_</a>	 Alignment		99.3	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aig2-like domain-containing protein 1; <b>PDBTitle:</b> human gamma-glutamylamine cyclotransferase
8	<a href="#">d1vkba_</a>	 Alignment		99.3	16	<b>Fold:</b> Gamma-glutamyl cyclotransferase-like <b>Superfamily:</b> Gamma-glutamyl cyclotransferase-like <b>Family:</b> Gamma-glutamyl cyclotransferase-like
9	<a href="#">d1v30a_</a>	 Alignment		99.2	13	<b>Fold:</b> Gamma-glutamyl cyclotransferase-like <b>Superfamily:</b> Gamma-glutamyl cyclotransferase-like <b>Family:</b> Gamma-glutamyl cyclotransferase-like
10	<a href="#">c5c5zA_</a>	 Alignment		96.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna amidotransferase; <b>PDBTitle:</b> crystal structure analysis of c4763, a uropathogenic e. coli-specific2 protein
11	<a href="#">c2gacA_</a>	 Alignment		22.9	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosylasparaginase; <b>PDBTitle:</b> t152c mutant glycosylasparaginase from flavobacterium2 meningosepticum

12	<a href="#">c4p9gA_</a>	Alignment		17.5	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,4'-dihydroxyacetophenone dioxygenase; <b>PDBTitle:</b> structure of the 2,4'-dihydroxyacetophenone dioxygenase from 2 alcaligenes sp.
13	<a href="#">d2ejna1</a>	Alignment		13.7	31	<b>Fold:</b> Uteroglobin-like <b>Superfamily:</b> Uteroglobin-like <b>Family:</b> Uteroglobin-like
14	<a href="#">c6ig4B_</a>	Alignment		11.2	60	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphatidate cytidyltransferase, mitochondrial; <b>PDBTitle:</b> structure of mitochondrial cdp-dag synthase tam41, delta 74
15	<a href="#">c2k89A_</a>	Alignment		10.6	4	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> phospholipase a-2-activating protein; <b>PDBTitle:</b> solution structure of a novel ubiquitin-binding domain from 2 human plaa (pfuc, gly76-pro77 cis isomer)
16	<a href="#">c4yxaA_</a>	Alignment		9.2	27	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> surface presentation of antigens protein spao; <b>PDBTitle:</b> complex of spao(spao1,2 semet) and orgb(apar)::t4lysozyme fusion2 protein
17	<a href="#">d2gtvx1</a>	Alignment		8.4	0	<b>Fold:</b> Chorismate mutase II <b>Superfamily:</b> Chorismate mutase II <b>Family:</b> monomeric chorismate mutase
18	<a href="#">c3qbcB_</a>	Alignment		8.3	33	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine <b>PDBTitle:</b> structure and design of a new pterin site inhibitor of s. aureus hppk
19	<a href="#">d1cbka_</a>	Alignment		8.2	40	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK <b>Family:</b> 6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK
20	<a href="#">c1p4vA_</a>	Alignment		7.7	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n(4)-(beta-n-acetylglucosaminy)-l-asparaginase <b>PDBTitle:</b> crystal structure of the glycosylasparaginase precursor2 d151n mutant with glycine
21	<a href="#">c2p22D_</a>	Alignment	not modelled	7.7	50	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical 12.0 kda protein in ade3-ser2 intergenic <b>PDBTitle:</b> structure of the yeast esct-i heterotetramer core
22	<a href="#">d2nn6i1</a>	Alignment	not modelled	7.4	11	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
23	<a href="#">d1f9ya_</a>	Alignment	not modelled	7.1	50	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK <b>Family:</b> 6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK
24	<a href="#">d1b77a2</a>	Alignment	not modelled	6.3	27	<b>Fold:</b> DNA clamp <b>Superfamily:</b> DNA clamp <b>Family:</b> DNA polymerase processivity factor
25	<a href="#">d1czda2</a>	Alignment	not modelled	6.2	20	<b>Fold:</b> DNA clamp <b>Superfamily:</b> DNA clamp <b>Family:</b> DNA polymerase processivity factor
26	<a href="#">d1utga_</a>	Alignment	not modelled	5.6	42	<b>Fold:</b> Uteroglobin-like <b>Superfamily:</b> Uteroglobin-like <b>Family:</b> Uteroglobin-like
27	<a href="#">d1n7za_</a>	Alignment	not modelled	5.6	19	<b>Fold:</b> Baseplate structural protein gp8 <b>Superfamily:</b> Baseplate structural protein gp8 <b>Family:</b> Baseplate structural protein gp8
28	<a href="#">c5lspP_</a>	Alignment	not modelled	5.5	25	<b>PDB header:</b> cell cycle <b>Chain:</b> P: <b>PDB Molecule:</b> centromere protein c; <b>PDBTitle:</b> crystal structure of the human kinetochore mis12-cenp-c complex