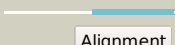

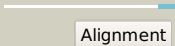
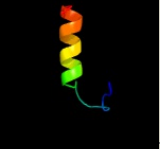
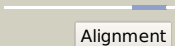
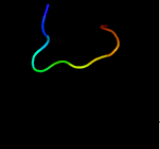
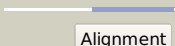
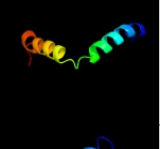
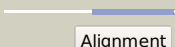
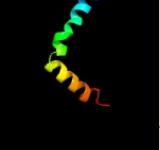
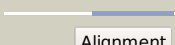
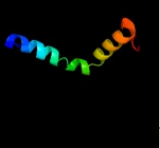
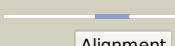
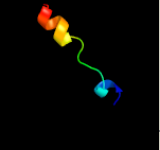
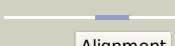
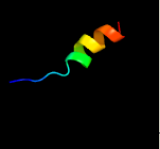

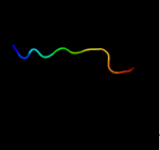
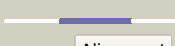





# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1036c_(-)_1160099_1160437
Date	Wed Jul 31 22:05:11 BST 2019
Unique Job ID	689491783f90c686

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5kinD_</a>	 Alignment		38.5	20	<b>PDB header:</b> lyase <b>Chain:</b> D; <b>PDB Molecule:</b> tryptophan synthase beta chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae
2	<a href="#">d1prtd_</a>	 Alignment		33.1	46	<b>Fold:</b> OB-fold <b>Superfamily:</b> Bacterial enterotoxins <b>Family:</b> Bacterial AB5 toxins, B-subunits
3	<a href="#">c6bxtB_</a>	 Alignment		29.2	58	<b>PDB header:</b> membrane protein <b>Chain:</b> B; <b>PDB Molecule:</b> mitochondrial association factor 1; <b>PDBTitle:</b> crystal structure of toxoplasma gondii mitochondrial association2 factor 1 a (maf1a) in complex with adpribose
4	<a href="#">c5tchH_</a>	 Alignment		28.6	20	<b>PDB header:</b> lyase <b>Chain:</b> H; <b>PDB Molecule:</b> tryptophan synthase beta chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase from m. tuberculosis -2 ligand-free form, trpa-g66v mutant
5	<a href="#">c1x1qA_</a>	 Alignment		27.8	28	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> tryptophan synthase beta chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase beta chain from thermus2 thermophilus hb8
6	<a href="#">d1qopb_</a>	 Alignment		24.0	25	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
7	<a href="#">c4hjdB_</a>	 Alignment		22.1	53	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> gcn4pli(alpha/beta/acyclic gamma); <b>PDBTitle:</b> gcn4pli derivative with alpha/beta/acyclic-gamma amino acid2 substitution pattern
8	<a href="#">c4hjdA_</a>	 Alignment		22.1	53	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> gcn4pli(alpha/beta/acyclic gamma); <b>PDBTitle:</b> gcn4pli derivative with alpha/beta/acyclic-gamma amino acid2 substitution pattern
9	<a href="#">c4ywcA_</a>	 Alignment		13.8	36	<b>PDB header:</b> transcription regulator <b>Chain:</b> A; <b>PDB Molecule:</b> transcription factor myc3; <b>PDBTitle:</b> crystal structure of myc3(5-242) fragment in complex with jaz9(218-2 239) peptide
10	<a href="#">c2krxA_</a>	 Alignment		13.7	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> asl3597 protein; <b>PDBTitle:</b> solution nmr structure of asl3597 from nostoc sp. pcc7120. northeast2 structural genomics consortium target id nsr244.
11	<a href="#">c5mlpA_</a>	 Alignment		12.8	20	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> structure of cdps from rickettsiella grylli

12	<a href="#">c3w20B_</a>	Alignment		10.5	58	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of a novel n-substituted l-amino acid dioxygenase2 from burkholderia ambifaria ammd
13	<a href="#">d1v8za1</a>	Alignment		9.1	23	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
14	<a href="#">c3pfyA_</a>	Alignment		8.4	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> otu domain-containing protein 5; <b>PDBTitle:</b> the catalytic domain of human otud5
15	<a href="#">c2lnmA_</a>	Alignment		8.0	23	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> protein tic 40, chloroplastic; <b>PDBTitle:</b> solution structure of the c-terminal np-repeat domain of tic40, a co-2 chaperone during protein import into chloroplasts
16	<a href="#">d1ho8a_</a>	Alignment		7.9	19	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> ARM repeat <b>Family:</b> Regulatory subunit H of the V-type ATPase
17	<a href="#">d1igwa_</a>	Alignment		7.7	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/isocitrate lyase-like
18	<a href="#">c5cuza_</a>	Alignment		6.9	40	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> methylmalonic aciduria and homocystinuria type d protein, <b>PDBTitle:</b> crystal structure of semet-substituted n-terminal truncated human b12-2 chaperone cbld (108-296)
19	<a href="#">d1luura1</a>	Alignment		6.4	46	<b>Fold:</b> STAT-like <b>Superfamily:</b> STAT <b>Family:</b> STAT
20	<a href="#">d1r5aa1</a>	Alignment		6.2	13	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
21	<a href="#">d1kp0a1</a>	Alignment	not modelled	6.1	43	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Creatinase/prolidase N-terminal domain <b>Family:</b> Creatinase/prolidase N-terminal domain
22	<a href="#">c3domC_</a>	Alignment	not modelled	6.0	45	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> rna polymerase ii transcription factor b subunit 2; <b>PDBTitle:</b> crystal structure of the complex between tfb5 and the c-terminal2 domain of tfb2
23	<a href="#">c4bopA_</a>	Alignment	not modelled	6.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> otu domain-containing protein 1; <b>PDBTitle:</b> structure of otud1 otu domain
24	<a href="#">c4ykbE_</a>	Alignment	not modelled	5.7	17	<b>PDB header:</b> plant protein <b>Chain:</b> E: <b>PDB Molecule:</b> tetrapyrrole-binding protein; <b>PDBTitle:</b> structure of gun4 from chlamydomonas reinhardtii
25	<a href="#">d1axda1</a>	Alignment	not modelled	5.7	26	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
26	<a href="#">c2lw1A_</a>	Alignment	not modelled	5.5	27	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter atp-binding protein uup; <b>PDBTitle:</b> the c-terminal domain of the uup protein is a dna-binding coiled coil2 motif
27	<a href="#">c2i6hA_</a>	Alignment	not modelled	5.5	40	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein atu0120; <b>PDBTitle:</b> structure of protein of unknown function atu0120 from agrobacterium2 tumefaciens
28	<a href="#">d2i6ha1</a>	Alignment	not modelled	5.5	40	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Atu0120-like
						<b>PDB header:</b> cell cycle, hydrolase

29	<a href="#">c3c0rC_</a>	Alignment	not modelled	5.4	16	<b>Chain:</b> C: <b>PDB Molecule:</b> ubiquitin thioesterase otu1; <b>PDBTitle:</b> structure of ovarian tumor (otu) domain in complex with ubiquitin
30	<a href="#">c2yg8B_</a>	Alignment	not modelled	5.4	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dna-3-methyladenine glycosidase ii, putative; <b>PDBTitle:</b> structure of an unusual 3-methyladenine dna glycosylase ii (alka) from2 deinococcus radiodurans
31	<a href="#">c3a98B_</a>	Alignment	not modelled	5.3	58	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> engulfment and cell motility protein 1; <b>PDBTitle:</b> crystal structure of the complex of the interacting regions of dock22 and elmo1
32	<a href="#">c5jzeA_</a>	Alignment	not modelled	5.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> rna-dependent rna polymerase; <b>PDBTitle:</b> erve virus viral otu domain protease in complex with mouse isg15
33	<a href="#">c6n1fD_</a>	Alignment	not modelled	5.2	50	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> oxidoreductase, 2og-fe(ii) oxygenase family; <b>PDBTitle:</b> crystal structure of oxidoreductase, 2og-fe(ii) oxygenase family, from2 burkholderia pseudomallei
34	<a href="#">d1v2aa1</a>	Alignment	not modelled	5.1	10	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain