
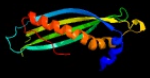
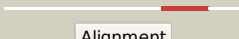
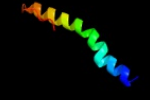
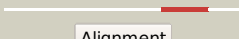


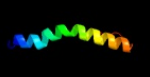

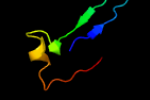



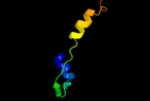










# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1957_(-) _2202591_2203136
Date	Mon Aug 5 13:25:05 BST 2019
Unique Job ID	7e45cd7fe25d0869

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5mtwD_</a>	 Alignment		100.0	100	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> secb-like chaperone rv1957; <b>PDBTitle:</b> mycobacterium tuberculosis rv1957 secb-like chaperone in complex with2 a chad peptide from rv1956 higa1 antitoxin
2	<a href="#">d1ozba_</a>	 Alignment		90.7	28	<b>Fold:</b> SecB-like <b>Superfamily:</b> SecB-like <b>Family:</b> Bacterial protein-export protein SecB
3	<a href="#">d1ozbg_</a>	 Alignment		90.5	28	<b>Fold:</b> SecB-like <b>Superfamily:</b> SecB-like <b>Family:</b> Bacterial protein-export protein SecB
4	<a href="#">d1qyna_</a>	 Alignment		90.4	23	<b>Fold:</b> SecB-like <b>Superfamily:</b> SecB-like <b>Family:</b> Bacterial protein-export protein SecB
5	<a href="#">c4o7kA_</a>	 Alignment		24.3	31	<b>PDB header:</b> antitumor protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein osa; <b>PDBTitle:</b> crystal structure of oncogenic suppression activity protein - a2 plasmid fertility inhibition factor
6	<a href="#">c1jqsB_</a>	 Alignment		17.9	54	<b>PDB header:</b> ribosome <b>Chain:</b> B: <b>PDB Molecule:</b> elongation factor g; <b>PDBTitle:</b> fitting of I11 protein and elongation factor g (domain g'2 and v) in the cryo-em map of e. coli 70s ribosome bound3 with ef-g and gmppcp, a nonhydrolysable gtp analog
7	<a href="#">c6eu9C_</a>	 Alignment		17.7	32	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> retinoic acid receptor; <b>PDBTitle:</b> crystal structure of platynereis dumerilii rar ligand-binding domain2 in complex with all-trans retinoic acid
8	<a href="#">c5a79A_</a>	 Alignment		14.1	26	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> capsid protein; <b>PDBTitle:</b> novel inter-subunit contacts in barley stripe mosaic virus revealed by2 cryo-em
9	<a href="#">d1wiew_</a>	 Alignment		12.7	27	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> SH3-domain <b>Family:</b> SH3-domain
10	<a href="#">c6bxwA_</a>	 Alignment		11.2	28	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> mitochondrial association factor 1; <b>PDBTitle:</b> crystal structure of toxoplasma gondii mitochondrial association2 factor 1 b (maf1b) in complex with adpribose
11	<a href="#">c3dd7D_</a>	 Alignment		10.9	78	<b>PDB header:</b> ribosome inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> prevent host death protein; <b>PDBTitle:</b> structure of doch66y in complex with the c-terminal domain of phd

12	<a href="#">d1ou0a_</a>	Alignment		10.2	43	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Precorrin-8X methylmutase CbiC/CobH <b>Family:</b> Precorrin-8X methylmutase CbiC/CobH
13	<a href="#">d1f2va_</a>	Alignment		10.0	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Precorrin-8X methylmutase CbiC/CobH <b>Family:</b> Precorrin-8X methylmutase CbiC/CobH
14	<a href="#">c2afvB_</a>	Alignment		9.4	43	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> cobalamin biosynthesis precorrin isomerase; <b>PDBTitle:</b> the crystal structure of putative precorrin isomerase cbic2 in cobalamin biosynthesis
15	<a href="#">c4au1A_</a>	Alignment		9.0	7	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> precorrin-8x methylmutase; <b>PDBTitle:</b> crystal structure of cobh (precorrin-8x methyl mutase)2 complexed with c5 desmethyl-hba
16	<a href="#">c3e7dC_</a>	Alignment		8.9	14	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> cobh, precorrin-8x methylmutase; <b>PDBTitle:</b> crystal structure of precorrin-8x methyl mutase cbic/cobh from2 brucella melitensis
17	<a href="#">d1v9ca_</a>	Alignment		8.8	57	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Precorrin-8X methylmutase CbiC/CobH <b>Family:</b> Precorrin-8X methylmutase CbiC/CobH
18	<a href="#">c3qzrC_</a>	Alignment		8.2	55	<b>PDB header:</b> hormone receptor <b>Chain:</b> C: <b>PDB Molecule:</b> abscisic acid receptor pyl5; <b>PDBTitle:</b> crystal structure of native abscisic acid receptor pyl5 at 2.62 angstrom
19	<a href="#">c5n9jC_</a>	Alignment		7.9	29	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> mediator of rna polymerase ii transcription subunit 19; <b>PDBTitle:</b> core mediator of transcriptional regulation
20	<a href="#">d1wbl1a3</a>	Alignment		7.8	73	<b>Fold:</b> Elongation factor/aminomethyltransferase common domain <b>Superfamily:</b> EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain <b>Family:</b> EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
21	<a href="#">d2veaa3</a>	Alignment	not modelled	7.5	50	<b>Fold:</b> Profilin-like <b>Superfamily:</b> PYP-like sensor domain (PAS domain) <b>Family:</b> BphP N-terminal domain-like
22	<a href="#">d1neka3</a>	Alignment	not modelled	7.3	24	<b>Fold:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain <b>Superfamily:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
23	<a href="#">c3dd7B_</a>	Alignment	not modelled	7.1	86	<b>PDB header:</b> ribosome inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> prevent host death protein; <b>PDBTitle:</b> structure of doch66y in complex with the c-terminal domain of phd
24	<a href="#">c5ldwC_</a>	Alignment	not modelled	7.0	46	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nahd dehydrogenase [ubiquinone] iron-sulfur protein 3, <b>PDBTitle:</b> structure of mammalian respiratory complex i, class1
25	<a href="#">d2bs2a3</a>	Alignment	not modelled	6.9	15	<b>Fold:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain <b>Superfamily:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
26	<a href="#">c2x2iB_</a>	Alignment	not modelled	6.2	34	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-1,4-glucan lyase isozyme 1; <b>PDBTitle:</b> crystal structure of the gracilariopsis lemaneiformis alpha-1,4-2 glucan lyase with acarbose
27	<a href="#">c2phgB_</a>	Alignment	not modelled	6.1	67	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> alpha trans-inducing protein; <b>PDBTitle:</b> model for vp16 binding to tfiib
						<b>PDB header:</b> protein transport

28	<a href="#">c2l4wA_</a>	Alignment	not modelled	5.6	54	<b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> nmr structure of the xanthomonas virb7
29	<a href="#">d1xn8a_</a>	Alignment	not modelled	5.5	19	<b>Fold:</b> Hypothetical protein YqbG <b>Superfamily:</b> Hypothetical protein YqbG <b>Family:</b> Hypothetical protein YqbG
30	<a href="#">c6ijoG_</a>	Alignment	not modelled	5.4	39	<b>PDB header:</b> photosynthesis <b>Chain:</b> G: <b>PDB Molecule:</b> psag; <b>PDBTitle:</b> photosystem i of chlamydomonas reinhardtii
31	<a href="#">c2n0pA_</a>	Alignment	not modelled	5.2	38	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein aq_1974; <b>PDBTitle:</b> solution structure of aquifex aeolicus aq1974
32	<a href="#">c1x0gA_</a>	Alignment	not modelled	5.2	22	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> isca; <b>PDBTitle:</b> crystal structure of isca with the [2fe-2s] cluster