

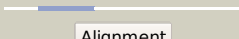
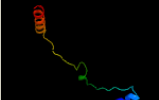
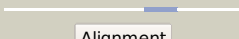



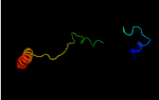



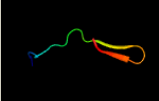



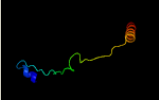

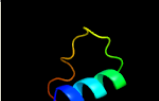

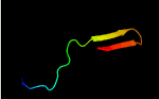


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1289_(-)_1442773_1443405
Date	Wed Jul 31 22:05:38 BST 2019
Unique Job ID	6a66dc5cd22b8753

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3oa8B_</a>	 Alignment		29.3	18	<b>PDB header:</b> heme-binding protein/heme-binding protei <b>Chain:</b> B; <b>PDB Molecule:</b> soxx; <b>PDBTitle:</b> diheme soxax
2	<a href="#">c2du3A_</a>	 Alignment		24.3	13	<b>PDB header:</b> ligase/rna <b>Chain:</b> A; <b>PDB Molecule:</b> o-phosphoseryl-trna synthetase; <b>PDBTitle:</b> crystal structure of archaeoglobus fulgidus o-phosphoseryl-2 trna synthetase complexed with trnacys and o-phosphoserine
3	<a href="#">c4tvxT_</a>	 Alignment		20.2	38	<b>PDB header:</b> <b>PDB COMPND:</b>
4	<a href="#">c4n77A_</a>	 Alignment		19.3	54	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of cas protein
5	<a href="#">c2du7C_</a>	 Alignment		17.5	13	<b>PDB header:</b> ligase <b>Chain:</b> C; <b>PDB Molecule:</b> o-phosphoseryl-trna synthetase; <b>PDBTitle:</b> crystal structure of methanococcus jannacshii o-phosphoseryl-trna2 synthetase
6	<a href="#">c2mn2A_</a>	 Alignment		17.4	9	<b>PDB header:</b> antitoxin <b>Chain:</b> A; <b>PDB Molecule:</b> ymob; <b>PDBTitle:</b> 3d structure of ymob, a modulator of biofilm formation
7	<a href="#">c4iykA_</a>	 Alignment		16.2	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative carbohydrate binding protein2 (bacuni_04699) from bacteroides uniformis atcc 8492 at 2.00 a3 resolution
8	<a href="#">d2vo1a1</a>	 Alignment		16.0	28	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
9	<a href="#">c2du4B_</a>	 Alignment		15.3	13	<b>PDB header:</b> ligase/rna <b>Chain:</b> B; <b>PDB Molecule:</b> o-phosphoseryl-trna synthetase; <b>PDBTitle:</b> crystal structure of archaeoglobus fulgidus o-phosphoseryl-2 trna synthetase complexed with trnacys
10	<a href="#">c5u07N_</a>	 Alignment		15.1	13	<b>PDB header:</b> immune system <b>Chain:</b> N; <b>PDB Molecule:</b> crispr-associated protein, cas5e family; <b>PDBTitle:</b> crispr rna-guided surveillance complex
11	<a href="#">c3hn5B_</a>	 Alignment		14.7	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> putative exported protein bf0290; <b>PDBTitle:</b> crystal structure of bf0290 (yp_210027.1) from bacteroides fragilis2 nctc 9343 at 1.70 a resolution

12	<a href="#">c2y3nB_</a>	Alignment		12.0	35	<b>PDB header:</b> structrual protein/hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cellulosomal family-48 processive glycoside hydrolase; <b>PDBTitle:</b> type ii cohesin-dockerin domain from bacteroides cellosolvans
13	<a href="#">d2gnra1</a>	Alignment		11.9	16	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> SSO2064-like
14	<a href="#">c6dk9l_</a>	Alignment		11.8	16	<b>PDB header:</b> lyase <b>Chain:</b> I: <b>PDB Molecule:</b> dna damage-inducible protein; <b>PDBTitle:</b> yeast ddi2 cyanamide hydratase
15	<a href="#">c4yoka_</a>	Alignment		11.3	21	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative flagellar protein flis; <b>PDBTitle:</b> crystal structure of a duf3823 family protein (parmer_04126) from2 parabacteroides merdae atcc 43184 at 1.80 a resolution
16	<a href="#">c6qbyA_</a>	Alignment		11.2	15	<b>PDB header:</b> cytosolic protein <b>Chain:</b> A: <b>PDB Molecule:</b> tubulinyln-tyr carboxypeptidase 2; <b>PDBTitle:</b> crystal structure of vash 2 in complex with svbp
17	<a href="#">c2llhA_</a>	Alignment		11.2	38	<b>PDB header:</b> dna binding protein, chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> nucleophosmin; <b>PDBTitle:</b> nmr structure of npm1_c70
18	<a href="#">c2v1sD_</a>	Alignment		10.7	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> mitochondrial import receptor subunit tom20 homolog; <b>PDBTitle:</b> crystal structure of rat tom20-aldh presequence complex
19	<a href="#">c2vxdA_</a>	Alignment		10.3	38	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleophosmin; <b>PDBTitle:</b> the structure of the c-terminal domain of nucleophosmin
20	<a href="#">c4dh2B_</a>	Alignment		9.5	22	<b>PDB header:</b> cell adhesion/protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> dockerin type 1; <b>PDBTitle:</b> crystal structure of coh-olpc(cthe_0452)-doc435(cthe_0435) complex: a2 novel type i cohesin-dockerin complex from clostridium thermocellum3 atcc 27405
21	<a href="#">d1om2a_</a>	Alignment	not modelled	8.9	14	<b>Fold:</b> Open three-helical up-and-down bundle <b>Superfamily:</b> Mitochondrial import receptor subunit Tom20 <b>Family:</b> Mitochondrial import receptor subunit Tom20
22	<a href="#">c6j4uA_</a>	Alignment	not modelled	7.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tubulinyln-tyr carboxypeptidase 1; <b>PDBTitle:</b> structural basis of tubulin deetyrosination by vasohibins-svbp enzyme2 complex and functional implications
23	<a href="#">c4fxtB_</a>	Alignment	not modelled	7.8	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a duf3823 family protein (bacova_02663) from2 bacteroides ovatus atcc 8483 at 2.77 a resolution
24	<a href="#">c2x3mA_</a>	Alignment	not modelled	7.5	80	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein orf239; <b>PDBTitle:</b> crystal structure of hypothetical protein orf239 from pyrobaculum2 spherical virus
25	<a href="#">c2dnqA_</a>	Alignment	not modelled	7.5	5	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna-binding protein 4b; <b>PDBTitle:</b> solution structure of rna binding domain 1 in rna-binding2 protein 30
26	<a href="#">c2ab9A_</a>	Alignment	not modelled	7.3	57	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> pro-sfti-1; <b>PDBTitle:</b> discovery, structural determination and processing of the2 precursor protein that produces the cyclic trypsin3 inhibitor sfti-1
27	<a href="#">d1cf7a_</a>	Alignment	not modelled	7.2	55	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Cell cycle transcription factor e2f-dp
28	<a href="#">d3bbda1</a>	Alignment	not modelled	7.2	21	<b>Fold:</b> alpha/beta knot <b>Superfamily:</b> alpha/beta knot <b>Family:</b> EMG1/NEP1-like <b>PDB header:</b> transferase

29	<a href="#">c5faiA_</a>	Alignment	not modelled	6.8	19	<b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal rna small subunit methyltransferase nep1; <b>PDBTitle:</b> emg1 n1-specific pseudouridine methyltransferase
30	<a href="#">d1xrxal</a>	Alignment	not modelled	6.5	30	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> SeqA N-terminal domain-like
31	<a href="#">c1xrxD_</a>	Alignment	not modelled	6.5	30	<b>PDB header:</b> replication inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> seqa protein; <b>PDBTitle:</b> crystal structure of a dna-binding protein
32	<a href="#">d2dkya1</a>	Alignment	not modelled	6.2	26	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> SAM/Pointed domain <b>Family:</b> Variant SAM domain
33	<a href="#">c4eiuA_</a>	Alignment	not modelled	6.1	29	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized hypothetical protein; <b>PDBTitle:</b> crystal structure of a duf3823 family protein (bacuni_03093) from bacteroides uniformis atcc 8492 at 1.90 a resolution
34	<a href="#">c2jmbA_</a>	Alignment	not modelled	6.0	50	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein atu4866; <b>PDBTitle:</b> solution structure of the protein atu4866 from agrobacterium2 tumefaciens
35	<a href="#">d2h80a1</a>	Alignment	not modelled	6.0	30	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> SAM/Pointed domain <b>Family:</b> Variant SAM domain
36	<a href="#">d2cpta1</a>	Alignment	not modelled	5.9	15	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> MIT domain <b>Family:</b> MIT domain
37	<a href="#">c4g6vE_</a>	Alignment	not modelled	5.9	19	<b>PDB header:</b> toxin <b>Chain:</b> E: <b>PDB Molecule:</b> adhesin/hemolysin; <b>PDBTitle:</b> cdia-ct/cdii toxin and immunity complex from burkholderia pseudomallei
38	<a href="#">c3j0xl_</a>	Alignment	not modelled	5.8	22	<b>PDB header:</b> ribosome <b>Chain:</b> I: <b>PDB Molecule:</b> 30s ribosomal protein s6; <b>PDBTitle:</b> structural characterization of mrna-trna translocation intermediates2 (30s ribosome of class 4b of the six classes)
39	<a href="#">c4n7zB_</a>	Alignment	not modelled	5.5	31	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> centrosomal protein of 192 kda; <b>PDBTitle:</b> crystal structure of human plk4 cryptic polo box (cpb) in complex with2 a cep192 n-terminal fragment
40	<a href="#">c5m2sB_</a>	Alignment	not modelled	5.5	30	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> doc8: type i dockerin repeat domain from family 9 glycoside <b>PDBTitle:</b> r. flavefaciens' third scab cohesin in complex with a group 1 dockerin
41	<a href="#">d1jb0e_</a>	Alignment	not modelled	5.5	45	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Electron transport accessory proteins <b>Family:</b> Photosystem I accessory protein E (PsaE)
42	<a href="#">d2j5aa1</a>	Alignment	not modelled	5.5	22	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Ribosomal protein S6 <b>Family:</b> Ribosomal protein S6
43	<a href="#">d1qjha_</a>	Alignment	not modelled	5.3	9	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Ribosomal protein S6 <b>Family:</b> Ribosomal protein S6
44	<a href="#">c5lxvB_</a>	Alignment	not modelled	5.3	34	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> carbohydrate-binding protein wp_009985128; <b>PDBTitle:</b> crystal structure of ruminococcus flavefaciens scaffoldin c cohesin in2 complex with a dockerin from an uncharacterized cbm-containing3 protein
45	<a href="#">c2cbjA_</a>	Alignment	not modelled	5.2	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hyaluronidase; <b>PDBTitle:</b> structure of the clostridium perfringens nagj family 84 glycoside2 hydrolase, a homologue of human o-glcnacase in complex with pugnac
46	<a href="#">d2jq9a1</a>	Alignment	not modelled	5.2	19	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> MIT domain <b>Family:</b> MIT domain
47	<a href="#">c4uyqB_</a>	Alignment	not modelled	5.2	16	<b>PDB header:</b> cell adhesion/protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> cellulosomal scaffoldin adaptor protein b; <b>PDBTitle:</b> high resolution structure of the third cohesin scac in complex with2 the scab dockerin with a mutation in the c-terminal helix (in to si)3 from acetivibrio cellulolyticus displaying a type i interaction.
48	<a href="#">c2k58B_</a>	Alignment	not modelled	5.1	26	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> neuronal acetylcholine receptor subunit beta-2; <b>PDBTitle:</b> nmr structures of the first transmembrane domain of the2 neuronal acetylcholine receptor beta 2 subunit