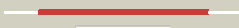
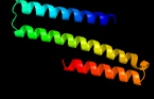





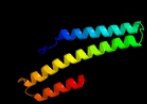





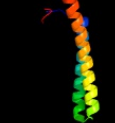
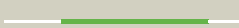




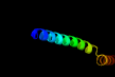
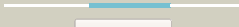

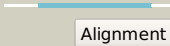
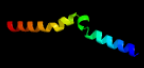
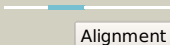

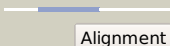
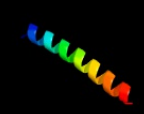
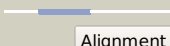
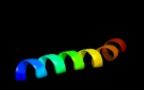
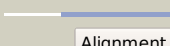

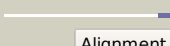

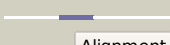

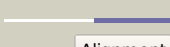

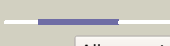

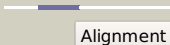
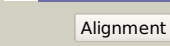
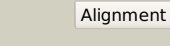

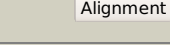
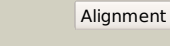

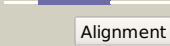
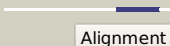


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0190 (-) _221869_222159
Date	Tue Jul 23 14:50:24 BST 2019
Unique Job ID	772340ab2de38c3e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4adzA_</a>	 Alignment		100.0	58	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> csor; <b>PDBTitle:</b> crystal structure of the apo form of a copper-sensitive operon2 regulator (csor) protein from streptomyces lividans
2	<a href="#">c5lbnD_</a>	 Alignment		100.0	21	<b>PDB header:</b> transcription <b>Chain:</b> D; <b>PDB Molecule:</b> transcriptional repressor frmr; <b>PDBTitle:</b> the asymmetric tetrameric structure of the formaldehyde sensing2 transcriptional repressor frmr from escherichia coli
3	<a href="#">c4m1pA_</a>	 Alignment		100.0	42	<b>PDB header:</b> transcription repressor <b>Chain:</b> A; <b>PDB Molecule:</b> copper-sensitive operon repressor (csor); <b>PDBTitle:</b> crystal structure of the copper-sensing repressor csor with cu(i) from2 geobacillus thermodenitrificans ng80-2
4	<a href="#">c5fmnB_</a>	 Alignment		100.0	38	<b>PDB header:</b> dna binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> inrs; <b>PDBTitle:</b> the nickel-responsive transcriptional regulator inrs
5	<a href="#">c5lcyD_</a>	 Alignment		100.0	23	<b>PDB header:</b> transcription <b>Chain:</b> D; <b>PDB Molecule:</b> frmr; <b>PDBTitle:</b> formaldehyde-responsive regulator frmr e64h variant from salmonella2 enterica serovar typhimurium
6	<a href="#">c2hh7A_</a>	 Alignment		100.0	39	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein csor; <b>PDBTitle:</b> crystal structure of cu(i) bound csor from mycobacterium tuberculosis.
7	<a href="#">c3aaiB_</a>	 Alignment		99.9	34	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> copper homeostasis operon regulatory protein; <b>PDBTitle:</b> x-ray crystal structure of csor from thermus thermophilus hb8
8	<a href="#">d1paqa_</a>	 Alignment		52.0	8	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> ARM repeat <b>Family:</b> MIF4G domain-like
9	<a href="#">c1paqA_</a>	 Alignment		52.0	8	<b>PDB header:</b> translation <b>Chain:</b> A; <b>PDB Molecule:</b> translation initiation factor eif-2b epsilon <b>PDBTitle:</b> crystal structure of the catalytic fragment of eukaryotic2 initiation factor 2b epsilon
10	<a href="#">c4u8us_</a>	 Alignment		44.9	2	<b>PDB header:</b> oxygen storage/transport <b>Chain:</b> S; <b>PDB Molecule:</b> globin d chain; <b>PDBTitle:</b> the crystallographic structure of the giant hemoglobin from2 glossoscolex paulistus at 3.2 a resolution.
11	<a href="#">c5frhA_</a>	 Alignment		38.9	9	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> anti-sigma factor rsra; <b>PDBTitle:</b> solution structure of oxidised rsra

12	<a href="#">c4aj5M_</a>	 Alignment		38.2	12	<b>PDB header:</b> cell cycle <b>Chain:</b> M: <b>PDB Molecule:</b> spindle and kinetochore-associated protein 2; <b>PDBTitle:</b> crystal structure of the ska core complex
13	<a href="#">c2p5tA_</a>	 Alignment		37.7	44	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator peza; <b>PDBTitle:</b> molecular and structural characterization of the pezat chromosomal2 toxin-antitoxin system of the human pathogen streptococcus pneumoniae
14	<a href="#">c4n6jA_</a>	 Alignment		23.7	11	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> striatin-3; <b>PDBTitle:</b> crystal structure of human striatin-3 coiled coil domain
15	<a href="#">c4n6jB_</a>	 Alignment		22.6	13	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> striatin-3; <b>PDBTitle:</b> crystal structure of human striatin-3 coiled coil domain
16	<a href="#">c3juia_</a>	 Alignment		21.4	10	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor eif-2b subunit epsilon; <b>PDBTitle:</b> crystal structure of the c-terminal domain of human translation2 initiation factor eif2b epsilon subunit
17	<a href="#">c3fajA_</a>	 Alignment		19.1	9	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> structure of the structural protein p131 of the archaeal virus2 acidianus two-tailed virus (atv)
18	<a href="#">c4fc9B_</a>	 Alignment		19.0	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> structure of the c-terminal domain of the type iii effector xcv32202 (xopl)
19	<a href="#">c4a1qB_</a>	 Alignment		18.3	16	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> orf e73; <b>PDBTitle:</b> solution structure of e73 protein from sulfolobus spindle-2 shaped virus ragged hills, a hyperthermophilic3 crenarchaeal virus from yellowstone national park
20	<a href="#">c2nv2U_</a>	 Alignment		17.7	29	<b>PDB header:</b> lyase/transferase <b>Chain:</b> U: <b>PDB Molecule:</b> pyridoxal biosynthesis lyase pdxs; <b>PDBTitle:</b> structure of the plp synthase complex pdx1/2 (yaad/e) from bacillus2 subtilis
21	<a href="#">c3swyB_</a>	 Alignment	not modelled	16.1	32	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> cyclic nucleotide-gated cation channel alpha-3; <b>PDBTitle:</b> cnga3 626-672 containing clz domain
22	<a href="#">c4yioB_</a>	 Alignment	not modelled	16.1	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> superoxide dismutase; <b>PDBTitle:</b> x-ray structure of the iron/manganese cambialistic superoxide2 dismutase from streptococcus thermophilus
23	<a href="#">c4aaiB_</a>	 Alignment	not modelled	16.1	15	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> orf e73; <b>PDBTitle:</b> thermostable protein from hyperthermophilic virus ssv-rh
24	<a href="#">c2n5xA_</a>	 Alignment	not modelled	15.1	12	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> hsp90 co-chaperone cdc37; <b>PDBTitle:</b> c-terminal domain of cdc37 cochaperone
25	<a href="#">c5vf3Z_</a>	 Alignment	not modelled	13.7	38	<b>PDB header:</b> virus <b>Chain:</b> Z: <b>PDB Molecule:</b> highly immunogenic outer capsid protein; <b>PDBTitle:</b> bacteriophage t4 isometric capsid
26	<a href="#">c2gtlO_</a>	 Alignment	not modelled	12.9	4	<b>PDB header:</b> oxygen storage/transport <b>Chain:</b> O: <b>PDB Molecule:</b> extracellular hemoglobin linker I3 subunit; <b>PDBTitle:</b> lumbricus erythrocruurin at 3.5a resolution
27	<a href="#">d2igsa1</a>	 Alignment	not modelled	11.6	18	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> PA2222-like
28	<a href="#">d1ivsa1</a>	 Alignment	not modelled	11.5	13	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> tRNA-binding arm <b>Family:</b> Valyl-tRNA synthetase (ValRS) C-terminal domain
29	<a href="#">c2mhwA_</a>	 Alignment	not modelled	9.3	32	<b>PDB header:</b> antimicrobial protein, membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> antimicrobial peptide;

						<b>PDBTitle:</b> the solution nmr structure of maximin-4 in sds micelles
30	<a href="#">d1sr2a_</a>	Alignment	not modelled	9.1	8	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Histidine-containing phosphotransfer domain, HPT domain <b>Family:</b> Sensor-like histidine kinase YojN, C-terminal domain <b>PDB header:</b> viral protein <b>Chain:</b> F: <b>PDB Molecule:</b> phosphoprotein; <b>PDBTitle:</b> crystal structure of the nipah virus phosphoprotein tetramerization2 domain
31	<a href="#">c4n5bF_</a>	Alignment	not modelled	8.9	23	<b>PDB header:</b> plant protein <b>Chain:</b> E: <b>PDB Molecule:</b> pyridoxal 5'-phosphate synthase-like subunit pdx1.2; <b>PDBTitle:</b> pdx1.2/pdx1.3 complex (intermediate)
32	<a href="#">c6hxoE_</a>	Alignment	not modelled	8.4	24	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> potassium voltage-gated channel subfamily kqt member 4; <b>PDBTitle:</b> crystal structure of a coiled-coil tetramerization domain from kv7.42 channels
33	<a href="#">c2ovcA_</a>	Alignment	not modelled	8.4	30	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> AgIA-like glucosidase
34	<a href="#">d1up7a2</a>	Alignment	not modelled	8.0	18	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> homer protein homolog 1; <b>PDBTitle:</b> crystal structure of the carboxy terminus of homer1
35	<a href="#">c3cveC_</a>	Alignment	not modelled	7.5	22	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> golgi to er traffic protein 2; <b>PDBTitle:</b> s. cerevisiae get3- <i>adp-alf4</i> - complex with a cytosolic get2 fragment
36	<a href="#">c3zs9D_</a>	Alignment	not modelled	7.4	40	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> magnesium transporter mrs2, mitochondrial; <b>PDBTitle:</b> structural and functional characterization of the yeast mg2+ channel2 mrs2
37	<a href="#">c3rkgA_</a>	Alignment	not modelled	7.2	18	<b>PDB header:</b> plant protein <b>Chain:</b> F: <b>PDB Molecule:</b> pyridoxal 5'-phosphate synthase subunit pdx1.3; <b>PDBTitle:</b> pdx1.2/pdx1.3 complex (pdx1.3:k97a)
38	<a href="#">c6hyeF_</a>	Alignment	not modelled	6.7	21	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Histidine-containing phosphotransfer domain, HPT domain <b>Family:</b> Aerobic respiration control sensor protein, ArcB
39	<a href="#">d2a0ba_</a>	Alignment	not modelled	6.4	12	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> initiation-control protein yaba; <b>PDBTitle:</b> crystal structure of yaba amino-terminal domain from bacillus subtilis
40	<a href="#">c5dolB_</a>	Alignment	not modelled	6.4	16	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin-like protein; <b>PDBTitle:</b> crystal structure of a dimeric ferredoxin-like protein (bb1511) from2 bordetella bronchiseptica rb50 at 1.90 a resolution
41	<a href="#">c2qycA_</a>	Alignment	not modelled	6.0	10	<b>PDB header:</b> rna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> signal recognition particle subunit srp68; <b>PDBTitle:</b> structure of the srp68-rbd from chaetomium thermophilum
42	<a href="#">c4p3gC_</a>	Alignment	not modelled	5.7	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> telomere length regulator taz1; <b>PDBTitle:</b> crystal structure of the dimerization domain of s. pombe taz1
43	<a href="#">c4zmkA_</a>	Alignment	not modelled	5.6	30	<b>PDB header:</b> cell cycle <b>Chain:</b> J: <b>PDB Molecule:</b> cell cycle protein gpsb; <b>PDBTitle:</b> b. subtilis gpsb c-terminal domain
44	<a href="#">c5an5J_</a>	Alignment	not modelled	5.6	38	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> cgmp-gated cation channel alpha-1; <b>PDBTitle:</b> cnga1 621-690 containing clz domain
45	<a href="#">c3swfA_</a>	Alignment	not modelled	5.6	22	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> spindle pole body component spc42; <b>PDBTitle:</b> yeast spc42 c-terminal antiparallel coiled-coil
46	<a href="#">c6od2A_</a>	Alignment	not modelled	5.3	40	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> fat acid-binding protein; <b>PDBTitle:</b> the crystal structure of a fat acid (stearic acid)-binding protein2 from eubacterium ventriosum atcc 27560.
47	<a href="#">c3nyiA_</a>	Alignment	not modelled	5.3	11	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Histidine-containing phosphotransfer domain, HPT domain <b>Family:</b> Phosphorelay protein-like
48	<a href="#">d1wn0a1</a>	Alignment	not modelled	5.2	11	<b>Fold:</b> Cell division protein MinE topological specificity domain <b>Superfamily:</b> Cell division protein MinE topological specificity domain <b>Family:</b> Cell division protein MinE topological specificity domain
49	<a href="#">d1ev0a_</a>	Alignment	not modelled	5.2	17	<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
50	<a href="#">c4hjdB_</a>	Alignment	not modelled	5.1	33	<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
51	<a href="#">c4hjdA_</a>	Alignment	not modelled	5.1	33	<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