
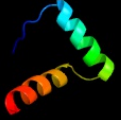


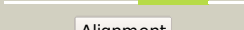

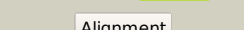


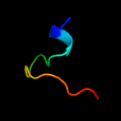




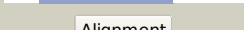

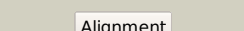
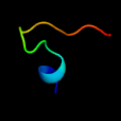
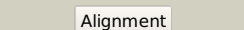


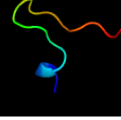

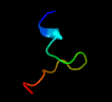
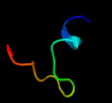



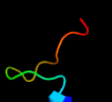
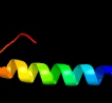



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0123 (-) _148854_149222
Date	Tue Jul 23 14:50:16 BST 2019
Unique Job ID	49aab1bef1444be8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2k5jB_</a>	 Alignment		74.4	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein yiif; <b>PDBTitle:</b> solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
2	<a href="#">c2rbfB_</a>	 Alignment		65.2	15	<b>PDB header:</b> oxidoreductase/dna <b>Chain:</b> B; <b>PDB Molecule:</b> bifunctional protein puta; <b>PDBTitle:</b> structure of the ribbon-helix-helix domain of escherichia coli puta2 (puta52) complexed with operator dna (o2)
3	<a href="#">c6iyaD_</a>	 Alignment		63.6	33	<b>PDB header:</b> antitoxin <b>Chain:</b> D; <b>PDB Molecule:</b> transcriptional regulator copg family; <b>PDBTitle:</b> structure of the dna binding domain of antitoxin copaso
4	<a href="#">c2k9iB_</a>	 Alignment		61.8	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein orf56; <b>PDBTitle:</b> nmr structure of plasmid copy control protein orf56 from sulfobolus2 islandicus
5	<a href="#">c5aj3p_</a>	 Alignment		33.9	35	<b>PDB header:</b> ribosome <b>Chain:</b> P; <b>PDB Molecule:</b> mitoribosomal protein bs16m, mrps16; <b>PDBTitle:</b> structure of the small subunit of the mammalian mitoribosome
6	<a href="#">c3e7kF_</a>	 Alignment		31.8	69	<b>PDB header:</b> membrane protein <b>Chain:</b> F; <b>PDB Molecule:</b> trpm7 channel; <b>PDBTitle:</b> crystal structure of an antiparallel coiled-coil tetramerization2 domain from trpm7 channels
7	<a href="#">c3kk4B_</a>	 Alignment		23.1	29	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein bp1543; <b>PDBTitle:</b> uncharacterized protein bp1543 from bordetella pertussis tohama i
8	<a href="#">c3f41B_</a>	 Alignment		22.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> phytase; <b>PDBTitle:</b> structure of the tandemly repeated protein tyrosine2 phosphatase like phytase from mitsuokella multacida
9	<a href="#">d2uubr1</a>	 Alignment		21.0	69	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Ribosomal protein S18 <b>Family:</b> Ribosomal protein S18
10	<a href="#">c5aj3R_</a>	 Alignment		20.9	33	<b>PDB header:</b> ribosome <b>Chain:</b> R; <b>PDB Molecule:</b> mitoribosomal protein bs18m, mrps18c; <b>PDBTitle:</b> structure of the small subunit of the mammalian mitoribosome
11	<a href="#">d2qalr1</a>	 Alignment		20.8	38	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Ribosomal protein S18 <b>Family:</b> Ribosomal protein S18

12	<a href="#">d1q9ja2</a>	Alignment		18.6	13	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> NRPS condensation domain (amide synthase)
13	<a href="#">c6dzkr</a>	Alignment		18.3	41	<b>PDB header:</b> ribosome <b>Chain:</b> R: <b>PDB Molecule:</b> <b>PDBTitle:</b> cryo-em structure of mycobacterium smegmatis c(minus) 30s ribosomal2 subunit with mpy
14	<a href="#">d1i94r</a>	Alignment		18.0	65	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Ribosomal protein S18 <b>Family:</b> Ribosomal protein S18
15	<a href="#">d1y0na</a>	Alignment		17.4	50	<b>Fold:</b> YehU-like <b>Superfamily:</b> YehU-like <b>Family:</b> YehU-like
16	<a href="#">c5o5jR</a>	Alignment		17.1	29	<b>PDB header:</b> ribosome <b>Chain:</b> R: <b>PDB Molecule:</b> 30s ribosomal protein s18 2; <b>PDBTitle:</b> structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
17	<a href="#">c3j0xU</a>	Alignment		16.7	40	<b>PDB header:</b> ribosome <b>Chain:</b> U: <b>PDB Molecule:</b> 30s ribosomal protein s18; <b>PDBTitle:</b> structural characterization of mrna-trna translocation intermediates2 (30s ribosome of class 4b of the six classes)
18	<a href="#">c3df1R</a>	Alignment		13.7	38	<b>PDB header:</b> ribosome <b>Chain:</b> R: <b>PDB Molecule:</b> 30s ribosomal protein s18; <b>PDBTitle:</b> crystal structure of the bacterial ribosome from escherichia coli in2 complex with hygromycin b. this file contains the 30s subunit of the3 first 70s ribosome, with hygromycin b bound. the entire crystal4 structure contains two 70s ribosomes.
19	<a href="#">d1h3ob</a>	Alignment		13.0	24	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> TBP-associated factors, TAFs
20	<a href="#">c3bbnR</a>	Alignment		12.9	44	<b>PDB header:</b> ribosome <b>Chain:</b> R: <b>PDB Molecule:</b> ribosomal protein s18; <b>PDBTitle:</b> homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
21	<a href="#">d2ay0a1</a>	Alignment	not modelled	12.6	14	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> PutA pre-N-terminal region-like
22	<a href="#">c6hqaK</a>	Alignment	not modelled	11.7	40	<b>PDB header:</b> transcription <b>Chain:</b> K: <b>PDB Molecule:</b> subunit (61/68 kda) of tfiid and saga complexes; <b>PDBTitle:</b> molecular structure of promoter-bound yeast tfiid
23	<a href="#">d2fug21</a>	Alignment	not modelled	10.6	34	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> NQO2-like
24	<a href="#">c2vsqA</a>	Alignment	not modelled	10.2	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> surfactin synthetase subunit 3; <b>PDBTitle:</b> structure of surfactin a synthetase c (srfa-c), a nonribosomal peptide2 synthetase termination module
25	<a href="#">c5mjyE</a>	Alignment	not modelled	9.7	44	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> zinc finger fyve domain-containing protein 9; <b>PDBTitle:</b> crystal structure of the his domain protein tyrosine phosphatase (hd-2 ptp/ptpn23) bro1 domain (sara complex structure)
26	<a href="#">c5mjyF</a>	Alignment	not modelled	9.7	44	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> zinc finger fyve domain-containing protein 9; <b>PDBTitle:</b> crystal structure of the his domain protein tyrosine phosphatase (hd-2 ptp/ptpn23) bro1 domain (sara complex structure)
27	<a href="#">c6a6xC</a>	Alignment	not modelled	9.6	39	<b>PDB header:</b> toxin <b>Chain:</b> C: <b>PDB Molecule:</b> antitoxin maze7; <b>PDBTitle:</b> the crystal structure of the mtb maze-mazf-mt9 complex
						<b>PDB header:</b> structural genomics

28	<a href="#">c3wqtB_</a>	Alignment	not modelled	8.7	24	<b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsa; <b>PDBTitle:</b> staphylococcus aureus ftsa complexed with amppnp
29	<a href="#">d1u8va2</a>	Alignment	not modelled	7.5	36	<b>Fold:</b> Acyl-CoA dehydrogenase NM domain-like <b>Superfamily:</b> Acyl-CoA dehydrogenase NM domain-like <b>Family:</b> Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains
30	<a href="#">d1tkna_</a>	Alignment	not modelled	7.1	29	<b>Fold:</b> STAT-like <b>Superfamily:</b> CAPPD, an extracellular domain of amyloid beta A4 protein <b>Family:</b> CAPPD, an extracellular domain of amyloid beta A4 protein
31	<a href="#">c1qz7B_</a>	Alignment	not modelled	6.9	75	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> axin; <b>PDBTitle:</b> beta-catenin binding domain of axin in complex with beta-2 catenin
32	<a href="#">d1wi0a_</a>	Alignment	not modelled	6.4	37	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> CAD & PB1 domains <b>Family:</b> PB1 domain
33	<a href="#">c4uzzB_</a>	Alignment	not modelled	6.3	55	<b>PDB header:</b> motor protein <b>Chain:</b> B: <b>PDB Molecule:</b> intraflagellar transporter-like protein; <b>PDBTitle:</b> crystal structure of the tift52-46 complex
34	<a href="#">c2aj1A_</a>	Alignment	not modelled	6.3	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable cadmium-transporting atpase; <b>PDBTitle:</b> solution structure of apocada
35	<a href="#">c6ckaB_</a>	Alignment	not modelled	6.2	34	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> paratox; <b>PDBTitle:</b> crystal structure of paratox
36	<a href="#">c4ic7B_</a>	Alignment	not modelled	6.1	37	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dual specificity mitogen-activated protein kinase kinase 5; <b>PDBTitle:</b> crystal structure of the erk5 kinase domain in complex with an mkk52 binding fragment
37	<a href="#">c6avhA_</a>	Alignment	not modelled	6.1	14	<b>PDB header:</b> ligase, plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> gh3.15 acyl acid amido synthetase; <b>PDBTitle:</b> gh3.15 acyl acid amido synthetase
38	<a href="#">c1nd9A_</a>	Alignment	not modelled	5.9	40	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor if-2; <b>PDBTitle:</b> solution structure of the n-terminal subdomain of f2 translation initiation factor if2
39	<a href="#">d1nd9a_</a>	Alignment	not modelled	5.9	40	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> N-terminal subdomain of bacterial translation initiation factor IF2
40	<a href="#">c3k4iC_</a>	Alignment	not modelled	5.8	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterized protein pspto_3204 from2 pseudomonas syringae pv. tomato str. dc3000
41	<a href="#">c4oo2D_</a>	Alignment	not modelled	5.7	64	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> chlorophenol-4-monooxygenase; <b>PDBTitle:</b> streptomyces globisporus c-1027 fad dependent (s)-3-chloro-β-2 tyrosine-s-sgcc2 c-5 hydroxylase sgcc apo form
42	<a href="#">c1u8vA_</a>	Alignment	not modelled	5.6	36	<b>PDB header:</b> lyase, isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> gamma-aminobutyrate metabolism dehydratase/isomerase; <b>PDBTitle:</b> crystal structure of 4-hydroxybutyryl-coa dehydratase from clostridium2 aminobutyricum: radical catalysis involving a [4fe-4s] cluster and3 flavin
43	<a href="#">d1jh3a_</a>	Alignment	not modelled	5.4	44	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
44	<a href="#">c1qeyD_</a>	Alignment	not modelled	5.3	64	<b>PDB header:</b> gene regulation <b>Chain:</b> D: <b>PDB Molecule:</b> protein (regulatory protein mnt); <b>PDBTitle:</b> nmr structure determination of the tetramerization domain2 of the mnt repressor: an asymmetric a-helical assembly in3 slow exchange
45	<a href="#">c1qeyB_</a>	Alignment	not modelled	5.3	64	<b>PDB header:</b> gene regulation <b>Chain:</b> B: <b>PDB Molecule:</b> protein (regulatory protein mnt); <b>PDBTitle:</b> nmr structure determination of the tetramerization domain2 of the mnt repressor: an asymmetric a-helical assembly in3 slow exchange
46	<a href="#">c1qeyA_</a>	Alignment	not modelled	5.3	64	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> protein (regulatory protein mnt); <b>PDBTitle:</b> nmr structure determination of the tetramerization domain2 of the mnt repressor: an asymmetric a-helical assembly in3 slow exchange
47	<a href="#">c1qeyC_</a>	Alignment	not modelled	5.3	64	<b>PDB header:</b> gene regulation <b>Chain:</b> C: <b>PDB Molecule:</b> protein (regulatory protein mnt); <b>PDBTitle:</b> nmr structure determination of the tetramerization domain2 of the mnt repressor: an asymmetric a-helical assembly in3 slow exchange
48	<a href="#">d2b5id2</a>	Alignment	not modelled	5.3	36	<b>Fold:</b> Complement control module/SCR domain <b>Superfamily:</b> Complement control module/SCR domain <b>Family:</b> Complement control module/SCR domain
49	<a href="#">c2dmeA_</a>	Alignment	not modelled	5.0	30	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> phd finger protein 3; <b>PDBTitle:</b> solution structure of the tfiis domain ii of human phd2 finger protein 3