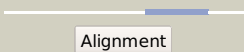

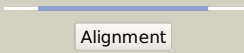

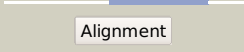





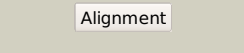

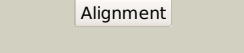



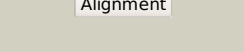

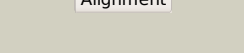

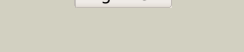

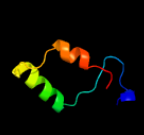

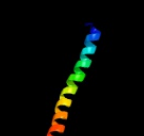
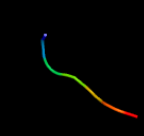

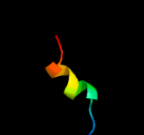

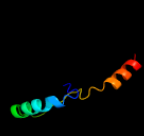
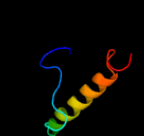


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0607 (-) _702816_703202
Date	Fri Jul 26 01:50:16 BST 2019
Unique Job ID	4945088985b1d1a2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3ktbD_</a>	 Alignment		29.2	11	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> arsenical resistance operon trans-acting repressor; <b>PDBTitle:</b> crystal structure of arsenical resistance operon trans-acting2 repressor from bacteroides vulgatus atcc 8482
2	<a href="#">d2gs4a1</a>	 Alignment		27.4	20	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ycif-like
3	<a href="#">c2bdqA_</a>	 Alignment		27.1	12	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> copper homeostasis protein cutc; <b>PDBTitle:</b> crystal structure of the putative copper homeostasis protein cutc from2 streptococcus agalactiae, northeast structural genomics target sar15.
4	<a href="#">c5vxxA_</a>	 Alignment		26.9	38	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> peroxisomal membrane protein pex15; <b>PDBTitle:</b> peroxisomal membrane protein pex15
5	<a href="#">c6g2jY_</a>	 Alignment		26.3	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> Y: <b>PDB Molecule:</b> mcg5603; <b>PDBTitle:</b> mouse mitochondrial complex i in the active state
6	<a href="#">c5ldwY_</a>	 Alignment		24.7	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> Y: <b>PDB Molecule:</b> nadh dehydrogenase [ubiquinone] 1 alpha subcomplex subunit <b>PDBTitle:</b> structure of mammalian respiratory complex i, class1
7	<a href="#">c1wwuA_</a>	 Alignment		20.3	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein flj21935; <b>PDBTitle:</b> solution structure of the sam_pnt domain of human protein2 flj21935
8	<a href="#">c2pg8C_</a>	 Alignment		19.9	42	<b>PDB header:</b> ligand binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> dpgc; <b>PDBTitle:</b> crystal structure of r254k mutant of dpgc with bound substrate analog
9	<a href="#">d1yl7a2</a>	 Alignment		18.2	26	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> Dihydropicolinate reductase-like
10	<a href="#">c3trkA_</a>	 Alignment		17.4	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nonstructural polyprotein; <b>PDBTitle:</b> structure of the chikungunya virus nsp2 protease
11	<a href="#">d1sxja1</a>	 Alignment		15.8	12	<b>Fold:</b> post-AAA+ oligomerization domain-like <b>Superfamily:</b> post-AAA+ oligomerization domain-like <b>Family:</b> DNA polymerase III clamp loader subunits, C-terminal domain

12	<a href="#">d2foka4</a>	Alignment		14.5	22	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> Restriction endonuclease FokI, C-terminal (catalytic) domain
13	<a href="#">c3fn2A_</a>	Alignment		14.5	47	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> putative sensor histidine kinase domain; <b>PDBTitle:</b> crystal structure of a putative sensor histidine kinase domain from2 clostridium symbiosum atcc 14940
14	<a href="#">c5gzxD_</a>	Alignment		14.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> (r)-2-haloacid dehalogenase; <b>PDBTitle:</b> the complex structure of d-2-haloacid dehalogenase mutant with d-2-cpa
15	<a href="#">c3lwwA_</a>	Alignment		14.3	57	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> glutamate--cysteine ligase; <b>PDBTitle:</b> glutathione-inhibited scgcl
16	<a href="#">c3kgkA_</a>	Alignment		13.8	28	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> arsenical resistance operon trans-acting repressor arsd; <b>PDBTitle:</b> crystal structure of arsd
17	<a href="#">d1nxha_</a>	Alignment		13.8	14	<b>Fold:</b> Hypothetical protein MTH393 <b>Superfamily:</b> Hypothetical protein MTH393 <b>Family:</b> Hypothetical protein MTH393
18	<a href="#">c4m55F_</a>	Alignment		13.5	25	<b>PDB header:</b> lyase <b>Chain:</b> F; <b>PDB Molecule:</b> udp-glucuronic acid decarboxylase 1; <b>PDBTitle:</b> crystal structure of human udp-xylose synthase r236h substitution
19	<a href="#">d2yvta1</a>	Alignment		13.1	17	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> TT1561-like
20	<a href="#">c5yoxB_</a>	Alignment		12.6	26	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> hd domain-containing protein ygl101w; <b>PDBTitle:</b> hd domain-containing protein ygk1(ygl101w)
21	<a href="#">c2e8mA_</a>	Alignment	not modelled	10.3	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> epidermal growth factor receptor kinase <b>PDBTitle:</b> solution structure of the c-terminal sam-domain of2 epidermal growth receptor pathway substrate 8
22	<a href="#">c2q9lA_</a>	Alignment	not modelled	10.1	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of imazg from vibrio dat 722: ctag-imazg (p43212)
23	<a href="#">d2gyqa1</a>	Alignment	not modelled	10.1	18	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ycif-like
24	<a href="#">c3fwbB_</a>	Alignment	not modelled	9.9	21	<b>PDB header:</b> cell cycle, transcription <b>Chain:</b> B; <b>PDB Molecule:</b> nuclear mrna export protein sac3; <b>PDBTitle:</b> sac3:sus1:cdc31 complex
25	<a href="#">c3ro3B_</a>	Alignment	not modelled	9.9	40	<b>PDB header:</b> protein binding <b>Chain:</b> B; <b>PDB Molecule:</b> peptide of protein inscuteable homolog; <b>PDBTitle:</b> crystal structure of lgn/minscuteable complex
26	<a href="#">c6nvoA_</a>	Alignment	not modelled	9.0	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> nuclease mpe; <b>PDBTitle:</b> crystal structure of pseudomonas putida nuclease mpe
27	<a href="#">d1diha2</a>	Alignment	not modelled	8.9	32	<b>Fold:</b> Fwde/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> Dihydrodipicolinate reductase-like
28	<a href="#">c4jhcC_</a>	Alignment	not modelled	8.8	47	<b>PDB header:</b> translation <b>Chain:</b> C; <b>PDB Molecule:</b> sb:cb157 protein; <b>PDBTitle:</b> crystal structure of danio rerio slp1 in complex with slpb
						<b>Fold:</b> Prismane protein-like

29	<a href="#">d1oaoa_</a>	Alignment	not modelled	8.5	31	<b>Superfamily:</b> Prismane protein-like <b>Family:</b> Carbon monoxide dehydrogenase
30	<a href="#">d1gc5a_</a>	Alignment	not modelled	8.3	15	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> ADP-specific Phosphofructokinase/Glucokinase
31	<a href="#">d2bwba1</a>	Alignment	not modelled	8.3	50	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
32	<a href="#">c2lo0B_</a>	Alignment	not modelled	8.2	38	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of the get5 carboxyl domain from a. fumigatus
33	<a href="#">d1yt3a2</a>	Alignment	not modelled	8.2	30	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> HRDC-like <b>Family:</b> RNase D C-terminal domains
34	<a href="#">d1kyfa1</a>	Alignment	not modelled	7.9	42	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Clathrin adaptor appendage domain <b>Family:</b> Alpha-adaptin ear subdomain-like
35	<a href="#">c1wymA_</a>	Alignment	not modelled	7.8	13	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> transgelin-2; <b>PDBTitle:</b> solution structure of the ch domain of human transgelin-2
36	<a href="#">c3bjxB_</a>	Alignment	not modelled	7.6	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> halocarboxylic acid dehalogenase dehi; <b>PDBTitle:</b> structure of a group i haloacid dehalogenase from2 pseudomonas putida strain pp3
37	<a href="#">d1s5da_</a>	Alignment	not modelled	7.6	17	<b>Fold:</b> ADP-ribosylation <b>Superfamily:</b> ADP-ribosylation <b>Family:</b> ADP-ribosylating toxins
38	<a href="#">c4zdtB_</a>	Alignment	not modelled	7.6	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> structure-specific endonuclease subunit slx4; <b>PDBTitle:</b> crystal structure of the ring finger domain of slx1 in complex with2 the c-terminal domain of slx4
39	<a href="#">c5fvkD_</a>	Alignment	not modelled	7.4	36	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> vps4-associated protein 1; <b>PDBTitle:</b> crystal structure of vps4-vfa1 complex from s.cerevisiae at 1.66 a2 resolution.
40	<a href="#">d1veja1</a>	Alignment	not modelled	6.7	30	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
41	<a href="#">c1wr1B_</a>	Alignment	not modelled	6.6	50	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> ubiquitin-like protein dsk2; <b>PDBTitle:</b> the complex structure of dsk2p uba with ubiquitin
42	<a href="#">c6elqA_</a>	Alignment	not modelled	6.5	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> carbon monoxide dehydrogenase; <b>PDBTitle:</b> carbon monoxide dehydrogenase iv from carboxydotherrmus2 hydrogenoformans
43	<a href="#">c3echC_</a>	Alignment	not modelled	6.5	57	<b>PDB header:</b> transcription, transcription regulation <b>Chain:</b> C: <b>PDB Molecule:</b> 25-mer fragment of protein armr; <b>PDBTitle:</b> the marr-family repressor mexr in complex with its antirepressor armr
44	<a href="#">c4niqD_</a>	Alignment	not modelled	6.5	36	<b>PDB header:</b> protein transport <b>Chain:</b> D: <b>PDB Molecule:</b> vps4-associated protein 1; <b>PDBTitle:</b> crystal structure of vps4 mit-vfa1 mim2
45	<a href="#">c5fvkC_</a>	Alignment	not modelled	6.5	36	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> vps4-associated protein 1; <b>PDBTitle:</b> crystal structure of vps4-vfa1 complex from s.cerevisiae at 1.66 a2 resolution.
46	<a href="#">c4niqC_</a>	Alignment	not modelled	6.4	36	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> vps4-associated protein 1; <b>PDBTitle:</b> crystal structure of vps4 mit-vfa1 mim2
47	<a href="#">c4ccsA_</a>	Alignment	not modelled	6.4	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> cbix; <b>PDBTitle:</b> the structure of cbix, the terminal enzyme for biosynthesis2 of siroheme in denitrifying bacteria
48	<a href="#">c4guaB_</a>	Alignment	not modelled	6.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> non-structural polyprotein; <b>PDBTitle:</b> alphavirus p23pro-zbd
49	<a href="#">c5mq9A_</a>	Alignment	not modelled	6.2	23	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yacp; <b>PDBTitle:</b> crystal structure of rae1 (yacp) from bacillus subtilis (w164l mutant)
50	<a href="#">c1yv0I_</a>	Alignment	not modelled	6.2	25	<b>PDB header:</b> contractile protein <b>Chain:</b> I: <b>PDB Molecule:</b> troponin i, fast skeletal muscle; <b>PDBTitle:</b> crystal structure of skeletal muscle troponin in the ca2+-free state
51	<a href="#">c6b6xA_</a>	Alignment	not modelled	6.2	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> carbon monoxide dehydrogenase; <b>PDBTitle:</b> crystal structure of desulfovibrio vulgaris carbon monoxide2 dehydrogenase, dithionite-reduced (protein batch 2), canonical c-3 cluster
52	<a href="#">c3sf4F_</a>	Alignment	not modelled	6.1	40	<b>PDB header:</b> signaling protein/protein binding <b>Chain:</b> F: <b>PDB Molecule:</b> protein inscuteable homolog; <b>PDBTitle:</b> crystal structure of the complex between the conserved cell polarity2 proteins inscuteable and lgn
53	<a href="#">d1p94a_</a>	Alignment	not modelled	6.1	56	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
54	<a href="#">c6nd4D_</a>	Alignment	not modelled	6.1	29	<b>PDB header:</b> ribosome <b>Chain:</b> D: <b>PDB Molecule:</b> bud21; <b>PDBTitle:</b> conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
55	<a href="#">c6gtsC_</a>	Alignment	not modelled	6.0	31	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> duf1778 domain-containing protein;

						<b>PDBTitle:</b> structure of the atat-atar complex bound dna
56	<a href="#">c5ejcD_</a>	Alignment	not modelled	5.9	44	<b>PDB header:</b> signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> hamartin; <b>PDBTitle:</b> crystal structural of the tsc1-tbc1d7 complex
57	<a href="#">c2hwkA_</a>	Alignment	not modelled	5.7	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> helicase nsp2; <b>PDBTitle:</b> crystal structure of venezuelan equine encephalitis alphavirus nsp22 protease domain
58	<a href="#">d2dnaa1_</a>	Alignment	not modelled	5.7	30	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
59	<a href="#">d1ujoa_</a>	Alignment	not modelled	5.7	16	<b>Fold:</b> CH domain-like <b>Superfamily:</b> Calponin-homology domain, CH-domain <b>Family:</b> Calponin-homology domain, CH-domain
60	<a href="#">d1u7ka_</a>	Alignment	not modelled	5.5	18	<b>Fold:</b> Retrovirus capsid protein, N-terminal core domain <b>Superfamily:</b> Retrovirus capsid protein, N-terminal core domain <b>Family:</b> Retrovirus capsid protein, N-terminal core domain
61	<a href="#">c3gznb_</a>	Alignment	not modelled	5.3	15	<b>PDB header:</b> protein binding/ligase <b>Chain:</b> B: <b>PDB Molecule:</b> nedd8-activating enzyme e1 catalytic subunit; <b>PDBTitle:</b> structure of nedd8-activating enzyme in complex with nedd8 and mln4924
62	<a href="#">d1su7a_</a>	Alignment	not modelled	5.3	25	<b>Fold:</b> Prismane protein-like <b>Superfamily:</b> Prismane protein-like <b>Family:</b> Carbon monoxide dehydrogenase
63	<a href="#">d1vm6a2_</a>	Alignment	not modelled	5.2	25	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> Dihydrodipicolinate reductase-like
64	<a href="#">c1tz5A_</a>	Alignment	not modelled	5.1	27	<b>PDB header:</b> hormone/growth factor <b>Chain:</b> A: <b>PDB Molecule:</b> chimera of pancreatic hormone and neuropeptide y; <b>PDBTitle:</b> [pnpy19-23]-hpp bound to dpc micelles