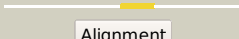
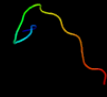
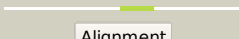

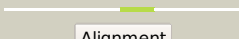







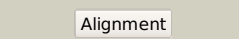

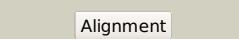
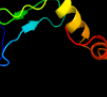
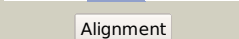


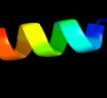
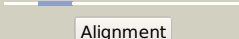

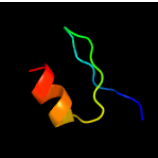
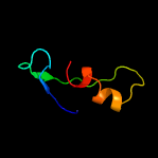

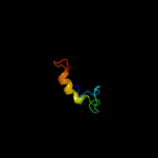







Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3527_(-)_3963784_3964233
Date	Fri Aug 9 18:20:20 BST 2019
Unique Job ID	88923609b15355ab

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3h0gL_	 Alignment		70.5	29	PDB header: transcription Chain: L: PDB Molecule: dna-directed rna polymerases i, ii, and iii subunit rpabc4; PDBTitle: rna polymerase ii from schizosaccharomyces pombe
2	c5x51X_	 Alignment		66.0	35	PDB header: transferase Chain: X: PDB Molecule: rna polymerase subunit, found in rna polymerase complexes PDBTitle: rna polymerase ii from komagataella pastoris (type-3 crystal)
3	c5flmL_	 Alignment		65.8	29	PDB header: transcription Chain: L: PDB Molecule: dna-directed rna polymerases i, ii, and iii subunit rpabc4; PDBTitle: structure of transcribing mammalian rna polymerase ii
4	c2ja6L_	 Alignment		59.9	24	PDB header: transferase Chain: L: PDB Molecule: dna-directed rna polymerases i, ii, and iii 7.7 kda PDBTitle: cpd lesion containing rna polymerase ii elongation complex b
5	c2l6lA_	 Alignment		34.0	15	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily c member 24; PDBTitle: solution structure of human j-protein co-chaperone, dph4
6	d1f2ka_	 Alignment		25.3	25	Fold: Profilin-like Superfamily: Profilin (actin-binding protein) Family: Profilin (actin-binding protein)
7	d1ppja2	 Alignment		24.2	23	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: MPP-like
8	c3davA_	 Alignment		23.7	15	PDB header: protein binding Chain: A: PDB Molecule: profilin; PDBTitle: schizosaccharomyces pombe profilin crystallized from sodium formate
9	c3nojA_	 Alignment		23.7	24	PDB header: lyase Chain: A: PDB Molecule: 4-carboxy-4-hydroxy-2-oxoadipate aldolase/oxaloacetate PDBTitle: the structure of hmg/cha aldolase from the protocatechuate degradation2 pathway of pseudomonas putida
10	c5wbuQ_	 Alignment		20.8	62	PDB header: transferase Chain: Q: PDB Molecule: proline-rich akt1 substrate 1; PDBTitle: crystal structure of mtor(deltan)-mlst8-pras40(alpha-helix & beta-2 strand) complex
11	c5wbuR_	 Alignment		20.8	62	PDB header: transferase Chain: R: PDB Molecule: proline-rich akt1 substrate 1; PDBTitle: crystal structure of mtor(deltan)-mlst8-pras40(alpha-helix & beta-2 strand) complex

12	d2csha2	Alignment		20.7	20	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
13	c3w0fA	Alignment		19.3	31	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease 8-like 3; PDBTitle: crystal structure of mouse endonuclease viii-like 3 (mneil3)
14	d1ypra	Alignment		17.9	13	Fold: Profilin-like Superfamily: Profilin (actin-binding protein) Family: Profilin (actin-binding protein)
15	c5vhvB	Alignment		17.8	23	PDB header: hydrolase/dna Chain: B: PDB Molecule: alkylpurine dna glycosylase alkC; PDBTitle: pseudomonas fluorescens alkylpurine dna glycosylase alkC bound to dna2 containing an oxocarbenium-intermediate analog
16	c2kvfA	Alignment		17.4	25	PDB header: transcription Chain: A: PDB Molecule: zinc finger and btb domain-containing protein 32; PDBTitle: structure of the three-cys2his2 domain of mouse testis zinc2 finger protein
17	d1g5ua	Alignment		17.3	23	Fold: Profilin-like Superfamily: Profilin (actin-binding protein) Family: Profilin (actin-binding protein)
18	c2yewG	Alignment		16.5	33	PDB header: virus Chain: G: PDB Molecule: capsid protein; PDBTitle: modeling barmah forest virus structural proteins
19	c2kj8A	Alignment		15.0	16	PDB header: dna binding protein Chain: A: PDB Molecule: putative prophage cps-53 integrase; PDBTitle: nmr structure of fragment 87-196 from the putative phage2 integrase ints of e. coli: northeast structural genomics3 consortium target er652a, psi-2
20	d1wyka	Alignment		13.8	33	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
21	c2l09A	Alignment	not modelled	13.6	28	PDB header: oxidoreductase Chain: A: PDB Molecule: asr4154 protein; PDBTitle: solution nmr structure of protein asr4154 from nostoc sp. pcc71202 northeast structural genomics consortium target id nsr143
22	d1acfa	Alignment	not modelled	13.6	21	Fold: Profilin-like Superfamily: Profilin (actin-binding protein) Family: Profilin (actin-binding protein)
23	c1kxfA	Alignment	not modelled	13.2	33	PDB header: viral protein Chain: A: PDB Molecule: sindbis virus capsid protein; PDBTitle: sindbis virus capsid, (wild-type) residues 1-264, tetragonal crystal2 form (form ii)
24	d1lep5a	Alignment	not modelled	13.1	33	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
25	d1vcpa	Alignment	not modelled	12.9	33	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
26	d1hxra	Alignment	not modelled	12.7	36	Fold: Mss4-like Superfamily: Mss4-like Family: RabGEF Mss4
27	c3zeyV	Alignment	not modelled	12.5	31	PDB header: ribosome Chain: V: PDB Molecule: ribosomal protein s26, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
28	d3bkjh1	Alignment	not modelled	12.5	29	Fold: Immunoglobulin-like beta-sandwich Superfamily: immunoglobulin Family: C1 set domains (antibody constant domain-like)
						Fold: Profilin-like

29	d1d1ja_	Alignment	not modelled	12.3	13	Superfamily: Profilin (actin-binding protein) Family: Profilin (actin-binding protein)
30	d2fu5a1	Alignment	not modelled	12.3	36	Fold: Mss4-like Superfamily: Mss4-like Family: RabGEF Mss4
31	d1vq0a2	Alignment	not modelled	12.0	17	Fold: HSP33 redox switch-like Superfamily: HSP33 redox switch-like Family: HSP33 redox switch-like
32	d1cqaa_	Alignment	not modelled	11.9	21	Fold: Profilin-like Superfamily: Profilin (actin-binding protein) Family: Profilin (actin-binding protein)
33	d1vzya2	Alignment	not modelled	11.3	17	Fold: HSP33 redox switch-like Superfamily: HSP33 redox switch-like Family: HSP33 redox switch-like
34	c6mx7C_	Alignment	not modelled	11.2	33	PDB header: virus Chain: C: PDB Molecule: capsid; PDBTitle: cryoem structure of chimeric eastern equine encephalitis virus:2 genome-binding capsid n-terminal domain
35	c2kaoA_	Alignment	not modelled	11.1	21	PDB header: oxidoreductase Chain: A: PDB Molecule: methionine-r-sulfoxide reductase b1; PDBTitle: structure of reduced mouse methionine sulfoxide reductase b12 (sec95cys mutant)
36	d2gmga1	Alignment	not modelled	10.7	40	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PF0610-like
37	c2i5oA_	Alignment	not modelled	10.2	42	PDB header: transferase Chain: A: PDB Molecule: dna polymerase eta; PDBTitle: solution structure of the ubiquitin-binding zinc finger2 (ubz) domain of the human dna y-polymerase eta
38	c5xyia_	Alignment	not modelled	9.7	25	PDB header: ribosome Chain: A: PDB Molecule: 40s ribosomal protein sa; PDBTitle: small subunit of trichomonas vaginalis ribosome
39	c3hcb_	Alignment	not modelled	9.6	25	PDB header: oxidoreductase Chain: B: PDB Molecule: peptide methionine sulfoxide reductase; PDBTitle: structure of msrb from xanthomonas campestris (oxidized2 form)
40	c1vq0A_	Alignment	not modelled	9.0	17	PDB header: chaperone Chain: A: PDB Molecule: 33 kda chaperonin; PDBTitle: crystal structure of 33 kda chaperonin (heat shock protein 33 homolog)2 (hsp33) (tm1394) from thermotoga maritima at 2.20 a resolution
41	d1nvpd1	Alignment	not modelled	8.9	13	Fold: Transcription factor IIA (TFIIA), alpha-helical domain Superfamily: Transcription factor IIA (TFIIA), alpha-helical domain Family: Transcription factor IIA (TFIIA), alpha-helical domain
42	c4uj3B_	Alignment	not modelled	8.6	18	PDB header: transport protein Chain: B: PDB Molecule: rab-3a-interacting protein; PDBTitle: crystal structure of human rab11-rabin8-fip3
43	d1xjha_	Alignment	not modelled	8.5	22	Fold: HSP33 redox switch-like Superfamily: HSP33 redox switch-like Family: HSP33 redox switch-like
44	d1twfj_	Alignment	not modelled	8.0	38	Fold: DNA/RNA-binding 3-helical bundle Superfamily: RNA polymerase subunit RPB10 Family: RNA polymerase subunit RPB10
45	d1nh2d1	Alignment	not modelled	7.9	25	Fold: Transcription factor IIA (TFIIA), alpha-helical domain Superfamily: Transcription factor IIA (TFIIA), alpha-helical domain Family: Transcription factor IIA (TFIIA), alpha-helical domain
46	c2eluA_	Alignment	not modelled	7.9	50	PDB header: transcription Chain: A: PDB Molecule: zinc finger protein 406; PDBTitle: solution structure of the 5th c2h2 zinc finger of human2 zinc finger protein 406
47	d1ef4a_	Alignment	not modelled	7.9	38	Fold: DNA/RNA-binding 3-helical bundle Superfamily: RNA polymerase subunit RPB10 Family: RNA polymerase subunit RPB10
48	c3j38a_	Alignment	not modelled	7.8	31	PDB header: ribosome Chain: A: PDB Molecule: 40s ribosomal protein sa; PDBTitle: structure of the d. melanogaster 40s ribosomal proteins
49	d2cy3a_	Alignment	not modelled	7.7	50	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Cytochrome c3-like
50	d2hfqa1	Alignment	not modelled	7.7	71	Fold: NE1680-like Superfamily: NE1680-like Family: NE1680-like
51	c2hfqa_	Alignment	not modelled	7.7	71	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: nmr structure of protein ne1680 from nitrosomonas europaea:2 northeast structural genomics consortium target net5
52	d1xm0a1	Alignment	not modelled	7.4	25	Fold: Mss4-like Superfamily: Mss4-like Family: SelR domain
53	c3u5ga_	Alignment	not modelled	7.3	25	PDB header: ribosome Chain: A: PDB Molecule: 40s ribosomal protein s0-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome b
54	c5xxua_	Alignment	not modelled	7.2	19	PDB header: ribosome Chain: A: PDB Molecule: ribosomal protein us2; PDBTitle: small subunit of toxoplasma gondii ribosome
55	c2xzn5_	Alignment	not modelled	7.2	25	PDB header: ribosome Chain: 5: PDB Molecule: ribosomal protein s26e containing protein; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. thisfile3 contains the 40s subunit

						and initiation factor for4 molecule 2 Fold: Dodecin subunit-like Superfamily: Amyloid beta a4 protein copper binding domain (domain 2) Family: Amyloid beta a4 protein copper binding domain (domain 2)
56	d2fklA1	Alignment	not modelled	7.0	35	PDB header: electron transport Chain: A: PDB Molecule: cytochrome c7; PDBTitle: ppce, a cytochrome c7 from geobacter sulfurreducens
57	c3h34A	Alignment	not modelled	7.0	44	PDB header: transcription Chain: V: PDB Molecule: dna-directed rna polymerase subunit n; PDBTitle: crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis
58	c4qiWV	Alignment	not modelled	6.9	31	Fold: Zinc-binding domain of translation initiation factor 2 beta Superfamily: Zinc-binding domain of translation initiation factor 2 beta Family: Zinc-binding domain of translation initiation factor 2 beta
59	d1k81a	Alignment	not modelled	6.7	11	PDB header: dna binding protein Chain: A: PDB Molecule: zinc finger and btb domain-containing protein 17; PDBTitle: solution structure of miz-1 zinc finger 2
60	c2n25A	Alignment	not modelled	6.5	57	PDB header: transcription Chain: A: PDB Molecule: zinc finger and btb domain-containing protein 32; PDBTitle: structure of the three-cys2his2 domain of mouse testis zinc2 finger protein
61	c2kvhA	Alignment	not modelled	6.5	30	Fold: AN1-like Zinc finger Superfamily: AN1-like Zinc finger Family: AN1-like Zinc finger
62	d1wfhA	Alignment	not modelled	6.5	50	PDB header: dna binding protein, chaperone Chain: C: PDB Molecule: protein psib; PDBTitle: x-ray crystal structure of the bacterial conjugation factor psib, a2 negative regulator of reca
63	c3nctC	Alignment	not modelled	6.4	50	PDB header: translation, transferase Chain: N: PDB Molecule: dna-directed rna polymerase subunit n; PDBTitle: archaeal rna polymerase from sulfolobus solfataricus
64	c2pmzN	Alignment	not modelled	6.4	40	PDB header: apoptosis, signaling protein Chain: A: PDB Molecule: calcyclin-binding protein; PDBTitle: solution structure of the core domain of calcyclin binding2 protein; siah-interacting protein (sip)
65	c1x5mA	Alignment	not modelled	6.3	20	PDB header: transcription Chain: A: PDB Molecule: polymerase basic protein 2; PDBTitle: the 627-domain from influenza a virus polymerase pb22 subunit with glu-627
66	c2vy8A	Alignment	not modelled	6.2	18	PDB header: transferase Chain: A: PDB Molecule: transcriptional regulatory protein; PDBTitle: crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate
67	c3tsuA	Alignment	not modelled	6.2	33	PDB header: viral peptide Chain: A: PDB Molecule: nef1-25; PDBTitle: nmr solution structure of nef1-25, 20 structures
68	c1zecA	Alignment	not modelled	6.1	71	Fold: Uteroglobin-like Superfamily: Uteroglobin-like Family: Uteroglobin-like
69	d2ejna1	Alignment	not modelled	6.1	22	PDB header: motor protein Chain: A: PDB Molecule: minor pilin comp; PDBTitle: global fold of the type iv pilin comp from neisseria meningitidis
70	c2m3kA	Alignment	not modelled	6.0	17	PDB header: immune system Chain: A: PDB Molecule: acan1; PDBTitle: nmr solution structure of acan1 from the ancylostoma caninum hookworm
71	c6driA	Alignment	not modelled	6.0	71	PDB header: oxidoreductase Chain: M: PDB Molecule: hydrogenase-2 large chain; PDBTitle: e. coli hydrogenase-2 (as isolated form).
72	c6ehqM	Alignment	not modelled	5.9	23	PDB header: hydrolase Chain: A: PDB Molecule: lysosomal alpha-mannosidase; PDBTitle: the structure of the bovine lysosomal a-mannosidase suggests a novel2 mechanism for low ph activation
73	c1o7dA	Alignment	not modelled	5.8	19	PDB header: transcription Chain: P: PDB Molecule: dna-directed rna polymerase subunit p; PDBTitle: crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis
74	c4qiWp	Alignment	not modelled	5.8	27	PDB header: electron transport Chain: A: PDB Molecule: cytochrome c; PDBTitle: crystal structure of the cytochrome c552 from moderate2 thermophilic bacterium, hydrogenophilus thermoluteolus
75	c2d0sA	Alignment	not modelled	5.7	27	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Cytochrome c3-like
76	d3caoA	Alignment	not modelled	5.6	60	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
77	d1ycca	Alignment	not modelled	5.5	30	Fold: Another 3-helical bundle Superfamily: IscX-like Family: IscX-like
78	d1uj8a1	Alignment	not modelled	5.5	40	PDB header: signaling protein Chain: A: PDB Molecule: cereblon isoform 4; PDBTitle: cereblon isoform 4 from magnetospirillum gryphiswaldense in2 complex with lenalidomide
79	c4v30A	Alignment	not modelled	5.4	27	PDB header: immune system Chain: A: PDB Molecule: ack1; PDBTitle: solution structure of shk-like immunomodulatory peptide from2 ancylostoma caninum (hookworm)
80	c2md0A	Alignment	not modelled	5.4	71	PDB header: transcription Chain: A: PDB Molecule: zinc finger and btb domain-containing protein 17; PDBTitle: solution structure of miz-1 zinc finger 5
81	c2m0dA	Alignment	not modelled	5.3	30	

82	c2jtxA_	Alignment	not modelled	5.3	29	PDB header: transcription Chain: A: PDB Molecule: transcription initiation factor iie subunit PDBTitle: nmr structure of the tfiie-alpha carboxyl terminus
83	c2dcuB_	Alignment	not modelled	5.3	11	PDB header: translation Chain: B: PDB Molecule: translation initiation factor 2 beta subunit; PDBTitle: crystal structure of translation initiation factor aif2betagamma2 heterodimer with gdp
84	c4cv5A_	Alignment	not modelled	5.3	29	PDB header: cell cycle Chain: A: PDB Molecule: general negative regulator of transcription subunit 1; PDBTitle: yeast not1 cn9bd-caf40 complex
85	c2k8dA_	Alignment	not modelled	5.3	33	PDB header: oxidoreductase Chain: A: PDB Molecule: peptide methionine sulfoxide reductase msrb; PDBTitle: solution structure of a zinc-binding methionine sulfoxide reductase
86	c2w9kA_	Alignment	not modelled	5.3	15	PDB header: electron transport Chain: A: PDB Molecule: cytochrome c; PDBTitle: crithidia fasciculata cytochrome c
87	d1rk8c_	Alignment	not modelled	5.2	43	Fold: WW domain-like Superfamily: Pym (Within the bgcn gene intron protein, WIBG), N-terminal domain Family: Pym (Within the bgcn gene intron protein, WIBG), N-terminal domain
88	c1rk8C_	Alignment	not modelled	5.2	43	PDB header: translation Chain: C: PDB Molecule: within the bgcn gene intron protein; PDBTitle: structure of the cytosolic protein pym bound to the mago-2 y14 core of the exon junction complex
89	c3h4nB_	Alignment	not modelled	5.2	50	PDB header: electron transport Chain: B: PDB Molecule: cytochrome c7; PDBTitle: ppdc, a cytochrome c7 from geobacter sulfurreducens
90	c2oxoA_	Alignment	not modelled	5.1	19	PDB header: dna binding protein Chain: A: PDB Molecule: integrase; PDBTitle: crystallization and structure determination of the core-2 binding domain of bacteriophage lambda integrase