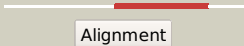

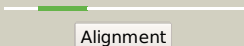

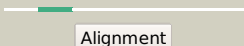

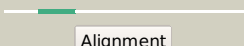

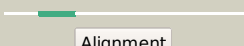

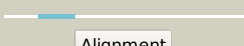

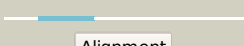






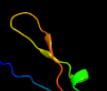

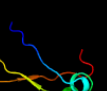











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0966c_(-)_1077237_1077839
Date	Wed Jul 31 22:05:03 BST 2019
Unique Job ID	2072465cbee4a10f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4qrkA_	 Alignment		98.6	21	PDB header: cell adhesion Chain: A; PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative cell adhesion protein (clospo_03726)2 from clostridium sporogenes atcc 15579 at 1.95 a resolution
2	d2pp4a1	 Alignment		55.8	9	Fold: TAFH domain-like Superfamily: TAFH domain-like Family: TAFH domain-like
3	d2p12a1	 Alignment		41.2	25	Fold: FomD barrel-like Superfamily: FomD-like Family: FomD-like
4	d2caza1	 Alignment		40.4	15	Fold: Long alpha-hairpin Superfamily: Endosomal sorting complex assembly domain Family: VPS23 C-terminal domain
5	c2cazD_	 Alignment		40.0	15	PDB header: protein transport Chain: D; PDB Molecule: suppressor protein stp22 of temperature-sensitive alpha- PDBTitle: escrt-i core
6	d2f6ma1	 Alignment		39.8	15	Fold: Long alpha-hairpin Superfamily: Endosomal sorting complex assembly domain Family: VPS23 C-terminal domain
7	d2p6va1	 Alignment		35.4	21	Fold: TAFH domain-like Superfamily: TAFH domain-like Family: TAFH domain-like
8	c1ponB_	 Alignment		27.0	14	PDB header: calcium-binding protein Chain: B; PDB Molecule: troponin c; PDBTitle: site iii-site iv troponin c heterodimer, nmr
9	c3i38K_	 Alignment		26.2	14	PDB header: chaperone Chain: K; PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
10	c3i38B_	 Alignment		24.8	14	PDB header: chaperone Chain: B; PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
11	c3i38D_	 Alignment		24.7	14	PDB header: chaperone Chain: D; PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578

12	c3i38A_	Alignment		24.7	14	PDB header: chaperone Chain: A; PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
13	c3i38G_	Alignment		24.7	14	PDB header: chaperone Chain: G; PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
14	c2p22A_	Alignment		22.8	19	PDB header: transport protein Chain: A; PDB Molecule: suppressor protein stp22 of temperature-sensitive alpha-escrt-i heterotetramer core PDBTitle: structure of the yeast escrt-i heterotetramer core
15	c3i38E_	Alignment		22.3	14	PDB header: chaperone Chain: E; PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
16	c3i38C_	Alignment		22.3	14	PDB header: chaperone Chain: C; PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
17	c4egeA_	Alignment		21.5	50	PDB header: hydrolase Chain: A; PDB Molecule: dipeptidase pepe; PDBTitle: crystal structure of dipeptidase pepe from mycobacterium ulcerans
18	c3e56A_	Alignment		21.4	44	PDB header: unknown function Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: the 2.0 angstrom resolution crystal structure of npr1517, a putative2 heterocyst differentiation inhibitor from nostoc punctiforme
19	d2cazb1	Alignment		20.7	11	Fold: Long alpha-hairpin Superfamily: Endosomal sorting complex assembly domain Family: VPS28 N-terminal domain
20	c2cazb_	Alignment		20.7	11	PDB header: protein transport Chain: B; PDB Molecule: vacuolar protein sorting-associated protein vps28; PDBTitle: escrt-i core
21	c3i38L_	Alignment	not modelled	20.2	14	PDB header: chaperone Chain: L; PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
22	d1kxpd3	Alignment	not modelled	20.1	26	Fold: Serum albumin-like Superfamily: Serum albumin-like Family: Serum albumin-like
23	c3i38F_	Alignment	not modelled	19.4	14	PDB header: chaperone Chain: F; PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
24	d2f6mb1	Alignment	not modelled	19.1	10	Fold: Long alpha-hairpin Superfamily: Endosomal sorting complex assembly domain Family: VPS28 N-terminal domain
25	c3znul_	Alignment	not modelled	18.4	14	PDB header: lyase Chain: I; PDB Molecule: 5-chloromuconolactone dehalogenase; PDBTitle: crystal structure of clcf in crystal form 2
26	c5j73A_	Alignment	not modelled	17.8	23	PDB header: de novo protein Chain: A; PDB Molecule: protein design 214hc2_9; PDBTitle: de novo design of protein homo-oligomers with modular hydrogen bond2 network-mediated specificity
27	c4nxiB_	Alignment	not modelled	16.6	32	PDB header: oxidoreductase Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: rv2466c mediates the activation of tp053 to kill replicating and non-2 replicating mycobacterium tuberculosis
28	c6cumA_	Alignment	not modelled	16.4	23	PDB header: transferase Chain: A; PDB Molecule: lao/ao transport system atpase; PDBTitle: crystal structure of a c-terminal proteolytic fragment of a protein2 annotated as an lao/ao transport system atpase but likely meab and3 mmaa-like gtpase from mycobacterium smegmatis

29	c3i38H_	Alignment	not modelled	16.3	14	PDB header: chaperone Chain: H: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
30	c6e5fA_	Alignment	not modelled	15.4	16	PDB header: lipid binding protein Chain: A: PDB Molecule: lipid binding protein lpqj; PDBTitle: crystal structure of lpqj involved in cell envelope biogenesis of2 mycobacterium tuberculosis
31	c2kq1A_	Alignment	not modelled	14.8	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: bh0266 protein; PDBTitle: solution structure of protein bh0266 from bacillus2 halodurans. northeast structural genomics consortium target3 bhr97a
32	c5xtaC_	Alignment	not modelled	14.2	23	PDB header: oxidoreductase Chain: C: PDB Molecule: virk protein; PDBTitle: crystal structure of lpg1832, a virk family protein from legionella2 pneumophila
33	c3i38J_	Alignment	not modelled	14.2	14	PDB header: chaperone Chain: J: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
34	d2bh1x1	Alignment	not modelled	14.2	25	Fold: Alpha-lytic protease prodomain-like Superfamily: EspE N-terminal domain-like Family: GSP11 protein E N-terminal domain-like
35	c2bh1Y_	Alignment	not modelled	14.2	25	PDB header: transport protein Chain: Y: PDB Molecule: general secretion pathway protein e, PDBTitle: x-ray structure of the general secretion pathway complex of2 the n-terminal domain of epse and the cytosolic domain of3 epsl of vibrio cholerae
36	c3li6D_	Alignment	not modelled	13.9	13	PDB header: metal binding protein Chain: D: PDB Molecule: calcium-binding protein; PDBTitle: crystal structure and trimer-monomer transition of n-terminal domain2 of ehcap1 from entamoeba histolytica
37	d1ctda_	Alignment	not modelled	13.9	13	Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like
38	d3orca_	Alignment	not modelled	13.4	26	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
39	c6mi5X_	Alignment	not modelled	13.2	15	PDB header: metal binding protein Chain: X: PDB Molecule: lanmodulin; PDBTitle: nmr solution structure of lanmodulin (lanm) complexed with2 yttrium(iii) ions
40	c3sqlB_	Alignment	not modelled	13.0	17	PDB header: hydrolase Chain: B: PDB Molecule: glycosyl hydrolase family 3; PDBTitle: crystal structure of glycoside hydrolase from synechococcus
41	d1ug3a1	Alignment	not modelled	12.7	24	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: MIF4G domain-like
42	c2f7nA_	Alignment	not modelled	11.9	8	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding stress response protein, dps family; PDBTitle: structure of d. radiodurans dps-1
43	d1mlia_	Alignment	not modelled	11.9	14	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Muconalactone isomerase, MLI
44	c5eu0B_	Alignment	not modelled	11.9	15	PDB header: toxin Chain: B: PDB Molecule: antitoxin 1; PDBTitle: fic domain of bep1 from bartonella rochalimae in complex with b1aa
45	c3vdoB_	Alignment	not modelled	10.8	20	PDB header: dna binding protein/protein binding Chain: B: PDB Molecule: anti-sigma-k factor rskA; PDBTitle: structure of extra-cytoplasmic function(ecf) sigma factor sigk in2 complex with its negative regulator rskA from mycobacterium3 tuberculosis
46	c4yyfC_	Alignment	not modelled	10.7	22	PDB header: hydrolase Chain: C: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: the crystal structure of a glycosyl hydrolase of gh3 family member2 from [mycobacterium smegmatis str. mc2 155
47	c2vrgA_	Alignment	not modelled	10.6	10	PDB header: transport Chain: A: PDB Molecule: multiple coagulation factor deficiency protein 2; PDBTitle: structure of human mcf2
48	c3lz8A_	Alignment	not modelled	10.6	14	PDB header: chaperone Chain: A: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone dnaj from klebsiella pneumoniae2 subsp. pneumoniae mgh 78578 at 2.9 a resolution.
49	c2y6tE_	Alignment	not modelled	10.5	20	PDB header: hydrolase/inhibitor Chain: E: PDB Molecule: ecotin; PDBTitle: molecular recognition of chymotrypsin by the serine protease inhibitor2 ecotin from yersinia pestis
50	c6b2zd_	Alignment	not modelled	10.5	44	PDB header: membrane protein Chain: D: PDB Molecule: atp synthase subunit c, mitochondrial; PDBTitle: cryo-em structure of the dimeric fo region of yeast mitochondrial atp2 synthase
51	c3lsgD_	Alignment	not modelled	10.4	11	PDB header: transcription regulator Chain: D: PDB Molecule: two-component response regulator yesn; PDBTitle: the crystal structure of the c-terminal domain of the two-2 component response regulator yesn from fusobacterium3 nucleatum subsp. nucleatum atcc 25586
52	d1xxfc_	Alignment	not modelled	10.2	20	Fold: Ecotin, trypsin inhibitor Superfamily: Ecotin, trypsin inhibitor Family: Ecotin, trypsin inhibitor
53	c5i2oA_	Alignment	not modelled	10.0	14	PDB header: metal binding protein Chain: A: PDB Molecule: ef-hand domain-containing protein d2; PDBTitle: structure of ef-hand containing protein
						PDB header: cell cycle

54	c4n7vC_	Alignment	not modelled	9.9	55	Chain: C: PDB Molecule: centrosomal protein of 152 kda; PDBTitle: crystal structure of human plk4 cryptic polo box (cpb) in complex with2 a cep152 n-terminal fragment PDB header: transport protein
55	c6qfjA_	Alignment	not modelled	9.8	25	Chain: A: PDB Molecule: magnetosome membrane protein mamb, putative co/zinc/cd cation PDBTitle: mamb ctd magnetosome protein [desulfamplus magnetovallimortis bw-1]
56	d1slua_	Alignment	not modelled	9.8	20	Fold: Ecotin, trypsin inhibitor Superfamily: Ecotin, trypsin inhibitor Family: Ecotin, trypsin inhibitor
57	d1jmx1	Alignment	not modelled	9.8	33	Fold: Cytochrome c Superfamily: Cytochrome c Family: Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
58	d2csba1	Alignment	not modelled	9.7	21	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Topoisomerase V repeat domain
59	c3l6aA_	Alignment	not modelled	9.7	18	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 4 gamma 2; PDBTitle: crystal structure of the c-terminal region of human p97
60	c4v0xB_	Alignment	not modelled	9.7	36	PDB header: hydrolase/hydrolase regulator Chain: B: PDB Molecule: protein phosphatase 1 regulatory subunit 15b; PDBTitle: the crystal structure of mouse pp1g in complex with truncated human2 ppp1r15b (631-684)
61	c3aqjQ_	Alignment	not modelled	9.4	17	PDB header: metal binding protein Chain: Q: PDB Molecule: baseplate assembly protein v; PDBTitle: crystal structure of a c-terminal domain of the bacteriophage p2 tail2 spike protein, gpv
62	c6odmK_	Alignment	not modelled	9.1	30	PDB header: viral protein Chain: K: PDB Molecule: capsid vertex component 2; PDBTitle: herpes simplex virus type 1 (hsv-1) portal vertex-adjacent2 capsid/catc, asymmetric unit
63	c5hqhA_	Alignment	not modelled	9.1	23	PDB header: unknown function Chain: A: PDB Molecule: lmo2119 protein; PDBTitle: 1.32 angstrom crystal structure of ybbr like domain of lmo2119 protein2 from listeria monocytogenes.
64	d1tjoa_	Alignment	not modelled	9.1	11	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ferritin
65	c5bzaA_	Alignment	not modelled	9.1	13	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: crystal structure of cbsa from thermotoga neapolitana
66	d1s6ja_	Alignment	not modelled	8.8	19	Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like
67	d1c3ga2	Alignment	not modelled	8.6	14	Fold: HSP40/Dnaj peptide-binding domain Superfamily: HSP40/Dnaj peptide-binding domain Family: HSP40/Dnaj peptide-binding domain
68	c3ndqA_	Alignment	not modelled	8.5	22	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor a protein 1; PDBTitle: structure of human tfiis domain ii
69	c3iq1A_	Alignment	not modelled	8.5	13	PDB header: metal transport Chain: A: PDB Molecule: dps family protein; PDBTitle: crystal structure of dps protein from vibrio cholerae o1, a member of2 a broad superfamily of ferritin-like diiron-carboxylate proteins
70	c2mxtA_	Alignment	not modelled	8.5	21	PDB header: splicing Chain: A: PDB Molecule: heterogeneous nuclear ribonucleoprotein q; PDBTitle: nmr structure of the acidic domain of syncrip (hnrnpq)
71	c5cuvB_	Alignment	not modelled	8.5	16	PDB header: metal binding protein Chain: B: PDB Molecule: acidocalcisomal pyrophosphatase; PDBTitle: crystal structure of trypanosoma cruzi vacuolar soluble2 pyrophosphatases in apo form
72	c3nctC_	Alignment	not modelled	8.4	22	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
73	c3i38l_	Alignment	not modelled	8.4	14	PDB header: chaperone Chain: I: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
74	d1pvaa_	Alignment	not modelled	8.3	18	Fold: EF Hand-like Superfamily: EF-hand Family: Parvalbumin
75	c3wo8B_	Alignment	not modelled	8.2	13	PDB header: hydrolase Chain: B: PDB Molecule: beta-n-acetylglucosaminidase; PDBTitle: crystal structure of the beta-n-acetylglucosaminidase from thermotoga2 maritima
76	d1ezsa_	Alignment	not modelled	8.2	20	Fold: Ecotin, trypsin inhibitor Superfamily: Ecotin, trypsin inhibitor Family: Ecotin, trypsin inhibitor
77	d1f54a_	Alignment	not modelled	8.2	9	Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like
78	d1ou9a_	Alignment	not modelled	8.1	26	Fold: SspB-like Superfamily: SspB-like Family: Stringent starvation protein B, SspB
79	d2owpa1	Alignment	not modelled	8.1	10	Fold: Cystatin-like Superfamily: NTF2-like Family: BxeB1374-like
						PDB header: hydrolase

80	c4il1A_	Alignment	not modelled	8.0	25	Chain: A: PDB Molecule: calmodulin, calcineurin subunit b type 1, serine/threonine- PDBTitle: crystal structure of the rat calcineurin
81	c1t71A_	Alignment	not modelled	7.9	10	PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydropteroyltriglutamate--homocysteine PDBTitle: crystal structure of cobalamin-independent methionine synthase from t.2 maritima
82	d1br1b_	Alignment	not modelled	7.9	12	Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like
83	c2bpbB_	Alignment	not modelled	7.9	29	PDB header: oxidoreductase Chain: B: PDB Molecule: sulfite[:cytochrome c oxidoreductase subunit b; PDBTitle: sulfite dehydrogenase from starkeya novella
84	c3l7sA_	Alignment	not modelled	7.8	8	PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydropteroyltriglutamate--homocysteine PDBTitle: crystal structure of mete coordinated with zinc from streptococcus2 mutans
85	c3fpnA_	Alignment	not modelled	7.7	16	PDB header: dna binding protein Chain: A: PDB Molecule: geobacillus stearothermophilus uvra interaction domain; PDBTitle: crystal structure of uvra-uvrb interaction domains
86	d5pala_	Alignment	not modelled	7.7	18	Fold: EF Hand-like Superfamily: EF-hand Family: Parvalbumin
87	c3ppgA_	Alignment	not modelled	7.7	10	PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydropteroyltriglutamate--homocysteine PDBTitle: crystal structure of the candida albicans methionine synthase by2 surface entropy reduction, alanine variant with zinc
88	c3u1dA_	Alignment	not modelled	7.6	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the structure of a protein with a gntr superfamily winged-helix-turn-2 helix domain from halomicrobium mukohataei.
89	c5hjhB_	Alignment	not modelled	7.5	0	PDB header: metal binding protein Chain: B: PDB Molecule: ferritin, dps family protein; PDBTitle: dps4 from nostoc punctiforme in complex with fe ions
90	c1wr2A_	Alignment	not modelled	7.5	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ph1789; PDBTitle: crystal structure of ph1788 from pyrococcus horikoshii ot3
91	d1ulza1	Alignment	not modelled	7.3	11	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
92	c4o14A_	Alignment	not modelled	7.3	12	PDB header: lipid binding protein Chain: A: PDB Molecule: proline-rich 28 kda antigen; PDBTitle: crystal structure of secreted proline rich antigen mtc28 (rv0040c)2 from mycobacterium tuberculosis
93	c3h96B_	Alignment	not modelled	7.3	32	PDB header: flavoprotein Chain: B: PDB Molecule: f420-h2 dependent reductase a; PDBTitle: msmeg_3358 f420 reductase
94	c4annA_	Alignment	not modelled	7.2	20	PDB header: membrane protein Chain: A: PDB Molecule: essb; PDBTitle: crystal structure staphylococcus aureus essb cytoplasmic fragment
95	c2k2aA_	Alignment	not modelled	7.2	15	PDB header: contractile protein Chain: A: PDB Molecule: troponin c; PDBTitle: solution structure of the apo c terminal domain of lethocerus troponin2 c isoform f1
96	c2iosA_	Alignment	not modelled	7.2	18	PDB header: antitumor protein Chain: A: PDB Molecule: programmed cell death 4, pdcd4; PDBTitle: crystal structure of the c-terminal ma3 domain of pdcd42 (mouse); form 3
97	c4wpxA_	Alignment	not modelled	7.2	14	PDB header: cell cycle Chain: A: PDB Molecule: cell division control protein 31-like protein; PDBTitle: chaetomium thermophilum trex2 cid domain complex
98	c4ednL_	Alignment	not modelled	7.0	60	PDB header: signaling protein/cell adhesion Chain: L: PDB Molecule: paxillin; PDBTitle: crystal structure of beta-parvin ch2 domain in complex with paxillin2 ld1 motif
99	c2ncpA_	Alignment	not modelled	7.0	26	PDB header: metal binding protein Chain: A: PDB Molecule: 25 kda calcium-binding protein; PDBTitle: nmr solution structure for the c-terminal domain of tetrahymena tcb22 in the presence of calcium