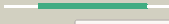

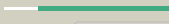
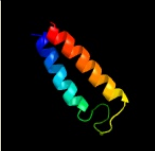

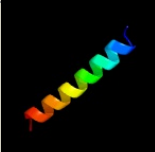

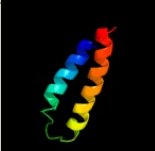


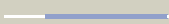
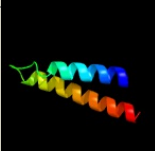

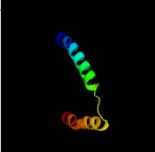

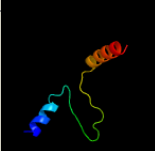



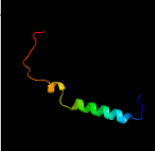

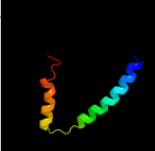


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0898c_(-)_1002444_1002707
Date	Fri Jul 26 01:50:49 BST 2019
Unique Job ID	35499dfdadf84089

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4pxjB_	 Alignment		42.9	21	PDB header: protein binding Chain: B: PDB Molecule: c-jun-amino-terminal kinase-interacting protein 3; PDBTitle: crystallographic structure of the lzii fragment (anti-parallel2 orientation) from jip3
2	d1kvka2	 Alignment		42.1	15	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Mevalonate kinase
3	c2v8sV_	 Alignment		38.3	12	PDB header: protein transport Chain: V: PDB Molecule: vesicle transport through interaction with PDBTitle: vti1b habc domain - epsinr enth domain complex
4	d1vcsa1	 Alignment		36.0	25	Fold: STAT-like Superfamily: t-snare proteins Family: t-snare proteins
5	d1k1fa_	 Alignment		29.2	25	Fold: Bcr-Abl oncoprotein oligomerization domain Superfamily: Bcr-Abl oncoprotein oligomerization domain Family: Bcr-Abl oncoprotein oligomerization domain
6	c3onjA_	 Alignment		26.7	25	PDB header: protein transport Chain: A: PDB Molecule: t-snare vti1; PDBTitle: crystal structure of yeast vti1p_habc domain
7	c3qzcA_	 Alignment		24.7	15	PDB header: signaling protein Chain: A: PDB Molecule: periplasmic protein cpxp; PDBTitle: structure of the periplasmic stress response protein cpxp
8	d1jkwa2	 Alignment		24.7	21	Fold: Cyclin-like Superfamily: Cyclin-like Family: Cyclin
9	c5e9fD_	 Alignment		24.2	18	PDB header: lyase Chain: D: PDB Molecule: isocitrate lyase; PDBTitle: structural insights of isocitrate lyases from magnaporthe oryzae
10	c4eo3A_	 Alignment		21.9	21	PDB header: oxidoreductase Chain: A: PDB Molecule: bacterioferritin comigratory protein/nadh dehydrogenase; PDBTitle: peroxiredoxin nitroreductase fusion enzyme
11	c3itfA_	 Alignment		21.7	15	PDB header: signaling protein Chain: A: PDB Molecule: periplasmic adaptor protein cpxp; PDBTitle: structural basis for the inhibitory function of the cpxp adaptor2 protein

12	c2mp6A_	Alignment		20.1	45	PDB header: signaling protein Chain: A: PDB Molecule: suppressor of cytokine signaling 5; PDBTitle: structure and function of the jak interaction region in the2 intrinsically disordered n-terminus of socs5
13	c5a16A_	Alignment		20.0	42	PDB header: structural protein Chain: A: PDB Molecule: anastral spindle 2; PDBTitle: central coiled-coil domain (cccd) of drosophila melanogaster ana2. a2 natural, parallel, tetrameric coiled-coil bundle.
14	d3fapb_	Alignment		17.5	38	Fold: Four-helical up-and-down bundle Superfamily: FKBP12-rapamycin-binding domain of FKBP-rapamycin-associated protein (FRAP) Family: FKBP12-rapamycin-binding domain of FKBP-rapamycin-associated protein (FRAP)
15	c2xqoA_	Alignment		17.1	24	PDB header: hydrolase Chain: A: PDB Molecule: cellulosome enzyme, dockerin type i; PDBTitle: ctcel124: a cellulase from clostridium thermocellum
16	c4h62V_	Alignment		16.8	50	PDB header: transcription Chain: V: PDB Molecule: mediator of rna polymerase ii transcription subunit 22; PDBTitle: structure of the saccharomyces cerevisiae mediator subcomplex2 med17c/med11c/med22c
17	c2q9rA_	Alignment		15.7	21	PDB header: unknown function Chain: A: PDB Molecule: protein of unknown function; PDBTitle: crystal structure of a duf416 family protein (sba1_3149) from2 shewanella baltica os155 at 1.91 a resolution
18	c6c0fw_	Alignment		15.2	39	PDB header: ribosome Chain: W: PDB Molecule: nucleolar gtp-binding protein 1; PDBTitle: yeast nucleolar pre-60s ribosomal subunit (state 2)
19	c4fg5B_	Alignment		14.6	27	PDB header: hydrolase Chain: B: PDB Molecule: e3 alpha-esterase-7 caboxylesterase; PDBTitle: crystal structure of the alpha-esterase-7 carboxylesterase, e3, from2 lucilia cuprina
20	c6e28D_	Alignment		13.3	29	PDB header: signaling protein Chain: D: PDB Molecule: caspase recruitment domain-containing protein 9; PDBTitle: the card9 card domain-swapped dimer
21	c5a2gB_	Alignment	not modelled	11.9	27	PDB header: hydrolase Chain: B: PDB Molecule: carboxylic ester hydrolase; PDBTitle: an esterase from anaerobic clostridium hathewayi can2 hydrolyze aliphatic aromatic polyesters
22	c4bxtH_	Alignment	not modelled	11.7	39	PDB header: viral protein Chain: H: PDB Molecule: phosphoprotein p; PDBTitle: crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain
23	c5oiyF_	Alignment	not modelled	11.6	39	PDB header: viral protein Chain: F: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 2.2 a
24	c5oixH_	Alignment	not modelled	11.3	39	PDB header: viral protein Chain: H: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 1.6 a
25	c5oixD_	Alignment	not modelled	11.3	39	PDB header: viral protein Chain: D: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 1.6 a
26	c4bxtA_	Alignment	not modelled	11.3	39	PDB header: viral protein Chain: A: PDB Molecule: phosphoprotein p; PDBTitle: crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain
27	c5oiyD_	Alignment	not modelled	11.3	39	PDB header: viral protein Chain: D: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 2.2 a
28	c4bxtC_	Alignment	not modelled	11.2	39	PDB header: viral protein Chain: C: PDB Molecule: phosphoprotein p; PDBTitle: crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain
						PDB header: structural genomics, unknown function

29	c2epiA	Alignment	not modelled	10.1	21	Chain: A: PDB Molecule: upf0045 protein mj1052; PDBTitle: crystal structure of hypothetical protein mj1052 from 2 methanocaldococcus jannaschii (form 2)
30	c3fjuB	Alignment	not modelled	9.2	100	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: carboxypeptidase a inhibitor; PDBTitle: ascaris suum carboxypeptidase inhibitor in complex with human 2 carboxypeptidase a1
31	c1tr8A	Alignment	not modelled	9.1	64	PDB header: chaperone Chain: A: PDB Molecule: conserved protein (mth177); PDBTitle: crystal structure of archaeal nascent polypeptide-associated complex 2 (aenac)
32	c5hytC	Alignment	not modelled	9.0	35	PDB header: immune system Chain: C: PDB Molecule: precursor to protein sir22; PDBTitle: structure of human c4b-binding protein alpha chain ccp domains 1 and 22 in complex with the hypervariable region of group a streptococcus m223 protein
33	c5hytE	Alignment	not modelled	9.0	35	PDB header: immune system Chain: E: PDB Molecule: precursor to protein sir22; PDBTitle: structure of human c4b-binding protein alpha chain ccp domains 1 and 22 in complex with the hypervariable region of group a streptococcus m223 protein
34	c4x3mB	Alignment	not modelled	8.8	29	PDB header: transferase Chain: B: PDB Molecule: rna 2'-o ribose methyltransferase; PDBTitle: crystal structure of ttha0275 from thermus thermophilus (hb8) in 2 complex with adenosine in space group p212121
35	c5hytA	Alignment	not modelled	8.7	35	PDB header: immune system Chain: A: PDB Molecule: precursor to protein sir22; PDBTitle: structure of human c4b-binding protein alpha chain ccp domains 1 and 22 in complex with the hypervariable region of group a streptococcus m223 protein
36	c5hytG	Alignment	not modelled	8.7	35	PDB header: immune system Chain: G: PDB Molecule: precursor to protein sir22; PDBTitle: structure of human c4b-binding protein alpha chain ccp domains 1 and 22 in complex with the hypervariable region of group a streptococcus m223 protein
37	c1dtcA	Alignment	not modelled	8.6	36	PDB header: toxin Chain: A: PDB Molecule: acetyl-delta-toxin; PDBTitle: delta-toxin and analogues as peptide models for protein ion2 channels
38	c2dtbA	Alignment	not modelled	8.6	36	PDB header: toxin Chain: A: PDB Molecule: delta-toxin; PDBTitle: delta-toxin and analogues as peptide models for protein ion2 channels
39	d1gz7a	Alignment	not modelled	8.6	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
40	d1thga	Alignment	not modelled	8.6	27	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
41	c2kamA	Alignment	not modelled	8.6	36	PDB header: toxin Chain: A: PDB Molecule: delta-hemolysin; PDBTitle: nmr structure of delta-toxin from staphylococcus aureus in 2 cd3oh
42	c4a56A	Alignment	not modelled	8.4	13	PDB header: protein transport Chain: A: PDB Molecule: pullulanase secretion protein puls; PDBTitle: crystal structure of the type 2 secretion system pilotin2 from klebsiella oxytoca
43	d1oqya1	Alignment	not modelled	8.4	36	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
44	c3t6gC	Alignment	not modelled	8.2	58	PDB header: signaling protein, cell adhesion Chain: C: PDB Molecule: sh2 domain-containing protein 3c; PDBTitle: structure of the complex between nsp3 (shep1) and p130cas
45	d1vk8a	Alignment	not modelled	8.0	21	Fold: Ferredoxin-like Superfamily: MTH1187/YkoF-like Family: MTH1187-like
46	c3jslA	Alignment	not modelled	8.0	9	PDB header: ligase Chain: A: PDB Molecule: dna ligase; PDBTitle: crystal structure of the adenylation domain of nad ⁺ -2 dependent dna ligase from staphylococcus aureus
47	c3utkA	Alignment	not modelled	7.6	26	PDB header: protein transport Chain: A: PDB Molecule: lipoprotein outs; PDBTitle: structure of the pilotin of the type ii secretion system
48	c5oiyC	Alignment	not modelled	7.4	39	PDB header: viral protein Chain: C: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 2.2 a
49	c5oiyG	Alignment	not modelled	7.4	39	PDB header: viral protein Chain: G: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 2.2 a
50	c4bxD	Alignment	not modelled	7.4	39	PDB header: viral protein Chain: D: PDB Molecule: phosphoprotein p; PDBTitle: crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain
51	c5oixA	Alignment	not modelled	7.4	39	PDB header: viral protein Chain: A: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 1.6 a
52	c5oixE	Alignment	not modelled	7.4	39	PDB header: viral protein Chain: E: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 1.6 a
53	c5oiyE	Alignment	not modelled	7.4	39	PDB header: viral protein Chain: E: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 2.2 a
54	c6akkA	Alignment	not modelled	7.4	40	PDB header: protein binding Chain: A: PDB Molecule: suppressor of ikbke 1; PDBTitle: crystal structure of the second coiled-coil domain of sike1

55	c5oixF_	Alignment	not modelled	7.3	39	PDB header: viral protein Chain: F: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 1.6 a
56	c5oiyH_	Alignment	not modelled	7.2	39	PDB header: viral protein Chain: H: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 2.2 a
57	c4bxtE_	Alignment	not modelled	7.2	39	PDB header: viral protein Chain: E: PDB Molecule: phosphoprotein p; PDBTitle: crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain
58	c4bxtF_	Alignment	not modelled	7.2	39	PDB header: viral protein Chain: F: PDB Molecule: phosphoprotein p; PDBTitle: crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain
59	c5oixB_	Alignment	not modelled	7.2	39	PDB header: viral protein Chain: B: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 1.6 a
60	c4bxtB_	Alignment	not modelled	7.2	39	PDB header: viral protein Chain: B: PDB Molecule: phosphoprotein p; PDBTitle: crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain
61	c4bxtG_	Alignment	not modelled	7.2	39	PDB header: viral protein Chain: G: PDB Molecule: phosphoprotein p; PDBTitle: crystal structure of the human metapneumovirus2 phosphoprotein tetramerization domain
62	c5oiyB_	Alignment	not modelled	7.2	39	PDB header: viral protein Chain: B: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 2.2 a
63	c5oiyA_	Alignment	not modelled	7.2	39	PDB header: viral protein Chain: A: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 2.2 a
64	d1dqua_	Alignment	not modelled	7.2	12	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
65	c5oixC_	Alignment	not modelled	7.1	39	PDB header: viral protein Chain: C: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 1.6 a
66	d1lxja_	Alignment	not modelled	7.0	29	Fold: Ferredoxin-like Superfamily: MTH1187/YkoF-like Family: MTH1187-like
67	c2wzvB_	Alignment	not modelled	7.0	38	PDB header: oxidoreductase Chain: B: PDB Molecule: nfnb protein; PDBTitle: crystal structure of the fnm-dependent nitroreductase nfnb2 from mycobacterium smegmatis
68	d1yqha1	Alignment	not modelled	7.0	36	Fold: Ferredoxin-like Superfamily: MTH1187/YkoF-like Family: MTH1187-like
69	c5oixG_	Alignment	not modelled	6.9	39	PDB header: viral protein Chain: G: PDB Molecule: phosphoprotein; PDBTitle: structure of the hmpv p oligomerization domain at 1.6 a
70	c4be4A_	Alignment	not modelled	6.7	31	PDB header: hydrolase Chain: A: PDB Molecule: sterol esterase; PDBTitle: closed conformation of o. piceae sterol esterase
71	c3nmdB_	Alignment	not modelled	6.7	39	PDB header: transferase Chain: B: PDB Molecule: cgmp dependent protein kinase; PDBTitle: crystal structure of the leucine zipper domain of cgmp dependent2 protein kinase i beta
72	d1lukca_	Alignment	not modelled	6.6	38	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
73	c3a5dM_	Alignment	not modelled	6.6	19	PDB header: hydrolase Chain: M: PDB Molecule: v-type atp synthase beta chain; PDBTitle: inter-subunit interaction and quaternary rearrangement2 defined by the central stalk of prokaryotic v1-atpase
74	c2npuA_	Alignment	not modelled	6.4	38	PDB header: transferase Chain: A: PDB Molecule: fkbp12-rapamycin complex-associated protein; PDBTitle: the solution structure of the rapamycin-binding domain of2 mtor (frb)
75	c1odrA_	Alignment	not modelled	6.4	70	PDB header: lipid transport Chain: A: PDB Molecule: apoa-i peptide; PDBTitle: peptide of human apoa-i residues 166-185. nmr, 5 structures2 at ph 6.0, 37 degrees celsius and peptide:dpc mole ratio3 of 1:40
76	c1odqA_	Alignment	not modelled	6.4	70	PDB header: lipid transport Chain: A: PDB Molecule: apoa-i peptide; PDBTitle: peptide of human apoa-i residues 166-185. nmr, 5 structures2 at ph 3.7, 37 degrees celsius and peptide:sds mole ratio3 of 1:40
77	c1odpA_	Alignment	not modelled	6.4	70	PDB header: lipid transport Chain: A: PDB Molecule: apoa-i peptide; PDBTitle: peptide of human apoa-i residues 166-185. nmr, 5 structures2 at ph 6.6, 37 degrees celsius and peptide:sds mole ratio3 of 1:40
78	c5vr2A_	Alignment	not modelled	6.4	31	PDB header: signaling protein Chain: A: PDB Molecule: myocilin; PDBTitle: mouse myocilin leucine zipper c-terminal 7 heptad repeat
79	d2dk4a1	Alignment	not modelled	6.2	41	Fold: LEM/SAP HeH motif Superfamily: PRP4-like Family: PRP4-like
80	c4olkB_	Alignment	not modelled	6.1	44	PDB header: hydrolase Chain: B: PDB Molecule: endolysin; PDBTitle: the chap domain of lysgh15

81	c3t6gA_	Alignment	not modelled	6.1	58	PDB header: signaling protein, cell adhesion Chain: A: PDB Molecule: sh2 domain-containing protein 3c; PDBTitle: structure of the complex between nsp3 (shep1) and p130cas
82	c2ztbB_	Alignment	not modelled	6.0	17	PDB header: toxin Chain: B: PDB Molecule: crystal protein; PDBTitle: crystal structure of the parasporin-2 bacillus thuringiensis toxin2 that recognizes cancer cells
83	d2bcea_	Alignment	not modelled	6.0	27	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
84	c2h0uA_	Alignment	not modelled	5.9	25	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-flavin oxidoreductase; PDBTitle: crystal structure of nad(p)h-flavin oxidoreductase from helicobacter2 pylori
85	c5co4A_	Alignment	not modelled	5.9	22	PDB header: transferase Chain: A: PDB Molecule: putative trna (cytidine(34)-2'-o)-methyltransferase; PDBTitle: structural insights into the 2-oh methylation of c/u34 on trna
86	d1f6wa_	Alignment	not modelled	5.8	27	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
87	c3sqjB_	Alignment	not modelled	5.7	17	PDB header: hydrolase Chain: B: PDB Molecule: glycosyl hydrolase family 3; PDBTitle: crystal structure of glycoside hydrolase from synechococcus
88	c4gdoC_	Alignment	not modelled	5.7	32	PDB header: structural protein Chain: C: PDB Molecule: plectin; PDBTitle: structure of a fragment of the rod domain of plectin
89	c5w1uA_	Alignment	not modelled	5.7	23	PDB header: hydrolase Chain: A: PDB Molecule: carboxylic ester hydrolase; PDBTitle: culex quinquefasciatus carboxylesterase b2
90	d1tr9a_	Alignment	not modelled	5.6	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: NagZ-like
91	c3biwD_	Alignment	not modelled	5.5	31	PDB header: cell adhesion/cell adhesion Chain: D: PDB Molecule: neuroigin-1; PDBTitle: crystal structure of the neuroigin-1/neurexin-1beta synaptic adhesion2 complex
92	c6n2mA_	Alignment	not modelled	5.5	26	PDB header: signaling protein Chain: A: PDB Molecule: caspase recruitment domain-containing protein 9; PDBTitle: nmr solution structure of the homodimeric, autoinhibited state of the2 card9 card and first coiled-coil
93	c3qc1A_	Alignment	not modelled	5.4	15	PDB header: signaling protein Chain: A: PDB Molecule: immunoglobulin-binding protein 1; PDBTitle: protein phosphatase subunit: alpha4
94	c5x61A_	Alignment	not modelled	5.4	31	PDB header: hydrolase Chain: A: PDB Molecule: acetylcholinesterase; PDBTitle: crystal structure of acetylcholinesterase catalytic subunit of the2 malaria vector anopheles gambiae, 3.4 a
95	c6edjD_	Alignment	not modelled	5.2	28	PDB header: virus like particle Chain: D: PDB Molecule: external core antigen; PDBTitle: cryo-em structure of woodchuck hepatitis virus capsid
96	d1crla_	Alignment	not modelled	5.1	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
97	c2hdiB_	Alignment	not modelled	5.1	41	PDB header: protein transport,antimicrobial protein Chain: B: PDB Molecule: colicin-ia; PDBTitle: crystal structure of the colicin i receptor cir from e.coli in complex2 with receptor binding domain of colicin ia.
98	d2iboa1	Alignment	not modelled	5.1	29	Fold: Ferredoxin-like Superfamily: MTH1187/YkoF-like Family: MTH1187-like
99	d1f5qb2	Alignment	not modelled	5.1	60	Fold: Cyclin-like Superfamily: Cyclin-like Family: Cyclin