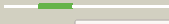
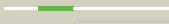
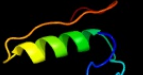
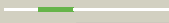






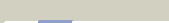
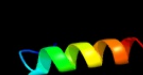



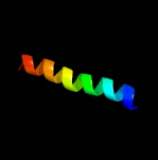
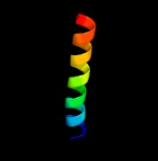

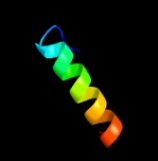
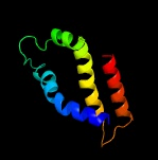
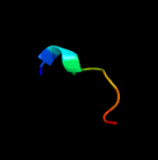
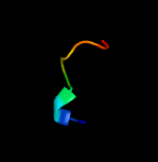
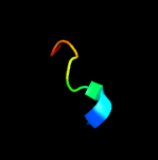


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3723_(-)_4168714_4169478
Date	Fri Aug 9 18:20:42 BST 2019
Unique Job ID	767e2df216381ab8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ctoA_	 Alignment		59.8	50	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: novel protein; PDBTitle: solution structure of the hmg box like domain from human2 hypothetical protein flj14904
2	c4nfuB_	 Alignment		59.4	41	PDB header: signaling protein Chain: B: PDB Molecule: senescence-associated carboxylesterase 101; PDBTitle: structure of the central plant immunity signaling node eds1 in complex2 with its interaction partner sag101
3	c4nfuA_	 Alignment		54.6	38	PDB header: signaling protein Chain: A: PDB Molecule: eds1; PDBTitle: structure of the central plant immunity signaling node eds1 in complex2 with its interaction partner sag101
4	c3ngmB_	 Alignment		35.3	33	PDB header: hydrolase Chain: B: PDB Molecule: extracellular lipase; PDBTitle: crystal structure of lipase from gibberella zeae
5	c3uuuA_	 Alignment		35.1	45	PDB header: hydrolase Chain: A: PDB Molecule: lip1, secretory lipase (family 3); PDBTitle: crystal structure of mono- and diacylglycerol lipase from malassezia2 globosa
6	c3o0dF_	 Alignment		33.4	37	PDB header: hydrolase Chain: F: PDB Molecule: triacylglycerol lipase; PDBTitle: crystal structure of lip2 lipase from yarrowia lipolytica at 1.7 a2 resolution
7	c5xk2A_	 Alignment		31.7	32	PDB header: hydrolase Chain: A: PDB Molecule: diacylglycerol lipase; PDBTitle: crystal structure of mono- and diacylglycerol lipase from aspergillus2 oryzae
8	d1tiaa_	 Alignment		27.9	26	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
9	d1lgva_	 Alignment		27.7	37	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
10	d3tgla_	 Alignment		25.7	32	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
11	c6qppA_	 Alignment		25.5	32	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: rhizomucor miehei lipase propeptide complex, native

12	d1tiba_	Alignment		25.0	53	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
13	c2kncB_	Alignment		24.7	26	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfaIb-beta3 transmembrane-cytoplasmic2 heterocomplex
14	c2rmzA_	Alignment		24.3	26	PDB header: cell adhesion Chain: A: PDB Molecule: integrin beta-3; PDBTitle: bicelle-embedded integrin beta3 transmembrane segment
15	c3g7nA_	Alignment		24.3	32	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of a triacylglycerol lipase from penicillium2 expansum at 1.3
16	c2yijA_	Alignment		23.6	27	PDB header: hydrolase Chain: A: PDB Molecule: phospholipase a1-iigamma; PDBTitle: crystal structure of phospholipase a1
17	d1kf6d_	Alignment		23.2	23	Fold: Heme-binding four-helical bundle Superfamily: Fumarate reductase respiratory complex transmembrane subunits Family: Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
18	d1dwma_	Alignment		23.0	60	Fold: CI-2 family of serine protease inhibitors Superfamily: CI-2 family of serine protease inhibitors Family: CI-2 family of serine protease inhibitors
19	c2ci2l_	Alignment		22.9	50	PDB header: proteinase inhibitor (chymotrypsin) Chain: I: PDB Molecule: chymotrypsin inhibitor 2; PDBTitle: crystal and molecular structure of the serine proteinase inhibitor ci-2 2 from barley seeds
20	c3rdyA_	Alignment		22.9	60	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: bwi-1=protease inhibitor/trypsin inhibitor; PDBTitle: crystal structure of buckwheat trypsin inhibitor rbt1 at 1.84 angstrom2 resolution
21	d1to2l_	Alignment	not modelled	22.9	50	Fold: CI-2 family of serine protease inhibitors Superfamily: CI-2 family of serine protease inhibitors Family: CI-2 family of serine protease inhibitors
22	d2snii_	Alignment	not modelled	22.7	50	Fold: CI-2 family of serine protease inhibitors Superfamily: CI-2 family of serine protease inhibitors Family: CI-2 family of serine protease inhibitors
23	d1ypci_	Alignment	not modelled	22.6	50	Fold: CI-2 family of serine protease inhibitors Superfamily: CI-2 family of serine protease inhibitors Family: CI-2 family of serine protease inhibitors
24	c1vbwA_	Alignment	not modelled	22.6	60	PDB header: protein binding Chain: A: PDB Molecule: trypsin inhibitor bgit; PDBTitle: crystal structure of bitter gourd trypsin inhibitor
25	d1csei_	Alignment	not modelled	22.5	40	Fold: CI-2 family of serine protease inhibitors Superfamily: CI-2 family of serine protease inhibitors Family: CI-2 family of serine protease inhibitors
26	c1hymA_	Alignment	not modelled	22.4	56	PDB header: hydrolase (serine proteinase) Chain: A: PDB Molecule: hydrolyzed cucurbita maxima trypsin inhibitor v; PDBTitle: hydrolyzed trypsin inhibitor (cmti-v, minimized average nmr structure)
27	d1uwca_	Alignment	not modelled	22.3	47	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
28	c5gw8A_	Alignment	not modelled	21.7	32	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical secretory lipase (family 3); PDBTitle: crystal structure of a putative dag-like lipase (mgmdl2) from2 malassezia globosa
						Fold: CI-2 family of serine protease inhibitors

29	d1egla_	Alignment	not modelled	19.6	40	Superfamily: Cl-2 family of serine protease inhibitors Family: Cl-2 family of serine protease inhibitors
30	c1tinA_	Alignment	not modelled	18.6	50	PDB header: serine protease inhibitor Chain: A: PDB Molecule: trypsin inhibitor v; PDBTitle: three-dimensional structure in solution of cucurbita maxima trypsin2 inhibitor-v determined by nmr spectroscopy
31	c6mhqE_	Alignment	not modelled	18.2	36	PDB header: membrane protein Chain: E: PDB Molecule: gap junction alpha-3 protein, connexin-46; PDBTitle: structure of connexin-46 intercellular gap junction channel at 3.42 angstrom resolution by cryoem
32	c1njpT_	Alignment	not modelled	18.0	23	PDB header: ribosome Chain: T: PDB Molecule: general stress protein ctc; PDBTitle: the crystal structure of the 50s large ribosomal subunit2 from deinococcus radiodurans complexed with a trna3 acceptor stem mimic (asm)
33	c3j39M_	Alignment	not modelled	16.6	38	PDB header: ribosome Chain: M: PDB Molecule: 60s ribosomal protein l14; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
34	c1cqtI_	Alignment	not modelled	15.8	35	PDB header: gene regulation/dna Chain: I: PDB Molecule: pou domain, class 2, associating factor 1; PDBTitle: crystal structure of a ternary complex containing an oca-b2 peptide, the oct-1 pou domain, and an octamer element
35	c3jcuJ_	Alignment	not modelled	14.5	25	PDB header: membrane protein Chain: J: PDB Molecule: photosystem ii reaction center protein j; PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
36	d1rr7a_	Alignment	not modelled	14.1	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Middle operon regulator, Mor
37	c1rr7A_	Alignment	not modelled	14.1	28	PDB header: transcription Chain: A: PDB Molecule: middle operon regulator; PDBTitle: crystal structure of the middle operon regulator protein of2 bacteriophage mu
38	c1u1iC_	Alignment	not modelled	13.7	26	PDB header: isomerase Chain: C: PDB Molecule: myo-inositol-1-phosphate synthase; PDBTitle: myo-inositol phosphate synthase mips from a. fulgidus
39	d1u1ia1	Alignment	not modelled	13.7	33	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
40	d2axtj1	Alignment	not modelled	13.0	20	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein J, Psbj Family: Psbj-like
41	c3a0hJ_	Alignment	not modelled	13.0	20	PDB header: electron transport Chain: J: PDB Molecule: photosystem ii reaction center protein j; PDBTitle: crystal structure of i-substituted photosystem ii complex
42	c1cqtJ_	Alignment	not modelled	12.7	35	PDB header: gene regulation/dna Chain: J: PDB Molecule: pou domain, class 2, associating factor 1; PDBTitle: crystal structure of a ternary complex containing an oca-b2 peptide, the oct-1 pou domain, and an octamer element
43	d3lr1a_	Alignment	not modelled	12.6	36	Fold: Insulin-like Superfamily: Insulin-like Family: Insulin-like
44	c5o9zE_	Alignment	not modelled	12.4	71	PDB header: splicing Chain: E: PDB Molecule: u4/u6 small nuclear ribonucleoprotein prp3; PDBTitle: cryo-em structure of a pre-catalytic human spliceosome primed for2 activation (b complex)
45	c2oryA_	Alignment	not modelled	12.4	32	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of m37 lipase
46	c5sxpF_	Alignment	not modelled	11.7	67	PDB header: signaling protein/ligase Chain: F: PDB Molecule: e3 ubiquitin-protein ligase itchy homolog; PDBTitle: structural basis for the interaction between itch prr and beta-pix
47	c1cirA_	Alignment	not modelled	11.7	63	PDB header: serine protease inhibitor Chain: A: PDB Molecule: chymotrypsin inhibitor 2; PDBTitle: complex of two fragments of ci2 [(1-40)(dot)(41-64)]
48	c5sxpG_	Alignment	not modelled	11.2	67	PDB header: signaling protein/ligase Chain: G: PDB Molecule: e3 ubiquitin-protein ligase itchy homolog; PDBTitle: structural basis for the interaction between itch prr and beta-pix
49	c5ovmA_	Alignment	not modelled	10.9	32	PDB header: chaperone Chain: A: PDB Molecule: lipase chaperone; PDBTitle: solution structure of lipase binding domain lid1 of foldase from2 pseudomonas aeruginosa
50	c5xnmj_	Alignment	not modelled	10.8	25	PDB header: membrane protein Chain: J: PDB Molecule: photosystem ii reaction center protein j; PDBTitle: structure of unstacked c2s2m2-type psii-lhcii supercomplex from pism2 sativum
51	c2mmbA_	Alignment	not modelled	10.6	42	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: nmr structure of the protein yp_001712342.1 from acinetobacter2 baumannii
52	c6n52B_	Alignment	not modelled	10.5	13	PDB header: membrane protein Chain: B: PDB Molecule: metabotropic glutamate receptor 5; PDBTitle: metabotropic glutamate receptor 5 apo form
53	c2q5tA_	Alignment	not modelled	10.4	33	PDB header: toxin Chain: A: PDB Molecule: cholix toxin; PDBTitle: full-length cholix toxin from vibrio cholerae
54	c5zazA_	Alignment	not modelled	10.2	26	PDB header: cell adhesion Chain: A: PDB Molecule: integrin beta-2; PDBTitle: solution structure of integrin b2 monomer tranmembrane domain in2 bicelle
						PDB header: viral protein/ translation Chain: D: PDB Molecule: eukaryotic protein synthesis initiation

55	c1lj2D_	Alignment	not modelled	9.7	27	factor; PDBTitle: recognition of eif4g by rotavirus nsp3 reveals a basis for2 mrna circularization
56	c6igzj_	Alignment	not modelled	9.4	33	PDB header: plant protein Chain: J: PDB Molecule: psaj; PDBTitle: structure of psi-lhci
57	c5ys3B_	Alignment	not modelled	8.9	24	PDB header: transport protein Chain: B: PDB Molecule: succinate-acetate permease; PDBTitle: 1.8 angstrom crystal structure of succinate-acetate permease from2 citrobacter koseri
58	c2lx0A_	Alignment	not modelled	8.9	55	PDB header: membrane protein Chain: A: PDB Molecule: membrane fusion protein p14; PDBTitle: arced helix (arch) nmr structure of the reovirus p14 fusion-associated2 small transmembrane (fast) protein transmembrane domain (tmd) in3 dodecyl phosphocholine (dpc) micelles
59	c2qjkM_	Alignment	not modelled	8.9	12	PDB header: electron transport Chain: M: PDB Molecule: cytochrome b; PDBTitle: crystal structure analysis of mutant rhodobacter2 sphaeroides bc1 with stigmatellin and antimycin
60	d2qam01	Alignment	not modelled	8.4	20	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L32p
61	c2mwqA_	Alignment	not modelled	8.3	57	PDB header: plant protein Chain: A: PDB Molecule: oxygen-evolving enhancer protein 3, chloroplastic; PDBTitle: solution structure of psbq from spinacia oleracea
62	c6mx7C_	Alignment	not modelled	8.2	45	PDB header: virus Chain: C: PDB Molecule: capsid; PDBTitle: cryoem structure of chimeric eastern equine encephalitis virus:2 genome-binding capsid n-terminal domain
63	c6epcN_	Alignment	not modelled	7.7	15	PDB header: hydrolase Chain: N: PDB Molecule: 26s proteasome non-atpase regulatory subunit 1; PDBTitle: ground state 26s proteasome (gs2)
64	c5fg0B_	Alignment	not modelled	7.5	14	PDB header: ligase Chain: B: PDB Molecule: e3 ubiquitin-protein ligase listerin; PDBTitle: structure of the conserved yeast listerin (ltn1) n-terminal domain,2 monoclinic form
65	c3j3v0_	Alignment	not modelled	7.5	36	PDB header: ribosome Chain: 0: PDB Molecule: 50s ribosomal protein l32; PDBTitle: atomic model of the immature 50s subunit from bacillus subtilis (state2 i-a)
66	c6hu9U_	Alignment	not modelled	7.4	19	PDB header: oxidoreductase/electron transport Chain: U: PDB Molecule: cytochrome b-c1 complex subunit 10; PDBTitle: iiii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
67	c5mlc7_	Alignment	not modelled	7.3	47	PDB header: ribosome Chain: 7: PDB Molecule: psrp5alpha, chloroplastic; PDBTitle: cryo-em structure of the spinach chloroplast ribosome reveals the2 location of plastid-specific ribosomal proteins and extensions
68	d1dc1a_	Alignment	not modelled	7.2	32	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Restriction endonuclease BsobI
69	c5xfsA_	Alignment	not modelled	7.1	26	PDB header: protein transport Chain: A: PDB Molecule: pe family protein pe8; PDBTitle: crystal structure of pe8-pppe15 in complex with esp95 from m.2 tuberculosis
70	c1y4eA_	Alignment	not modelled	7.1	57	PDB header: membrane protein Chain: A: PDB Molecule: sodium/hydrogen exchanger 1; PDBTitle: nmr structure of transmembrane segment iv of the nhe12 isoform of the na+/h+ exchanger
71	c6o4mB_	Alignment	not modelled	7.0	16	PDB header: toxin Chain: B: PDB Molecule: melittin; PDBTitle: racemic melittin
72	c2mltB_	Alignment	not modelled	7.0	16	PDB header: toxin (hemolytic polypeptide) Chain: B: PDB Molecule: melittin; PDBTitle: melittin
73	c2mw6A_	Alignment	not modelled	7.0	16	PDB header: toxin Chain: A: PDB Molecule: melittin; PDBTitle: structure of the bee venom toxin melittin with [(c5h5)ru]+ fragment2 attached to the tryptophan residue
74	c6o4mA_	Alignment	not modelled	7.0	16	PDB header: toxin Chain: A: PDB Molecule: melittin; PDBTitle: racemic melittin
75	c6dstA_	Alignment	not modelled	7.0	16	PDB header: toxin Chain: A: PDB Molecule: melittin; PDBTitle: recombinant melittin
76	c2mltA_	Alignment	not modelled	7.0	16	PDB header: toxin (hemolytic polypeptide) Chain: A: PDB Molecule: melittin; PDBTitle: melittin
77	c2g38A_	Alignment	not modelled	6.9	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pe family protein; PDBTitle: a pe/pppe protein complex from mycobacterium tuberculosis
78	d2g38a1	Alignment	not modelled	6.9	11	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
79	c1pjmA_	Alignment	not modelled	6.8	100	PDB header: protein transport Chain: A: PDB Molecule: retinoblastoma-associated protein; PDBTitle: mouse importin alpha-bipartite nls from human2 retinoblastoma protein complex
80	c4b1yM_	Alignment	not modelled	6.7	46	PDB header: structural protein Chain: M: PDB Molecule: phosphatase and actin regulator 1; PDBTitle: structure of the phactr1 rpel-3 bound to g-actin

81	c2mckA	Alignment	not modelled	6.7	44	PDB header: hydrolase Chain: A: PDB Molecule: polyprotein; PDBTitle: backbone 1h, 13c, and 15n chemical shift assignments for murine2 norovirus cr6 ns1/2 protein
82	c5h1sg	Alignment	not modelled	6.6	54	PDB header: ribosome Chain: G: PDB Molecule: 50s ribosomal protein l4, chloroplastic; PDBTitle: structure of the large subunit of the chloro-ribosome
83	d2j0151	Alignment	not modelled	6.6	50	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L32p
84	c5zghJ	Alignment	not modelled	6.5	25	PDB header: photosynthesis Chain: J: PDB Molecule: psaj; PDBTitle: cryo-em structure of the red algal psi-lhcr
85	d2e74h1	Alignment	not modelled	6.4	54	Fold: Single transmembrane helix Superfamily: PetN subunit of the cytochrome b6f complex Family: PetN subunit of the cytochrome b6f complex
86	c5vnyA	Alignment	not modelled	6.4	63	PDB header: endocytosis, protein binding Chain: A: PDB Molecule: lethal (2) giant discs 1, isoform b; PDBTitle: crystal structure of dm14-3 domain of Igd
87	c6e3yP	Alignment	not modelled	6.3	38	PDB header: signaling protein Chain: P: PDB Molecule: calcitonin gene-related peptide 1; PDBTitle: cryo-em structure of the active, gs-protein complexed, human cgrp2 receptor
88	c4i7zH	Alignment	not modelled	6.3	54	PDB header: photosynthesis Chain: H: PDB Molecule: cytochrome b6-f complex subunit 8; PDBTitle: crystal structure of cytochrome b6f in dopg, with disordered rieske2 iron-sulfur protein soluble domain
89	c4pv1H	Alignment	not modelled	6.3	54	PDB header: electron transport/inhibitor Chain: H: PDB Molecule: cytochrome b6-f complex subunit 8; PDBTitle: cytochrome b6f structure from m. lamimosus with the quinone analog2 inhibitor stigmatellin
90	c2kncA	Alignment	not modelled	6.3	30	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alfaIIB-beta3 transmembrane-cytoplasmic2 heterocomplex
91	c5wu5C	Alignment	not modelled	6.3	27	PDB header: transferase Chain: C: PDB Molecule: speckle targeted pip5k1a-regulated poly(a) polymerase; PDBTitle: crystal structure of apo human tut1, form iii
92	c3pq1A	Alignment	not modelled	6.3	27	PDB header: transferase Chain: A: PDB Molecule: poly(a) rna polymerase; PDBTitle: crystal structure of human mitochondrial poly(a) polymerase (papd1)
93	c6gwxA	Alignment	not modelled	6.2	75	PDB header: structural protein Chain: A: PDB Molecule: optimised ppa-tyr; PDBTitle: stabilising and understanding a miniprotein by rational design.
94	c5f5uH	Alignment	not modelled	6.2	38	PDB header: splicing Chain: H: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the snu23-prp38-mfap1(217-258) complex of2 chaetomium thermophilum
95	c1z8yl	Alignment	not modelled	6.2	35	PDB header: virus Chain: I: PDB Molecule: spike glycoprotein e1; PDBTitle: mapping the e2 glycoprotein of alphaviruses
96	c1z8yM	Alignment	not modelled	6.2	35	PDB header: virus Chain: M: PDB Molecule: spike glycoprotein e1; PDBTitle: mapping the e2 glycoprotein of alphaviruses
97	c1z8yK	Alignment	not modelled	6.2	35	PDB header: virus Chain: K: PDB Molecule: spike glycoprotein e1; PDBTitle: mapping the e2 glycoprotein of alphaviruses
98	c1z8yO	Alignment	not modelled	6.2	35	PDB header: virus Chain: O: PDB Molecule: spike glycoprotein e1; PDBTitle: mapping the e2 glycoprotein of alphaviruses
99	c2e75H	Alignment	not modelled	6.2	54	PDB header: photosynthesis Chain: H: PDB Molecule: cytochrome b6-f complex subunit 8; PDBTitle: crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.lamimosus