


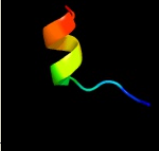







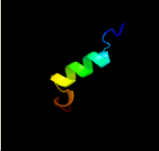



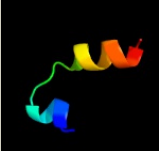

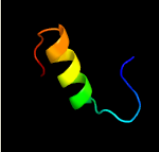

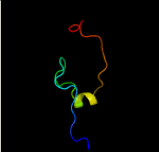



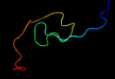

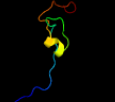
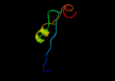
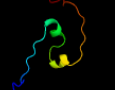

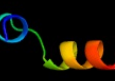
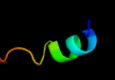


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2738c (-) _3051816_3052022
Date	Wed Aug 7 12:50:39 BST 2019
Unique Job ID	8523dddf75c058d2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6jx3B_	 Alignment		51.6	31	PDB header: peptide binding protein Chain: B; PDB Molecule: tfub1; PDBTitle: lasso peptide synthetase b1 complexed with the leader peptide
2	d1ecia_	 Alignment		43.6	42	Fold: Ectatomin subunits Superfamily: Ectatomin subunits Family: Ectatomin subunits
3	c5v1uB_	 Alignment		43.2	28	PDB header: protein binding Chain: B; PDB Molecule: tbib1; PDBTitle: tbib1 in complex with the tbia(beta) leader peptide
4	c4bx9C_	 Alignment		40.1	25	PDB header: protein transport Chain: C; PDB Molecule: svacuolar protein sorting-associated protein 16 homolog; PDBTitle: human vps33a in complex with a fragment of human vps16
5	c6fkgC_	 Alignment		39.6	16	PDB header: toxin Chain: C; PDB Molecule: rv1990c (mbca); PDBTitle: crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
6	c2nydB_	 Alignment		29.1	8	PDB header: unknown function Chain: B; PDB Molecule: upf0135 protein sa1388; PDBTitle: crystal structure of staphylococcus aureus hypothetical protein sa1388
7	c2p9xB_	 Alignment		25.6	28	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: hypothetical protein ph0832; PDBTitle: crystal structure of ph0832 from pyrococcus horikoshii ot3
8	c3ctdB_	 Alignment		22.0	32	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: putative atpase, aaa family; PDBTitle: crystal structure of a putative aaa family atpase from prochlorococcus2 marinus subsp. pastoris
9	c3g2bA_	 Alignment		21.1	20	PDB header: biosynthetic protein Chain: A; PDB Molecule: coenzyme pqq synthesis protein d; PDBTitle: crystal structure of pqqd from xanthomonas campestris
10	c4na3A_	 Alignment		20.6	30	PDB header: transferase Chain: A; PDB Molecule: polyketide synthase pksj; PDBTitle: crystal structure of the second ketosynthase from the bacillaene2 polyketide synthase bound to a hexanoyl substrate mimic
11	d3ctda1	 Alignment		18.1	32	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: MgsA/YrvN C-terminal domain-like

12	c6gw6B_	Alignment		17.5	20	PDB header: toxin Chain: B: PDB Molecule: xre antitoxin; PDBTitle: structure of the pseudomonas putida res-xre toxin-antitoxin complex
13	c4z37A_	Alignment		17.1	23	PDB header: transferase Chain: A: PDB Molecule: putative mixed polyketide synthase/non-ribosomal peptide PDBTitle: structure of the ketosynthase of module 2 of c0zgg5 (trans-at pks)2 from brevibacillus brevis
14	c3twkB_	Alignment		16.0	17	PDB header: hydrolase Chain: B: PDB Molecule: formamidopyrimidine-dna glycosylase 1; PDBTitle: crystal structure of arabidopsis thaliana fpg
15	c5erbB_	Alignment		15.9	31	PDB header: transferase Chain: B: PDB Molecule: polyketide synthase; PDBTitle: ketosynthase from module 5 of the bacillaene synthase from bacillus2 amyloliquefaciens fzb42
16	c4tl2A_	Alignment		15.3	36	PDB header: transferase Chain: A: PDB Molecule: at-less polyketide synthase; PDBTitle: crystal structure of ketosynthase domain from mgsf from streptomyces2 platensis
17	c4tktA_	Alignment		15.1	26	PDB header: transferase Chain: A: PDB Molecule: at-less polyketide synthase; PDBTitle: streptomyces platensis isomigrastatin ketosynthase domain mgsf ks6
18	c3p9a_	Alignment		14.5	38	PDB header: dna binding protein Chain: I: PDB Molecule: dna-packaging protein gp3; PDBTitle: an atomic view of the nonameric small terminase subunit of2 bacteriophage p22
19	d3bgea1	Alignment		14.0	37	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: MgsA/YrvN C-terminal domain-like
20	c3ismC_	Alignment		13.5	21	PDB header: hydrolase inhibitor/hydrolase Chain: C: PDB Molecule: cg4930; PDBTitle: crystal structure of the endog/endogi complex: mechanism of endog2 inhibition
21	c4qyrA_	Alignment	not modelled	13.4	29	PDB header: transferase Chain: A: PDB Molecule: at-less polyketide synthase; PDBTitle: streptomyces platensis isomigrastatin ketosynthase domain mgse ks3
22	c4b3nA_	Alignment	not modelled	13.3	19	PDB header: sugar binding protein/ligase Chain: A: PDB Molecule: maltose-binding periplasmic protein, tripartite motif- PDBTitle: crystal structure of rhesus trim5alpha pry/spry domain
23	d1rd5a_	Alignment	not modelled	12.9	26	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
24	c5e5nD_	Alignment	not modelled	12.9	29	PDB header: hydrolase Chain: D: PDB Molecule: polyketide synthase pksl; PDBTitle: ketosynthase from module 6 of the bacillaene synthase from bacillus2 subtilis 168 (c167s mutant, crystal form 1)
25	c3qyxD_	Alignment	not modelled	12.7	11	PDB header: transcription/dna Chain: D: PDB Molecule: esx-1 secretion-associated regulator espr; PDBTitle: crystal structure of mycobacterium tuberculosis espr in complex with a2 small dna fragment
26	d1ee8a1	Alignment	not modelled	12.5	13	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
27	c5e5nB_	Alignment	not modelled	12.0	36	PDB header: hydrolase Chain: B: PDB Molecule: polyketide synthase pksl; PDBTitle: ketosynthase from module 6 of the bacillaene synthase from bacillus2 subtilis 168 (c167s mutant, crystal form 1)
28	c1no3A_	Alignment	not modelled	11.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: lipoyxygenase-3; PDBTitle: refined structure of soybean lipoyxygenase-3 with 4-nitrocatechol at2 2.15 angstrom resolution
						PDB header: rna binding protein

29	c5b88A_	Alignment	not modelled	11.5	30	Chain: A: PDB Molecule: atp-dependent rna helicase dead; PDBTitle: rrm-like domain of dead-box protein, csda
30	d1rrha1	Alignment	not modelled	11.1	18	Fold: Lipoxigenase Superfamily: Lipoxigenase Family: Plant lipoxigenases
31	c3iz5w_	Alignment	not modelled	10.5	16	PDB header: ribosome Chain: W: PDB Molecule: 60s ribosomal protein l22 (l22e); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
32	c3izcw_	Alignment	not modelled	10.4	32	PDB header: ribosome Chain: W: PDB Molecule: 60s ribosomal protein rpl22 (l22e); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
33	c6fahD_	Alignment	not modelled	10.1	15	PDB header: flavoprotein Chain: D: PDB Molecule: caffel-coa reductase-etf complex subunit carc; PDBTitle: molecular basis of the flavin-based electron-bifurcating caffel-coa2 reductase reaction
34	c5gxtA_	Alignment	not modelled	9.4	19	PDB header: protein transport Chain: A: PDB Molecule: maltose-binding periplasmic protein,pigg; PDBTitle: crystal structure of pigg
35	c4a5uA_	Alignment	not modelled	9.4	21	PDB header: transferase/rna binding protein Chain: A: PDB Molecule: rna replicase polyprotein; PDBTitle: turnip yellow mosaic virus proteinase and escherichia coli 30s2 ribosomal s15
36	c4opeD_	Alignment	not modelled	9.3	34	PDB header: ligase, transferase Chain: D: PDB Molecule: nrps/pks; PDBTitle: streptomcyes albus ja3453 oxazolomycin ketosynthase domain ozmh ks7
37	c4wviA_	Alignment	not modelled	8.6	26	PDB header: hydrolase Chain: A: PDB Molecule: maltose-binding periplasmic protein,signal peptidase ib; PDBTitle: crystal structure of the type-i signal peptidase from staphylococcus2 aureus (spsb) in complex with a substrate peptide (pep2).
38	c3csgA_	Alignment	not modelled	8.6	19	PDB header: de novo protein, sugar binding protein Chain: A: PDB Molecule: maltose-binding protein monobody ys1 fusion; PDBTitle: crystal structure of monobody ys1(mbp-74)/maltose binding protein2 fusion complex
39	c4wkyB_	Alignment	not modelled	8.4	17	PDB header: transferase Chain: B: PDB Molecule: beta-ketoacyl synthase; PDBTitle: streptomcyes albus ja3453 oxazolomycin ketosynthase domain ozmn ks2
40	c5sxyA_	Alignment	not modelled	8.2	8	PDB header: chaperone Chain: A: PDB Molecule: bifunctional coenzyme pqq synthesis protein c/d; PDBTitle: the solution nmr structure for the pqqd truncation of methylobacterium2 extorquens pqqcd representing a functional and stand-alone3 ribosomally synthesized and post-translational modified (ripp)4 recognition element (rre)
41	d2proc1	Alignment	not modelled	8.1	27	Fold: Alpha-lytic protease prodomain-like Superfamily: Alpha-lytic protease prodomain Family: Alpha-lytic protease prodomain
42	c3hbmA_	Alignment	not modelled	7.9	5	PDB header: hydrolase Chain: A: PDB Molecule: udp-sugar hydrolase; PDBTitle: crystal structure of pseg from campylobacter jejuni
43	d3bula1	Alignment	not modelled	7.6	21	Fold: Methionine synthase domain-like Superfamily: Methionine synthase domain Family: Methionine synthase domain
44	d1k82a1	Alignment	not modelled	7.5	13	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
45	c3p14C_	Alignment	not modelled	7.5	25	PDB header: isomerase Chain: C: PDB Molecule: l-rhamnose isomerase; PDBTitle: crystal structure of l-rhamnose isomerase with a novel high thermo-2 stability from bacillus halodurans
46	c2qw6A_	Alignment	not modelled	7.5	31	PDB header: hydrolase Chain: A: PDB Molecule: aaa atpase, central region; PDBTitle: crystal structure of the c-terminal domain of an aaa atpase from2 enterococcus faecium do
47	d2qw6a1	Alignment	not modelled	7.5	31	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: MgsA/YrvN C-terminal domain-like
48	c3oaiB_	Alignment	not modelled	7.4	19	PDB header: membrane protein, cell adhesion Chain: B: PDB Molecule: maltose-binding periplasmic protein, myelin protein p0; PDBTitle: crystal structure of the extra-cellular domain of human myelin protein2 zero
49	c3msqC_	Alignment	not modelled	7.4	7	PDB header: biosynthetic protein Chain: C: PDB Molecule: putative ubiquinone biosynthesis protein; PDBTitle: crystal structure of a putative ubiquinone biosynthesis protein2 (npun02000094) from nostoc punctiforme pcc 73102 at 2.85 a resolution
50	c6itwA_	Alignment	not modelled	7.1	11	PDB header: antitoxin Chain: A: PDB Molecule: type vi immunity protein atu4351; PDBTitle: crystal structure of atu4351 from agrobacterium tumefaciens
51	d2r9ga1	Alignment	not modelled	7.0	26	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: MgsA/YrvN C-terminal domain-like
52	d1d8wa_	Alignment	not modelled	6.9	30	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: L-rhamnose isomerase
						PDB header: metal binding protein

53	c6bwqB_	Alignment	not modelled	6.8	25	Chain: B: PDB Molecule: pyridinium-3,5-bisthiocarboxylic acid mononucleotide nickel PDBTitle: larc2, the c-terminal domain of a cyclometalase involved in the2 synthesis of the npn cofactor of lactate racemase, in complex with3 mnctp
54	c1ty4D_	Alignment	not modelled	6.7	63	PDB header: apoptosis Chain: D: PDB Molecule: egg laying defective egl-1, programmed cell death PDBTitle: crystal structure of a ced-9/egl-1 complex
55	c2joiA_	Alignment	not modelled	6.7	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ta0095; PDBTitle: nmr solution structure of hypothetical protein ta0095 from2 thermoplasma acidophilum
56	d1nmpa_	Alignment	not modelled	6.7	18	Fold: NIF3 (NGG1p interacting factor 3)-like Superfamily: NIF3 (NGG1p interacting factor 3)-like Family: NIF3 (NGG1p interacting factor 3)-like
57	c3gx4X_	Alignment	not modelled	6.6	40	PDB header: dna binding protein/dna Chain: X: PDB Molecule: alkyltransferase-like protein 1; PDBTitle: crystal structure analysis of s. pombe atl in complex with dna
58	d1mwwa_	Alignment	not modelled	6.6	17	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: Hypothetical protein HI1388.1
59	d1u0bb1	Alignment	not modelled	6.5	25	Fold: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Superfamily: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Family: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
60	c1ty4C_	Alignment	not modelled	6.4	63	PDB header: apoptosis Chain: C: PDB Molecule: egg laying defective egl-1, programmed cell death PDBTitle: crystal structure of a ced-9/egl-1 complex
61	c4kmoB_	Alignment	not modelled	6.3	17	PDB header: transport protein Chain: B: PDB Molecule: putative vacuolar protein sorting-associated protein; PDBTitle: crystal structure of the vps33-vps16 hops subcomplex from chaetomium2 thermophilum
62	d1nvma1	Alignment	not modelled	6.3	16	Fold: RuvA C-terminal domain-like Superfamily: post-HMGL domain-like Family: DmpG/LeuA communication domain-like
63	c3k1A_	Alignment	not modelled	6.2	18	PDB header: ligase Chain: A: PDB Molecule: fancl; PDBTitle: crystal structure of fancl
64	c3zqsB_	Alignment	not modelled	6.1	18	PDB header: ligase Chain: B: PDB Molecule: e3 ubiquitin-protein ligase fancl; PDBTitle: human fancl central domain
65	c2gx8B_	Alignment	not modelled	6.0	24	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: nif3-related protein; PDBTitle: the crystal structure of bacillus cereus protein related to nif3
66	c5vglA_	Alignment	not modelled	6.0	16	PDB header: isomerase Chain: A: PDB Molecule: lachrymatory-factor synthase; PDBTitle: crystal structure of lachrymatory factor synthase from allium cepa
67	d1sr9a1	Alignment	not modelled	6.0	29	Fold: RuvA C-terminal domain-like Superfamily: post-HMGL domain-like Family: DmpG/LeuA communication domain-like
68	d3procl	Alignment	not modelled	5.9	19	Fold: Alpha-lytic protease prodomain-like Superfamily: Alpha-lytic protease prodomain Family: Alpha-lytic protease prodomain
69	c2ix4B_	Alignment	not modelled	5.9	24	PDB header: transferase Chain: B: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase; PDBTitle: arabidopsis thaliana mitochondrial beta-ketoacyl acp synthase hexanoic2 acid complex
70	c6d0hB_	Alignment	not modelled	5.8	18	PDB header: toxin Chain: B: PDB Molecule: pars: cog5642 (duf2384) antitoxin; PDBTitle: part: prs adp-ribosylating toxin bound to cognate antitoxin pars
71	c3c0vC_	Alignment	not modelled	5.8	37	PDB header: plant protein Chain: C: PDB Molecule: cytokinin-specific binding protein; PDBTitle: crystal structure of cytokinin-specific binding protein in complex2 with cytokinin and ta6br12
72	c4kegA_	Alignment	not modelled	5.7	21	PDB header: lipid binding protein Chain: A: PDB Molecule: maltose-binding periplasmic/palate lung and nasal PDBTitle: crystal structure of mbp fused human splunc1
73	c1dvaX_	Alignment	not modelled	5.5	90	PDB header: hydrolase/hydrolase inhibitor Chain: X: PDB Molecule: peptide e-76; PDBTitle: crystal structure of the complex between the peptide exosite inhibitor2 e-76 and coagulation factor viia
74	c1dvaY_	Alignment	not modelled	5.5	90	PDB header: hydrolase/hydrolase inhibitor Chain: Y: PDB Molecule: peptide e-76; PDBTitle: crystal structure of the complex between the peptide exosite inhibitor2 e-76 and coagulation factor viia
75	c3j61G_	Alignment	not modelled	5.2	43	PDB header: ribosome Chain: G: PDB Molecule: 60s ribosomal protein l8e; PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
76	c5elpA_	Alignment	not modelled	5.1	6	PDB header: hydrolase Chain: A: PDB Molecule: nrps/pks protein; PDBTitle: ketosynthase from module 1 of the bacillaene synthase from bacillus2 amyloliquefaciens fzb42
77	c1r7gA_	Alignment	not modelled	5.0	44	PDB header: membrane protein Chain: A: PDB Molecule: genome polyprotein; PDBTitle: nmr structure of the membrane anchor domain (1-31) of the2 nonstructural protein 5a (ns5a) of hepatitis c virus3 (minimized average structure, sample in 100mm dpc)