

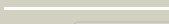




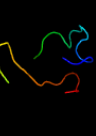

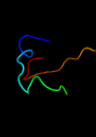

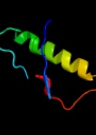

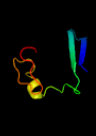

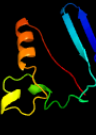

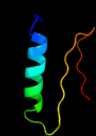





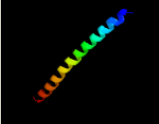
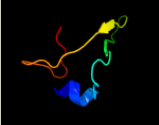
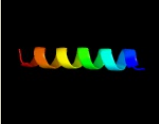

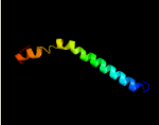
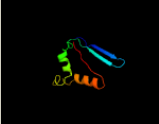

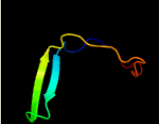


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0479c_(-)_567924_568970
Date	Tue Jul 23 14:50:56 BST 2019
Unique Job ID	b9e3b1eb11eb5c95

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2bv3a3	 Alignment		60.2	21	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components
2	c2qazC_	 Alignment		54.9	11	PDB header: hydrolase activator Chain: C: PDB Molecule: sspb protein; PDBTitle: structure of c. crescentus sspb ortholog
3	c2qasA_	 Alignment		53.0	11	PDB header: hydrolase activator Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of caulobacter crescentus sspb ortholog
4	d2nysa1	 Alignment		52.3	23	Fold: SspB-like Superfamily: SspB-like Family: AGR C 3712p-like
5	c2nysA_	 Alignment		52.3	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: agr_c_3712p; PDBTitle: x-ray crystal structure of protein agr_c_3712 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr88.
6	d2dy1a3	 Alignment		44.5	10	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components
7	c4ew8A_	 Alignment		38.7	19	PDB header: transferase Chain: A: PDB Molecule: sensor protein divl; PDBTitle: crystal structure of a c-terminal part of tyrosine kinase (divl) from2 caulobacter crescentus cb15 at 2.50 a resolution (psi community3 target, shapiro l.)
8	c4i5sA_	 Alignment		35.5	18	PDB header: transferase Chain: A: PDB Molecule: putative histidine kinase covs; vick-like protein; PDBTitle: structure and function of sensor histidine kinase
9	d1ghha_	 Alignment		31.4	13	Fold: DNA damage-inducible protein DinI Superfamily: DNA damage-inducible protein DinI Family: DNA damage-inducible protein DinI
10	d2pila_	 Alignment		31.2	16	Fold: Pili subunits Superfamily: Pili subunits Family: Pilin
11	c1spfA_	 Alignment		28.0	17	PDB header: lipoprotein(surface film) Chain: A: PDB Molecule: pulmonary surfactant-associated polypeptide c; PDBTitle: the nmr structure of the pulmonary surfactant-associated2 polypeptide sp-c in an apolar solvent contains a valyl-3 rich alpha-helix

12	c3d2rB_	Alignment		27.4	12	PDB header: transferase Chain: B: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 4; PDBTitle: crystal structure of pyruvate dehydrogenase kinase isoform 4 in2 complex with adp
13	c5o4uK_	Alignment		25.1	19	PDB header: cell adhesion Chain: K: PDB Molecule: flagellin; PDBTitle: the flagellin of pyrococcus furiosus
14	d1wlfa2	Alignment		23.9	17	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
15	c6btmA_	Alignment		23.4	14	PDB header: membrane protein Chain: A: PDB Molecule: alternative complex iii subunit a; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
16	c5ndaA_	Alignment		23.2	24	PDB header: protein Chain: A: PDB Molecule: rsp-c33leu -recombinant pulmonary surfactant-associated PDBTitle: nmr structural characterisation of pharmaceutically relevant proteins2 obtained through a novel recombinant production: the case of the3 pulmonary surfactant polypeptide c analogue rsp-c33leu.
17	c5f15A_	Alignment		21.2	15	PDB header: transferase Chain: A: PDB Molecule: 4-amino-4-deoxy-l-arabinose (l-ara4n) transferase; PDBTitle: crystal structure of arnt from cupriavidus metallidurans bound to2 undecaprenyl phosphate
18	c2q8fA_	Alignment		20.3	11	PDB header: transferase Chain: A: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 1; PDBTitle: structure of pyruvate dehydrogenase kinase isoform 1
19	d1oqwa_	Alignment		18.8	29	Fold: Pili subunits Superfamily: Pili subunits Family: Pilin
20	c2mvfA_	Alignment		17.4	15	PDB header: ribosomal protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: structural insight into an essential assembly factor network on the2 pre-ribosome
21	c4fmtB_	Alignment	not modelled	16.6	8	PDB header: transferase Chain: B: PDB Molecule: chpt protein; PDBTitle: crystal structure of a chpt protein (cc_3470) from caulobacter2 crescentus cb15 at 2.30 a resolution
22	c2mi2A_	Alignment	not modelled	16.2	38	PDB header: transport protein Chain: A: PDB Molecule: sec-independent protein translocase protein tatb; PDBTitle: solution structure of the e. coli tatb protein in dpc micelles
23	c3o0rC_	Alignment	not modelled	15.0	15	PDB header: immune system/oxidoreductase Chain: C: PDB Molecule: nitric oxide reductase subunit c; PDBTitle: crystal structure of nitric oxide reductase from pseudomonas2 aeruginosa in complex with antibody fragment
24	c6j4oB_	Alignment	not modelled	15.0	25	PDB header: hydrolase Chain: B: PDB Molecule: small vasohibin-binding protein; PDBTitle: structural basis of tubulin detyrosination by vasohibins-vbpb enzyme2 complex and functional implications
25	d1zgha1	Alignment	not modelled	14.5	18	Fold: FMT C-terminal domain-like Superfamily: FMT C-terminal domain-like Family: Post formyltransferase domain
26	c6fbIA_	Alignment	not modelled	13.9	24	PDB header: rna binding protein Chain: A: PDB Molecule: mina-1; PDBTitle: nmr solution structure of mina-1(254-334)
27	c3sokB_	Alignment	not modelled	13.9	19	PDB header: cell adhesion Chain: B: PDB Molecule: fimbrial protein; PDBTitle: dichelobacter nodosus pilin fima
28	c5z1lL_	Alignment	not modelled	13.8	16	PDB header: protein fibril Chain: L: PDB Molecule: flagellin; PDBTitle: cryo-em structure of methanococcus maripaludis archaeillum
29	c5tfyl_	Alignment	not modelled	13.5	9	PDB header: cell adhesion Chain: J: PDB Molecule: flagellin; PDBTitle: the archaeal flagellum of methanospirillum hungatei

						strain jf1.
30	c4qpkA_	Alignment	not modelled	12.8	7	PDB header: signaling protein Chain: A: PDB Molecule: phosphotransferase; PDBTitle: 1.7 angstrom structure of a bacterial phosphotransferase
31	c2mv6A_	Alignment	not modelled	12.5	42	PDB header: membrane protein Chain: A: PDB Molecule: erythropoietin receptor; PDBTitle: solution structure of the transmembrane domain and the juxta-membrane2 domain of the erythropoietin receptor in micelles
32	c2bu8A_	Alignment	not modelled	12.4	13	PDB header: transferase Chain: A: PDB Molecule: pyruvate dehydrogenase kinase isoenzyme 2; PDBTitle: crystal structures of human pyruvate dehydrogenase kinase 2 containing2 physiological and synthetic ligands
33	c2na6A_	Alignment	not modelled	12.1	43	PDB header: apoptosis Chain: A: PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: transmembrane domain of mouse fas/cd95 death receptor
34	c2na6C_	Alignment	not modelled	12.1	43	PDB header: apoptosis Chain: C: PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: transmembrane domain of mouse fas/cd95 death receptor
35	c6f0kA_	Alignment	not modelled	11.8	27	PDB header: membrane protein Chain: A: PDB Molecule: cytochrome c family protein; PDBTitle: alternative complex iii
36	c6gv9K_	Alignment	not modelled	11.3	11	PDB header: protein fibril Chain: K: PDB Molecule: prepilin peptidase-dependent protein d; PDBTitle: structure of the type iv pilus from enterohemorrhagic escherichia coli2 (ehec)
37	c2mrnB_	Alignment	not modelled	10.2	6	PDB header: dna binding protein Chain: B: PDB Molecule: antitoxin maze; PDBTitle: structure of truncated ecmaze
38	c2na6B_	Alignment	not modelled	10.2	43	PDB header: apoptosis Chain: B: PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: transmembrane domain of mouse fas/cd95 death receptor
39	c6mitC_	Alignment	not modelled	9.9	50	PDB header: lipid transport Chain: C: PDB Molecule: lipopolysaccharide export system protein lptc; PDBTitle: lptbfgc from enterobacter cloacae
40	c6ekvA_	Alignment	not modelled	9.8	11	PDB header: lipid binding protein Chain: A: PDB Molecule: toxin complex component orf-x2; PDBTitle: structure of orfx2 from clostridium botulinum a2
41	c6em5r_	Alignment	not modelled	9.8	15	PDB header: ribosome Chain: R: PDB Molecule: 60s ribosomal protein l19-a; PDBTitle: state d architectural model (nsa1-tap flag-ytm1) - visualizing the2 assembly pathway of nucleolar pre-60s ribosomes
42	c6ochB_	Alignment	not modelled	9.4	25	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: small vasohibin-binding protein; PDBTitle: crystal structure of vash1-svbp complex bound with parthenolide
43	c6c6lO_	Alignment	not modelled	9.4	29	PDB header: membrane protein Chain: O: PDB Molecule: v-type proton atpase subunit f; PDBTitle: yeast vacuolar atpase vo in lipid nanodisc
44	c3ipdB_	Alignment	not modelled	9.3	17	PDB header: exocytosis Chain: B: PDB Molecule: syntaxin-1a; PDBTitle: helical extension of the neuronal snare complex into the2 membrane, spacegroup i 21 21 21
45	c6qbyB_	Alignment	not modelled	9.2	25	PDB header: cytosolic protein Chain: B: PDB Molecule: small vasohibin-binding protein; PDBTitle: crystal structure of vash 2 in complex with svbp
46	c6nvqB_	Alignment	not modelled	9.2	25	PDB header: hydrolase Chain: B: PDB Molecule: small vasohibin-binding protein; PDBTitle: crystal structure of the vash1-svbp complex
47	c2e1mA_	Alignment	not modelled	9.1	11	PDB header: oxidoreductase Chain: A: PDB Molecule: l-glutamate oxidase; PDBTitle: crystal structure of l-glutamate oxidase from streptomyces sp. x-119-6
48	c6j4uB_	Alignment	not modelled	9.0	25	PDB header: hydrolase Chain: B: PDB Molecule: small vasohibin-binding protein; PDBTitle: structural basis of tubulin detyrosination by vasohibins-svbp enzyme2 complex and functional implications
49	c6j4qK_	Alignment	not modelled	9.0	24	PDB header: hydrolase Chain: K: PDB Molecule: small vasohibin-binding protein; PDBTitle: structural basis of tubulin detyrosination by vasohibins-svbp enzyme2 complex and functional implications
50	c6qbyD_	Alignment	not modelled	8.9	24	PDB header: cytosolic protein Chain: D: PDB Molecule: small vasohibin-binding protein; PDBTitle: crystal structure of vash 2 in complex with svbp
51	c2j7aC_	Alignment	not modelled	8.8	3	PDB header: oxidoreductase Chain: C: PDB Molecule: cytochrome c quinol dehydrogenase nrfh; PDBTitle: crystal structure of cytochrome c nitrite reductase nrfa2 complex from desulfovibrio vulgaris
52	d2od6a1	Alignment	not modelled	8.7	47	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Marine metagenome family DABB1
53	c4dbIB_	Alignment	not modelled	8.6	14	PDB header: transport protein Chain: B: PDB Molecule: vitamin b12 import system permease protein btuc; PDBTitle: crystal structure of e159q mutant of btucdf
54	c6qwJB_	Alignment	not modelled	8.6	12	PDB header: rna binding protein Chain: B: PDB Molecule: ekc/keops complex subunit lage3; PDBTitle: protein complex
						PDB header: hydrolase

55	c6j4sB_	Alignment	not modelled	8.3	25	Chain: B; PDB Molecule: small vasohibin-binding protein; PDBTitle: structural basis of tubulin deetyrosination by vasohibinsvbp enzyme2 complex and functional implications
56	c6j4qG_	Alignment	not modelled	8.2	25	PDB header: hydrolase Chain: G; PDB Molecule: small vasohibin-binding protein; PDBTitle: structural basis of tubulin deetyrosination by vasohibinsvbp enzyme2 complex and functional implications
57	c4xtrG_	Alignment	not modelled	8.2	16	PDB header: hydrolase/transport protein Chain: G; PDB Molecule: pep12p; PDBTitle: structure of get3 bound to the transmembrane domain of pep12
58	c6adqP_	Alignment	not modelled	8.1	26	PDB header: electron transport Chain: P; PDB Molecule: prokaryotic respiratory supercomplex associate factor 1 PDBTitle: respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
59	c6jzcD_	Alignment	not modelled	8.1	25	PDB header: cytosolic protein Chain: D; PDB Molecule: small vasohibin-binding protein; PDBTitle: structural basis of tubulin deetyrosination
60	c6j4qB_	Alignment	not modelled	8.0	25	PDB header: hydrolase Chain: B; PDB Molecule: small vasohibin-binding protein; PDBTitle: structural basis of tubulin deetyrosination by vasohibinsvbp enzyme2 complex and functional implications
61	c6j4qD_	Alignment	not modelled	7.9	25	PDB header: hydrolase Chain: D; PDB Molecule: small vasohibin-binding protein; PDBTitle: structural basis of tubulin deetyrosination by vasohibinsvbp enzyme2 complex and functional implications
62	d1ub4c_	Alignment	not modelled	7.9	6	Fold: Double-split beta-barrel Superfamily: AbrB/MazE/MraZ-like Family: Kis/PemI addiction antidote
63	c6j91A_	Alignment	not modelled	7.7	23	PDB header: peptide binding protein/hydrolase Chain: A; PDB Molecule: small vasohibin-binding protein; PDBTitle: structure of a hypothetical protease
64	c2jpwA_	Alignment	not modelled	7.7	50	PDB header: contractile protein Chain: A; PDB Molecule: troponin i, cardiac muscle; PDBTitle: solution structure of the bisphosphorylated cardiac2 specific n-extension of cardiac troponin i
65	c6j7bB_	Alignment	not modelled	7.6	25	PDB header: hydrolase Chain: B; PDB Molecule: small vasohibin-binding protein; PDBTitle: crystal structure of vash1-svbp in complex with epoxy
66	c6jzcC_	Alignment	not modelled	7.6	25	PDB header: cytosolic protein Chain: C; PDB Molecule: small vasohibin-binding protein; PDBTitle: structural basis of tubulin deetyrosination
67	c6jzdB_	Alignment	not modelled	7.6	25	PDB header: cytosolic protein Chain: B; PDB Molecule: small vasohibin-binding protein; PDBTitle: crystal structure of peptide-bound vash2-svbp complex
68	c5wd7A_	Alignment	not modelled	7.6	13	PDB header: membrane protein Chain: A; PDB Molecule: siad; PDBTitle: structure of a bacterial polysialyltransferase in complex with2 fondaparinux
69	d1ljma_	Alignment	not modelled	7.5	12	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: p53-like transcription factors Family: RUNT domain
70	c6j4vB_	Alignment	not modelled	7.4	25	PDB header: hydrolase Chain: B; PDB Molecule: small vasohibin-binding protein; PDBTitle: structural basis of tubulin deetyrosination by vasohibinsvbp enzyme2 complex and functional implications
71	c5eulE_	Alignment	not modelled	7.3	8	PDB header: protein transport Chain: E; PDB Molecule: preprotein translocase sece subunit; PDBTitle: structure of the sece-secy complex with a translocating polypeptide2 substrate
72	c2c2aA_	Alignment	not modelled	7.3	13	PDB header: transferase Chain: A; PDB Molecule: sensor histidine kinase; PDBTitle: structure of the entire cytoplasmic portion of a sensor2 histidine kinase protein
73	c5wdaL_	Alignment	not modelled	7.2	15	PDB header: protein transport Chain: L; PDB Molecule: general secretion pathway protein g; PDBTitle: structure of the pulg pseudopilus
74	c2ks1B_	Alignment	not modelled	7.1	26	PDB header: transferase Chain: B; PDB Molecule: epidermal growth factor receptor; PDBTitle: heterodimeric association of transmembrane domains of erbb1 and erbb22 receptors enabling kinase activation
75	c2l16A_	Alignment	not modelled	7.0	46	PDB header: protein transport Chain: A; PDB Molecule: sec-independent protein translocase protein tatad; PDBTitle: solution structure of bacillus subtilis tatad protein in dpc micelles
76	c4l0zA_	Alignment	not modelled	6.8	12	PDB header: transcription/dna Chain: A; PDB Molecule: runt-related transcription factor 1; PDBTitle: crystal structure of runx1 and ets1 bound to tcr alpha promoter2 (crystal form 2)
77	d1eaqa_	Alignment	not modelled	6.8	12	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: p53-like transcription factors Family: RUNT domain
78	d1mvfd_	Alignment	not modelled	6.8	6	Fold: Double-split beta-barrel Superfamily: AbrB/MazE/MraZ-like Family: Kis/PemI addiction antidote
79	c4v0bA_	Alignment	not modelled	6.7	10	PDB header: hydrolase Chain: A; PDB Molecule: atp-dependent zinc metalloprotease ftsh; PDBTitle: escherichia coli ftsh hexameric n-domain
80	c4pwuC_	Alignment	not modelled	6.4	24	PDB header: signaling protein Chain: C; PDB Molecule: modulator protein mzra; PDBTitle: crystal structure of a modulator protein mzra (kpn_03524) from2 klebsiella pneumoniae subsp. pneumoniae mgh 78578 at 2.45 a3 resolution

81	c2mxbA_	Alignment	not modelled	6.3	33	PDB header: membrane protein Chain: A: PDB Molecule: erythropoietin receptor; PDBTitle: structure of the transmembrane domain of the mouse erythropoietin2 receptor
82	c5ch4E_	Alignment	not modelled	6.3	6	PDB header: protein transport Chain: E: PDB Molecule: protein translocase subunit sece; PDBTitle: peptide-bound state of thermus thermophilus secyeg
83	c6agfB_	Alignment	not modelled	6.2	11	PDB header: membrane protein Chain: B: PDB Molecule: sodium channel subunit beta-1; PDBTitle: structure of the human voltage-gated sodium channel nav1.4 in complex2 with beta1
84	c2ddhA_	Alignment	not modelled	6.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: acyl-coa oxidase; PDBTitle: crystal structure of acyl-coa oxidase complexed with 3-oh-dodecanoate
85	c2gofA_	Alignment	not modelled	6.2	38	PDB header: viral protein Chain: A: PDB Molecule: vpu protein; PDBTitle: three-dimensional structure of the trans-membrane domain of2 vpu from hiv-1 in aligned phospholipid bicelles
86	c1pi8A_	Alignment	not modelled	6.2	38	PDB header: viral protein Chain: A: PDB Molecule: vpu protein; PDBTitle: structure of the channel-forming trans-membrane domain of2 virus protein "u" (vpu) from hiv-1
87	c1pjeA_	Alignment	not modelled	6.2	38	PDB header: viral protein Chain: A: PDB Molecule: vpu protein; PDBTitle: structure of the channel-forming trans-membrane domain of2 virus protein "u"(vpu) from hiv-1
88	c1pi7A_	Alignment	not modelled	6.2	38	PDB header: viral protein Chain: A: PDB Molecule: vpu protein; PDBTitle: structure of the channel-forming trans-membrane domain of2 virus protein "u" (vpu) from hiv-1
89	c2gohA_	Alignment	not modelled	6.2	38	PDB header: viral protein Chain: A: PDB Molecule: vpu protein; PDBTitle: three-dimensional structure of the trans-membrane domain of2 vpu from hiv-1 in aligned phospholipid bicelles
90	c5mx2R_	Alignment	not modelled	6.2	27	PDB header: oxidoreductase Chain: R: PDB Molecule: photosystem ii protein y; PDBTitle: photosystem ii depleted of the mn4cao5 cluster at 2.55 a resolution
91	c2lzsE_	Alignment	not modelled	6.1	25	PDB header: protein transport Chain: E: PDB Molecule: sec-independent protein translocase protein tata; PDBTitle: tata oligomer
92	d2hzab1	Alignment	not modelled	6.1	8	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
93	c3ah9D_	Alignment	not modelled	6.1	53	PDB header: structural protein Chain: D: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
94	c2mc7A_	Alignment	not modelled	6.1	17	PDB header: membrane protein Chain: A: PDB Molecule: regulatory peptide; PDBTitle: structure of salmonella mgtr
95	c1kcpA_	Alignment	not modelled	6.1	44	PDB header: neurotoxin Chain: A: PDB Molecule: kappa-conotoxin pviia; PDBTitle: 3d structure of k-conotoxin pviia, a novel potassium channel-blocking2 toxin from cone snails, nmr, 22 structures
96	d1kcpa_	Alignment	not modelled	6.1	44	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like Family: Conotoxin
97	c6ocgB_	Alignment	not modelled	6.1	27	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: small vasohibin-binding protein; PDBTitle: crystal structure of vash1-svbp complex bound with epoxy
98	c5mx2r_	Alignment	not modelled	6.0	24	PDB header: oxidoreductase Chain: R: PDB Molecule: photosystem ii protein y; PDBTitle: photosystem ii depleted of the mn4cao5 cluster at 2.55 a resolution
99	c6ochD_	Alignment	not modelled	5.9	27	PDB header: hydrolase/hydrolase inhibitor Chain: D: PDB Molecule: small vasohibin-binding protein; PDBTitle: crystal structure of vash1-svbp complex bound with parthenolide