
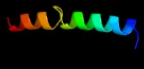
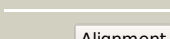
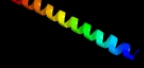
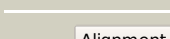

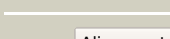
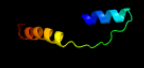

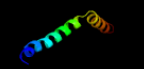





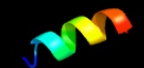

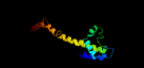



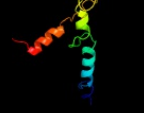
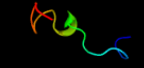



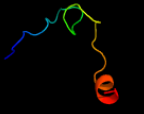
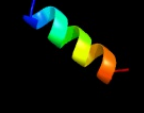





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0102_(-)_117711_119696
Date	Tue Jul 23 14:50:14 BST 2019
Unique Job ID	b791b6bcb6c4a31a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4flaC_	 Alignment		44.9	31	PDB header: transcription Chain: C: PDB Molecule: regulation of nuclear pre-mrna domain-containing protein PDBTitle: crystal structure of human rprd1b, carboxy-terminal domain
2	c5fwlE_	 Alignment		41.7	19	PDB header: chaperone Chain: E: PDB Molecule: hsp90 co-chaperone cdc37; PDBTitle: atomic cryoem structure of hsp90-cdc37-cdk4 complex
3	c5kxfA_	 Alignment		41.0	29	PDB header: rna binding protein Chain: A: PDB Molecule: flowering time control protein fpa; PDBTitle: crystal structure of the spoc domain of the arabidopsis flowering2 regulator fpa
4	c5n9mA_	 Alignment		34.1	9	PDB header: transferase Chain: A: PDB Molecule: cohyric acid synthase; PDBTitle: crystal structure of gatd - a glutamine amidotransferase from2 staphylococcus aureus involved in peptidoglycan amidation
5	c2w8aC_	 Alignment		32.0	7	PDB header: membrane protein Chain: C: PDB Molecule: glycine betaine transporter betp; PDBTitle: crystal structure of the sodium-coupled glycine betaine2 symporter betp from corynebacterium glutamicum with bound3 substrate
6	d1v4pa_	 Alignment		31.2	21	Fold: RRF/trna synthetase additional domain-like Superfamily: ThrRS/AlaRS common domain Family: AlaX-like
7	c6bn1B_	 Alignment		30.8	46	PDB header: signaling protein Chain: B: PDB Molecule: scaffold protein salvador; PDBTitle: salvador hippo sarah domain complex
8	c6ao5B_	 Alignment		30.8	38	PDB header: signaling protein Chain: B: PDB Molecule: protein salvador homolog 1; PDBTitle: crystal structure of human mst2 in complex with sav1 sarah domain
9	d1f6ga_	 Alignment		28.1	15	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
10	c4ainB_	 Alignment		27.4	9	PDB header: membrane protein Chain: B: PDB Molecule: glycine betaine transporter betp; PDBTitle: crystal structure of betp with asymmetric protomers.
11	c2jo1A_	 Alignment		25.3	23	PDB header: hydrolase regulator Chain: A: PDB Molecule: phospholemman; PDBTitle: structure of the na,k-atpase regulatory protein fxyd1 in2 micelles

12	c6hwhX	Alignment		22.1	42	PDB header: electron transport Chain: X: PDB Molecule: cytochrome c oxidase polypeptide 4; PDBTitle: structure of a functional obligate respiratory supercomplex from <i>Mycobacterium smegmatis</i>
13	c1ddxA	Alignment		21.3	18	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (prostaglandin h2 synthase-2); PDBTitle: crystal structure of a mixture of arachidonic acid and prostaglandin2 bound to the cyclooxygenase active site of cox-2: prostaglandin3 structure
14	c5z51A	Alignment		20.6	18	PDB header: transferase Chain: A: PDB Molecule: dna primase; PDBTitle: helicase binding domain of primase from <i>Mycobacterium tuberculosis</i>
15	c3pghD	Alignment		20.6	18	PDB header: oxidoreductase Chain: D: PDB Molecule: cyclooxygenase-2; PDBTitle: cyclooxygenase-2 (prostaglandin synthase-2) complexed with a non-2 selective inhibitor, flurbiprofen
16	d1cvua1	Alignment		20.6	18	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: Myeloperoxidase-like
17	d1gvna	Alignment		18.1	33	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Plasmid maintenance system epsilon/zeta, antidote epsilon subunit Family: Plasmid maintenance system epsilon/zeta, antidote epsilon subunit
18	d1q4ga1	Alignment		17.5	12	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: Myeloperoxidase-like
19	c6hc2L	Alignment		14.5	25	PDB header: cell cycle Chain: L: PDB Molecule: nuclear mitotic apparatus protein 1; PDBTitle: crystal structure of numa/ign hetero-hexamers
20	d1q90d	Alignment		13.7	17	Fold: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Superfamily: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
21	c4tq0D	Alignment	not modelled	13.0	24	PDB header: protein binding Chain: D: PDB Molecule: autophagy-related protein 16-1; PDBTitle: crystal structure of human atg5-atg16n69
22	c4tq0B	Alignment	not modelled	12.6	24	PDB header: protein binding Chain: B: PDB Molecule: autophagy-related protein 16-1; PDBTitle: crystal structure of human atg5-atg16n69
23	c2ksfA	Alignment	not modelled	11.0	21	PDB header: transferase Chain: A: PDB Molecule: sensor protein kdpd; PDBTitle: backbone structure of the membrane domain of e. coli histidine kinase2 receptor kdpd, center for structures of membrane proteins (csm)3 target 4312c
24	c2lonA	Alignment	not modelled	10.9	21	PDB header: membrane protein Chain: A: PDB Molecule: hig1 domain family member 1b; PDBTitle: backbone structure of human membrane protein hig1b
25	d2vcha1	Alignment	not modelled	10.7	5	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
26	c5npwF	Alignment	not modelled	10.3	24	PDB header: cell cycle Chain: F: PDB Molecule: autophagy-related protein 16-1; PDBTitle: structure of human atg5-atg16i1(atg5bd) complex (c2)
27	c5npvD	Alignment	not modelled	10.3	24	PDB header: cell cycle Chain: D: PDB Molecule: autophagy-related protein 16-1; PDBTitle: structure of human atg5-atg16i1(atg5bd) complex (i4)
28	c2lomA	Alignment	not modelled	10.3	15	PDB header: membrane protein Chain: A: PDB Molecule: hig1 domain family member 1a; PDBTitle: backbone structure of human membrane protein hig1a
						PDB header: cell cycle

29	c5npvB_	Alignment	not modelled	10.2	24	Chain: B; PDB Molecule: autophagy-related protein 16-1; PDBTitle: structure of human atg5-atg16l1(atg5bd) complex (i4)
30	c3c4rC_	Alignment	not modelled	9.8	21	PDB header: structural genomics, unknown function Chain: C; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein encoded by2 cryptic prophage
31	c2n28A_	Alignment	not modelled	9.8	18	PDB header: viral protein Chain: A; PDB Molecule: protein vpu; PDBTitle: solid-state nmr structure of vpu
32	c2oyuP_	Alignment	not modelled	9.6	12	PDB header: oxidoreductase Chain: P; PDB Molecule: prostaglandin g/h synthase 1; PDBTitle: indomethacin-(s)-alpha-ethyl-ethanolamide bound to cyclooxygenase-1
33	c3aqqB_	Alignment	not modelled	9.5	50	PDB header: unknown function Chain: B; PDB Molecule: zymogen granule protein 16 homolog b; PDBTitle: crystal structure of human pancreatic secretory protein zg16b
34	c1ht8B_	Alignment	not modelled	9.3	12	PDB header: oxidoreductase Chain: B; PDB Molecule: prostaglandin h2 synthase-1; PDBTitle: the 2.7 angstrom resolution model of ovine cox-1 complexed with2 alclofenac
35	c1pggB_	Alignment	not modelled	9.3	12	PDB header: oxidoreductase Chain: B; PDB Molecule: prostaglandin h2 synthase-1; PDBTitle: prostaglandin h2 synthase-1 complexed with 1-(4-iodobenzoyl)-5-2 methoxy-2-methylindole-3-acetic acid (iodoindomethacin), trans model
36	c5d3aA_	Alignment	not modelled	9.2	13	PDB header: motor protein Chain: A; PDB Molecule: kinesin-like protein kif21a; PDBTitle: kif21a regulatory coiled coil
37	c5zt3A_	Alignment	not modelled	8.9	19	PDB header: plant protein Chain: A; PDB Molecule: wa352; PDBTitle: crystal structure of wa352 from oryza sativa
38	c3m6cA_	Alignment	not modelled	8.3	18	PDB header: chaperone Chain: A; PDB Molecule: 60 kda chaperonin 1; PDBTitle: crystal structure of mycobacterium tuberculosis groel1 apical domain
39	d2e74b1	Alignment	not modelled	8.3	14	Fold: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Superfamily: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
40	c5whaF_	Alignment	not modelled	8.2	20	PDB header: protein binding Chain: F; PDB Molecule: miniprotein 225-11; PDBTitle: kras g12v, bound to gdp and miniprotein 225-11
41	d1sjpa2	Alignment	not modelled	8.0	12	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: GroEL-like chaperone, apical domain
42	c2rddB_	Alignment	not modelled	7.6	13	PDB header: membrane protein/transport protein Chain: B; PDB Molecule: upf0092 membrane protein yajc; PDBTitle: x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
43	c3rgbG_	Alignment	not modelled	7.5	20	PDB header: oxidoreductase Chain: G; PDB Molecule: methane monooxygenase subunit c2; PDBTitle: crystal structure of particulate methane monooxygenase from2 methylococcus capsulatus (bath)
44	c4tt1A_	Alignment	not modelled	7.4	21	PDB header: hydrolase Chain: A; PDB Molecule: deneddylase; PDBTitle: crystal structure of fragment 1600-1733 of hsv1 ul36, native
45	c2ncaA_	Alignment	not modelled	7.3	21	PDB header: chaperone Chain: A; PDB Molecule: hsp90 co-chaperone cdc37; PDBTitle: structural model for the n-terminal domain of human cdc37
46	c4a1a1_	Alignment	not modelled	7.3	17	PDB header: ribosome Chain: I; PDB Molecule: 60s ribosomal protein l13a; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rna,3 5.8s rna and proteins of molecule 3.
47	c3j3bO_	Alignment	not modelled	7.3	9	PDB header: ribosome Chain: O; PDB Molecule: 60s ribosomal protein l13a; PDBTitle: structure of the human 60s ribosomal proteins
48	c4r36A_	Alignment	not modelled	7.1	12	PDB header: transferase Chain: A; PDB Molecule: putative acyl-[acyl-carrier-protein]--udp-n- PDBTitle: crystal structure analysis of lpxa, a udp-n-acetylglucosamine2 acyltransferase from bacteroides fragilis 9343
49	c2mbhB_	Alignment	not modelled	7.1	17	PDB header: transcription Chain: B; PDB Molecule: krueppel-like factor 1; PDBTitle: nmr structure of eklf(22-40)/ubiquitin complex
50	c3mawB_	Alignment	not modelled	7.1	54	PDB header: viral protein Chain: B; PDB Molecule: fusion glycoprotein f0; PDBTitle: structure of the newcastle disease virus f protein in the post-fusion2 conformation
51	c4nawG_	Alignment	not modelled	7.1	25	PDB header: protein transport/ligase Chain: G; PDB Molecule: autophagy-related protein 16-1; PDBTitle: crystal structure of human atg12-atg5-atg16n in complex with a2 fragment of atg3
52	c4nawO_	Alignment	not modelled	7.1	25	PDB header: protein transport/ligase Chain: O; PDB Molecule: autophagy-related protein 16-1; PDBTitle: crystal structure of human atg12-atg5-atg16n in complex with a2 fragment of atg3
53	c5cdjA_	Alignment	not modelled	7.0	10	PDB header: chaperone Chain: A; PDB Molecule: rubisco large subunit-binding protein subunit alpha, PDBTitle: apical domain of chloroplast chaperonin 60a
54	c4gdkC_	Alignment	not modelled	6.9	25	PDB header: protein binding Chain: C; PDB Molecule: autophagy-related protein 16-1; PDBTitle: crystal structure of human atg12-atg5 conjugate in

						complex with an n-2 terminal fragment of atg16l1 PDB header: protein binding
55	c4gdIC_	Alignment	not modelled	6.9	25	Chain: C: PDB Molecule: autophagy-related protein 16-1; PDBTitle: crystal structure of human atg12-atg5 conjugate in complex with an n-2 terminal fragment of atg16l1
56	c4nawC_	Alignment	not modelled	6.9	25	PDB header: protein transport/ligase Chain: C: PDB Molecule: autophagy-related protein 16-1; PDBTitle: crystal structure of human atg12-atg5-atg16n in complex with a2 fragment of atg3
57	c5oc0A_	Alignment	not modelled	6.9	12	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome b561; PDBTitle: structure of e. coli superoxide oxidase
58	c4gdkF_	Alignment	not modelled	6.9	25	PDB header: protein binding Chain: F: PDB Molecule: autophagy-related protein 16-1; PDBTitle: crystal structure of human atg12-atg5 conjugate in complex with an n-2 terminal fragment of atg16l1
59	d1kida_	Alignment	not modelled	6.9	10	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: GroEL-like chaperone, apical domain
60	c6iedA_	Alignment	not modelled	6.9	9	PDB header: membrane protein Chain: A: PDB Molecule: heme a synthase; PDBTitle: crystal structure of heme a synthase from bacillus subtilis
61	c6e4hA_	Alignment	not modelled	6.8	33	PDB header: oncoprotein Chain: A: PDB Molecule: partner and localizer of brca2; PDBTitle: solution nmr structure of the coiled-coil palb2 homodimer
62	c5lnkZ_	Alignment	not modelled	6.7	19	PDB header: oxidoreductase Chain: Z: PDB Molecule: mitochondrial complex i, pdsw subunit; PDBTitle: entire ovine respiratory complex i
63	d1we3a2	Alignment	not modelled	6.6	10	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: GroEL-like chaperone, apical domain
64	c5y88R_	Alignment	not modelled	6.5	23	PDB header: splicing Chain: R: PDB Molecule: protein cwc16; PDBTitle: cryo-em structure of the intron-lariat spliceosome ready for2 disassembly from s.cerevisiae at 3.5 angstrom
65	c2jlnA_	Alignment	not modelled	6.5	5	PDB header: membrane protein Chain: A: PDB Molecule: mhp1; PDBTitle: structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
66	d1z9ha1	Alignment	not modelled	6.4	13	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
67	d1hr6a2	Alignment	not modelled	6.2	6	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: MPP-like
68	d2gv8a1	Alignment	not modelled	6.1	12	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
69	c3j39O_	Alignment	not modelled	6.0	13	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l13a; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
70	c3iz5K_	Alignment	not modelled	5.9	22	PDB header: ribosome Chain: K: PDB Molecule: 60s ribosomal protein l13a (l13p); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
71	c3lofF_	Alignment	not modelled	5.9	16	PDB header: chaperone Chain: F: PDB Molecule: heat shock 70 kda protein 1; PDBTitle: c-terminal domain of human heat shock 70kda protein 1b.
72	c3vviB_	Alignment	not modelled	5.9	29	PDB header: transport protein Chain: B: PDB Molecule: non selective cation channel homologous to trp channel; PDBTitle: crystal structure of the coiled-coil domain of the transient receptor2 potential channel from gibberella zeae (trpgz)
73	c3vviD_	Alignment	not modelled	5.9	29	PDB header: transport protein Chain: D: PDB Molecule: non selective cation channel homologous to trp channel; PDBTitle: crystal structure of the coiled-coil domain of the transient receptor2 potential channel from gibberella zeae (trpgz)
74	c3vviE_	Alignment	not modelled	5.9	29	PDB header: transport protein Chain: E: PDB Molecule: non selective cation channel homologous to trp channel; PDBTitle: crystal structure of the coiled-coil domain of the transient receptor2 potential channel from gibberella zeae (trpgz)
75	c3vviA_	Alignment	not modelled	5.9	29	PDB header: transport protein Chain: A: PDB Molecule: non selective cation channel homologous to trp channel; PDBTitle: crystal structure of the coiled-coil domain of the transient receptor2 potential channel from gibberella zeae (trpgz)
76	c3vviC_	Alignment	not modelled	5.9	29	PDB header: transport protein Chain: C: PDB Molecule: non selective cation channel homologous to trp channel; PDBTitle: crystal structure of the coiled-coil domain of the transient receptor2 potential channel from gibberella zeae (trpgz)
77	c3vviH_	Alignment	not modelled	5.9	29	PDB header: transport protein Chain: H: PDB Molecule: non selective cation channel homologous to trp channel; PDBTitle: crystal structure of the coiled-coil domain of the transient receptor2 potential channel from gibberella zeae (trpgz)
78	c3vviF_	Alignment	not modelled	5.9	29	PDB header: transport protein Chain: F: PDB Molecule: non selective cation channel homologous to trp channel; PDBTitle: crystal structure of the coiled-coil domain of the transient receptor2 potential channel from gibberella zeae (trpgz)
						PDB header: transport protein Chain: G: PDB Molecule: non selective cation channel homologous

79	c3vviG_	Alignment	not modelled	5.9	29	to trp channel; PDBTitle: crystal structure of the coiled-coil domain of the transient receptor2 potential channel from gibberella zeae (trpgz)
80	c2ht2B_	Alignment	not modelled	5.8	7	PDB header: membrane protein Chain: B: PDB Molecule: h(+)/cl(-) exchange transporter clca; PDBTitle: structure of the escherichia coli clc chloride channel2 y445h mutant and fab complex
81	c4btgB_	Alignment	not modelled	5.8	21	PDB header: virus Chain: B: PDB Molecule: major inner protein p1; PDBTitle: coordinates of the bacteriophage phi6 capsid subunits (p1a and p1b)2 fitted into the cryoem reconstruction of the procapsid at 4.4 a3 resolution
82	c5dg3D_	Alignment	not modelled	5.8	17	PDB header: transferase Chain: D: PDB Molecule: acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine o- PDBTitle: structure of pseudomonas aeruginosa lpxa in complex with udp-3-o-(r-3-2 hydroxydecanoyl)-glcnac
83	c3vouB_	Alignment	not modelled	5.7	13	PDB header: transport protein Chain: B: PDB Molecule: ion transport 2 domain protein, voltage-gated sodium PDBTitle: the crystal structure of nak-navsulp chimera channel
84	d1dxwa_	Alignment	not modelled	5.6	15	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
85	c3zf7d_	Alignment	not modelled	5.6	14	PDB header: ribosome Chain: D: PDB Molecule: PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
86	c2p3xA_	Alignment	not modelled	5.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: polyphenol oxidase, chloroplast; PDBTitle: crystal structure of grenache (vitis vinifera) polyphenol2 oxidase
87	d2csba5	Alignment	not modelled	5.6	38	Fold: Topoisomerase V catalytic domain-like Superfamily: Topoisomerase V catalytic domain-like Family: Topoisomerase V catalytic domain-like
88	d1b93a_	Alignment	not modelled	5.5	44	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Methylglyoxal synthase, MgsA
89	c6bl5A_	Alignment	not modelled	5.5	6	PDB header: viral protein Chain: A: PDB Molecule: head decoration protein; PDBTitle: head decoration protein from the hyperthermophilic phage p74-26
90	c5zfvF_	Alignment	not modelled	5.5	21	PDB header: transport protein Chain: F: PDB Molecule: 22-mer peptide from biopolymer transport protein exbd; PDBTitle: structure of the exbb/exbd pentameric complex (exbb5exbd1tm)
91	d1l8ya_	Alignment	not modelled	5.5	18	Fold: HMG-box Superfamily: HMG-box Family: HMG-box
92	c5f42B_	Alignment	not modelled	5.5	14	PDB header: transferase Chain: B: PDB Molecule: acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine o- PDBTitle: activity and crystal structure of francisella novicida udp-n-2 acetylglucosamine acyltransferase
93	c5xqgC_	Alignment	not modelled	5.4	26	PDB header: lyase Chain: C: PDB Molecule: pcrglx protein; PDBTitle: crystal structure of a pl 26 exo-rhamnogalacturonan lyase from2 penicillium chrysogenum complexed with unsaturated galacturonosyl3 rhamnose
94	d1rw2a_	Alignment	not modelled	5.4	29	Fold: alpha-alpha superhelix Superfamily: C-terminal domain of Ku80 Family: C-terminal domain of Ku80
95	c2f9jP_	Alignment	not modelled	5.4	30	PDB header: rna binding protein Chain: P: PDB Molecule: splicing factor 3b subunit 1; PDBTitle: 3.0 angstrom resolution structure of a y22m mutant of the spliceosomal2 protein p14 bound to a region of sf3b155
96	d1a0rp_	Alignment	not modelled	5.3	7	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Phosducin
97	d1bt3a_	Alignment	not modelled	5.3	12	Fold: Di-copper centre-containing domain Superfamily: Di-copper centre-containing domain Family: Catechol oxidase
98	c4odaD_	Alignment	not modelled	5.3	13	PDB header: hydrolase/replication Chain: D: PDB Molecule: dna polymerase processivity factor component a20; PDBTitle: crystal structure of the vaccinia virus dna polymerase holoenzyme2 subunit d4 in complex with the a20 n-terminus
99	c3m6zA_	Alignment	not modelled	5.2	38	PDB header: isomerase Chain: A: PDB Molecule: topoisomerase v; PDBTitle: crystal structure of an n-terminal 44 kda fragment of topoisomerase v2 in the presence of guanidium hydrochloride