
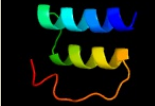
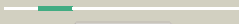
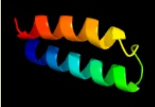



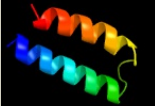

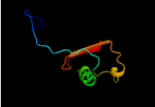



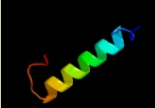





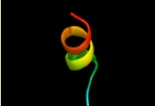

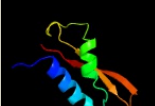



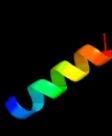
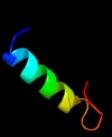
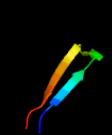


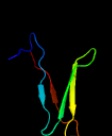


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0048c_(-)_51828_52697
Date	Tue Jul 23 14:50:07 BST 2019
Unique Job ID	4a44232ef896e475

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2pp4a1	 Alignment		47.5	19	Fold: TAFH domain-like Superfamily: TAFH domain-like Family: TAFH domain-like
2	d2caza1	 Alignment		47.3	18	Fold: Long alpha-hairpin Superfamily: Endosomal sorting complex assembly domain Family: VPS23 C-terminal domain
3	d2f6ma1	 Alignment		47.1	18	Fold: Long alpha-hairpin Superfamily: Endosomal sorting complex assembly domain Family: VPS23 C-terminal domain
4	c2cazD_	 Alignment		47.0	18	PDB header: protein transport Chain: D: PDB Molecule: suppressor protein stp22 of temperature-sensitive alpha- PDBTitle: escrt-i core
5	c3s6kA_	 Alignment		28.5	14	PDB header: transferase Chain: A: PDB Molecule: acetylglutamate kinase; PDBTitle: crystal structure of xcnags
6	d2p6va1	 Alignment		23.9	17	Fold: TAFH domain-like Superfamily: TAFH domain-like Family: TAFH domain-like
7	c4egeA_	 Alignment		23.1	29	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidase pepe; PDBTitle: crystal structure of dipeptidase pepe from mycobacterium ulcerans
8	c5vj7B_	 Alignment		20.1	20	PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin-nadp(+) reductase subunit alpha; PDBTitle: ferredoxin nadp oxidoreductase (xfn)
9	d2pnwa1	 Alignment		18.2	53	Fold: Double psi beta-barrel Superfamily: Barwin-like endoglucanases Family: MLTA-like
10	c1ponB_	 Alignment		17.0	21	PDB header: calcium-binding protein Chain: B: PDB Molecule: troponin c; PDBTitle: site iii-site iv troponin c heterodimer, nmr
11	c2odrC_	 Alignment		16.4	17	PDB header: ligase Chain: C: PDB Molecule: phosphoseryl-trna synthetase; PDBTitle: methanococcus maripaludis phosphoseryl-trna synthetase

12	d1vbka2	Alignment		16.4	22	Fold: THUMP domain Superfamily: THUMP domain-like Family: THUMP domain
13	d1nosa_	Alignment		16.3	27	Fold: Nitric oxide (NO) synthase oxygenase domain Superfamily: Nitric oxide (NO) synthase oxygenase domain Family: Nitric oxide (NO) synthase oxygenase domain
14	d2p12a1	Alignment		15.5	25	Fold: FomD barrel-like Superfamily: FomD-like Family: FomD-like
15	c3e56A_	Alignment		15.2	44	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the 2.0 angstrom resolution crystal structure of npr1517, a putative2 heterocyst differentiation inhibitor from nostoc punctiforme
16	d1j6ua2	Alignment		14.0	17	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
17	d2g5da1	Alignment		13.9	29	Fold: Double psi beta-barrel Superfamily: Barwin-like endoglucanases Family: MLTA-like
18	c6f6jC_	Alignment		13.7	18	PDB header: oxidoreductase Chain: C: PDB Molecule: l-lysine 3-hydroxylase; PDBTitle: crystal structure of the fe(ii)/alpha-ketoglutarate dependent2 dioxygenase kdo1 with fe(ii)/succinate/(3s)-3-hydroxy-l-lysine
19	c3l20A_	Alignment		13.1	29	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a hypothetical protein from staphylococcus aureus
20	d2azeb1	Alignment		11.8	6	Fold: E2F-DP heterodimerization region Superfamily: E2F-DP heterodimerization region Family: E2F dimerization segment
21	c5jcaS_	Alignment	not modelled	11.5	20	PDB header: oxidoreductase Chain: S: PDB Molecule: nadh-dependent ferredoxin:nadp oxidoreductase (nfn1) PDBTitle: nadp(h) bound nadh-dependent ferredoxin:nadp oxidoreductase (nfn1)2 from pyrococcus furiosus
22	c2p22A_	Alignment	not modelled	11.4	18	PDB header: transport protein Chain: A: PDB Molecule: suppressor protein stp22 of temperature-sensitive alpha- PDBTitle: structure of the yeast escrt-i heterotetramer core
23	c3czbA_	Alignment	not modelled	11.0	35	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative transglycosylase; PDBTitle: crystal structure of putative transglycosylase from caulobacter2 crescentus
24	c3ff0A_	Alignment	not modelled	10.1	18	PDB header: biosynthetic protein Chain: A: PDB Molecule: phenazine biosynthesis protein phzb 2; PDBTitle: crystal structure of a phenazine biosynthesis-related protein (phzb2)2 from pseudomonas aeruginosa at 1.90 a resolution
25	d1l1kta_	Alignment	not modelled	9.5	26	Fold: Head-binding domain of phage P22 tailspike protein Superfamily: Head-binding domain of phage P22 tailspike protein Family: Head-binding domain of phage P22 tailspike protein
26	c5cwwC_	Alignment	not modelled	9.3	30	PDB header: transport protein Chain: C: PDB Molecule: nucleoporin nup159; PDBTitle: crystal structure of the chaetomium thermophilum heterotrimeric nup822 ntd-nup159 tail-nup145n apd complex
27	c3fo8D_	Alignment	not modelled	9.2	27	PDB header: viral protein Chain: D: PDB Molecule: tail sheath protein gp18; PDBTitle: crystal structure of the bacteriophage t4 tail sheath protein_2 protease resistant fragment gp18pr
28	c4ylfA_	Alignment	not modelled	9.0	10	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase b (nad(+)), electron transfer PDBTitle: insights into flavin-based electron bifurcation via the

						nadh-dependent2 reduced ferredoxin-nadp oxidoreductase structure
29	d1kxpd3	Alignment	not modelled	8.9	21	Fold: Serum albumin-like Superfamily: Serum albumin-like Family: Serum albumin-like
30	c4n7vC	Alignment	not modelled	8.5	50	PDB header: cell cycle Chain: C: PDB Molecule: centrosomal protein of 152 kda; PDBTitle: crystal structure of human plk4 cryptic polo box (cpb) in complex with2 a cep152 n-terminal fragment
31	d2bh1x1	Alignment	not modelled	8.3	25	Fold: Alpha-lytic protease prodomain-like Superfamily: EspE N-terminal domain-like Family: GSPll protein E N-terminal domain-like
32	c2bh1Y	Alignment	not modelled	8.3	25	PDB header: transport protein Chain: Y: PDB Molecule: general secretion pathway protein e.; PDBTitle: x-ray structure of the general secretion pathway complex of2 the n-terminal domain of epse and the cytosolic domain of3 epsl of vibrio cholerae
33	c1zaxZ	Alignment	not modelled	8.1	22	PDB header: structural protein Chain: Z: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
34	c1zawU	Alignment	not modelled	8.0	22	PDB header: structural protein Chain: U: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
35	c1zawW	Alignment	not modelled	8.0	22	PDB header: structural protein Chain: W: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
36	c1zawV	Alignment	not modelled	8.0	22	PDB header: structural protein Chain: V: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
37	c4xaeB	Alignment	not modelled	8.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: feruloyl coa ortho-hydroxylase 1; PDBTitle: structure of feruloyl-coa 6-hydroxylase (f6h) from arabidopsis2 thaliana
38	c4p74D	Alignment	not modelled	8.0	17	PDB header: ligase/ligase inhibitor Chain: D: PDB Molecule: phenylalanine--trna ligase alpha subunit; PDBTitle: phers in complex with compound 3a
39	c2odrD	Alignment	not modelled	7.9	17	PDB header: ligase Chain: D: PDB Molecule: phosphoseryl-trna synthetase; PDBTitle: methanococcus maripaludis phosphoseryl-trna synthetase
40	c6cumA	Alignment	not modelled	7.9	27	PDB header: transferase Chain: A: PDB Molecule: lao/ao transport system atpase; PDBTitle: crystal structure of a c-terminal proteolytic fragment of a protein2 annotated as an lao/ao transport system atpase but likely meab and3 mmaa-like gtpase from mycobacterium smegmatis
41	c1zaxW	Alignment	not modelled	7.9	22	PDB header: structural protein Chain: W: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
42	d1zavu1	Alignment	not modelled	7.9	22	Fold: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain
43	c1zavU	Alignment	not modelled	7.9	22	PDB header: structural protein Chain: U: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p21
44	c1zavV	Alignment	not modelled	7.9	22	PDB header: structural protein Chain: V: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p21
45	c1zaxV	Alignment	not modelled	7.9	22	PDB header: structural protein Chain: V: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
46	c1zavW	Alignment	not modelled	7.9	22	PDB header: structural protein Chain: W: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p21
47	c1zaxU	Alignment	not modelled	7.9	22	PDB header: structural protein Chain: U: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
48	c3li6D	Alignment	not modelled	7.8	29	PDB header: metal binding protein Chain: D: PDB Molecule: calcium-binding protein; PDBTitle: crystal structure and trimer-monomer transition of n-terminal domain2 of ehcbp1 from entamoeba histolytica
49	c4yyfC	Alignment	not modelled	7.8	19	PDB header: hydrolase Chain: C: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: the crystal structure of a glycosyl hydrolase of gh3 family member2 from [mycobacterium smegmatis str. mc2 155
50	c2dhyA	Alignment	not modelled	7.7	7	PDB header: immune system Chain: A: PDB Molecule: cue domain-containing protein 1; PDBTitle: solution structure of the cue domain in the human cue2 domain containing protein 1 (cuedc1)
51	c3b4oB	Alignment	not modelled	7.6	14	PDB header: biosynthetic protein Chain: B: PDB Molecule: phenazine biosynthesis protein a/b; PDBTitle: crystal structure of phenazine biosynthesis protein phza/b2 from burkholderia cepacia r18194, apo form
52	d1s6ja	Alignment	not modelled	7.6	10	Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like
53	d1ylea1	Alignment	not modelled	7.5	18	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: Asta-like
						PDB header: ribosome

54	c1rqtA_	Alignment	not modelled	7.5	27	Chain: A: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: nmr structure of dimeric n-terminal domain of ribosomal2 protein l7 from e.coli
55	c1rqtB_	Alignment	not modelled	7.5	27	PDB header: ribosome Chain: B: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: nmr structure of dimeric n-terminal domain of ribosomal2 protein l7 from e.coli
56	d1rqtA_	Alignment	not modelled	7.5	27	Fold: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain
57	d3orca_	Alignment	not modelled	7.4	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
58	d2hw4a1	Alignment	not modelled	7.3	33	Fold: PHP14-like Superfamily: PHP14-like Family: janus/Ocnus
59	c6b2zd_	Alignment	not modelled	7.2	30	PDB header: membrane protein Chain: D: PDB Molecule: atp synthase subunit c, mitochondrial; PDBTitle: cryo-em structure of the dimeric fo region of yeast mitochondrial atp2 synthase
60	c4hicA_	Alignment	not modelled	7.2	26	PDB header: unknown function Chain: A: PDB Molecule: trak; PDBTitle: crystal structure of the potential transfer protein trak from gram-2 positive conjugative plasmid pip501
61	d1dd4c_	Alignment	not modelled	7.1	22	Fold: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain
62	c2fqhA_	Alignment	not modelled	7.1	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ta0938; PDBTitle: nmr structure of hypothetical protein ta0938 from2 thermoplasma acidophilum
63	d1dd3a1	Alignment	not modelled	7.1	22	Fold: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain
64	c1dd3C_	Alignment	not modelled	7.0	25	PDB header: ribosome Chain: C: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: crystal structure of ribosomal protein l12 from thermotoga maritima
65	c1dd3D_	Alignment	not modelled	7.0	25	PDB header: ribosome Chain: D: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: crystal structure of ribosomal protein l12 from thermotoga maritima
66	d2hh8a1	Alignment	not modelled	7.0	18	Fold: YdfO-like Superfamily: YdfO-like Family: YdfO-like
67	d1jj2h_	Alignment	not modelled	7.0	14	Fold: alpha/beta-Hammerhead Superfamily: Ribosomal protein L16p/L10e Family: Ribosomal protein L10e
68	c3sqhB_	Alignment	not modelled	6.8	25	PDB header: hydrolase Chain: B: PDB Molecule: glycosyl hydrolase family 3; PDBTitle: crystal structure of glycoside hydrolase from synechococcus
69	c3mvaA_	Alignment	not modelled	6.8	17	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate:l-alanyl-gamma-d-glutamyl-medo- PDBTitle: crystal structure of a domain from a putative udp-n-acetylmuramate:l-2 alanyl-gamma-d-glutamyl-medo-diaminopimelate ligase from haemophilus3 ducreyi 35000hp
70	c2ld7A_	Alignment	not modelled	6.8	26	PDB header: transcription Chain: A: PDB Molecule: histone deacetylase complex subunit sap30; PDBTitle: solution structure of the msin3a pah3-sap30 sid complex
71	c3e90B_	Alignment	not modelled	6.6	22	PDB header: hydrolase Chain: B: PDB Molecule: ns3 protease; PDBTitle: west nile vi rus ns2b-ns3protease in complexed with2 inhibitor naph-kr-h
72	d1u7ia_	Alignment	not modelled	6.4	14	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: 3-demethylubiquinone-9 3-methyltransferase
73	c1t7IA_	Alignment	not modelled	6.3	26	PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydropteroyltriglutamate--homocysteine PDBTitle: crystal structure of cobalamin-independent methionine synthase from t.2 maritima
74	d2ijob1	Alignment	not modelled	6.3	21	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
75	c1wr2A_	Alignment	not modelled	6.0	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ph1789; PDBTitle: crystal structure of ph1788 from pyrococcus horikoshii ot3
76	d1p3da2	Alignment	not modelled	5.9	17	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
77	c3ppgA_	Alignment	not modelled	5.8	16	PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydropteroyltriglutamate--homocysteine PDBTitle: crystal structure of the candida albicans methionine synthase by2 surface entropy reduction, alanine variant with zinc PDB header: structural genomics, hydrolase

78	c2hw4A_	Alignment	not modelled	5.7	35	Chain: A: PDB Molecule: 14 kda phosphohistidine phosphatase; PDBTitle: crystal structure of human phosphohistidine phosphatase
79	c5bzaA_	Alignment	not modelled	5.7	10	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: crystal structure of cbsa from thermotoga neapolitana
80	c4pzjA_	Alignment	not modelled	5.6	4	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, lysr family; PDBTitle: 1.60 angstrom resolution crystal structure of a transcriptional2 regulator of the lysr family from eggerthella lenta dsm 2243
81	d2fp7b1	Alignment	not modelled	5.6	21	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
82	c3h3hA_	Alignment	not modelled	5.5	4	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized snoal-like protein; PDBTitle: crystal structure of a snoal-like protein of unknown function2 (bth_ii0226) from burkholderia thailandensis e264 at 1.60 a3 resolution
83	c3m1eA_	Alignment	not modelled	5.5	9	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: crystal structure of benm_dbd
84	c6odmK_	Alignment	not modelled	5.4	15	PDB header: viral protein Chain: K: PDB Molecule: capsid vertex component 2; PDBTitle: herpes simplex virus type 1 (hsv-1) portal vertex-adjacent2 capsid/catc, asymmetric unit
85	d1okia1	Alignment	not modelled	5.4	20	Fold: gamma-Crystallin-like Superfamily: gamma-Crystallin-like Family: Crystallins/Ca-binding development proteins
86	c2odrB_	Alignment	not modelled	5.4	17	PDB header: ligase Chain: B: PDB Molecule: phosphoseryl-trna synthetase; PDBTitle: methanococcus maripaludis phosphoseryl-trna synthetase
87	c3lkwA_	Alignment	not modelled	5.4	27	PDB header: viral protein,hydrolase Chain: A: PDB Molecule: fusion protein of nonstructural protein 2b and PDBTitle: crystal structure of dengue virus 1 ns2b/ns3 protease active site2 mutant
88	c6f5dH_	Alignment	not modelled	5.4	19	PDB header: hydrolase Chain: H: PDB Molecule: atp synthase subunit delta, mitochondrial; PDBTitle: trypanosoma brucei f1-atpase
89	d3cjrbl	Alignment	not modelled	5.3	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Ribosomal protein L11, C-terminal domain Family: Ribosomal protein L11, C-terminal domain
90	c2vkyB_	Alignment	not modelled	5.3	26	PDB header: viral protein Chain: B: PDB Molecule: tail protein, piigcn4; PDBTitle: headbinding domain of phage p22 tailspike c-terminally fused to2 isoleucine zipper piigcn4 (chimera i)
91	d1ctda_	Alignment	not modelled	5.1	38	Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like
92	c4ednO_	Alignment	not modelled	5.1	55	PDB header: signaling protein/cell adhesion Chain: O: PDB Molecule: paxillin; PDBTitle: crystal structure of beta-parvin ch2 domain in complex with paxillin2 ld1 motif
93	c5craB_	Alignment	not modelled	5.1	8	PDB header: hydrolase Chain: B: PDB Molecule: sdea; PDBTitle: structure of the sdea dub domain
94	c5lc0B_	Alignment	not modelled	5.0	27	PDB header: hydrolase Chain: B: PDB Molecule: ns2b-ns3 protease,ns2b-ns3 protease; PDBTitle: crystal structure of zika virus ns2b-ns3 protease in complex with a2 boronate inhibitor
95	d1dd4d_	Alignment	not modelled	5.0	25	Fold: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain