
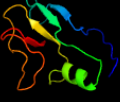
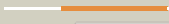
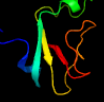

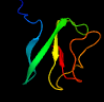

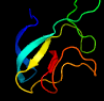

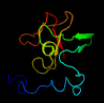

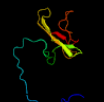
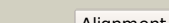

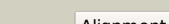







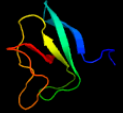
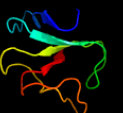
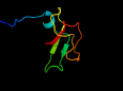

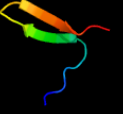
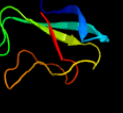
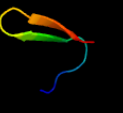




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2597_(-)_2926365_2926985
Date	Wed Aug 7 12:50:23 BST 2019
Unique Job ID	64a5413c2b5b3342

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2cp6a1	 Alignment		84.7	24	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
2	d2cowa1	 Alignment		80.9	26	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
3	d1whka_	 Alignment		66.0	11	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
4	c4b6mA_	 Alignment		64.2	20	PDB header: structural protein Chain: A: PDB Molecule: tubulin-specific chaperone, putative; PDBTitle: trypanosoma brucei tubulin binding cofactor b cap-gly domain
5	d1whja_	 Alignment		60.4	13	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
6	d2cp5a1	 Alignment		58.8	16	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
7	d2coza1	 Alignment		58.7	20	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
8	d2hqha1	 Alignment		58.0	24	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
9	d2coya1	 Alignment		56.4	24	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
10	d1ed7a_	 Alignment		56.3	25	Fold: WW domain-like Superfamily: Carbohydrate binding domain Family: Carbohydrate binding domain
11	c2e4hA_	 Alignment		54.0	23	PDB header: structural protein Chain: A: PDB Molecule: restin; PDBTitle: solution structure of cytoskeletal protein in complex with2 tubulin tail

12	d2cp0a1	Alignment		53.6	20	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
13	d2cp2a1	Alignment		51.2	24	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
14	c2z0wA	Alignment		50.7	16	PDB header: protein binding Chain: A; PDB Molecule: cap-gly domain-containing linker protein 4; PDBTitle: crystal structure of the 2nd cap-gly domain in human restin-2 like protein 2 reveals a swapped-dimer
15	d2f9ha1	Alignment		48.8	24	Fold: PTSIIA/GutA-like Superfamily: PTSIIA/GutA-like Family: PTSIIA/GutA-like
16	c4h87A	Alignment		47.2	24	PDB header: peptide binding protein Chain: A; PDB Molecule: kanadapтин; PDBTitle: crystal structure of a fha domain of kanadapтин (slc4a1ap) from homo2 sapiens at 1.55 a resolution
17	d2e3ha1	Alignment		47.2	22	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
18	d1p9ka	Alignment		46.9	26	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ybcj-like
19	d2cp3a1	Alignment		43.7	21	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
20	d2e3ia1	Alignment		42.3	21	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
21	d1ixda	Alignment	not modelled	41.4	16	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
22	d1c0ma2	Alignment	not modelled	41.1	21	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
23	d1tova	Alignment	not modelled	37.2	18	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
24	c3cwzB	Alignment	not modelled	35.3	14	PDB header: transport protein Chain: B; PDB Molecule: rab6-interacting protein 1; PDBTitle: structure of rab6(gtp)-r6ip1 complex
25	d1whha	Alignment	not modelled	26.3	15	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
26	c2nv4A	Alignment	not modelled	25.3	19	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: upf0066 protein af_0241; PDBTitle: crystal structure of upf0066 protein af0241 in complex with 2 s-adenosylmethionine. northeast structural genomics3 consortium target gr27
27	d2f4ma1	Alignment	not modelled	23.8	19	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
28	c3e0eA	Alignment	not modelled	23.7	22	PDB header: replication Chain: A; PDB Molecule: replication protein a; PDBTitle: crystal structure of a domain of replication protein a from 2 methanococcus maripaludis. northeast structural genomics3 target mrr110b

29	c3okxA	Alignment	not modelled	22.1	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: yaeb-like protein rpa0152; PDBTitle: crystal structure of yaeb-like protein from rhodospseudomonas palustris
30	c2ls01	Alignment	not modelled	22.0	16	PDB header: hydrolase Chain: 1: PDB Molecule: zoocin a endopeptidase; PDB Fragment: unp residues 170-285; PDBTitle: solution structure of the target recognition domain of zoocin a
31	d2affa1	Alignment	not modelled	20.5	14	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
32	c5dniB	Alignment	not modelled	20.4	37	PDB header: lyase Chain: B: PDB Molecule: putative (+)-tartrate dehydratase subunit beta; PDBTitle: crystal structure of methanocaldococcus jannaschii fumarate hydratase2 beta subunit
33	d1cz5a1	Alignment	not modelled	20.3	18	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
34	c3a5zF	Alignment	not modelled	20.1	24	PDB header: ligase Chain: F: PDB Molecule: elongation factor p; PDBTitle: crystal structure of escherichia coli genx in complex with elongation2 factor p
35	c2mkvA	Alignment	not modelled	20.1	15	PDB header: transport protein Chain: A: PDB Molecule: sodium/potassium-transporting atpase subunit gamma; PDBTitle: structure of the na,k-atpase regulatory protein fxyd2b in micelles
36	d2vv5a1	Alignment	not modelled	19.5	32	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Mechanosensitive channel protein MscS (YggB), middle domain
37	d1k0ha	Alignment	not modelled	19.2	25	Fold: Phage tail proteins Superfamily: Phage tail proteins Family: gpFII-like
38	c6fc6A	Alignment	not modelled	18.8	14	PDB header: cell cycle Chain: A: PDB Molecule: nuclear fusion protein bik1; PDBTitle: bik1 cap-gly domain with etf peptide from bim1
39	d1x3za1	Alignment	not modelled	18.5	19	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
40	c4a0eB	Alignment	not modelled	18.4	14	PDB header: transport protein Chain: B: PDB Molecule: type iii secretion protein; PDBTitle: crystal structure of the cytoplasmic n-terminal domain of yersinia2 pestis yscd
41	c3dm3A	Alignment	not modelled	18.2	20	PDB header: replication Chain: A: PDB Molecule: replication factor a; PDBTitle: crystal structure of a domain of a replication factor a2 protein, from methanocaldococcus jannaschii. northeast3 structural genomics target mjrl18e
42	d2icha1	Alignment	not modelled	17.8	25	Fold: AttH-like Superfamily: AttH-like Family: AttH-like
43	d2isba1	Alignment	not modelled	16.7	26	Fold: The "swivelling" beta/beta/alpha domain Superfamily: FumA C-terminal domain-like Family: FumA C-terminal domain-like
44	d1vyva1	Alignment	not modelled	15.5	11	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
45	c1r21A	Alignment	not modelled	15.5	14	PDB header: cell cycle Chain: A: PDB Molecule: antigen ki-67; PDBTitle: solution structure of human ki67 fha domain
46	c2wkdA	Alignment	not modelled	15.1	18	PDB header: dna binding protein Chain: A: PDB Molecule: orf34p2; PDBTitle: crystal structure of a double ile-to-met mutant of protein orf34 from2 lactococcus phage p2
47	d1eika	Alignment	not modelled	14.1	25	Fold: RPB5-like RNA polymerase subunit Superfamily: RPB5-like RNA polymerase subunit Family: RPB5
48	c3ounA	Alignment	not modelled	13.8	30	PDB header: protein binding/transferase Chain: A: PDB Molecule: putative uncharacterized protein tb39.8; PDBTitle: crystal structure of the fhaa fha domain complexed with the2 intracellular domain of rv3910
49	d1rl2a2	Alignment	not modelled	13.7	27	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
50	d2qamc2	Alignment	not modelled	13.5	27	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
51	c3poaA	Alignment	not modelled	13.5	30	PDB header: peptide binding protein Chain: A: PDB Molecule: putative uncharacterized protein tb39.8; PDBTitle: structural and functional analysis of phosphothreonine-dependent fha2 domain interactions
52	d1vioa2	Alignment	not modelled	13.2	7	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Pseudouridine synthase RsuA N-terminal domain
53	d2zjra2	Alignment	not modelled	13.1	42	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
54	c6msoD	Alignment	not modelled	12.3	21	PDB header: lyase/lyase inhibitor Chain: D: PDB Molecule: fumarate hydratase; PDBTitle: crystal structure of mitochondrial fumarate hydratase from leishmania2 major in a complex with inhibitor thiomalate

55	c4owtB_	Alignment	not modelled	12.3	23	PDB header: dna binding protein Chain: B: PDB Molecule: soxs complex subunit b1; PDBTitle: structural basis of soxs1 complex assembly
56	d1goia1	Alignment	not modelled	12.2	42	Fold: WW domain-like Superfamily: Carbohydrate binding domain Family: Carbohydrate binding domain
57	c3mk7F_	Alignment	not modelled	11.7	6	PDB header: oxidoreductase Chain: F: PDB Molecule: cytochrome c oxidase, cbb3-type, subunit p; PDBTitle: the structure of cbb3 cytochrome oxidase
58	c3eswA_	Alignment	not modelled	11.6	19	PDB header: hydrolase Chain: A: PDB Molecule: peptide-n(4)-(n-acetyl-beta-glucosaminyl)asparagine PDBTitle: complex of yeast pngase with glcnac2-iac.
59	d2cqaa1	Alignment	not modelled	11.4	8	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: TIP49 domain
60	c2q5xA_	Alignment	not modelled	11.3	40	PDB header: protein transport Chain: A: PDB Molecule: nuclear pore complex protein nup98; PDBTitle: crystal structure of the c-terminal domain of hnup98
61	c6cahA_	Alignment	not modelled	11.2	29	PDB header: protein binding Chain: A: PDB Molecule: abc transporter atp-binding/permease protein rv1747; PDBTitle: nmr-based structure of the fha-2 domain from mycobacterium2 tuberculosis abc transporter rv1747
62	d2piaa1	Alignment	not modelled	11.1	15	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
63	d2ff4a3	Alignment	not modelled	11.1	10	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
64	c1vw4M_	Alignment	not modelled	10.8	20	PDB header: ribosome Chain: M: PDB Molecule: 54s ribosomal protein img1, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
65	c5vgzF_	Alignment	not modelled	10.6	21	PDB header: hydrolase Chain: F: PDB Molecule: 26s proteasome regulatory subunit 6a; PDBTitle: conformational landscape of the p28-bound human proteasome regulatory2 particle
66	c1mhsA_	Alignment	not modelled	10.6	17	PDB header: membrane protein, proton transport Chain: A: PDB Molecule: plasma membrane atpase; PDBTitle: model of neurospora crassa proton atpase
67	d1tvca1	Alignment	not modelled	10.6	23	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
68	c2mk5A_	Alignment	not modelled	10.3	26	PDB header: hydrolase Chain: A: PDB Molecule: endolysin; PDBTitle: solution structure of a protein domain
69	c4djiA_	Alignment	not modelled	10.3	19	PDB header: transport protein Chain: A: PDB Molecule: probable glutamate/gamma-aminobutyrate antiporter; PDBTitle: structure of glutamate-gaba antiporter gadc
70	c1jb7A_	Alignment	not modelled	10.2	11	PDB header: dna-binding protein/dna Chain: A: PDB Molecule: telomere-binding protein alpha subunit; PDBTitle: dna g-quartets in a 1.86 a resolution structure of an oxytricha nova2 telomeric protein-dna complex
71	c1ph4A_	Alignment	not modelled	10.2	11	PDB header: dna binding protein/dna Chain: A: PDB Molecule: telomere-binding protein alpha subunit; PDBTitle: crystal structure of the oxytricha nova telomere end-binding protein2 complexed with noncognate ssdna ggggttttgccg
72	c2jp3A_	Alignment	not modelled	10.2	19	PDB header: transcription Chain: A: PDB Molecule: fxyd domain-containing ion transport regulator 4; PDBTitle: solution structure of the human fxyd4 (chif) protein in sds2 micelles
73	c4in3C_	Alignment	not modelled	9.9	25	PDB header: protein transport Chain: C: PDB Molecule: chitin biosynthesis protein chs5; PDBTitle: crystal structure of the chs5-bch1 exomer cargo adaptor complex
74	d1s04a_	Alignment	not modelled	9.9	42	Fold: PUA domain-like Superfamily: PUA domain-like Family: ProFAR isomerase associated domain
75	c2d49A_	Alignment	not modelled	9.8	38	PDB header: hydrolase Chain: A: PDB Molecule: chitinase c; PDBTitle: solution structure of the chitin-binding domain of 2 streptomyces griseus chitinase c
76	c3cyyA_	Alignment	not modelled	9.8	14	PDB header: peptide binding protein Chain: A: PDB Molecule: tight junction protein zo-1; PDBTitle: the crystal structure of zo-1 pdz2 in complex with the cx43 peptide
77	d1krha1	Alignment	not modelled	9.8	31	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
78	c4qiwH_	Alignment	not modelled	9.7	13	PDB header: transcription Chain: H: PDB Molecule: dna-directed rna polymerase subunit h; PDBTitle: crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis
79	c3ij3A_	Alignment	not modelled	9.6	33	PDB header: hydrolase Chain: A: PDB Molecule: cytosol aminopeptidase; PDBTitle: 1.8 angstrom resolution crystal structure of cytosol aminopeptidase2 from coxiella burnetii
80	c5vgzC_	Alignment	not modelled	9.6	13	PDB header: hydrolase Chain: C: PDB Molecule: 26s proteasome regulatory subunit 8; PDBTitle: conformational landscape of the p28-bound human proteasome regulatory2 particle

81	c1z9zA_	Alignment	not modelled	9.6	19	PDB header: structural protein Chain: A: PDB Molecule: cytoskeleton assembly control protein sla1; PDBTitle: crystal structure of yeast sla1 sh3 domain 3
82	d2bmwa1	Alignment	not modelled	9.6	36	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
83	c3kf8D_	Alignment	not modelled	9.5	27	PDB header: structural protein Chain: D: PDB Molecule: protein ten1; PDBTitle: crystal structure of c. tropicalis stn1-ten1 complex
84	c3gqsB_	Alignment	not modelled	9.5	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: adenylate cyclase-like protein; PDBTitle: crystal structure of the fha domain of ct664 protein from chlamydia2 trachomatis
85	c5ounA_	Alignment	not modelled	9.1	15	PDB header: hydrolase Chain: A: PDB Molecule: ruvb-like protein 2; PDBTitle: nmr solution structure of the external dii domain of rvb2 from2 saccharomyces cerevisiae
86	d1hmja_	Alignment	not modelled	8.9	20	Fold: RPB5-like RNA polymerase subunit Superfamily: RPB5-like RNA polymerase subunit Family: RPB5
87	c3ebrA_	Alignment	not modelled	8.8	20	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized rmlc-like cupin; PDBTitle: crystal structure of an rmlc-like cupin protein (reut_a0381) from2 ralstonia eutropha jmp134 at 2.60 a resolution
88	c2q1dX_	Alignment	not modelled	8.7	19	PDB header: lyase Chain: X: PDB Molecule: 2-keto-3-deoxy-d-arabinonate dehydratase; PDBTitle: 2-keto-3-deoxy-d-arabinonate dehydratase complexed with magnesium and2 2,5-dioxopentanoate
89	d1gvha2	Alignment	not modelled	8.6	15	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
90	d2d6fa1	Alignment	not modelled	8.6	24	Fold: Sm-like fold Superfamily: GatD N-terminal domain-like Family: GatD N-terminal domain-like
91	c5wxkB_	Alignment	not modelled	8.6	22	PDB header: transferase Chain: B: PDB Molecule: elongation factor p; PDBTitle: earp bound with domain i of ef-p
92	c3kzwD_	Alignment	not modelled	8.5	7	PDB header: hydrolase Chain: D: PDB Molecule: cytosol aminopeptidase; PDBTitle: crystal structure of cytosol aminopeptidase from staphylococcus aureus2 col
93	d1cxa2	Alignment	not modelled	8.5	15	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
94	c5l2rA_	Alignment	not modelled	8.4	32	PDB header: lyase Chain: A: PDB Molecule: fumarate hydratase; PDBTitle: crystal structure of fumarate hydratase from leishmania major
95	c3j20R_	Alignment	not modelled	8.4	21	PDB header: ribosome Chain: R: PDB Molecule: 30s ribosomal protein s17p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
96	c4hw9E_	Alignment	not modelled	8.4	21	PDB header: membrane protein Chain: E: PDB Molecule: mechanosensitive channel mscs; PDBTitle: crystal structure of helicobacter pylori mscs (closed state)
97	c3h8gC_	Alignment	not modelled	8.1	27	PDB header: hydrolase Chain: C: PDB Molecule: cytosol aminopeptidase; PDBTitle: bestatin complex structure of leucine aminopeptidase from pseudomonas2 putida
98	c4nz3A_	Alignment	not modelled	8.0	27	PDB header: hydrolase Chain: A: PDB Molecule: deacetylase da1; PDBTitle: structure of vibrio cholerae chitin de-n-acetylase in complex with2 di(n-acetyl-d-glucosamine) (cbs) in p 21 21 21
99	c6a8wA_	Alignment	not modelled	8.0	29	PDB header: protein binding Chain: A: PDB Molecule: vacuolar protein sorting-associated protein 64; PDBTitle: crystal structure of the fha domain of far9