
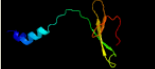
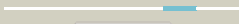












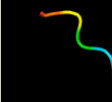

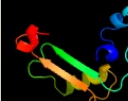

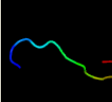




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1132_(-)_1257330_1259060
Date	Wed Jul 31 22:05:21 BST 2019
Unique Job ID	b8e57904c04f01ee

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2r6gf1	 Alignment		56.9	15	Fold: MaIF N-terminal region-like Superfamily: MaIF N-terminal region-like Family: MaIF N-terminal region-like
2	c3hi2C_	 Alignment		38.8	33	PDB header: dna binding protein/toxin Chain: C: PDB Molecule: hth-type transcriptional regulator mqsA(ygit); PDBTitle: structure of the n-terminal domain of the e. coli antitoxin mqsA2 (ygit/b3021) in complex with the e. coli toxin mqsR (ygiu/b3022)
3	d1fo1a2	 Alignment		37.6	35	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Non-canonical RBD domain
4	c4gvsA_	 Alignment		34.6	21	PDB header: hydrolase Chain: A: PDB Molecule: methenyltetrahydromethanopterin cyclohydrolase; PDBTitle: x-ray structure of the archaeoglobus fulgidus methenyl-2 tetrahydromethanopterin cyclohydrolase in complex with n5-formyl-3 tetrahydromethanopterin
5	d1qlma_	 Alignment		33.8	21	Fold: Methenyltetrahydromethanopterin cyclohydrolase Superfamily: Methenyltetrahydromethanopterin cyclohydrolase Family: Methenyltetrahydromethanopterin cyclohydrolase
6	c2hja_	 Alignment		32.8	38	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ykff; PDBTitle: solution nmr structure of protein ykff from escherichia coli.2 northeast structural genomics target er397.
7	d2hja1	 Alignment		32.8	38	Fold: dsRBD-like Superfamily: YcfA/nrd intein domain Family: Ykff-like
8	d1b4ra_	 Alignment		26.8	83	Fold: Immunoglobulin-like beta-sandwich Superfamily: PKD domain Family: PKD domain
9	c4fioA_	 Alignment		25.5	16	PDB header: hydrolase Chain: A: PDB Molecule: methenyltetrahydromethanopterin cyclohydrolase; PDBTitle: crystal structure of methenyltetrahydromethanopterin cyclohydrolase2 from methanobrevibacter ruminantium
10	d1vkwa_	 Alignment		24.9	33	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: Putative nitroreductase TM1586
11	c3iacA_	 Alignment		24.8	23	PDB header: isomerase Chain: A: PDB Molecule: glucuronate isomerase; PDBTitle: 2.2 angstrom crystal structure of glucuronate isomerase from 2 salmonella typhimurium.

12	c2l6pA_	Alignment		21.7	22	PDB header: structure genomics, unknown function Chain: A: PDB Molecule: phac1, phac2 and phad genes; PDBTitle: nmr solution structure of the protein np_253742.1
13	d1j2jb_	Alignment		20.1	28	Fold: Spectrin repeat-like Superfamily: GAT-like domain Family: GAT domain
14	d1wgoa_	Alignment		19.7	50	Fold: Immunoglobulin-like beta-sandwich Superfamily: PKD domain Family: PKD domain
15	c5jpbj_	Alignment		19.2	36	PDB header: ribosome Chain: I: PDB Molecule: u3 small nucleolar rna-associated protein 21; PDBTitle: cryo-em structure of the 90s pre-ribosome
16	c6rdf7_	Alignment		18.3	31	PDB header: proton transport Chain: 7: PDB Molecule: mitochondrial atp synthase associated protein asa7; PDBTitle: cryoem structure of polytomella f-atp synthase, primary rotary state2 3, monomer-masked refinement
17	c2zpaB_	Alignment		18.0	36	PDB header: transferase Chain: B: PDB Molecule: uncharacterized protein ypfi; PDBTitle: crystal structure of trna(met) cytidine acetyltransferase
18	c1x27F_	Alignment		17.7	23	PDB header: signaling protein Chain: F: PDB Molecule: proto-oncogene tyrosine-protein kinase lck; PDBTitle: crystal structure of lck sh2-sh3 with sh2 binding site of p130cas
19	c2l6nA_	Alignment		17.6	35	PDB header: structure genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein yp_001092504.1; PDBTitle: nmr solution structure of the protein yp_001092504.1
20	c4yubB_	Alignment		17.3	15	PDB header: ligase Chain: B: PDB Molecule: nicotinate phosphoribosyltransferase; PDBTitle: crystal structure of human nicotinic acid phosphoribosyltransferase
21	c4umoB_	Alignment	not modelled	17.1	21	PDB header: signaling protein Chain: B: PDB Molecule: potassium voltage-gated channel subfamily kqt member 1; PDBTitle: crystal structure of the kv7.1 proximal c-terminal domain in complex2 with calmodulin
22	c3iynR_	Alignment	not modelled	16.5	56	PDB header: virus Chain: R: PDB Molecule: hexon-associated protein; PDBTitle: 3.6-angstrom cryoem structure of human adenovirus type 5
23	c5n4cF_	Alignment	not modelled	16.0	47	PDB header: hydrolase Chain: F: PDB Molecule: alpha-amanitin proprotein; PDBTitle: prolyl oligopeptidase b from galerina marginata bound to 35mer2 hydrolysis and macrocyclization substrate - s577a mutant
24	d1kpta_	Alignment	not modelled	15.4	17	Fold: Yeast killer toxins Superfamily: Yeast killer toxins Family: Virally encoded KP4 toxin
25	d1c0pa1	Alignment	not modelled	15.3	11	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: D-aminoacid oxidase, N-terminal domain
26	c3iynQ_	Alignment	not modelled	14.9	56	PDB header: virus Chain: Q: PDB Molecule: hexon-associated protein; PDBTitle: 3.6-angstrom cryoem structure of human adenovirus type 5
27	c4xedA_	Alignment	not modelled	14.7	50	PDB header: protein binding Chain: A: PDB Molecule: peptidase m14, carboxypeptidase a; PDBTitle: pkd domain of m14-like peptidase from thermoplasmatales archaeon scgc2 ab-540-f20
28	c4ep5A_	Alignment	not modelled	14.7	17	PDB header: hydrolase Chain: A: PDB Molecule: crossover junction endodeoxyribonuclease ruvc; PDBTitle: thermus thermophilus ruvc structure

29	c3chxE	Alignment	not modelled	14.7	14	PDB header: membrane protein Chain: E: PDB Molecule: pmob; PDBTitle: crystal structure of methylinus trichosporium ob3b particulate2 methane monooxygenase (pmmo)
30	c1nafA	Alignment	not modelled	13.8	28	PDB header: signaling protein, membrane protein Chain: A: PDB Molecule: adp-ribosylation factor binding protein gga1; PDBTitle: crystal structure of the human gga1 gat domain
31	c4l9dB	Alignment	not modelled	13.4	67	PDB header: cell adhesion Chain: B: PDB Molecule: protease; PDBTitle: crystal structure of the pkd1 domain from vibrio cholerae2 metalloprotease prtV
32	d1l0qa1	Alignment	not modelled	13.3	83	Fold: Immunoglobulin-like beta-sandwich Superfamily: PKD domain Family: PKD domain
33	d1loxza	Alignment	not modelled	12.9	28	Fold: Spectrin repeat-like Superfamily: GAT-like domain Family: GAT domain
34	c1oxzA	Alignment	not modelled	12.9	28	PDB header: membrane protein Chain: A: PDB Molecule: adp-ribosylation factor binding protein gga1; PDBTitle: crystal structure of the human gga1 gat domain
35	c5SubdB	Alignment	not modelled	12.8	67	PDB header: dna binding protein Chain: B: PDB Molecule: rctb replication initiator protein; PDBTitle: crystal structure of the n-terminal domain (domain 1) of rctb, rctb-1-2 124-148m
36	d1c3ha	Alignment	not modelled	11.7	10	Fold: TNF-like Superfamily: TNF-like Family: TNF-like
37	c1avoA	Alignment	not modelled	11.6	54	PDB header: proteasome activator Chain: A: PDB Molecule: 11s regulator; PDBTitle: proteasome activator reg(alpha)
38	c5hbaA	Alignment	not modelled	11.5	14	PDB header: immune system Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: globular domain of zebrafish complement 1qa protein
39	c5tvfF	Alignment	not modelled	11.4	29	PDB header: lyase Chain: F: PDB Molecule: s-adenosylmethionine decarboxylase proenzyme-like, PDBTitle: crystal structure of trypanosoma brucei adometdc/prozyme heterodimer2 in complex with inhibitor cgp 40215
40	c4z9nB	Alignment	not modelled	11.3	12	PDB header: transport protein Chain: B: PDB Molecule: amino acid abc transporter, periplasmic amino acid-binding PDBTitle: abc transporter / periplasmic binding protein from brucella ovis with2 glutathione bound
41	d1ttja	Alignment	not modelled	11.3	14	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
42	c3luuA	Alignment	not modelled	11.1	30	PDB header: biosynthetic protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein with unknown function which belongs to2 pfam duf971 family (afe_2189) from acidithiobacillus ferrooxidans3 atcc 23270 at 1.93 a resolution
43	d1oz9a	Alignment	not modelled	10.9	24	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Predicted metal-dependent hydrolase
44	c6aemB	Alignment	not modelled	10.6	67	PDB header: unknown function Chain: B: PDB Molecule: pkd domain; PDBTitle: crystal structure of the pkd1 domain of vibrio anguillarum epp
45	c3nhnA	Alignment	not modelled	10.6	26	PDB header: transferase Chain: A: PDB Molecule: tyrosine-protein kinase hck; PDBTitle: crystal structure of the src-family kinase hck sh3-sh2-linker2 regulatory region
46	c3oakD	Alignment	not modelled	10.6	100	PDB header: transcription Chain: D: PDB Molecule: transcription elongation factor spt6; PDBTitle: crystal structure of a spn1 (iws1)-spt6 complex
47	d1r2ra	Alignment	not modelled	10.6	14	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
48	d1pk6c	Alignment	not modelled	10.4	10	Fold: TNF-like Superfamily: TNF-like Family: TNF-like
49	c4ohqB	Alignment	not modelled	10.3	11	PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase, chloroplastic; PDBTitle: crystal structure of chloroplast triose phosphate isomerase from2 arabidopsis thaliana
50	c3oakC	Alignment	not modelled	10.2	100	PDB header: transcription Chain: C: PDB Molecule: transcription elongation factor spt6; PDBTitle: crystal structure of a spn1 (iws1)-spt6 complex
51	c3gzaA	Alignment	not modelled	10.2	25	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein with a ntf2-like fold; PDBTitle: crystal structure of an uncharacterized protein with a cystatin-like2 fold (cc_2572) from caulobacter vibrioides at 1.40 a resolution
52	d1rgoa2	Alignment	not modelled	10.0	33	Fold: CCCH zinc finger Superfamily: CCCH zinc finger Family: CCCH zinc finger
53	c4mknA	Alignment	not modelled	9.8	11	PDB header: isomerase Chain: A: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of chloroplastic triosephosphate isomerase from2 chlamydomonas reinhardtii at 1.1 a of resolution
						PDB header: protein binding

54	c5xywD_	Alignment	not modelled	9.8	57	Chain: D: PDB Molecule: gd21652; PDBTitle: crystal structure of drosophila simulans rhino chromoshadow domain in2 complex with n-terminal domain
55	c4whnB_	Alignment	not modelled	9.7	21	PDB header: transferase Chain: B: PDB Molecule: apxc; PDBTitle: structure of toxin-activating acyltransferase (taat)
56	c2q3vB_	Alignment	not modelled	9.5	24	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein at2g34160; PDBTitle: ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at2g34160
57	c3m9yB_	Alignment	not modelled	9.5	8	PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from methicillin2 resistant staphylococcus aureus at 1.9 angstrom resolution
58	c5kc5A_	Alignment	not modelled	9.5	24	PDB header: signaling protein Chain: A: PDB Molecule: cerebellin-1; PDBTitle: crystal structure of the cbln1 c1q domain trimer
59	d1mo0a_	Alignment	not modelled	9.2	14	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
60	d1b9ba_	Alignment	not modelled	9.1	14	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
61	c4y9aB_	Alignment	not modelled	9.1	14	PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from streptomyces2 coelicolor
62	c4oumA_	Alignment	not modelled	9.0	24	PDB header: signaling protein Chain: A: PDB Molecule: caprin-2; PDBTitle: crystal structure of human caprin-2 c1q domain
63	d1suxa_	Alignment	not modelled	9.0	14	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
64	c2wltA_	Alignment	not modelled	9.0	19	PDB header: hydrolase Chain: A: PDB Molecule: l-asparaginase; PDBTitle: the crystal structure of helicobacter pylori l-asparaginase at 1.4 a2 resolution
65	c2mc3A_	Alignment	not modelled	8.5	17	PDB header: hydrolase Chain: A: PDB Molecule: mus81 endonuclease homolog (yeast), isoform cra_b; PDBTitle: nmr solution structure of the winged-helix domain from mus812 structure-specific endonuclease
66	c4d7yA_	Alignment	not modelled	8.4	10	PDB header: signaling protein Chain: A: PDB Molecule: c1q-related factor; PDBTitle: crystal structure of mouse c1q1 globular domain
67	d1sw3a_	Alignment	not modelled	8.3	14	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
68	c2ka3C_	Alignment	not modelled	8.3	19	PDB header: structural protein Chain: C: PDB Molecule: emilin-1; PDBTitle: structure of emilin-1 c1q-like domain
69	c4i19A_	Alignment	not modelled	8.2	26	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from streptomyces2 carzinostaticus subsp. neocarzinostaticus.
70	c4obtA_	Alignment	not modelled	8.0	14	PDB header: isomerase Chain: A: PDB Molecule: triosephosphate isomerase, cytosolic; PDBTitle: crystal structure of arabidopsis thaliana cytosolic triose phosphate2 isomerase
71	d1b5ea_	Alignment	not modelled	7.9	12	Fold: Thymidylate synthase/dCMP hydroxymethylase Superfamily: Thymidylate synthase/dCMP hydroxymethylase Family: Thymidylate synthase/dCMP hydroxymethylase
72	d2p02a3	Alignment	not modelled	7.9	20	Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase
73	d1n55a_	Alignment	not modelled	7.8	14	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
74	d1qm4a3	Alignment	not modelled	7.8	16	Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase
75	c5zg5B_	Alignment	not modelled	7.8	11	PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase sadsubaaa mutant from2 opisthorchis viverrini
76	c3j3bG_	Alignment	not modelled	7.7	44	PDB header: ribosome Chain: G: PDB Molecule: 60s ribosomal protein l7a; PDBTitle: structure of the human 60s ribosomal proteins
77	c2m3dA_	Alignment	not modelled	7.7	10	PDB header: hydrolase Chain: A: PDB Molecule: nucleolar rna helicase 2; PDBTitle: nmr structure of the guc domain from human dead box polypeptide 21
78	c3qstA_	Alignment	not modelled	7.6	17	PDB header: isomerase Chain: A: PDB Molecule: triosephosphate isomerase, putative; PDBTitle: crystal structure of trichomonas vaginalis triosephosphate isomerase2 tvag_096350 gene (val-45 variant)
79	d1m6ja_	Alignment	not modelled	7.6	11	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
						PDB header: signaling protein Chain: A: PDB Molecule: complement c1a tumor necrosis factor-

80	c4f3jA_	Alignment	not modelled	7.6	9	related protein 5; PDBTitle: crystal structure of trimeric gc1q domain of human c1qtnf5 associated2 with late-onset retinal macular degeneration
81	d1fngb2	Alignment	not modelled	7.5	33	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
82	d1kfia4	Alignment	not modelled	7.5	25	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain
83	d1pk6a_	Alignment	not modelled	7.5	14	Fold: TNF-like Superfamily: TNF-like Family: TNF-like
84	c4ediC_	Alignment	not modelled	7.5	16	PDB header: transport protein Chain: C: PDB Molecule: ethanolamine utilization protein; PDBTitle: disulfide bonded eutl from clostridium perfringens
85	c4esjA_	Alignment	not modelled	7.5	38	PDB header: hydrolase/dna Chain: A: PDB Molecule: type-2 restriction enzyme dpni; PDBTitle: restriction endonuclease dpni in complex with target dna
86	d2btma_	Alignment	not modelled	7.4	14	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
87	c4a1eF_	Alignment	not modelled	7.4	39	PDB header: ribosome Chain: F: PDB Molecule: rpl7a; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
88	c2kzwA_	Alignment	not modelled	7.4	83	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of q8psa4 from methanosarcina mazei, northeast2 structural genomics consortium target mar143a
89	c2q74B_	Alignment	not modelled	7.4	24	PDB header: hydrolase Chain: B: PDB Molecule: inositol-1-monophosphatase; PDBTitle: mycobacterium tuberculosis suhb
90	d1u5la_	Alignment	not modelled	7.4	36	Fold: Prion-like Superfamily: Prion-like Family: Prion-like
91	c3x0uB_	Alignment	not modelled	7.4	20	PDB header: toxin Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of pirb
92	c2yt6A_	Alignment	not modelled	7.4	19	PDB header: cell cycle Chain: A: PDB Molecule: adult male urinary bladder cdna, riken full- PDBTitle: solution structure of the sh3_1 domain of yamaguchi sarcoma2 viral (v-yes) oncogene homolog 1
93	d1mxaa3	Alignment	not modelled	7.3	25	Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase
94	d1kv5a_	Alignment	not modelled	7.3	14	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
95	d1q1va_	Alignment	not modelled	7.2	24	Fold: Another 3-helical bundle Superfamily: DEK C-terminal domain Family: DEK C-terminal domain
96	c1l0qC_	Alignment	not modelled	7.2	83	PDB header: protein binding Chain: C: PDB Molecule: surface layer protein; PDBTitle: tandem yvtn beta-propeller and pkd domains from an archaeal surface2 layer protein
97	d1pk6b_	Alignment	not modelled	7.2	14	Fold: TNF-like Superfamily: TNF-like Family: TNF-like
98	c2x3mA_	Alignment	not modelled	7.1	19	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein orf239; PDBTitle: crystal structure of hypothetical protein orf239 from pyrobaculum2 spherical virus
99	c1qeyD_	Alignment	not modelled	7.1	19	PDB header: gene regulation Chain: D: PDB Molecule: protein (regulatory protein mnt); PDBTitle: nmr structure determination of the tetramerization domain2 of the mnt repressor: an asymmetric a-helical assembly in3 slow exchange