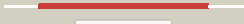

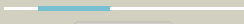
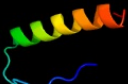








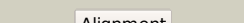











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2117 (-) _2377156_2377449
Date	Mon Aug 5 13:25:23 BST 2019
Unique Job ID	2b099088c4c8934c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1j27a_	 Alignment		100.0	23	Fold: Ferredoxin-like Superfamily: Hypothetical protein TT1725 Family: Hypothetical protein TT1725
2	c3m20A_	 Alignment		38.1	13	PDB header: isomerase Chain: A: PDB Molecule: 4-oxalocrotonate tautomerase, putative; PDBTitle: crystal structure of dmpl from archaeoglobus fulgidus determined to 2.27 angstroms resolution
3	c4lkbA_	 Alignment		35.0	23	PDB header: isomerase Chain: A: PDB Molecule: hypothetical protein alr4568/putative 4-oxalocrotonate PDBTitle: crystal structure of a putative 4-oxalocrotonate tautomerase from 2 nostoc sp. pcc 7120
4	d3bypa1	 Alignment		34.9	17	Fold: Alpha-lytic protease prodomain-like Superfamily: Cation efflux protein cytoplasmic domain-like Family: Cation efflux protein cytoplasmic domain-like
5	c6qekB_	 Alignment		33.8	14	PDB header: transport protein Chain: B: PDB Molecule: magnetosome protein; PDBTitle: putative membrane transporter, magnetosome protein mamm ctd2 [desulfamplus magnetovallimortis bw-1]
6	d1mwwa_	 Alignment		26.7	20	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: Hypothetical protein HI1388.1
7	c4fdxB_	 Alignment		22.0	21	PDB header: isomerase Chain: B: PDB Molecule: 4-oxalocrotonase tautomerase isozyme; PDBTitle: kinetic and structural characterization of the 4-oxalocrotonate2 tautomerase isozymes from methylibium petroleiphilum
8	c1p58E_	 Alignment		19.7	23	PDB header: virus Chain: E: PDB Molecule: envelope protein m; PDBTitle: complex organization of dengue virus membrane proteins as revealed by 2 9.5 angstrom cryo-em reconstruction
9	c2flzC_	 Alignment		19.1	11	PDB header: hydrolase Chain: C: PDB Molecule: cis-3-chloroacrylic acid dehalogenase; PDBTitle: the x-ray structure of cis-3-chloroacrylic acid dehalogenase (cis-2 caad) with a sulfate ion bound in the active site
10	c1p58F_	 Alignment		18.8	23	PDB header: virus Chain: F: PDB Molecule: envelope protein m; PDBTitle: complex organization of dengue virus membrane proteins as revealed by 2 9.5 angstrom cryo-em reconstruction
11	c4fazB_	 Alignment		18.0	18	PDB header: isomerase Chain: B: PDB Molecule: 4-oxalocrotonate isomerase protein; PDBTitle: kinetic and structural characterization of the 4-oxalocrotonate2 tautomerase isozymes from methylibium petroleiphilum

12	c2op8A_	Alignment		17.8	18	PDB header: isomerase Chain: A: PDB Molecule: probable tautomerase ywhb; PDBTitle: crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase
13	c3ry0A_	Alignment		17.5	19	PDB header: isomerase Chain: A: PDB Molecule: putative tautomerase; PDBTitle: crystal structure of tomn, a 4-oxalocrotonate tautomerase homologue in 2 tomaymycin biosynthetic pathway
14	c2vd2A_	Alignment		17.1	22	PDB header: transferase Chain: A: PDB Molecule: atp phosphoribosyltransferase; PDBTitle: the crystal structure of hisg from b. subtilis
15	c5m8hH_	Alignment		17.1	19	PDB header: transferase Chain: H: PDB Molecule: atp phosphoribosyltransferase; PDBTitle: atp phosphoribosyltransferase (hiszg atpprt) from psychrobacter2 arcticus
16	d2bm0a4	Alignment		17.0	38	Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: EF-G/eEF-2 domains III and V
17	d1ve4a1	Alignment		16.7	44	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
18	d1iwga3	Alignment		16.3	13	Fold: Ferredoxin-like Superfamily: Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains Family: Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
19	c2mcfA_	Alignment		15.1	17	PDB header: unknown function Chain: A: PDB Molecule: tgam_1934; PDBTitle: nmr structure of tgam_1934
20	d1otfa_	Alignment		13.6	12	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
21	d2v0ea1	Alignment	not modelled	13.0	13	Fold: GYF/BRK domain-like Superfamily: BRK domain-like Family: BRK domain-like
22	c5ho5D_	Alignment	not modelled	12.9	6	PDB header: metal transport Chain: D: PDB Molecule: magnetosome protein mamb; PDBTitle: mamb
23	d2ckaa1	Alignment	not modelled	12.4	31	Fold: GYF/BRK domain-like Superfamily: BRK domain-like Family: BRK domain-like
24	c2ckaA_	Alignment	not modelled	12.4	31	PDB header: hydrolase Chain: A: PDB Molecule: chromodomain-helicase-dna-binding protein 8; PDBTitle: solution structures of the brk domains of the human chromo2 helicase domain 7 and 8, reveals structural similarity3 with gyf domain suggesting a role in protein interaction
25	d1zbsa2	Alignment	not modelled	11.9	9	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
26	d1knya2	Alignment	not modelled	11.8	6	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Kanamycin nucleotidyltransferase (KNTase), N-terminal domain
27	c3icIA_	Alignment	not modelled	11.2	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: eal/ggdef domain protein; PDBTitle: x-ray structure of protein (eal/ggdef domain protein) from 2 m.capsulatus, northeast structural genomics consortium target mcr174c
28	c4kunB_	Alignment	not modelled	11.0	16	PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein lpp1115;

					PDBTitle: crystal structure of legionella pneumophila lpp1115 / kaib
29	d2fgca2	Alignment	not modelled	10.9	20 Fold: Ferredoxin-like Superfamily: ACT-like Family: llvH-like
30	d1r5pa_	Alignment	not modelled	10.9	16 Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: KaiB-like
31	d1iwga1	Alignment	not modelled	10.9	3 Fold: Ferredoxin-like Superfamily: Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains Family: Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
32	c2ckcA_	Alignment	not modelled	10.1	13 PDB header: hydrolase Chain: A: PDB Molecule: chromodomain-helicase-dna-binding protein 7; PDBTitle: solution structures of the brk domains of the human chromo2 helicase domain 7 and 8, reveals structural similarity3 with gyf domain suggesting a role in protein interaction
33	d2ckca1	Alignment	not modelled	10.1	13 Fold: GYF/BRK domain-like Superfamily: BRK domain-like Family: BRK domain-like
34	c2lvwA_	Alignment	not modelled	10.1	16 PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase isozyme 1 small subunit; PDBTitle: solution nmr studies of the dimeric regulatory subunit ilvn of the2 e.coli acetohydroxyacid synthase i (ahas i)
35	c1vw44_	Alignment	not modelled	9.9	11 PDB header: ribosome Chain: 4: PDB Molecule: 54s ribosomal protein l51, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
36	c3mb2G_	Alignment	not modelled	9.5	28 PDB header: isomerase Chain: G: PDB Molecule: 4-oxalocrotonate tautomerase family enzyme - alpha subunit; PDBTitle: kinetic and structural characterization of a heterohexamer 4-2 oxalocrotonate tautomerase from chloroflexus aurantiacus j-10-fl:3 implications for functional and structural diversity in the4 tautomerase superfamily
37	c5unqF_	Alignment	not modelled	9.2	18 PDB header: hydrolase Chain: F: PDB Molecule: putative tautomerase; PDBTitle: crystal structure of pt0534 inactivated by 2-oxo-3-pentynoate
38	d1z7me1	Alignment	not modelled	9.1	28 Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
39	c5wx8B_	Alignment	not modelled	8.9	17 PDB header: dna binding protein Chain: B: PDB Molecule: immediate-early protein 2; PDBTitle: human herpesvirus 6a immediate early protein 2 c-terminal domain
40	d2pc6a2	Alignment	not modelled	8.8	7 Fold: Ferredoxin-like Superfamily: ACT-like Family: llvH-like
41	c2l2lA_	Alignment	not modelled	8.1	21 PDB header: transferase Chain: A: PDB Molecule: transcriptional repressor p66-alpha; PDBTitle: solution structure of the coiled-coil complex between mbd2 and2 p66alpha
42	c3mlcC_	Alignment	not modelled	7.9	18 PDB header: isomerase Chain: C: PDB Molecule: fg41 malonate semialdehyde decarboxylase; PDBTitle: crystal structure of fg41msad inactivated by 3-chloropropiolate
43	c5bndA_	Alignment	not modelled	7.7	27 PDB header: transport protein Chain: A: PDB Molecule: abc transporter, atp-binding protein; PDBTitle: crystal structure of the c-terminal domain of tagh
44	c5uifC_	Alignment	not modelled	7.7	6 PDB header: hydrolase Chain: C: PDB Molecule: ps01740; PDBTitle: crystal structure of native ps01740
45	c2x4kB_	Alignment	not modelled	7.2	16 PDB header: isomerase Chain: B: PDB Molecule: 4-oxalocrotonate tautomerase; PDBTitle: crystal structure of sar1376, a putative 4-oxalocrotonate2 tautomerase from the methicillin-resistant staphylococcus3 aureus (mrsa)
46	c6d9mA_	Alignment	not modelled	7.0	18 PDB header: hydrolase Chain: A: PDB Molecule: fusion protein of endolysin,response receiver sensor PDBTitle: t4-lysozyme fusion to geobacter ggdef
47	c2zztA_	Alignment	not modelled	7.0	18 PDB header: transport protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the cytosolic domain of the cation2 diffusion facilitator family protein
48	d2f1fa1	Alignment	not modelled	7.0	17 Fold: Ferredoxin-like Superfamily: ACT-like Family: llvH-like
49	d1bjpa_	Alignment	not modelled	6.9	19 Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
50	c3ezkB_	Alignment	not modelled	6.8	25 PDB header: hydrolase Chain: B: PDB Molecule: dna packaging protein gp17; PDBTitle: bacteriophage t4 gp17 motor assembly based on crystal structures and2 cryo-em reconstructions
51	c2f1fA_	Alignment	not modelled	6.8	13 PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase isozyme iii small subunit; PDBTitle: crystal structure of the regulatory subunit of acetohydroxyacid2 synthase isozyme iii from e. coli
52	d2aala1	Alignment	not modelled	6.7	26 Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF

				Family:MSAD-like		
53	d2v0fa1	Alignment	not modelled	6.6	25	Fold: GYF/BRK domain-like Superfamily: BRK domain-like Family: BRK domain-like
54	c5ensA	Alignment	not modelled	6.5	7	PDB header: transport protein Chain: A: PDB Molecule: multidrug efflux pump subunit acrb,multidrug efflux pump PDBTitle: rhodamine bound structure of bacterial efflux pump.
55	d1rp3a1	Alignment	not modelled	6.5	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma3 domain
56	c2kzfA	Alignment	not modelled	6.5	18	PDB header: ribosomal protein Chain: A: PDB Molecule: ribosome-binding factor a; PDBTitle: solution nmr structure of the thermotoga maritima protein tm0855 a2 putative ribosome binding factor a
57	c3mgjA	Alignment	not modelled	6.4	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein mj1480; PDBTitle: crystal structure of the saccharop_dh_n domain of mj1480 protein from2 methanococcus jannaschii. northeast structural genomics consortium3 target mjr83a.
58	c3j2pD	Alignment	not modelled	6.2	23	PDB header: viral protein Chain: D: PDB Molecule: small envelope protein m; PDBTitle: cryoem structure of dengue virus envelope protein heterotetramer
59	c2ormA	Alignment	not modelled	6.1	9	PDB header: isomerase Chain: A: PDB Molecule: probable tautomerase hp0924; PDBTitle: crystal structure of the 4-oxalocrotonate tautomerase homologue dmpi2 from helicobacter pylori.
60	c6gxzD	Alignment	not modelled	6.1	20	PDB header: chaperone Chain: D: PDB Molecule: pih1 domain-containing protein 1; PDBTitle: crystal structure of the human rpap3(tp2)-pih1d1(cs) complex
61	d1o63a	Alignment	not modelled	6.0	28	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
62	d2dl6a1	Alignment	not modelled	5.6	31	Fold: GYF/BRK domain-like Superfamily: BRK domain-like Family: BRK domain-like
63	c5ireD	Alignment	not modelled	5.6	18	PDB header: virus Chain: D: PDB Molecule: m protein; PDBTitle: the cryo-em structure of zika virus
64	c5wsnD	Alignment	not modelled	5.4	23	PDB header: virus Chain: D: PDB Molecule: m protein; PDBTitle: structure of japanese encephalitis virus
65	c2jnvA	Alignment	not modelled	5.4	18	PDB header: metal transport Chain: A: PDB Molecule: nifu-like protein 1, chloroplast; PDBTitle: solution structure of c-terminal domain of nifu-like2 protein from oryza sativa
66	d1qd1a1	Alignment	not modelled	5.2	10	Fold: Ferredoxin-like Superfamily: Formiminotransferase domain of formiminotransferase-cyclodeaminase. Family: Formiminotransferase domain of formiminotransferase-cyclodeaminase.
67	d2z1ea1	Alignment	not modelled	5.2	13	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like
68	c2vd3B	Alignment	not modelled	5.1	17	PDB header: transferase Chain: B: PDB Molecule: atp phosphoribosyltransferase; PDBTitle: the structure of histidine inhibited hisg from2 methanobacterium thermoautotrophicum
69	d1lfra	Alignment	not modelled	5.1	12	Fold: Immunoglobulin-like beta-sandwich Superfamily: Lamin A/C globular tail domain Family: Lamin A/C globular tail domain