


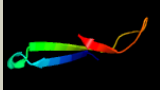



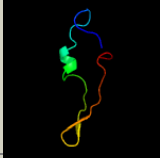

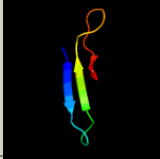





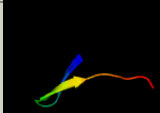

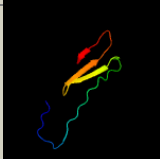

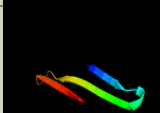

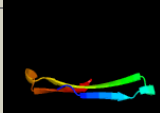
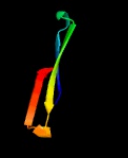
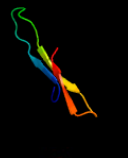



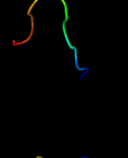
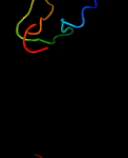
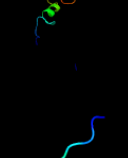
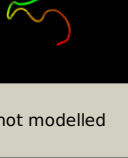


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1914c (-) _2159928_2160335
Date	Fri Aug 2 13:30:53 BST 2019
Unique Job ID	95c91c5fd34f3d4a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6fcoB_	 Alignment		47.7	21	PDB header: transport protein Chain: B: PDB Molecule: mitochondrial frataxin-like protein; PDBTitle: structural and functional characterisation of frataxin (fxn) like2 protein from chaetomium thermophilum
2	d2fq1a1	 Alignment		27.7	22	Fold: N domain of copper amine oxidase-like Superfamily: Frataxin/Nqo15-like Family: Frataxin-like
3	d1ekga_	 Alignment		26.7	14	Fold: N domain of copper amine oxidase-like Superfamily: Frataxin/Nqo15-like Family: Frataxin-like
4	c3iz6A_	 Alignment		24.2	20	PDB header: ribosome Chain: A: PDB Molecule: 40s ribosomal protein sa (s2p); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
5	d2ga5a1	 Alignment		22.7	19	Fold: N domain of copper amine oxidase-like Superfamily: Frataxin/Nqo15-like Family: Frataxin-like
6	c4zrmB_	 Alignment		22.5	12	PDB header: isomerase Chain: B: PDB Molecule: udp-glucose 4-epimerase; PDBTitle: crystal structure of udp-glucose 4-epimerase (tm0509) from2 hyperthermophilic eubacterium thermotoga maritima
7	c5aj3h_	 Alignment		22.5	18	PDB header: ribosome Chain: H: PDB Molecule: PDBTitle: structure of the small subunit of the mammalian mitoribosome
8	c4h5bB_	 Alignment		20.5	29	PDB header: unknown function Chain: B: PDB Molecule: dr_1245 protein; PDBTitle: crystal structure of dr_1245 from deinococcus radiodurans
9	c4e0eB_	 Alignment		18.2	18	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a duf4450 family protein (bt_4147) from2 bacteroides thetaiotaomicron vpi-5482 at 2.90 a resolution
10	c4jpdA_	 Alignment		17.8	15	PDB header: metal binding protein Chain: A: PDB Molecule: protein cyay; PDBTitle: the structure of cyay from burkholderia cenocepacia
11	d1ew4a_	 Alignment		16.5	11	Fold: N domain of copper amine oxidase-like Superfamily: Frataxin/Nqo15-like Family: Frataxin-like

12	c4hs5B_	Alignment		15.1	11	PDB header: metal binding protein Chain: B: PDB Molecule: protein cyay; PDBTitle: frataxin from psychromonas ingrahamii as a model to study stability2 modulation within cyay protein family
13	c5kz5H_	Alignment		15.0	13	PDB header: transferase/oxidoreductase Chain: H: PDB Molecule: frataxin, mitochondrial; PDBTitle: architecture of the human mitochondrial iron-sulfur cluster assembly2 machinery: the complex formed by the iron donor, the sulfur donor,3 and the scaffold
14	c2pzb_	Alignment		14.4	17	PDB header: sugar binding protein Chain: B: PDB Molecule: putative nucleotide sugar epimerase/dehydratase; PDBTitle: crystal structure of the bordetella bronchiseptica enzyme wbmgi2 complex with nad and udp
15	c6f46A_	Alignment		13.9	78	PDB header: apoptosis Chain: A: PDB Molecule: bcl-2-like protein 1; PDBTitle: structure of the transmembrane helix of bclxl in phospholipid2 nanodiscs
16	c6nusA_	Alignment		13.1	21	PDB header: viral protein Chain: A: PDB Molecule: nsp12; PDBTitle: sars-coronavirus nsp12 bound to nsp8 co-factor
17	d1nvmb1	Alignment		11.0	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
18	c3j6vB_	Alignment		10.6	31	PDB header: ribosome Chain: B: PDB Molecule: 28s ribosomal protein s2, mitochondrial; PDBTitle: cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
19	c2o61A_	Alignment		9.7	15	PDB header: transcription/dna Chain: A: PDB Molecule: transcription factor p65/interferon regulatory factor PDBTitle: crystal structure of nfkb, irf7, irf3 bound to the interferon-b2 enhancer
20	c4jn6B_	Alignment		9.6	20	PDB header: lyase/oxidoreductase Chain: B: PDB Molecule: acetaldehyde dehydrogenase; PDBTitle: crystal structure of the aldolase-dehydrogenase complex from2 mycobacterium tuberculosis hrv37
21	c6chgB_	Alignment	not modelled	9.1	15	PDB header: transferase Chain: B: PDB Molecule: klla0c10945p; PDBTitle: crystal structure of the yeast compass catalytic module
22	d1a6ca2	Alignment	not modelled	9.0	12	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Comoviridae-like VP
23	c3uv0B_	Alignment	not modelled	8.9	22	PDB header: protein binding Chain: B: PDB Molecule: mutator 2, isoform b; PDBTitle: crystal structure of the drosophila mu2 fha domain
24	c4ksnC_	Alignment	not modelled	8.7	50	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: sdbc; PDBTitle: c-terminal domain of sdbc protein from legionella pneumophila.
25	c4cwuT_	Alignment	not modelled	8.4	14	PDB header: virus Chain: T: PDB Molecule: core-capsid bridging protein; PDBTitle: crystal structure derived models of adenovirus cement proteins at 3.8a
26	d1orra_	Alignment	not modelled	8.2	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
27	c4bz4D_	Alignment	not modelled	8.0	43	PDB header: copper-binding protein Chain: D: PDB Molecule: copper-repressible polypeptide; PDBTitle: cora is a surface-associated copper-binding protein2 important in methylomicrobium album bg8 copper acquisition
28	c4gu8G_	Alignment	not modelled	8.0	29	PDB header: sugar binding protein Chain: G: PDB Molecule: burkholderia oklahomensis agglutinin (boa); PDBTitle: crystal structure of burkholderia oklahomensis agglutinin (boa)

29	c5yalA_	Alignment	not modelled	8.0	30	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: ferulic acid esterase from streptomyces cinnamoneus at 1.5 a2 resolution
30	c2vduE_	Alignment	not modelled	7.8	14	PDB header: transferase Chain: E: PDB Molecule: trna (guanine-n(7)-)-methyltransferase; PDBTitle: structure of trm8-trm82, the yeast trna m7g methylation2 complex
31	c1nvmB_	Alignment	not modelled	7.8	13	PDB header: lyase/oxidoreductase Chain: B: PDB Molecule: acetaldehyde dehydrogenase (acylating); PDBTitle: crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
32	c2p5uC_	Alignment	not modelled	7.6	17	PDB header: isomerase Chain: C: PDB Molecule: udp-glucose 4-epimerase; PDBTitle: crystal structure of thermus thermophilus hb8 udp-glucose 4-epimerase2 complex with nad
33	c2mw1A_	Alignment	not modelled	7.5	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lipocalin-like protein; PDBTitle: nmr structure of the protein np_809137.1 from bacteroides2 thetaiotaomicron
34	c3h2zA_	Alignment	not modelled	6.9	28	PDB header: oxidoreductase Chain: A: PDB Molecule: mannitol-1-phosphate 5-dehydrogenase; PDBTitle: the crystal structure of mannitol-1-phosphate dehydrogenase from2 shigella flexneri
35	c4qlbD_	Alignment	not modelled	6.8	34	PDB header: transferase Chain: D: PDB Molecule: probable glycogen [starch] synthase; PDBTitle: structural basis for the recruitment of glycogen synthase by2 glycogenin
36	c5jnmA_	Alignment	not modelled	6.5	24	PDB header: oxidoreductase Chain: A: PDB Molecule: mannitol-1-phosphate 5-dehydrogenase; PDBTitle: crystal structure of mtld from staphylococcus aureus at 1.7-angstrom2 resolution
37	c2pk3B_	Alignment	not modelled	6.4	15	PDB header: oxidoreductase Chain: B: PDB Molecule: gdp-6-deoxy-d-lyxo-4-hexulose reductase; PDBTitle: crystal structure of a gdp-4-keto-6-deoxy-d-mannose reductase
38	d2uubb1	Alignment	not modelled	6.3	34	Fold: Flavodoxin-like Superfamily: Ribosomal protein S2 Family: Ribosomal protein S2
39	c5o5jV_	Alignment	not modelled	6.3	28	PDB header: ribosome Chain: V: PDB Molecule: 30s ribosomal protein s2; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
40	c2q1wC_	Alignment	not modelled	6.3	12	PDB header: sugar binding protein Chain: C: PDB Molecule: putative nucleotide sugar epimerase/dehydratase; PDBTitle: crystal structure of the bordetella bronchiseptica enzyme wbmh in2 complex with nad+
41	c3e20C_	Alignment	not modelled	6.2	15	PDB header: translation Chain: C: PDB Molecule: eukaryotic peptide chain release factor subunit 1; PDBTitle: crystal structure of s.pombe erf1/erf3 complex
42	c1n7gB_	Alignment	not modelled	6.0	13	PDB header: lyase Chain: B: PDB Molecule: gdp-d-mannose-4,6-dehydratase; PDBTitle: crystal structure of the gdp-mannose 4,6-dehydratase2 ternary complex with nadph and gdp-rhamnose.
43	c2o6dB_	Alignment	not modelled	5.7	24	PDB header: membrane protein, protein binding Chain: B: PDB Molecule: 34 kda membrane antigen; PDBTitle: structure of native rtp34 from treponema pallidum
44	d1hn0a3	Alignment	not modelled	5.6	50	Fold: Hyaluronate lyase-like, C-terminal domain Superfamily: Hyaluronate lyase-like, C-terminal domain Family: Hyaluronate lyase-like, C-terminal domain
45	c2lw6A_	Alignment	not modelled	5.4	42	PDB header: apoptosis Chain: A: PDB Molecule: avrpiz-t protein; PDBTitle: solution structure of an avirulence protein avrpiz-t from pathogen2 magnaportheorzyae
46	c4twrA_	Alignment	not modelled	5.1	14	PDB header: isomerase Chain: A: PDB Molecule: nad binding site:nad-dependent epimerase/dehydratase:udp- PDBTitle: structure of udp-glucose 4-epimerase from brucella abortus