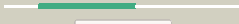
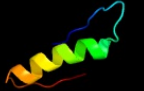
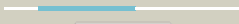
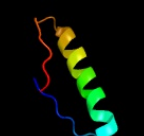
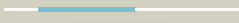


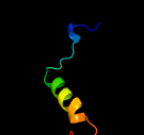

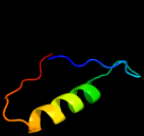
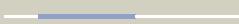
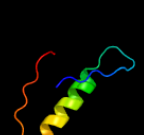
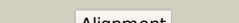
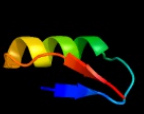

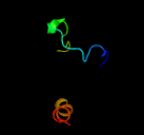





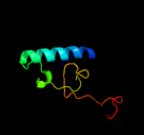






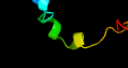

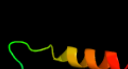


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0750 (-)_842036_842281
Date	Fri Jul 26 01:50:32 BST 2019
Unique Job ID	d5c9d0a24d8fcf10

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1yqha1	 Alignment		42.6	11	Fold: Ferredoxin-like Superfamily: MTH1187/YkoF-like Family: MTH1187-like
2	d1vk8a_	 Alignment		37.4	20	Fold: Ferredoxin-like Superfamily: MTH1187/YkoF-like Family: MTH1187-like
3	d2iboal	 Alignment		36.8	11	Fold: Ferredoxin-like Superfamily: MTH1187/YkoF-like Family: MTH1187-like
4	c4qysA_	 Alignment		35.8	42	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase beta chain 2; PDBTitle: trpb2 enzymes
5	d1lxna_	 Alignment		24.1	17	Fold: Ferredoxin-like Superfamily: MTH1187/YkoF-like Family: MTH1187-like
6	c2epiA_	 Alignment		22.3	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0045 protein mj1052; PDBTitle: crystal structure pf hypothetical protein mj1052 from2 methanocaldococcus jannascii (form 2)
7	d3clsd2	 Alignment		21.1	33	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: C-terminal domain of the electron transfer flavoprotein alpha subunit
8	c4plaA_	 Alignment		17.3	34	PDB header: transferase,hydrolase Chain: A: PDB Molecule: chimera protein of phosphatidylinositol 4-kinase type 2- PDBTitle: crystal structure of phosphatidyl inositol 4-kinase ii alpha in2 complex with atp
9	c6b4eC_	 Alignment		16.5	63	PDB header: transport protein Chain: C: PDB Molecule: nucleoporin nup42; PDBTitle: crystal structure of saccharomyces cerevisiae gle1 ctd-nup42 gbm2 complex
10	c2lqtA_	 Alignment		15.0	18	PDB header: unknown function Chain: A: PDB Molecule: coiled-coil-helix-coiled-coil-helix domain-containing PDBTitle: solution structure of chchd7
11	d1gnta_	 Alignment		14.4	27	Fold: Prismane protein-like Superfamily: Prismane protein-like Family: Hybrid cluster protein (prismane protein)

12	c3ulcA	Alignment		12.4	47	PDB header: membrane protein Chain: A; PDB Molecule: target of rapamycin complex 2 subunit avo1; PDBTitle: crystal structure of the pleckstrin homology domain of saccharomyces2 cerevisiae avo1, a torc2 subunit, in the p3121 crystal form
13	d2rh2a1	Alignment		12.2	47	Fold: SH3-like barrel Superfamily: Electron transport accessory proteins Family: R67 dihydrofolate reductase
14	d1efpa2	Alignment		11.7	30	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: C-terminal domain of the electron transfer flavoprotein alpha subunit
15	d1lxja	Alignment		9.6	17	Fold: Ferredoxin-like Superfamily: MTH1187/YkoF-like Family: MTH1187-like
16	d2apoa2	Alignment		9.5	50	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase II TruB
17	c4uedB	Alignment		9.4	28	PDB header: translation Chain: B; PDB Molecule: eukaryotic translation factor 4e-binding protein 1; PDBTitle: complex of human eif4e with the 4e binding protein 4e-bp1
18	d1wura1	Alignment		8.6	30	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: GTP cyclohydrolase I
19	c1wm9D	Alignment		8.6	30	PDB header: hydrolase Chain: D; PDB Molecule: gtp cyclohydrolase i; PDBTitle: structure of gtp cyclohydrolase i from thermus thermophilus hb8
20	c3seeA	Alignment		8.2	45	PDB header: sugar binding protein Chain: A; PDB Molecule: hypothetical sugar binding protein; PDBTitle: crystal structure of a putative sugar binding protein (bt_4411) from2 bacteroides thetaiotaomicron vpi-5482 at 1.25 a resolution
21	c4ar1A	Alignment	not modelled	7.9	33	PDB header: hydrolase Chain: A; PDB Molecule: colh protein; PDBTitle: crystal structure of the peptidase domain of collagenase h from2 clostridium histolyticum at 2.01 angstrom resolution.
22	c2n1dA	Alignment	not modelled	7.6	29	PDB header: protein binding Chain: A; PDB Molecule: mrg/morf4l-binding protein; PDBTitle: solution structure of the mrg15-mrgbp complex
23	d1gnla	Alignment	not modelled	7.4	27	Fold: Prismane protein-like Superfamily: Prismane protein-like Family: Hybrid cluster protein (prismane protein)
24	d1r3ea2	Alignment	not modelled	7.4	41	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase II TruB
25	c1lzlL	Alignment	not modelled	7.1	17	PDB header: photosynthesis Chain: L; PDB Molecule: photosystem ii: subunit psbb; PDBTitle: crystal structure of photosystem ii
26	c4wcbB	Alignment	not modelled	7.0	50	PDB header: translation Chain: B; PDB Molecule: ribosomal silencing factor rsfs; PDBTitle: ribosomal silencing factor during starvation or stationary phase2 (rsfs) from mycobacterium tuberculosis
27	d1k8wa5	Alignment	not modelled	6.7	29	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase II TruB
28	d1efva2	Alignment	not modelled	6.7	33	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: C-terminal domain of the electron transfer flavoprotein alpha subunit
29	c1k8wA	Alignment	not modelled	6.5	26	PDB header: lyase/rna Chain: A; PDB Molecule: trna pseudouridine synthase b;

29	c1k0wA_	Alignment	not modelled	6.5	30	PDBTitle: crystal structure of the e. coli pseudouridine synthase2 trub bound to a t stem-loop rna
30	d1a8ra_	Alignment	not modelled	6.4	20	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: GTP cyclohydrolase I
31	c1sgvA_	Alignment	not modelled	6.3	36	PDB header: lyase Chain: A: PDB Molecule: trna pseudouridine synthase b; PDBTitle: structure of trna psi55 pseudouridine synthase (trub)
32	d2id1a1	Alignment	not modelled	6.3	44	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: !ojap/YbeB-like
33	d2ey4a2	Alignment	not modelled	6.2	36	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase II TruB
34	c5wk1L_	Alignment	not modelled	6.2	38	PDB header: virus Chain: L: PDB Molecule: capsid stabilizing protein; PDBTitle: structure of the major capsid protein and the capsid stabilizing2 protein of the marine siphovirus tw1
35	c3abqA_	Alignment	not modelled	6.0	34	PDB header: lyase Chain: A: PDB Molecule: ethanolamine ammonia-lyase heavy chain; PDBTitle: crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with cn-cbl and 2-amino-1-propanol
36	d1sgva2	Alignment	not modelled	5.7	36	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase II TruB
37	c4uqfB_	Alignment	not modelled	5.7	33	PDB header: hydrolase Chain: B: PDB Molecule: gtp cyclohydrolase 1; PDBTitle: crystal structure of listeria monocytogenes gtp cyclohydrolase i
38	c2yy3B_	Alignment	not modelled	5.7	33	PDB header: translation Chain: B: PDB Molecule: elongation factor 1-beta; PDBTitle: crystal structure of translation elongation factor ef-1 beta from2 pyrococcus horikoshii
39	d2o5aa1	Alignment	not modelled	5.6	50	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: !ojap/YbeB-like
40	d1wpla_	Alignment	not modelled	5.6	33	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: GTP cyclohydrolase I
41	c1is7F_	Alignment	not modelled	5.6	33	PDB header: hydrolase/protein binding Chain: F: PDB Molecule: gtp cyclohydrolase i; PDBTitle: crystal structure of rat gtpchi/gfrp stimulatory complex
42	c2lzsE_	Alignment	not modelled	5.4	33	PDB header: protein transport Chain: E: PDB Molecule: sec-independent protein translocase protein tata; PDBTitle: tata oligomer
43	c2bruB_	Alignment	not modelled	5.3	28	PDB header: oxidoreductase Chain: B: PDB Molecule: nad(p) transhydrogenase subunit alpha; PDBTitle: complex of the domain i and domain iii of escherichia coli2 transhydrogenase
44	c3upsA_	Alignment	not modelled	5.3	50	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: !ojap-like protein; PDBTitle: crystal structure of !ojap-like protein from zymomonas mobilis
45	c3ed6B_	Alignment	not modelled	5.3	27	PDB header: oxidoreductase Chain: B: PDB Molecule: betaine aldehyde dehydrogenase; PDBTitle: 1.7 angstrom resolution crystal structure of betaine aldehyde2 dehydrogenase (betb) from staphylococcus aureus