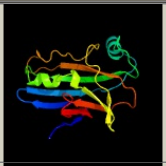
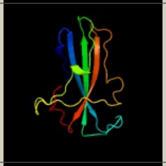
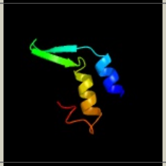
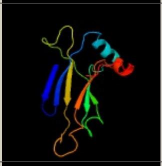
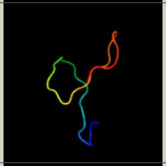
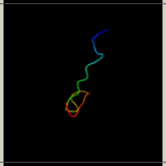
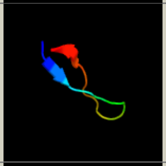
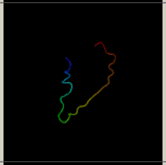
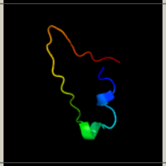
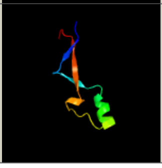
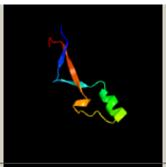
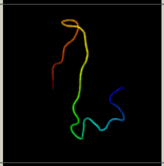
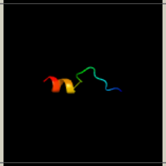
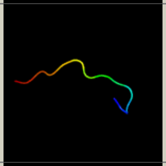
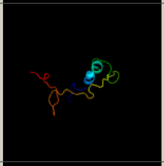
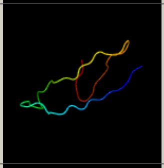
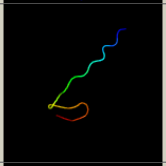
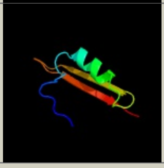
Email	mdejesus@rockefeller.edu
Description	RVBD2668_(-)_2984743_2985264
Date	Wed Aug 7 12:50:32 BST 2019
Unique Job ID	6ead294746f1ee90

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1lmia_	Alignment		96.8	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Antigen MPT63/MPB63 (immunoprotective extracellular protein) **Family:**Antigen MPT63/MPB63 (immunoprotective extracellular protein)
2	c3cfuA_	Alignment		60.7	17	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**uncharacterized lipoprotein yjha; **PDBTitle:** crystal structure of the yjha protein from bacillus subtilis.2 northeast structural genomics consortium target sr562
3	c5gpdA_	Alignment		41.9	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**sterol regulatory element-binding protein 1; **PDBTitle:** crystal structure of the binding domain of srebp from fission yeast
4	c2eefA_	Alignment		32.6	14	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**protein phosphatase 1, regulatory (inhibitor) **PDBTitle:** solution structure of the cbm_21 domain from human protein2 phosphatase 1, regulatory (inhibitor) subunit 3b
5	c6dkqA_	Alignment		23.2	31	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**heme-binding protein shr; **PDBTitle:** crystal structure of the shr hemoglobin interacting domain 2
6	c4ktbA_	Alignment		20.4	40	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** the crystal structure of posible asymmetric diadenosine tetraphosphate2 (ap(4)a) hydrolases from jonesia denitrificans dsm 20603
7	d2nn6g2	Alignment		18.9	50	**Fold:**Barrel-sandwich hybrid **Superfamily:**Ribosomal L27 protein-like **Family:**ECR1 N-terminal domain-like
8	c2cwrA_	Alignment		17.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase; **PDBTitle:** crystal structure of chitin biding domain of chitinase from2 pyrococcus furiosus
9	c5yy3A_	Alignment		16.9	9	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein asqi; **PDBTitle:** crystal structure of asqi
10	d2cbpa_	Alignment		16.7	19	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
11	d1s21a_	Alignment		14.7	30	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**AvrPphF ORF2, a type III effector

12	c1s21A_	Alignment		14.7	30	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**orf2; **PDBTitle:** crystal structure of avrpphf orf2, a type iii effector from p.2 syringae
13	c1x9rA_	Alignment		13.9	31	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**umecyanin; **PDBTitle:** umecyanin from horse raddish- crystal structure of the2 oxidised form
14	d1sg5a1	Alignment		13.6	42	**Fold:**Rof/RNase P subunit-like **Superfamily:**Rof/RNase P subunit-like **Family:**Rof-like
15	d1j5ya2	Alignment		13.5	38	**Fold:**HPr-like **Superfamily:**Putative transcriptional regulator TM1602, C-terminal domain **Family:**Putative transcriptional regulator TM1602, C-terminal domain
16	c5lc5q_	Alignment		11.8	17	**PDB header:**oxidoreductase **Chain:** Q: **PDB Molecule:**nadh dehydrogenase [ubiquinone] iron-sulfur protein 4, **PDBTitle:** structure of mammalian respiratory complex i, class2
17	c6f7eA_	Alignment		10.9	17	**PDB header:**carbohydrate **Chain:** A: **PDB Molecule:**putative secreted cellulose binding protein; **PDBTitle:** nmr solution structure of the cellulose-binding family 2 carbohydrate2 binding domain (cbm2) from sclpmo9c
18	c2b44A_	Alignment		10.7	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycyl-glycine endopeptidase lytm; **PDBTitle:** truncated s. aureus lytm, p 32 2 1 crystal form
19	c1wd6B_	Alignment		10.1	42	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein ydhr; **PDBTitle:** crystal structure of jw1657 from escherichia coli
20	c3iwcD_	Alignment		9.8	20	**PDB header:**lyase **Chain:** D: **PDB Molecule:**s-adenosylmethionine decarboxylase; **PDBTitle:** t. maritima adometdc complex with s-adenosylmethionine methyl ester
21	d1a0da_	Alignment	not modelled	9.4	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
22	c5vnyA_	Alignment	not modelled	9.2	42	**PDB header:**endocytosis, protein binding **Chain:** A: **PDB Molecule:**lethal (2) giant discs 1, isoform b; **PDBTitle:** crystal structure of dm14-3 domain of lgd
23	c2a7uA_	Alignment	not modelled	8.6	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp synthase alpha chain; **PDBTitle:** nmr solution structure of the e.coli f-atpase delta subunit n-terminal2 domain in complex with alpha subunit n-terminal 22 residues
24	c3eq1A_	Alignment	not modelled	8.2	47	**PDB header:**transferase **Chain:** A: **PDB Molecule:**porphobilinogen deaminase; **PDBTitle:** the crystal structure of human porphobilinogen deaminase at2 2.8a resolution
25	c2xznZ_	Alignment	not modelled	8.2	67	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**rps21e; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
26	c5flgA_	Alignment	not modelled	8.1	50	**PDB header:**ligase **Chain:** A: **PDB Molecule:**6-carboxyhexanoate--coa ligase; **PDBTitle:** crystal structure of the 6-carboxyhexanoate-coa ligase (biow)from2 bacillus subtilis in complex with amppnp
27	d1jzta_	Alignment	not modelled	7.8	28	**Fold:**YjeF N-terminal domain-like **Superfamily:**YjeF N-terminal domain-like **Family:**YjeF N-terminal domain-like
28	c1rrjA_	Alignment	not modelled	7.6	47	**PDB header:**isomerase/dna **Chain:** A: **PDB Molecule:**dna topoisomerase i; **PDBTitle:** structural mechanisms of camptothecin resistance by2

						mutations in human topoisomerase i
29	c4qpvB_	Alignment	not modelled	7.4	23	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a duf1672 family protein (sav1486) from2 staphylococcus aureus subsp. aureus mu50 at 1.80 a resolution
30	c5j5uC_	Alignment	not modelled	7.3	20	**PDB header:**chitin-binding protein **Chain:** C: **PDB Molecule:**ragb/susd domain protein; **PDBTitle:** fjoh_4561 chitin-binding protein
31	c3i09A_	Alignment	not modelled	7.2	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**periplasmic branched-chain amino acid-binding protein; **PDBTitle:** crystal structure of a periplasmic binding protein (bma2936) from2 burkholderia mallei at 1.80 a resolution
32	d1kf6d_	Alignment	not modelled	7.0	22	**Fold:**Heme-binding four-helical bundle **Superfamily:**Fumarate reductase respiratory complex transmembrane subunits **Family:**Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
33	c2gu1A_	Alignment	not modelled	6.9	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc peptidase; **PDBTitle:** crystal structure of a zinc containing peptidase from2 vibrio cholerae
34	c1jerA_	Alignment	not modelled	6.7	23	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cucumber stellacyanin; **PDBTitle:** cucumber stellacyanin, cu2+, ph 7.0
35	d1jera_	Alignment	not modelled	6.7	23	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
36	d1cr5a2	Alignment	not modelled	6.7	17	**Fold:**Cdc48 domain 2-like **Superfamily:**Cdc48 domain 2-like **Family:**Cdc48 domain 2-like
37	c3j38V_	Alignment	not modelled	6.5	58	**PDB header:**ribosome **Chain:** V: **PDB Molecule:**40s ribosomal protein s21; **PDBTitle:** structure of the d. melanogaster 40s ribosomal proteins
38	c5kvpA_	Alignment	not modelled	6.4	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zoocin a endopeptidase; **PDBTitle:** solution structure of the catalytic domain of zoocin a
39	c4yzwA_	Alignment	not modelled	6.0	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**agap004976-pa; **PDBTitle:** crystal structure of agppo8
40	d2bz1a1	Alignment	not modelled	6.0	36	**Fold:**RibA-like **Superfamily:**RibA-like **Family:**RibA-like
41	d2byea1	Alignment	not modelled	6.0	45	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
42	c6fhvA_	Alignment	not modelled	5.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucoamylase; **PDBTitle:** crystal structure of penicillium oxalicum glucoamylase
43	c2yopB_	Alignment	not modelled	5.8	19	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**protein fam3b; **PDBTitle:** long wavelength s-sad structure of fam3b pander
44	c4c8dA_	Alignment	not modelled	5.7	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysine-specific demethylase 3b; **PDBTitle:** crystal structure of jmjc domain of human histone 3 lysine-specific2 demethylase 3b (kdm3b)
45	c3nqyA_	Alignment	not modelled	5.6	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**secreted metalloprotease mcp02; **PDBTitle:** crystal structure of the autoprocessed complex of vibriolysin mcp-022 with a single point mutation e346a
46	c2i1tA_	Alignment	not modelled	5.5	40	**PDB header:**toxin **Chain:** A: **PDB Molecule:**jingzhaotoxin-3; **PDBTitle:** solution structure of jingzhaotoxin-iii, a novel toxin2 inhibiting both nav and kv channels
47	d1zhva1	Alignment	not modelled	5.5	10	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Atu0741-like
48	d2inca1	Alignment	not modelled	5.3	24	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ribonucleotide reductase-like
49	d1khba1	Alignment	not modelled	5.3	21	**Fold:**PEP carboxykinase-like **Superfamily:**PEP carboxykinase-like **Family:**PEP carboxykinase C-terminal domain
50	d1oisa_	Alignment	not modelled	5.3	35	**Fold:**Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment **Superfamily:**Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment **Family:**Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment
51	c3zeyR_	Alignment	not modelled	5.2	30	**PDB header:**ribosome **Chain:** R: **PDB Molecule:**40s ribosomal protein s21, putative; **PDBTitle:** high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
52	d1bhea_	Alignment	not modelled	5.2	31	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Galacturonase
53	c2djmA_	Alignment	not modelled	5.2	50	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**glucoamylase a; **PDBTitle:** solution structure of n-terminal starch-binding domain of2 glucoamylase from rhizopus oryzae
						PDB header:hydrolase

54	c5olpB_	Alignment	not modelled	5.2	17	**Chain:** B: **PDB Molecule:**pectate lyase; **PDBTitle:** galacturonidase
55	c3pf6C_	Alignment	not modelled	5.1	33	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein pp-luz7_gp033; **PDBTitle:** the structure of uncharacterized protein pp-luz7_gp033 from2 pseudomonas phage luz7.