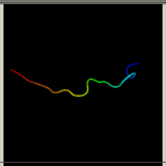
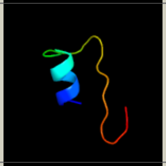
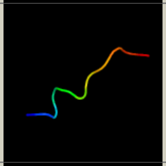
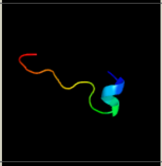
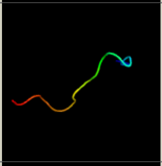
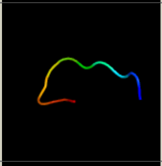
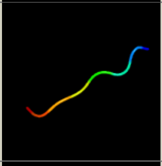
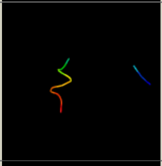
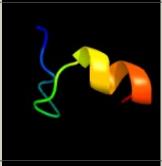
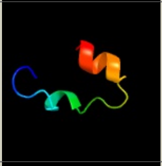
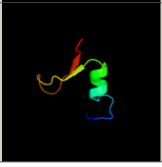
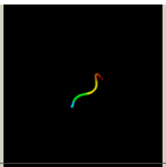
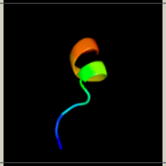
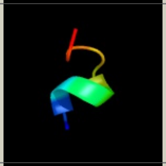
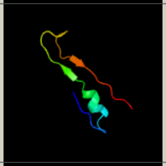
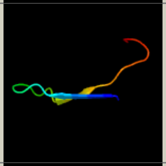
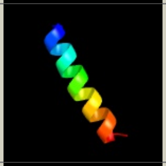
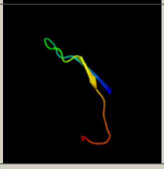
Email	mdejesus@rockefeller.edu
Description	RVBD2799_(-)_3107778_3108407
Date	Wed Aug 7 12:50:46 BST 2019
Unique Job ID	69498bd2c7c359ad

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2pbea1	Alignment		35.1	50	**Fold:**PAP/OAS1 substrate-binding domain **Superfamily:**PAP/OAS1 substrate-binding domain **Family:**AadK C-terminal domain-like
2	d1chka_	Alignment		21.7	32	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Chitosanase
3	c2rpsA_	Alignment		18.3	90	**PDB header:**immune system **Chain:** A: **PDB Molecule:**chemokine; **PDBTitle:** solution structure of a novel insect chemokine isolated from2 integument
4	c3j6vO_	Alignment		15.8	28	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**28s ribosomal protein s15, mitochondrial; **PDBTitle:** cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
5	c4m6tA_	Alignment		15.5	44	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**rna polymerase ii-associated factor 1 homolog, linker, rna **PDBTitle:** structure of human paf1 and leo1 complex
6	d1wjpa3	Alignment		14.6	55	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
7	c5lcsA_	Alignment		12.7	63	**PDB header:**immune system **Chain:** A: **PDB Molecule:**gallinacin-7; **PDBTitle:** nmr structure of chicken avbd7 defensin
8	c2okqB_	Alignment		12.6	64	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ybaa; **PDBTitle:** crystal structure of unknown conserved ybaa protein from shigella2 flexneri
9	d3dssb1	Alignment		11.6	32	**Fold:**alpha/alpha toroid **Superfamily:**Terpenoid cyclases/Protein prenyltransferases **Family:**Protein prenyltransferases
10	d1kl9a1	Alignment		10.7	38	**Fold:**SAM domain-like **Superfamily:**eIF2alpha middle domain-like **Family:**eIF2alpha middle domain-like
11	d1m4ma_	Alignment		10.2	24	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat

12	c6cnuB_	Alignment		10.0	83	**PDB header:**toxin **Chain:** B: **PDB Molecule:**jztx-v; **PDBTitle:** crystal structure of jztx-v
13	d1s4ka_	Alignment		9.8	36	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**YdiL-like
14	d1n1ba1	Alignment		9.7	30	**Fold:**alpha/alpha toroid **Superfamily:**Terpenoid cyclases/Protein prenyltransferases **Family:**Terpenoid cyclase N-terminal domain
15	d1ypzf2	Alignment		9.5	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C1 set domains (antibody constant domain-like)
16	c3psqA_	Alignment		9.3	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical exported protein; **PDBTitle:** crystal structure of spy0129, a streptococcus pyogenes class b sortase2 involved in pilus biogenesis
17	d5easa1	Alignment		9.1	60	**Fold:**alpha/alpha toroid **Superfamily:**Terpenoid cyclases/Protein prenyltransferases **Family:**Terpenoid cyclase N-terminal domain
18	c4gkgA_	Alignment		8.4	45	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**c4-dicarboxylate transport sensor protein dctb; **PDBTitle:** crystal structure of the s-helix linker
19	c2n59A_	Alignment		8.2	21	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein csgh; **PDBTitle:** solution structure of r. palustris csgh
20	c5yfkA_	Alignment		8.1	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized protein sortase b; **PDBTitle:** x-ray structure of a mutant form c232s of clostridium perfringens2 sortase b
21	c6cgwA_	Alignment	not modelled	7.8	83	**PDB header:**toxin **Chain:** A: **PDB Molecule:**beta/kappa-theraphotoxin-cg2a; **PDBTitle:** solution nmr structure of jztx-v, a nav 1.7 inhibitory peptide
22	d1tqza1	Alignment	not modelled	7.8	28	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Necap1 N-terminal domain-like
23	c2juyA_	Alignment	not modelled	7.8	47	**PDB header:**antitumor protein **Chain:** A: **PDB Molecule:**neopetrosiamide a; **PDBTitle:** nmr ensemble of neopetrosiamide a
24	c6chcA_	Alignment	not modelled	7.5	83	**PDB header:**toxin **Chain:** A: **PDB Molecule:**beta/kappa-theraphotoxin-cg2a; **PDBTitle:** jztx-v toxin peptide, wild-type
25	d2oqza1	Alignment	not modelled	7.3	39	**Fold:**Sortase **Superfamily:**Sortase **Family:**Sortase
26	c5z5kB_	Alignment	not modelled	7.2	83	**PDB header:**apoptosis/inbititor **Chain:** B: **PDB Molecule:**draxin; **PDBTitle:** structure of the dcc-draxin complex
27	c1zhqB_	Alignment	not modelled	7.0	14	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**mannan-binding lectin; **PDBTitle:** crystal structure of apo mvl
28	c3zfsA_	Alignment	not modelled	6.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**f420-reducing hydrogenase, subunit alpha; **PDBTitle:** cryo-em structure of the f420-reducing nife-hydrogenase from a2 methanogenic archaeon with bound substrate
29	d1n0ua5	Alignment	not modelled	6.8	23	**Fold:**Ferredoxin-like **Superfamily:**EF-G C-terminal domain-like

						Family:EF-G/eEF-2 domains III and V
30	c4c3oC_	Alignment	not modelled	6.7	30	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**hydrogenase-1 large subunit; **PDBTitle:** structure and function of an oxygen tolerant nife hydrogenase from2 salmonella
31	c4dwcA_	Alignment	not modelled	6.6	24	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**e(rns) glycoprotein; **PDBTitle:** crystal structure of the glycoprotein erns from the pestivirus bvdv-12 in complex with zn ions
32	c5yy0A_	Alignment	not modelled	6.6	20	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**cytosolic nife-hydrogenase, alpha subunit; **PDBTitle:** crystal structure of the hyhl-hypa complex (form ii)
33	c1v7fA_	Alignment	not modelled	6.6	67	**PDB header:**toxin **Chain:** A: **PDB Molecule:**phrixotoxin 1; **PDBTitle:** solution structure of phrixotoxin 1
34	d1v7fa_	Alignment	not modelled	6.6	67	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**omega toxin-like **Family:**Spider toxins
35	d2vana2	Alignment	not modelled	6.6	21	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**DNA polymerase beta-like
36	c4oltA_	Alignment	not modelled	6.4	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitosanase; **PDBTitle:** chitosanase complex structure
37	d1qwza_	Alignment	not modelled	6.4	26	**Fold:**Sortase **Superfamily:**Sortase **Family:**Sortase
38	c6ehqM_	Alignment	not modelled	6.3	20	**PDB header:**oxidoreductase **Chain:** M: **PDB Molecule:**hydrogenase-2 large chain; **PDBTitle:** e. coli hydrogenase-2 (as isolated form).
39	c4v3aC_	Alignment	not modelled	6.3	26	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**pleurotolysin b; **PDBTitle:** membrane bound pleurotolysin prepore (tmh1 lock) trapped with2 engineered disulphide cross-link
40	c5jcvA_	Alignment	not modelled	6.2	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lmo2181 protein; **PDBTitle:** sortase b from listeria monocytogenes.
41	d2raxa1	Alignment	not modelled	6.0	24	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
42	c2n2aA_	Alignment	not modelled	5.9	21	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** spatial structure of her2/erbb2 dimeric transmembrane domain in the2 presence of cytoplasmic juxtamembrane domains
43	c1lupA_	Alignment	not modelled	5.7	67	**PDB header:**toxin **Chain:** A: **PDB Molecule:**gsmtx2; **PDBTitle:** solution structure of a toxin (gsmtx2) from the tarantula,2 grammostola spatulata, which inhibits mechanosensitive ion3 channels
44	c2l66B_	Alignment	not modelled	5.7	30	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, abrb family; **PDBTitle:** the dna-recognition fold of sso7c4 suggests a new member of spovt-abrb2 superfamily from archaea.
45	c3q38A_	Alignment	not modelled	5.6	44	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**capsid protein; **PDBTitle:** crystal structure of p domain from norwalk virus strain vietnam 026 in2 complex with hbga type b (triglycan)
46	d1yq9h1	Alignment	not modelled	5.6	15	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
47	c2kdpA_	Alignment	not modelled	5.5	58	**PDB header:**transcription **Chain:** A: **PDB Molecule:**histone deacetylase complex subunit sap30; **PDBTitle:** solution structure of the sap30 zinc finger motif
48	d1frfl_	Alignment	not modelled	5.4	20	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
49	c3useL_	Alignment	not modelled	5.4	24	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**hydrogenase-1 large chain; **PDBTitle:** crystal structure of e. coli hydrogenase-1 in its as-isolated form
50	d2q1ma1	Alignment	not modelled	5.2	16	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
51	d1tcra2	Alignment	not modelled	5.1	26	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C1 set domains (antibody constant domain-like)
52	c2df7H_	Alignment	not modelled	5.1	29	**PDB header:**virus like particle **Chain:** H: **PDB Molecule:**structural polyprotein vp2; **PDBTitle:** crystal structure of infectious bursal disease virus vp2 subviral2 particle