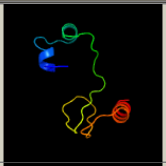
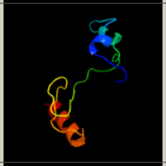
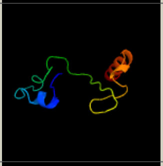
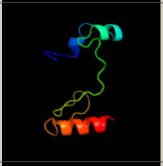
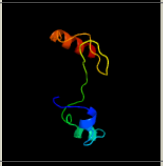
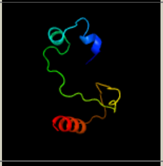
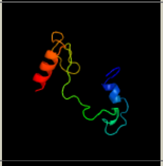
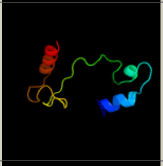
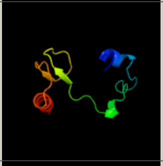
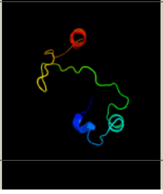
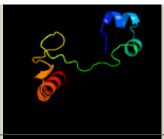
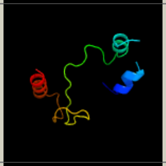
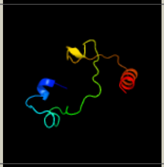
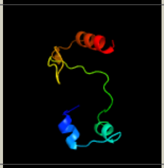
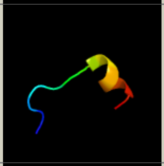
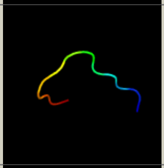
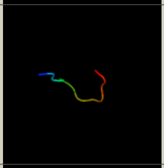
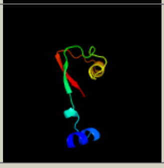
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1087A_(-)_1214045_1214365
Date	Wed Jul 31 22:05:16 BST 2019
Unique Job ID	03fe196990340803

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vg2C_	Alignment		99.8	44	**PDB header:**transferase **Chain:** C: **PDB Molecule:**undecaprenyl pyrophosphate synthetase; **PDBTitle:** rv2361 with ipp
2	c6jcnB_	Alignment		99.8	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dehydrodolichyl diphosphate synthase complex subunit nus1; **PDBTitle:** yeast dehydrodolichyl diphosphate synthase complex subunit nus1
3	d1f75a_	Alignment		99.8	36	**Fold:**Undecaprenyl diphosphate synthase **Superfamily:**Undecaprenyl diphosphate synthase **Family:**Undecaprenyl diphosphate synthase
4	d1ueha_	Alignment		99.8	27	**Fold:**Undecaprenyl diphosphate synthase **Superfamily:**Undecaprenyl diphosphate synthase **Family:**Undecaprenyl diphosphate synthase
5	c2d2rA_	Alignment		99.8	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**undecaprenyl pyrophosphate synthase; **PDBTitle:** crystal structure of helicobacter pylori undecaprenyl pyrophosphate2 synthase
6	c4h8eA_	Alignment		99.8	35	**PDB header:**transferase/transferase inhibitor **Chain:** A: **PDB Molecule:**undecaprenyl pyrophosphate synthase; **PDBTitle:** structure of s. aureus undecaprenyl diphosphate synthase in complex2 with fpp and sulfate
7	c2vfwB_	Alignment		99.8	76	**PDB header:**transferase **Chain:** B: **PDB Molecule:**short-chain z-isoprenyl diphosphate synthetase; **PDBTitle:** rv1086 native
8	c5hc7A_	Alignment		99.8	42	**PDB header:**transferase/transferase inhibitor **Chain:** A: **PDB Molecule:**prenyltransference for protein; **PDBTitle:** crystal structure of lavandulyl diphosphate synthase from lavandula x2 intermedia in complex with s-thiolo-isopentenyldiphosphate
9	c6acsA_	Alignment		99.7	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ditrans,polycis-undecaprenyl-diphosphate synthase ((2e,6e)- **PDBTitle:** poly-cis-prenyltransferase
10	c1jp3A_	Alignment		99.7	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**undecaprenyl pyrophosphate synthase; **PDBTitle:** structure of e.coli undecaprenyl pyrophosphate synthase
11	c4q9mA_	Alignment		99.7	42	**PDB header:**transferase/transferase inhibitor **Chain:** A: **PDB Molecule:**isoprenyl transferase; **PDBTitle:** crystal structure of upps in complex with fpp and an allosteric2 inhibitor

12	c5xk9F_	Alignment		99.7	23	**PDB header:**transferase **Chain:** F: **PDB Molecule:**undecaprenyl diphosphate synthase; **PDBTitle:** crystal structure of isosesquilavandulyl diphosphate synthase from2 streptomyces sp. strain cnh-189 in complex with gspp and dmapp
13	c5hxpA_	Alignment		99.7	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**(2z,6z)-farnesyl diphosphate synthase, chloroplastic; **PDBTitle:** crystal structure of z,z-farnesyl diphosphate synthase (d71m, e75a and2 h103y mutants) complexed with ipp
14	c3ugsB_	Alignment		99.7	30	**PDB header:**transferase **Chain:** B: **PDB Molecule:**undecaprenyl pyrophosphate synthase; **PDBTitle:** crystal structure of a probable undecaprenyl diphosphate synthase2 (upps) from campylobacter jejuni
15	c5gukA_	Alignment		99.6	26	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**cyclolavandulyl diphosphate synthase; **PDBTitle:** crystal structure of apo form of cyclolavandulyl diphosphate synthase2 (clds) from streptomyces sp. cl190
16	c2ksnA_	Alignment		35.8	29	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ubiquitin domain-containing protein 2; **PDBTitle:** solution structure of the n-terminal domain of dc-ubp/ubtd2
17	c4n6rA_	Alignment		14.2	46	**PDB header:**dna binding protein/transcription **Chain:** A: **PDB Molecule:**vosa; **PDBTitle:** crystal structure of vosa-velb-complex
18	c4n6rB_	Alignment		13.1	54	**PDB header:**dna binding protein/transcription **Chain:** B: **PDB Molecule:**velb; **PDBTitle:** crystal structure of vosa-velb-complex
19	d1ofua1	Alignment		11.1	19	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
20	d1tgoa2	Alignment		11.1	22	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**DNA polymerase I
21	d1a6qa1	Alignment	not modelled	10.8	38	**Fold:**Another 3-helical bundle **Superfamily:**Protein serine/threonine phosphatase 2C, C-terminal domain **Family:**Protein serine/threonine phosphatase 2C, C-terminal domain
22	c3qrzC_	Alignment	not modelled	10.6	38	**PDB header:**hormone receptor **Chain:** C: **PDB Molecule:**abscisic acid receptor pyl5; **PDBTitle:** crystal structure of native abscisic acid receptor pyl5 at 2.62 angstrom
23	c2wmmA_	Alignment	not modelled	10.3	9	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**chromosome partition protein mukb; **PDBTitle:** crystal structure of the hinge domain of mukb
24	c2vwkA_	Alignment	not modelled	9.9	22	**PDB header:**dna replication **Chain:** A: **PDB Molecule:**dna polymerase; **PDBTitle:** uracil recognition in archaeal dna polymerases captured by2 x-ray crystallography. v93q polymerase variant
25	c5znsA_	Alignment	not modelled	9.8	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitin deacetylase; **PDBTitle:** insect chitin deacetylase
26	d1w5fa1	Alignment	not modelled	9.6	22	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
27	c3btpA_	Alignment	not modelled	9.4	19	**PDB header:**dna binding protein, chaperone **Chain:** A: **PDB Molecule:**single-strand dna-binding protein; **PDBTitle:** crystal structure of agrobacterium tumefaciens vire2 in complex with2 its chaperone vire1: a novel fold and implications for dna binding
28	d2vapa1	Alignment	not modelled	8.2	24	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
29	c4c1bC_	Alignment	not modelled	7.8	33	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**orf1-encoded protein;

29	c4c1bC_	Alignment	not modelled	7.8	33	**PDBTitle:** esterase domain of the zfl2-1 orf1 protein from the zebrafish zfl2-12 retrotransposon
30	c3gzfD_	Alignment	not modelled	7.7	33	**PDB header:**viral protein **Chain:** D: **PDB Molecule:**replicase polyprotein 1ab; **PDBTitle:** structure of the c-terminal domain of nsp4 from feline coronavirus
31	d2vana2	Alignment	not modelled	7.3	29	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**DNA polymerase beta-like
32	c4n6qA_	Alignment	not modelled	7.3	46	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**vosa; **PDBTitle:** crystal structure of vosa velvet domain
33	c1nomA_	Alignment	not modelled	7.3	29	**PDB header:**nucleotidyltransferase **Chain:** A: **PDB Molecule:**dna polymerase beta; **PDBTitle:** dna polymerase beta (pol b) (e.c.2.7.7.7), 31-kd domain; soaked in the2 presence of mncl2 (5 millimolar)
34	c3d0fA_	Alignment	not modelled	7.2	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**penicillin-binding 1 transmembrane protein mrca; **PDBTitle:** structure of the big_1156.2 domain of putative penicillin-binding2 protein mrca from nitrosomonas europaea atcc 19718
35	c5z34A_	Alignment	not modelled	6.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitin deacetylase; **PDBTitle:** the structure of a chitin deacetylase from bombyx mori provide the2 first insight into insect chitin deacetylation mechanism
36	c3viqC_	Alignment	not modelled	6.5	35	**PDB header:**recombination activator **Chain:** C: **PDB Molecule:**swi5-dependent recombination dna repair protein 1; **PDBTitle:** crystal structure of swi5-sfr1 complex from fission yeast
37	c1usdA_	Alignment	not modelled	6.3	25	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**vasodilator-stimulated phosphoprotein; **PDBTitle:** human vasp tetramerisation domain l352m
38	c8iczA_	Alignment	not modelled	6.1	29	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**protein (dna polymerase beta (e.c.2.7.7.7)); **PDBTitle:** dna polymerase beta (pol b) (e.c.2.7.7.7) complexed with2 seven base pairs of dna; soaked in the presence of of datp3 (1 millimolar), mncl2 (5 millimolar), and lithium sulfate4 (75 millimolar)
39	d2fmpa3	Alignment	not modelled	6.1	29	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**DNA polymerase beta-like
40	c4xaiP_	Alignment	not modelled	6.0	43	**PDB header:**transcription **Chain:** P: **PDB Molecule:**grunge, isoform j; **PDBTitle:** crystal structure of red flour beetle nr2e1/tlx
41	d2p6va1	Alignment	not modelled	6.0	18	**Fold:**TAFH domain-like **Superfamily:**TAFH domain-like **Family:**TAFH domain-like
42	d2oq1a2	Alignment	not modelled	6.0	22	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
43	c5fmlA_	Alignment	not modelled	5.6	39	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**pb2 subunit of influenza b polymerase; **PDBTitle:** crystal structure of the endonuclease from the pa subunit of2 influenza b virus bound to the pb2 subunit nls peptide
44	c2k4mA_	Alignment	not modelled	5.5	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0146 protein mth_1000; **PDBTitle:** solution nmr structure of m. thermoautotrophicum protein mth_1000,2 northeast structural genomics consortium target tr8