

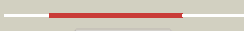







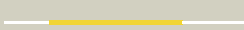


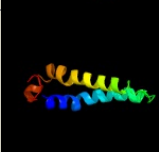


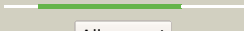




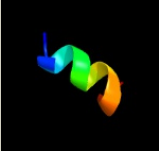


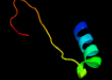

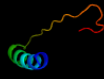
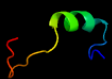


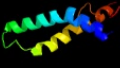


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1451_(ctaB)_1635035_1635961
Date	Fri Aug 2 13:30:03 BST 2019
Unique Job ID	9ead662b29829549

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4od5C_	 Alignment		100.0	19	PDB header: transferase Chain: C: PDB Molecule: 4-hydroxybenzoate octaprenyltransferase; PDBTitle: substrate-bound structure of a ubia homolog from aeropyrum pernix k1
2	c3ts7B_	 Alignment		93.6	12	PDB header: transferase Chain: B: PDB Molecule: geranyltranstransferase; PDBTitle: crystal structure of farnesyl diphosphate synthase (target efi-501951)2 from methylococcus capsulatus
3	c3m9uD_	 Alignment		92.7	13	PDB header: transferase Chain: D: PDB Molecule: farnesyl-diphosphate synthase; PDBTitle: crystal structure of geranylgeranyl pyrophosphate synthase from2 lactobacillus brevis atcc 367
4	c5xn5A_	 Alignment		91.7	10	PDB header: transferase Chain: A: PDB Molecule: os07g0580900 protein; PDBTitle: homo-dimer crystal structure of geranylgeranyl diphosphate synthases 12 from oryza sativa
5	c3dh4A_	 Alignment		80.1	12	PDB header: transport protein Chain: A: PDB Molecule: sodium/glucose cotransporter; PDBTitle: crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus
6	c3lsnA_	 Alignment		70.1	15	PDB header: transferase Chain: A: PDB Molecule: geranyltranstransferase; PDBTitle: crystal structure of putative geranyltranstransferase from pseudomonas2 fluorescens pf-5 complexed with magnesium
7	c4jyxE_	 Alignment		59.5	14	PDB header: transferase Chain: E: PDB Molecule: trans-hexaprenyltranstransferase; PDBTitle: crystal structure of polyprenyl synthase patl_3739 (target efi-509195)2 from pseudoalteromonas atlantica, complex with inorganic phosphate3 and an unknown ligand
8	c3ez3A_	 Alignment		53.7	9	PDB header: lyase Chain: A: PDB Molecule: farnesyl pyrophosphate synthase, putative; PDBTitle: crystal structure of plasmodium vivax geranylgeranylpyrophosphate2 synthase pvx_092040 with zoledronate and ipp bound
9	d1rqja_	 Alignment		52.7	13	Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Isoprenyl diphosphate synthases
10	c3oacD_	 Alignment		51.4	10	PDB header: transferase Chain: D: PDB Molecule: geranyl diphosphate synthase large subunit; PDBTitle: mint deletion mutant of heterotetrameric geranyl pyrophosphate2 synthase in complex with ligands
11	c2l4fA_	 Alignment		50.7	33	PDB header: protein binding Chain: A: PDB Molecule: defective in cullin neddylation protein 1; PDBTitle: nmr structure of the uba domain of s. cerevisiae dcn1 bound to2 ubiquitin

12	c4lfgB	Alignment		43.1	10	PDB header: transferase Chain: B: PDB Molecule: geranylgeranyl diphosphate synthase; PDBTitle: crystal structure of geranylgeranyl diphosphate synthase sub12742 (target efi-509455) from streptococcus uberis 0140j with bound3 magnesium and isopentyl diphosphate, fully liganded complex;
13	c2j1oA	Alignment		43.1	7	PDB header: transferase Chain: A: PDB Molecule: geranylgeranyl pyrophosphate synthetase; PDBTitle: geranylgeranyl diphosphate synthase from sinapis alba
14	d1dih2	Alignment		36.8	18	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Dihydrodipicolinate reductase-like
15	c5h9dB	Alignment		36.1	8	PDB header: transferase Chain: B: PDB Molecule: farnesyl pyrophosphate synthetase; PDBTitle: crystal structure of heptaprenyl diphosphate synthase from2 staphylococcus aureus
16	c5us6L	Alignment		33.9	11	PDB header: oxidoreductase Chain: L: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: structure of dihydrodipicolinate reductase from vibrio vulnificus2 bound to nadh and 2,6 pyridine dicarboxylic acid with intact3 polyhistidine tag
17	c4ksnC	Alignment		33.6	33	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: sdbc; PDBTitle: c-terminal domain of sdbc protein from legionella pneumophila.
18	c2o1oB	Alignment		33.0	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative farnesyl pyrophosphate synthase; PDBTitle: cryptosporidium parvum putative polyprenyl pyrophosphate synthase2 (cgd4_2550) in complex with risedronate.
19	c4kkmB	Alignment		32.8	12	PDB header: transferase Chain: B: PDB Molecule: polyprenyl synthetase; PDBTitle: crystal structure of a fpp/gfpp synthase (target efi-501952) from2 zymomonas mobilis, apo structure
20	c3p8rA	Alignment		32.8	16	PDB header: transferase Chain: A: PDB Molecule: geranyltranstransferase; PDBTitle: crystal structure of polyprenyl synthase from vibrio cholerae
21	c3llwA	Alignment	not modelled	32.1	10	PDB header: transferase Chain: A: PDB Molecule: geranyltranstransferase (ispa); PDBTitle: crystal structure of geranyltransferase from helicobacter pylori 26695
22	c2j1pB	Alignment	not modelled	27.6	11	PDB header: transferase Chain: B: PDB Molecule: geranylgeranyl pyrophosphate synthetase; PDBTitle: geranylgeranyl diphosphate synthase from sinapis alba in2 complex with ggpp
23	d1m9fd	Alignment	not modelled	26.4	17	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
24	d2axth1	Alignment	not modelled	25.4	27	Fold: Single transmembrane helix Superfamily: Photosystem II 10 kDa phosphoprotein PsbH Family: PsbH-like
25	c2axtH	Alignment	not modelled	25.4	27	PDB header: electron transport Chain: H: PDB Molecule: photosystem ii reaction center h protein; PDBTitle: crystal structure of photosystem ii from thermosynechococcus elongatus
26	d1m9dc	Alignment	not modelled	25.2	14	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
27	c4kk2B	Alignment	not modelled	23.1	11	PDB header: transferase Chain: B: PDB Molecule: monoterpene synthase fds-5, chloroplast - farnesyl PDBTitle: crystal structure of a chimeric fpp/gfpp synthase (target efi-502313c)2 from artemisia spiciformis (1-72:gi751454468,73-346:gi75233326), apo3 structure
28	c5jfqB	Alignment	not modelled	22.8	12	PDB header: oxidoreductase Chain: B: PDB Molecule: geranylgeranyl pyrophosphate synthetase; PDBTitle: geranylgeranyl pyrophosphate synthetase from archaeon

						geoglobus2 acetivorans
29	d2pxrc1	Alignment	not modelled	22.2	14	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
30	c4f62B	Alignment	not modelled	21.8	10	PDB header: transferase Chain: B: PDB Molecule: geranyltranstransferase; PDBTitle: crystal structure of a putative farnesyl-diphosphate synthase from2 marinomonas sp. med121 (target efi-501980)
31	c3wjnA	Alignment	not modelled	21.2	12	PDB header: transferase Chain: A: PDB Molecule: octaprenyl diphosphate synthase; PDBTitle: crystal structure of octaprenyl pyrophosphate synthase from2 escherichia coli with farnesyl s-thiol-pyrophosphate (fsp)
32	c4jzbA	Alignment	not modelled	20.7	10	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: farnesyl pyrophosphate synthase; PDBTitle: crystal structure of leshmaniasis major farnesyl diphosphate synthase2 in complex with 1-(2-hydroxy-2,2-diphosphonoethyl)-3-3 phenylpyridinium, ipp and ca2+
33	c5tenH	Alignment	not modelled	19.3	11	PDB header: oxidoreductase Chain: H: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: structure of 4-hydroxy-tetrahydrodipicolinate reductase from vibrio2 vulnificus with 2,5 furan dicarboxylic and nadh with intact3 polyhistidine tag
34	c1wy0A	Alignment	not modelled	18.7	12	PDB header: transferase Chain: A: PDB Molecule: geranylgeranyl pyrophosphate synthetase; PDBTitle: crystal structure of geranylgeranyl pyrophosphate synthetase from2 pyrococcus horikoshii ot3
35	c3oyrB	Alignment	not modelled	18.7	12	PDB header: transferase Chain: B: PDB Molecule: trans-isoprenyl diphosphate synthase; PDBTitle: crystal structure of polyprenyl synthase from caulobacter crescentus2 cb15 complexed with calcium and isoprenyl diphosphate
36	c4lltB	Alignment	not modelled	18.3	13	PDB header: transferase Chain: B: PDB Molecule: geranyltranstransferase; PDBTitle: crystal structure of a farnesyl diphosphate synthase from roseobacter2 denitrificans och 114, target efi-509393, with two ipp and calcium3 bound in active site
37	c3tc1A	Alignment	not modelled	18.0	10	PDB header: transferase Chain: A: PDB Molecule: octaprenyl pyrophosphate synthase; PDBTitle: crystal structure of octaprenyl pyrophosphate synthase from2 helicobacter pylori
38	c3mzvB	Alignment	not modelled	18.0	14	PDB header: transferase Chain: B: PDB Molecule: decaprenyl diphosphate synthase; PDBTitle: crystal structure of a decaprenyl diphosphate synthase from2 rhodobacter capsulatus
39	c3p8B	Alignment	not modelled	15.0	11	PDB header: transferase Chain: B: PDB Molecule: geranyltranstransferase; PDBTitle: crystal structure of polyprenyl synthase from enterococcus faecalis2 v583
40	c3aqbD	Alignment	not modelled	14.6	8	PDB header: transferase Chain: D: PDB Molecule: component b of hexaprenyl diphosphate synthase; PDBTitle: m. luteus b-p 26 heterodimeric hexaprenyl diphosphate synthase in2 complex with magnesium
41	c1drwA	Alignment	not modelled	13.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: escherichia coli dhpr/nhdh complex
42	c3cp6A	Alignment	not modelled	12.9	9	PDB header: transferase Chain: A: PDB Molecule: farnesyl pyrophosphate synthetase; PDBTitle: crystal structure of human farnesyl diphosphate synthase (t201a2 mutant) complexed with mg and biphosphonate inhibitor
43	c5yo8B	Alignment	not modelled	12.9	8	PDB header: lyase Chain: B: PDB Molecule: tetraprenyl-beta-curcumene synthase; PDBTitle: crystal structure of beta-c25/c30/c35-prene synthase
44	c3kraB	Alignment	not modelled	11.9	9	PDB header: transferase Chain: B: PDB Molecule: geranyl diphosphate synthase small subunit; PDBTitle: mint heterotetrameric geranyl pyrophosphate synthase in complex with2 magnesium
45	c2wlvA	Alignment	not modelled	11.0	15	PDB header: viral protein Chain: A: PDB Molecule: gag polyprotein; PDBTitle: structure of the n-terminal capsid domain of hiv-2
46	c3ijpA	Alignment	not modelled	11.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: crystal structure of dihydrodipicolinate reductase from bartonella2 henselae at 2.0a resolution
47	c1l6nA	Alignment	not modelled	10.4	12	PDB header: viral protein Chain: A: PDB Molecule: gag polyprotein; PDBTitle: structure of the n-terminal 283-residue fragment of the hiv-2 1 gag polyprotein
48	c6c57B	Alignment	not modelled	9.1	8	PDB header: transferase/transferase inhibitor Chain: B: PDB Molecule: geranylgeranyl pyrophosphate synthase; PDBTitle: crystal structure of mutant human geranylgeranyl pyrophosphate2 synthase (y246d) in complex with bisphosphonate inhibitor fv0109
49	c2xq2A	Alignment	not modelled	9.0	9	PDB header: transport protein Chain: A: PDB Molecule: sodium/glucose cotransporter; PDBTitle: structure of the k294a mutant of vsplt
50	c6cflw	Alignment	not modelled	8.4	12	PDB header: membrane protein Chain: I: PDB Molecule: mbh subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
51	d1vm6a2	Alignment	not modelled	8.1	14	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Dihydrodipicolinate reductase-like
52	c4f3yA	Alignment	not modelled	8.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: x-ray crystal structure of dihydrodipicolinate reductase from2 burkholderia thailandensis

53	c3ipiA_	Alignment	not modelled	7.9	12	PDB header: transferase Chain: A: PDB Molecule: geranyltranstransferase; PDBTitle: crystal structure of a geranyltranstransferase from the methanosarcina2 mazei
54	c4ywjB_	Alignment	not modelled	7.4	17	PDB header: oxidoreductase Chain: B: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: crystal structure of 4-hydroxy-tetrahydrodipicolinate reductase (htpa2 reductase) from pseudomonas aeruginosa
55	c3nf2A_	Alignment	not modelled	7.4	16	PDB header: transferase Chain: A: PDB Molecule: putative polyprenyl synthetase; PDBTitle: crystal structure of polyprenyl synthetase from streptomyces2 coelicolor a3(2)
56	c6j5ib_	Alignment	not modelled	7.0	13	PDB header: membrane protein Chain: B: PDB Molecule: atp synthase subunit alpha, mitochondrial; PDBTitle: cryo-em structure of the mammalian dp-state atp synthase
57	c2jlnA_	Alignment	not modelled	6.8	9	PDB header: membrane protein Chain: A: PDB Molecule: mhp1; PDBTitle: structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
58	c2zcpA_	Alignment	not modelled	6.8	4	PDB header: transferase Chain: A: PDB Molecule: dehydrosqualene synthase; PDBTitle: crystal structure of the c(30) carotenoid dehydrosqualene synthase2 from staphylococcus aureus complexed with farnesyl thiopyrophosphate
59	c3qy9C_	Alignment	not modelled	6.8	14	PDB header: oxidoreductase Chain: C: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: the crystal structure of dihydrodipicolinate reductase from2 staphylococcus aureus
60	c3oyrA_	Alignment	not modelled	6.6	16	PDB header: transferase Chain: A: PDB Molecule: trans-isoprenyl diphosphate synthase; PDBTitle: crystal structure of polyprenyl synthase from caulobacter crescentus2 cb15 complexed with calcium and isoprenyl diphosphate
61	d1fpsa_	Alignment	not modelled	6.5	11	Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Isoprenyl diphosphate synthases
62	c5ugiC_	Alignment	not modelled	6.4	19	PDB header: oxidoreductase Chain: C: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: crystal structure of htpa reductase from neisseria meningitidis
63	d1ezfa_	Alignment	not modelled	6.2	15	Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Squalene synthase
64	c2ftzA_	Alignment	not modelled	6.2	7	PDB header: transferase Chain: A: PDB Molecule: geranyltranstransferase; PDBTitle: crystal structure of geranyltranstransferase (ec 2.5.1.10) (tm0161)2 from thermotoga maritima at 1.90 a resolution
65	c6hu9x_	Alignment	not modelled	6.1	13	PDB header: oxidoreductase/electron transport Chain: X: PDB Molecule: PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
66	c6hu9l_	Alignment	not modelled	6.1	13	PDB header: oxidoreductase/electron transport Chain: L: PDB Molecule: cytochrome b-c1 complex subunit 1, mitochondrial; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
67	c1xv3A_	Alignment	not modelled	5.9	43	PDB header: antibiotic Chain: A: PDB Molecule: penaeidin-4d; PDBTitle: nmr structure of the synthetic penaeidin 4
68	c1wmwA_	Alignment	not modelled	5.5	13	PDB header: transferase Chain: A: PDB Molecule: geranylgeranyl diphosphate synthetase; PDBTitle: crystal structure of geranylgeranyl diphosphate synthase from thermus2 thermophilus
69	c2f94F_	Alignment	not modelled	5.2	9	PDB header: transferase Chain: F: PDB Molecule: farnesyl diphosphate synthase; PDBTitle: crystal structure of human fpps in complex with ibandronate
70	d2hjqa2	Alignment	not modelled	5.2	29	Fold: GINS/PriA/YqbF domain Superfamily: PriA/YqbF domain Family: YqbF N-terminal domain-like
71	c4h25F_	Alignment	not modelled	5.1	31	PDB header: immune system Chain: F: PDB Molecule: peptide; PDBTitle: tcr interaction with peptide mimics of nickel offers structure2 insights to nickel contact allergy
72	c4h25C_	Alignment	not modelled	5.1	31	PDB header: immune system Chain: C: PDB Molecule: peptide; PDBTitle: tcr interaction with peptide mimics of nickel offers structure2 insights to nickel contact allergy
73	d1v74a_	Alignment	not modelled	5.1	15	Fold: Colicin D/E5 nuclease domain Superfamily: Colicin D/E5 nuclease domain Family: Colicin D nuclease domain
74	c5dm5E_	Alignment	not modelled	5.1	21	PDB header: hydrolase Chain: E: PDB Molecule: putative acyl-coa thioester hydrolase; PDBTitle: crystal structure of the hexameric thioesterase y2039 from yersinia2 pestis