



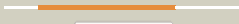











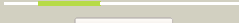



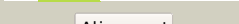

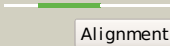

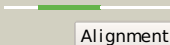

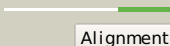
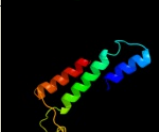
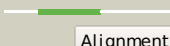


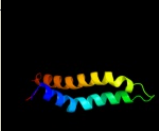
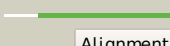


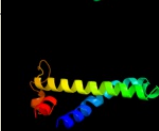




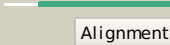




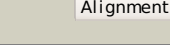
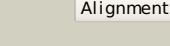



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3m9uD_</a>	 Alignment		94.9	12	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> farnesyl-diphosphate synthase; <b>PDBTitle:</b> crystal structure of geranylgeranyl pyrophosphate synthase2 from lactobacillus brevis atcc 367
2	<a href="#">c3ts7B_</a>	 Alignment		94.4	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> geranyltranstransferase; <b>PDBTitle:</b> crystal structure of farnesyl diphosphate synthase (target efi-501951)2 from methylococcus capsulatus
3	<a href="#">c3lsnA_</a>	 Alignment		87.8	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> geranyltranstransferase; <b>PDBTitle:</b> crystal structure of putative geranyltranstransferase from pseudomonas2 fluorescens pf-5 complexed with magnesium
4	<a href="#">dlv4ea_</a>	 Alignment		87.8	14	<b>Fold:</b> Terpenoid synthases <b>Superfamily:</b> Terpenoid synthases <b>Family:</b> Isoprenyl diphosphate synthases
5	<a href="#">dlrqja_</a>	 Alignment		83.1	13	<b>Fold:</b> Terpenoid synthases <b>Superfamily:</b> Terpenoid synthases <b>Family:</b> Isoprenyl diphosphate synthases
6	<a href="#">c2o1oB_</a>	 Alignment		71.1	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative farnesyl pyrophosphate synthase; <b>PDBTitle:</b> cryptosporidium parvum putative polyprenyl pyrophosphate2 synthase (cgd4_2550) in complex with risedronate.
7	<a href="#">clvhlA_</a>	 Alignment		71.0	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> farnesyl pyrophosphate synthase; <b>PDBTitle:</b> structure of the complex of trypanosoma cruzi farnesyl diphosphate2 synthase with risedronate, dmapp and mg+2
8	<a href="#">c2f94F_</a>	 Alignment		64.2	13	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> farnesyl diphosphate synthase; <b>PDBTitle:</b> crystal structure of human fpps in complex with ibandronate
9	<a href="#">c3aq0G_</a>	 Alignment		62.7	9	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> geranyl diphosphate synthase; <b>PDBTitle:</b> ligand-bound form of arabidopsis medium/long-chain length prenyl2 pyrophosphate synthase (surface polar residue mutant)
10	<a href="#">c3tc1A_</a>	 Alignment		61.1	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> octaprenyl pyrophosphate synthase; <b>PDBTitle:</b> crystal structure of octaprenyl pyrophosphate synthase from2 helicobacter pylori
11	<a href="#">c3cp6A_</a>	 Alignment		60.7	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> farnesyl pyrophosphate synthetase; <b>PDBTitle:</b> crystal structure of human farnesyl diphosphate synthase (t201a2 mutant) complexed with mg and biphosphonate inhibitor

12	<a href="#">dlfpsa_</a>	 Alignment		56.2	11	<b>Fold:</b> Terpenoid synthases <b>Superfamily:</b> Terpenoid synthases <b>Family:</b> Isoprenyl diphosphate synthases
13	<a href="#">c3ez3A_</a>	 Alignment		55.3	10	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> farnesyl pyrophosphate synthase, putative; <b>PDBTitle:</b> crystal structure of plasmodium vivax geranylgeranylpyrophosphate2 synthase pvx_092040 with zoledronate and ipp bound
14	<a href="#">c3kraB_</a>	 Alignment		52.4	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> geranyl diphosphate synthase small subunit; <b>PDBTitle:</b> mint heterotetrameric geranyl pyrophosphate synthase in2 complex with magnesium
15	<a href="#">c1wmwA_</a>	 Alignment		52.3	7	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> geranylgeranyl diphosphate synthetase; <b>PDBTitle:</b> crystal structure of geranylgeranyl diphosphate synthase from thermus2 thermophilus
16	<a href="#">c3p8rA_</a>	 Alignment		52.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> geranyltranstransferase; <b>PDBTitle:</b> crystal structure of polyprenyl synthase from vibrio cholerae
17	<a href="#">c3mzvB_</a>	 Alignment		50.7	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> decaprenyl diphosphate synthase; <b>PDBTitle:</b> crystal structure of a decaprenyl diphosphate synthase from2 rhodobacter capsulatus
18	<a href="#">c3nf2A_</a>	 Alignment		48.3	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative polyprenyl synthetase; <b>PDBTitle:</b> crystal structure of polyprenyl synthetase from streptomyces2 coelicolor a3(2)
19	<a href="#">c2ogdB_</a>	 Alignment		47.8	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> farnesyl pyrophosphate synthase; <b>PDBTitle:</b> t. brucei farnesyl diphosphate synthase complexed with bisphosphonate2 bph-527
20	<a href="#">c3rmgB_</a>	 Alignment		47.5	7	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> octaprenyl-diphosphate synthase; <b>PDBTitle:</b> crystal structure of geranylgeranyl pyrophosphate synthase from2 bacteroides thetaiotaomicron
21	<a href="#">d2q80a1</a>	 Alignment	not modelled	46.6	8	<b>Fold:</b> Terpenoid synthases <b>Superfamily:</b> Terpenoid synthases <b>Family:</b> Isoprenyl diphosphate synthases
22	<a href="#">c3n3dB_</a>	 Alignment	not modelled	45.9	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> geranylgeranyl pyrophosphate synthase; <b>PDBTitle:</b> crystal structure of geranylgeranyl pyrophosphate synthase from2 lactobacillus brevis atcc 367
23	<a href="#">c2j1pB_</a>	 Alignment	not modelled	44.3	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> geranylgeranyl pyrophosphate synthetase; <b>PDBTitle:</b> geranylgeranyl diphosphate synthase from sinapis alba in2 complex with ggpp
24	<a href="#">c3llwA_</a>	 Alignment	not modelled	36.4	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> geranyltranstransferase (ispa); <b>PDBTitle:</b> crystal structure of geranyltransferase from helicobacter2 pylori 26695
25	<a href="#">c3p8lB_</a>	 Alignment	not modelled	33.4	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> geranyltranstransferase; <b>PDBTitle:</b> crystal structure of polyprenyl synthase from enterococcus faecalis2 v583
26	<a href="#">c3lmdA_</a>	 Alignment	not modelled	31.8	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> geranylgeranyl pyrophosphate synthase; <b>PDBTitle:</b> crystal structure of geranylgeranyl pyrophosphate synthase2 from corynebacterium glutamicum atcc 13032
27	<a href="#">c2e8xB_</a>	 Alignment	not modelled	28.7	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> geranylgeranyl pyrophosphate synthetase; <b>PDBTitle:</b> s. cerevisiae geranylgeranyl pyrophosphate synthase in2 complex with magnesium and gpp
28	<a href="#">c3dh4A_</a>	 Alignment	not modelled	23.6	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium/glucose cotransporter; <b>PDBTitle:</b> crystal structure of sodium/sugar symporter with bound

						galactose from2 vibrio parahaemolyticus
29	<a href="#">c2j1oA_</a>	Alignment	not modelled	23.0	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> geranylgeranyl pyrophosphate synthetase; <b>PDBTitle:</b> geranylgeranyl diphosphate synthase from sinapis alba
30	<a href="#">c2xq2A_</a>	Alignment	not modelled	19.5	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium/glucose cotransporter; <b>PDBTitle:</b> structure of the k294a mutant of vsglt
31	<a href="#">c1wy0A_</a>	Alignment	not modelled	16.2	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> geranylgeranyl pyrophosphate synthetase; <b>PDBTitle:</b> crystal structure of geranylgeranyl pyrophosphate synthetase from2 pyrococcus horikoshii ot3
32	<a href="#">c3aqbD_</a>	Alignment	not modelled	15.1	12	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> component b of hexaprenyl diphosphate synthase; <b>PDBTitle:</b> m. luteus b-p 26 heterodimeric hexaprenyl diphosphate synthase in2 complex with magnesium
33	<a href="#">d1qlec_</a>	Alignment	not modelled	14.8	10	<b>Fold:</b> Cytochrome c oxidase subunit III-like <b>Superfamily:</b> Cytochrome c oxidase subunit III-like <b>Family:</b> Cytochrome c oxidase subunit III-like
34	<a href="#">c2ftzA_</a>	Alignment	not modelled	14.1	7	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> geranyltranstransferase; <b>PDBTitle:</b> crystal structure of geranyltranstransferase (ec 2.5.1.10) (tm0161)2 from thermotoga maritima at 1.90 a resolution
35	<a href="#">d1m9dc_</a>	Alignment	not modelled	13.1	15	<b>Fold:</b> Retrovirus capsid protein, N-terminal core domain <b>Superfamily:</b> Retrovirus capsid protein, N-terminal core domain <b>Family:</b> Retrovirus capsid protein, N-terminal core domain
36	<a href="#">d1diha2</a>	Alignment	not modelled	12.5	18	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> Dihydrodipicolinate reductase-like
37	<a href="#">c3oyrB_</a>	Alignment	not modelled	11.5	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> trans-isoprenyl diphosphate synthase; <b>PDBTitle:</b> crystal structure of polyprenyl synthase from caulobacter crescentus2 cb15 complexed with calcium and isoprenyl diphosphate
38	<a href="#">c1l6nA_</a>	Alignment	not modelled	10.4	12	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> gag polyprotein; <b>PDBTitle:</b> structure of the n-terminal 283-residue fragment of the hiv-2 1 gag polyprotein
39	<a href="#">d1m9fd_</a>	Alignment	not modelled	9.6	12	<b>Fold:</b> Retrovirus capsid protein, N-terminal core domain <b>Superfamily:</b> Retrovirus capsid protein, N-terminal core domain <b>Family:</b> Retrovirus capsid protein, N-terminal core domain
40	<a href="#">c2h8oA_</a>	Alignment	not modelled	8.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> geranyltranstransferase; <b>PDBTitle:</b> the 1.6a crystal structure of the geranyltransferase from2 agrobacterium tumefaciens
41	<a href="#">c2forB_</a>	Alignment	not modelled	7.7	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> geranyltranstransferase; <b>PDBTitle:</b> crystal structure of the shigella flexneri farnesyl pyrophosphate2 synthase complex with an isopentenyl pyrophosphate
42	<a href="#">c2wlvA_</a>	Alignment	not modelled	6.9	10	<b>PDB header:</b> virus protein <b>Chain:</b> A: <b>PDB Molecule:</b> gag polyprotein; <b>PDBTitle:</b> structure of the n-terminal capsid domain of hiv-2
43	<a href="#">d2pxrc1</a>	Alignment	not modelled	6.8	12	<b>Fold:</b> Retrovirus capsid protein, N-terminal core domain <b>Superfamily:</b> Retrovirus capsid protein, N-terminal core domain <b>Family:</b> Retrovirus capsid protein, N-terminal core domain
44	<a href="#">c2zcpA_</a>	Alignment	not modelled	6.7	0	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dehydrosqualene synthase; <b>PDBTitle:</b> crystal structure of the c(30) carotenoid dehydrosqualene2 synthase from staphylococcus aureus complexed with3 farnesyl thiopyrophosphate
45	<a href="#">c3lk5A_</a>	Alignment	not modelled	6.6	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> geranylgeranyl pyrophosphate synthase; <b>PDBTitle:</b> crystal structure of putative geranylgeranyl pyrophosphate synthase2 from corynebacterium glutamicum
46	<a href="#">d1ezfa_</a>	Alignment	not modelled	6.5	12	<b>Fold:</b> Terpenoid synthases <b>Superfamily:</b> Terpenoid synthases <b>Family:</b> Squalene synthase
47	<a href="#">c3lomA_</a>	Alignment	not modelled	6.4	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> geranyltranstransferase; <b>PDBTitle:</b> crystal structure of geranyltransferase from legionella2 pneumophila
48	<a href="#">c3oyrA_</a>	Alignment	not modelled	6.2	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trans-isoprenyl diphosphate synthase; <b>PDBTitle:</b> crystal structure of polyprenyl synthase from caulobacter crescentus2 cb15 complexed with calcium and isoprenyl diphosphate
49	<a href="#">c3am6C_</a>	Alignment	not modelled	5.8	9	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> rhodopsin-2; <b>PDBTitle:</b> crystal structure of the proton pumping rhodopsin ar2 from marine alga2 acetabularia acetabulum
50	<a href="#">c3ipiA_</a>	Alignment	not modelled	5.3	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> geranyltranstransferase; <b>PDBTitle:</b> crystal structure of a geranyltranstransferase from the2 methanosarcina mazei
51	<a href="#">d1te7a_</a>	Alignment	not modelled	5.1	22	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> yqfB-like
52	<a href="#">c3ucaB_</a>	Alignment	not modelled	5.1	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> geranyltranstransferase; <b>PDBTitle:</b> crystal structure of isoprenoid synthase (target efi-501974) from2 clostridium perfringens