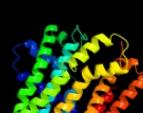


Phyre²

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Description	P22939
Date	Thu Jan 5 11:39:12 GMT 2012
Unique Job ID	0159194e84c36ebf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1rqja_			100.0	100	Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Isoprenyl diphosphate synthases
2	c2forB_			100.0	99	PDB header: transferase Chain: B; PDB Molecule: geranyltransterase; PDBTitle: crystal structure of the shigella flexneri farnesyl pyrophosphate2 synthase complex with an isopentenyl pyrophosphate
3	c3ts7B_			100.0	49	PDB header: transferase Chain: B; PDB Molecule: geranyltransterase; PDBTitle: crystal structure of farnesyl diphosphate synthase (target efi-501951)2 from methylococcus capsulatus
4	c1wy0A_			100.0	35	PDB header: transferase Chain: A; PDB Molecule: geranylgeranyl pyrophosphate synthetase; PDBTitle: crystal structure of geranylgeranyl pyrophosphate synthetase from2 pyrococcus horikoshii ot3
5	c3mzvB_			100.0	33	PDB header: transferase Chain: B; PDB Molecule: decaprenyl diphosphate synthase; PDBTitle: crystal structure of a decaprenyl diphosphate synthase from2 rhodobacter capsulatus
6	c3aqbD_			100.0	29	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
7	c3lsnA_			100.0	47	PDB header: transferase Chain: A; PDB Molecule: geranyltransterase; PDBTitle: crystal structure of putative geranyltransterase from pseudomonas2 fluorescens pf-5 complexed with magnesium
8	c3m9uD_			100.0	41	PDB header: transferase Chain: D; PDB Molecule: farnesyl-diphosphate synthase; PDBTitle: crystal structure of geranylgeranyl pyrophosphate synthase2 from lactobacillus brevis atcc 367
9	c3lomA_			100.0	35	PDB header: transferase Chain: A; PDB Molecule: geranyltransterase; PDBTitle: crystal structure of geranyltransferase from legionella2 pneumophila
10	c3oyrB_			100.0	33	PDB header: transferase Chain: B; PDB Molecule: trans-isoprenyl diphosphate synthase; PDBTitle: crystal structure of polypropenyl synthase from caulobacter crescentus2 cb15 complexed with calcium and isoprenyl diphosphate
11	c3nf2A_			100.0	33	PDB header: transferase Chain: A; PDB Molecule: putative polypropenyl synthetase; PDBTitle: crystal structure of polypropenyl synthetase from streptomyces2 coelicolor a3(2)

12	c2h8oA			100.0	43	PDB header: transferase Chain: A: PDB Molecule: geranyltrantransferase; PDBTitle: the 1.6a crystal structure of the geranyltransferase from2 agrobacterium tumefaciens
13	d1rtra			100.0	39	Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Isoprenyl diphosphate synthases
14	c2j1pB			100.0	43	PDB header: transferase Chain: B: PDB Molecule: geranylgeranyl pyrophosphate synthetase; PDBTitle: geranylgeranyl diphosphate synthase from sinapis alba in2 complex with gppp
15	d1fpsa			100.0	24	Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Isoprenyl diphosphate synthases
16	c3llwA			100.0	34	PDB header: transferase Chain: A: PDB Molecule: geranyltrantransferase (ispa); PDBTitle: crystal structure of geranyltransferase from helicobacter2 pylori 26695
17	c3ucaB			100.0	38	PDB header: transferase Chain: B: PDB Molecule: geranyltrantransferase; PDBTitle: crystal structure of isoprenoid synthase (target efi-501974) from2 clostridium perfringens
18	c1wmwA			100.0	26	PDB header: transferase Chain: A: PDB Molecule: geranylgeranyl diphosphate synthetase; PDBTitle: crystal structure of geranylgeranyl diphosphate synthetase from thermus2 thermophilus
19	c3cp6A			100.0	24	PDB header: transferase Chain: A: PDB Molecule: farnesyl pyrophosphate synthetase; PDBTitle: crystal structure of human farnesyl diphosphate synthase (t201a2 mutant) complexed with mg and bisphosphonate inhibitor
20	c2ogdB			100.0	22	PDB header: transferase Chain: B: PDB Molecule: farnesyl pyrophosphate synthase; PDBTitle: t. brucei farnesyl diphosphate synthase complexed with bisphosphonate2 bph-527
21	c1yhlA		not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: farnesyl pyrophosphate synthase; PDBTitle: structure of the complex of trypanosoma cruzi farnesyl diphosphate2 synthase with risedronate, dmapp and mg+2
22	c3m0gB		not modelled	100.0	46	PDB header: transferase Chain: B: PDB Molecule: farnesyl diphosphate synthase; PDBTitle: crystal structure of putative farnesyl diphosphate synthase from2 rhodobacter capsulatus
23	c2f94F		not modelled	100.0	24	PDB header: transferase Chain: F: PDB Molecule: farnesyl diphosphate synthase; PDBTitle: crystal structure of human fpps in complex with ibandronate
24	c3p8IB		not modelled	100.0	38	PDB header: transferase Chain: B: PDB Molecule: geranyltrantransferase; PDBTitle: crystal structure of polyprenyl synthase from enterococcus faecalis2 v583
25	d1v4ea		not modelled	100.0	28	Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Isoprenyl diphosphate synthases
26	c3ez3A		not modelled	100.0	21	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
27	c3npkB		not modelled	100.0	36	PDB header: transferase Chain: B: PDB Molecule: geranyltrantransferase; PDBTitle: the crystal structure of geranyltrantransferase from campylobacter2 jejuni
						PDB header: transferase Chain: B: PDB Molecule: geranylgeranyl pyrophosphate

28	c2e8xB	Alignment	not modelled	100.0	22	PDB header: synthetase; PDBTitle: <i>s. cerevisiae</i> geranylgeranyl pyrophosphate synthase in2 complex with magnesium and gpp
29	d2q80a1	Alignment	not modelled	100.0	25	Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Isoprenyl diphosphate synthases
30	c2o1oB	Alignment	not modelled	100.0	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative farnesyl pyrophosphate synthase; PDBTitle: cryptosporidium parvum putative polyprenyl pyrophosphate2 synthase (cgd4_2550) in complex with risedronate. PDB header: transferase
31	c3n3dB	Alignment	not modelled	100.0	30	Chain: B: PDB Molecule: geranylgeranyl pyrophosphate synthase; PDBTitle: crystal structure of geranylgeranyl pyrophosphate synthase from2 lactobacillus brevis atcc 367
32	c3ipiA	Alignment	not modelled	100.0	23	PDB header: transferase Chain: A: PDB Molecule: geranyltransterase; PDBTitle: crystal structure of a geranyltransterase from the2 methanosaicina maezi
33	c3p8rA	Alignment	not modelled	100.0	58	PDB header: transferase Chain: A: PDB Molecule: geranyltransterase; PDBTitle: crystal structure of polyprenyl synthase from vibrio cholerae
34	c3aq0G	Alignment	not modelled	100.0	27	PDB header: transferase Chain: G: PDB Molecule: geranyl diphosphate synthase; PDBTitle: ligand-bound form of arabidopsis medium/long-chain length prenyl2 pyrophosphate synthase (surface polar residue mutant)
35	c2azjB	Alignment	not modelled	100.0	21	PDB header: transferase Chain: B: PDB Molecule: geranylgeranyl pyrophosphate synthetase; PDBTitle: crystal structure for the mutant d81c of <i>sulfolobus2 solfataricus</i> hexaprenyl pyrophosphate synthase
36	c3Ik5A	Alignment	not modelled	100.0	30	PDB header: transferase Chain: A: PDB Molecule: geranylgeranyl pyrophosphate synthase; PDBTitle: crystal structure of putative geranylgeranyl pyrophosphate synthase2 from <i>corynebacterium glutamicum</i>
37	c2j1oA	Alignment	not modelled	100.0	43	PDB header: transferase Chain: A: PDB Molecule: geranylgeranyl pyrophosphate synthetase; PDBTitle: geranylgeranyl diphosphate synthase from <i>sinapis alba</i>
38	c3lmdA	Alignment	not modelled	100.0	31	PDB header: transferase Chain: A: PDB Molecule: geranylgeranyl pyrophosphate synthase; PDBTitle: crystal structure of geranylgeranyl pyrophosphate synthase2 from <i>corynebacterium glutamicum</i> atcc 13032
39	c3rmgB	Alignment	not modelled	100.0	27	PDB header: transferase Chain: B: PDB Molecule: octaprenyl-diphosphate synthase; PDBTitle: crystal structure of geranylgeranyl pyrophosphate synthase from2 <i>bacteroides thetaiotaomicron</i>
40	c3kraB	Alignment	not modelled	100.0	22	PDB header: transferase Chain: B: PDB Molecule: geranyl diphosphate synthase small subunit; PDBTitle: mint heterotetrameric geranyl pyrophosphate synthase in2 complex with magnesium
41	c3tc1A	Alignment	not modelled	100.0	28	PDB header: transferase Chain: A: PDB Molecule: octaprenyl pyrophosphate synthase; PDBTitle: crystal structure of octaprenyl pyrophosphate synthase from2 <i>helicobacter pylori</i>
42	c3qkcB	Alignment	not modelled	100.0	18	PDB header: transferase Chain: B: PDB Molecule: geranyl diphosphate synthase small subunit; PDBTitle: crystal structure of geranyl diphosphate synthase small subunit from2 <i>antirrhinum majus</i>
43	c3oyrA	Alignment	not modelled	100.0	28	PDB header: transferase Chain: A: PDB Molecule: trans-isoprenyl diphosphate synthase; PDBTitle: crystal structure of polyprenyl synthase from <i>caulobacter crescentus2</i> cb15 complexed with calcium and isoprenyl diphosphate
44	c2ftzA	Alignment	not modelled	100.0	30	PDB header: transferase Chain: A: PDB Molecule: geranyltransterase; PDBTitle: crystal structure of geranyltransterase (ec 2.5.1.10) (tm0161)2 from <i>thermotoga maritima</i> at 1.90 a resolution
45	d1ezfa	Alignment	not modelled	96.3	27	Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Squalene synthase
46	c2zcpA	Alignment	not modelled	95.7	14	PDB header: transferase Chain: A: PDB Molecule: dehydrosqualene synthase; PDBTitle: crystal structure of the c(30) carotenoid dehydrosqualene2 synthase from <i>staphylococcus aureus</i> complexed with3 farnesyl thiopyrophosphate
47	d1n1ba2	Alignment	not modelled	75.3	13	Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Terpenoid cyclase C-terminal domain
48	c1hx9A	Alignment	not modelled	72.7	16	PDB header: lyase Chain: A: PDB Molecule: 5-epi-aristolochene synthase; PDBTitle: crystal structure of teas w273s form 1
49	c3n0fA	Alignment	not modelled	70.3	12	PDB header: lyase Chain: A: PDB Molecule: isoprene synthase; PDBTitle: crystal structure of isoprene synthase from grey poplar leaves2 (<i>populus x canescens</i>)
50	c3saeA	Alignment	not modelled	67.5	15	PDB header: lyase Chain: A: PDB Molecule: alpha-bisabolene synthase; PDBTitle: structure of a three-domain sesquiterpene synthase: a prospective2 target for advanced biofuels production
51	c1n20A	Alignment	not modelled	66.9	12	PDB header: isomerase Chain: A: PDB Molecule: (+)-bornyl diphosphate synthase; PDBTitle: (+)-bornyl diphosphate synthase: complex with mg and 3-aza-2,3-dihydrogeranyl diphosphate
						Fold: Terpenoid synthases

52	d5easa2	Alignment	not modelled	59.7	16	Superfamily: Terpenoid synthases Family: Terpenoid cyclase C-terminal domain
53	c2ongA_	Alignment	not modelled	58.9	10	PDB header: lyase Chain: A: PDB Molecule: 4s-limonene synthase; PDBTitle: crystal structure of limonene synthase with 2-2 fluorogeranyl diphosphate (fgpp).
54	c3g4dB_	Alignment	not modelled	56.3	9	PDB header: lyase Chain: B: PDB Molecule: (+)-delta-cadinene synthase isozyme xc1; PDBTitle: crystal structure of (+)-delta-cadinene synthase from gossypium2 arboreum and evolutionary divergence of metal binding motifs for3 catalysis
55	d2o3la1	Alignment	not modelled	55.7	16	Fold: Left-handed superhelix Superfamily: BH3980-like Family: BH3980-like
56	c3p5rB_	Alignment	not modelled	55.6	13	PDB header: lyase Chain: B: PDB Molecule: taxadiene synthase; PDBTitle: crystal structure of taxadiene synthase from pacific yew (taxus2 brevifolia) in complex with mg2+ and 2-fluorogeranylgeranyl3 diphosphate
57	c3s9vD_	Alignment	not modelled	51.7	9	PDB header: lyase, isomerase Chain: D: PDB Molecule: abietadiene synthase, chloroplastic; PDBTitle: abietadiene synthase from abies grandis
58	d2hh6a1	Alignment	not modelled	43.7	29	Fold: Left-handed superhelix Superfamily: BH3980-like Family: BH3980-like
59	c2j5cB_	Alignment	not modelled	39.1	14	PDB header: lyase Chain: B: PDB Molecule: 1,8-cineole synthase; PDBTitle: rational conversion of substrate and product specificity2 in a monoterpane synthase. structural insights into the3 molecular basis of rapid evolution.
60	d2htja1	Alignment	not modelled	34.0	36	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: FaeA-like
61	c3byvA_	Alignment	not modelled	28.8	24	PDB header: transferase Chain: A: PDB Molecule: rhoptry kinase; PDBTitle: crystal structure of toxoplasma gondii specific rhoptry2 antigen kinase domain
62	c3q60A_	Alignment	not modelled	24.3	10	PDB header: transferase Chain: A: PDB Molecule: rop5b; PDBTitle: crystal structure of virulent allele rop5b pseudokinase domain bound2 to atp
63	d2o4ta1	Alignment	not modelled	23.8	23	Fold: Left-handed superhelix Superfamily: BH3980-like Family: BH3980-like
64	c3e7eA_	Alignment	not modelled	18.3	24	PDB header: transferase Chain: A: PDB Molecule: mitotic checkpoint serine/threonine-protein kinase bub1; PDBTitle: structure and substrate recruitment of the human spindle checkpoint2 kinase bub
65	c3lg5A_	Alignment	not modelled	18.1	11	PDB header: lyase Chain: A: PDB Molecule: epi-isozaene synthase; PDBTitle: f198a epi-isozaene synthase: complex with mg, inorganic2 pyrophosphate and benzyl triethyl ammonium cation
66	c2jiiA_	Alignment	not modelled	16.2	19	PDB header: transferase Chain: A: PDB Molecule: serine/threonine-protein kinase vrk3 molecule: vaccinia PDBTitle: structure of vaccinia related kinase 3
67	c2v62A_	Alignment	not modelled	16.0	24	PDB header: transferase Chain: A: PDB Molecule: serine/threonine-protein kinase vrk2; PDBTitle: structure of vaccinia-related kinase 2
68	c3dzoA_	Alignment	not modelled	12.8	24	PDB header: transferase Chain: A: PDB Molecule: rhoptry kinase domain; PDBTitle: crystal structure of a rhoptry kinase from toxoplasma gondii
69	c1tqmA_	Alignment	not modelled	10.3	29	PDB header: ribosome Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of a. fulgidus rio2 serine protein kinase bound to2 amppnp
70	c2j0kB_	Alignment	not modelled	9.8	14	PDB header: transferase Chain: B: PDB Molecule: focal adhesion kinase 1; PDBTitle: crystal structure of a fragment of focal adhesion kinase2 containing the ferm and kinase domains.
71	c2wtkC_	Alignment	not modelled	9.4	19	PDB header: transferase/metal-binding protein Chain: C: PDB Molecule: serine/threonine-protein kinase 11; PDBTitle: structure of the heterotrimeric lkb1-stradalpha-mo25alpha2 complex
72	c3qa8A_	Alignment	not modelled	8.4	33	PDB header: immune system, signalling protein Chain: A: PDB Molecule: mgc80376 protein; PDBTitle: crystal structure of inhibitor of kappa b kinase beta
73	c2ctoA_	Alignment	not modelled	8.3	30	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: novel protein; PDBTitle: solution structure of the hmgb box like domain from human2 hypothetical protein flj14904
74	c3c4yA_	Alignment	not modelled	8.2	24	PDB header: transferase Chain: A: PDB Molecule: rhodopsin kinase; PDBTitle: crystal structure of apo form of g protein coupled receptor kinase 12 at 7.51a
75	c3a1yF_	Alignment	not modelled	8.2	36	PDB header: ribosomal protein Chain: F: PDB Molecule: 50s ribosomal protein p1 (l12p); PDBTitle: the structure of protein complex
76	c2pzIA_	Alignment	not modelled	8.0	29	PDB header: transferase Chain: A: PDB Molecule: probable serine/threonine-protein kinase pkng; PDBTitle: crystal structure of protein kinase pkng from mycobacterium2 tuberculosis in complex with tetrahydrobenzothiophene ax20017

77	c3fbvL		Alignment	not modelled	7.8	38	PDB header: transferase, hydrolase Chain: L: PDB Molecule: serine/threonine-protein kinase/endoribonuclease ire1; PDBTitle: crystal structure of the oligomer formed by the kinase-ribonuclease 2 domain of ire1
78	d1ps1a		Alignment	not modelled	7.4	15	Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Aristolochene/pentalenene synthase
79	c2oa6B		Alignment	not modelled	7.3	14	PDB header: lyase Chain: B: PDB Molecule: aristolochene synthase; PDBTitle: aristolochene synthase from aspergillus terreus complexed with 2 pyrophosphate
80	c3op5B		Alignment	not modelled	7.3	24	PDB header: transferase Chain: B: PDB Molecule: serine/threonine-protein kinase vrk1; PDBTitle: human vaccinia-related kinase 1
81	c2acxB		Alignment	not modelled	7.1	19	PDB header: transferase Chain: B: PDB Molecule: g protein-coupled receptor kinase 6; PDBTitle: crystal structure of g protein coupled receptor kinase 6 bound to 2 amppnp
82	c1ym7C		Alignment	not modelled	6.9	19	PDB header: transferase Chain: C: PDB Molecule: beta-adrenergic receptor kinase 1; PDBTitle: g protein-coupled receptor kinase 2 (grk2)
83	c2ozoA		Alignment	not modelled	6.7	14	PDB header: transferase Chain: A: PDB Molecule: tyrosine-protein kinase zap-70; PDBTitle: autoinhibited intact human zap-70
84	c1u57A		Alignment	not modelled	6.6	13	PDB header: viral protein Chain: A: PDB Molecule: gag polyprotein; PDBTitle: nmr structure of the (345-392)gag sequence from hiv-1
85	c3cvjB		Alignment	not modelled	6.5	15	PDB header: isomerase Chain: B: PDB Molecule: putative phosphoheptose isomerase; PDBTitle: crystal structure of a putative phosphoheptose isomerase (bh3325) from bacillus halodurans c-125 at 2.00 a resolution
86	c2vwiC		Alignment	not modelled	6.5	29	PDB header: transferase Chain: C: PDB Molecule: serine/threonine-protein kinase osr1; PDBTitle: structure of the osr1 kinase, a hypertension drug target
87	c3i3aC		Alignment	not modelled	6.2	9	PDB header: transferase Chain: C: PDB Molecule: acyl-[acyl-carrier-protein]-udp-n-PDBTitle: structural basis for the sugar nucleotide and acyl chain 2 selectivity of leptospira interrogans lpxa
88	d1vjja1		Alignment	not modelled	6.1	67	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Transglutaminase N-terminal domain
89	d1g0da1		Alignment	not modelled	6.1	67	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Transglutaminase N-terminal domain
90	c3t98A		Alignment	not modelled	5.9	40	PDB header: protein transport Chain: A: PDB Molecule: nuclear pore complex protein nup54; PDBTitle: molecular architecture of the transport channel of the nuclear pore2 complex: nup54/nup58
91	c3pjAK		Alignment	not modelled	5.9	2	PDB header: hydrolase Chain: K: PDB Molecule: translin-associated protein x; PDBTitle: crystal structure of human c3po complex
92	d2g3za1		Alignment	not modelled	5.9	67	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Transglutaminase N-terminal domain
93	c2c47D		Alignment	not modelled	5.8	29	PDB header: transferase Chain: D: PDB Molecule: casein kinase 1 gamma 2 isoform; PDBTitle: structure of casein kinase 1 gamma 2
94	d1sq8a		Alignment	not modelled	5.7	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
95	c1hm4A		Alignment	not modelled	5.5	11	PDB header: lyase Chain: A: PDB Molecule: pentalenene synthase; PDBTitle: n219l pentalenene synthase
96	c2r17C		Alignment	not modelled	5.5	20	PDB header: protein transport Chain: C: PDB Molecule: vacuolar protein sorting-associated protein 35; PDBTitle: functional architecture of the retromer cargo-recognition complex
97	d1riqa1		Alignment	not modelled	5.4	20	Fold: Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS) Superfamily: Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS) Family: Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS)
98	c2vuwA		Alignment	not modelled	5.2	29	PDB header: transferase Chain: A: PDB Molecule: serine/threonine-protein kinase haspin; PDBTitle: structure of human haspin kinase domain