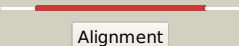



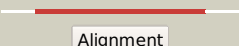





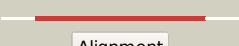













# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3397c_phyA_3814270_3815178
Date	Fri Aug 9 18:20:06 BST 2019
Unique Job ID	6b9125142521833b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2zcpA_</a>	 Alignment		100.0	26	<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 dehydrosqualene synthase2 from staphylococcus aureus complexed with farnesyl thiopyrophosphate
2	<a href="#">c5iysA_</a>	 Alignment		100.0	29	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> phytoene synthase; <b>PDBTitle:</b> crystal structure of a dehydrosqualene synthase in complex with ligand
3	<a href="#">c4hd1A_</a>	 Alignment		100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> squalene synthase hpnc; <b>PDBTitle:</b> crystal structure of squalene synthase hpnc from alicyclobacillus2 acidocaldarius
4	<a href="#">c3we9A_</a>	 Alignment		100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phytoene/squalene synthase yisp; <b>PDBTitle:</b> the crystal structure of yisp from bacillus subtilis subsp. subtilis2 strain 168
5	<a href="#">d1ezfa_</a>	 Alignment		100.0	18	<b>Fold:</b> Terpenoid synthases <b>Superfamily:</b> Terpenoid synthases <b>Family:</b> Squalene synthase
6	<a href="#">c3wccC_</a>	 Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> farnesyltransferase, putative; <b>PDBTitle:</b> the complex structure of tcsqs with ligand, e5700
7	<a href="#">c3aq0G_</a>	 Alignment		97.4	16	<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)
8	<a href="#">c3wjnA_</a>	 Alignment		97.4	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> octaprenyl diphosphate synthase; <b>PDBTitle:</b> crystal structure of octaprenyl pyrophosphate synthase from2 escherichia coli with farnesyl s-thiol-pyrophosphate (fspp)
9	<a href="#">c5jfqB_</a>	 Alignment		97.3	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> geranylgeranyl pyrophosphate synthetase; <b>PDBTitle:</b> geranylgeranyl pyrophosphate synthetase from archaeon geoglobus2 acetivorans
10	<a href="#">d2q80a1</a>	 Alignment		97.3	15	<b>Fold:</b> Terpenoid synthases <b>Superfamily:</b> Terpenoid synthases <b>Family:</b> Isoprenyl diphosphate synthases
11	<a href="#">c3tc1A_</a>	 Alignment		97.1	14	<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

12	<a href="#">c4lobA_</a>	Alignment		96.8	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polyprenyl synthetase; <b>PDBTitle:</b> crystal structure of polyprenyl diphosphate synthase a1s_2732 (target2 efi-509223) from acinetobacter baumannii
13	<a href="#">c5h9dB_</a>	Alignment		96.8	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> farnesyl pyrophosphate synthetase; <b>PDBTitle:</b> crystal structure of heptaprenyl diphosphate synthase from2 staphylococcus aureus
14	<a href="#">c3oyrB_</a>	Alignment		96.8	17	<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
15	<a href="#">c3n3dB_</a>	Alignment		96.7	20	<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
16	<a href="#">c3rmgB_</a>	Alignment		96.5	12	<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
17	<a href="#">c3m9uD_</a>	Alignment		96.5	19	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> farnesyl-diphosphate synthase; <b>PDBTitle:</b> crystal structure of geranylgeranyl pyrophosphate synthase from2 lactobacillus brevis atcc 367
18	<a href="#">c4lltB_</a>	Alignment		96.5	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> geranyltranstransferase; <b>PDBTitle:</b> crystal structure of a farnesyl diphosphate synthase from roseobacter2 denitrificans och 114, target efi-509393, with two ipp and calcium3 bound in active site
19	<a href="#">c3oacD_</a>	Alignment		96.4	17	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> geranyl diphosphate synthase large subunit; <b>PDBTitle:</b> mint deletion mutant of heterotetrameric geranyl pyrophosphate2 synthase in complex with ligands
20	<a href="#">d1v4ea_</a>	Alignment		96.2	13	<b>Fold:</b> Terpenoid synthases <b>Superfamily:</b> Terpenoid synthases <b>Family:</b> Isoprenyl diphosphate synthases
21	<a href="#">c1wy0A_</a>	Alignment	not modelled	96.1	15	<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
22	<a href="#">c4lfgB_</a>	Alignment	not modelled	96.1	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> geranylgeranyl diphosphate synthase; <b>PDBTitle:</b> crystal structure of geranylgeranyl diphosphate synthase sub12742 (target efi-509455) from streptococcus uberis 0140j with bound3 magnesium and isopentyl diphosphate, fully liganded complex;
23	<a href="#">c3mzvB_</a>	Alignment	not modelled	96.0	19	<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
24	<a href="#">c5xn5A_</a>	Alignment	not modelled	96.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> os07g0580900 protein; <b>PDBTitle:</b> homo-dimer crystal structure of geranylgeranyl diphosphate synthases 12 from oryza sativa
25	<a href="#">c4jyxE_</a>	Alignment	not modelled	95.9	12	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> trans-hexaprenyltranstransferase; <b>PDBTitle:</b> crystal structure of polyprenyl synthase patl_3739 (target efi-509195)2 from pseudoalteromonas atlantica, complex with inorganic phosphate3 and an unknown ligand
26	<a href="#">c2e8xB_</a>	Alignment	not modelled	95.9	13	<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
27	<a href="#">c3ts7B_</a>	Alignment	not modelled	95.7	15	<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
						<b>PDB header:</b> transferase

28	<a href="#">c3lmdA</a>	Alignment	not modelled	95.7	12	<b>Chain:</b> A: <b>PDB Molecule:</b> geranylgeranyl pyrophosphate synthase; <b>PDBTitle:</b> crystal structure of geranylgeranyl pyrophosphate synthase from2 corynebacterium glutamicum atcc 13032
29	<a href="#">c3nf2A</a>	Alignment	not modelled	95.6	17	<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)
30	<a href="#">c6b07B</a>	Alignment	not modelled	95.5	11	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> farnesyl diphosphate synthase; <b>PDBTitle:</b> crystal structure of cffpps2, a lepidopteran type-ii farnesyl2 diphosphate synthase, complexed with [1-phosphono-2-(1-propylpyridin-3-2-yl)ethyl]phosphonic acid (inhibitor 1d)
31	<a href="#">c3aqbD</a>	Alignment	not modelled	95.5	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
32	<a href="#">c6c57B</a>	Alignment	not modelled	95.4	18	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> geranylgeranyl pyrophosphate synthase; <b>PDBTitle:</b> crystal structure of mutant human geranylgeranyl pyrophosphate2 synthase (y246d) in complex with bisphosphonate inhibitor fv0109
33	<a href="#">d1rtra</a>	Alignment	not modelled	95.4	16	<b>Fold:</b> Terpenoid synthases <b>Superfamily:</b> Terpenoid synthases <b>Family:</b> Isoprenyl diphosphate synthases
34	<a href="#">c4dhdA</a>	Alignment	not modelled	95.2	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polyprenyl synthetase; <b>PDBTitle:</b> crystal structure of isoprenoid synthase a3msh1 (target efi-501992)2 from pyrobaculum calidifontis
35	<a href="#">c2azjB</a>	Alignment	not modelled	95.1	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> geranylgeranyl pyrophosphate synthetase; <b>PDBTitle:</b> crystal structure for the mutant d81c of sulfolobus2 solfataricus hexaprenyl pyrophosphate synthase
36	<a href="#">c5eroB</a>	Alignment	not modelled	94.9	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> fusicoccadiene synthase; <b>PDBTitle:</b> crystal structure of elongation domain of phomopsis amygdali2 fusicoccadiene synthase complexed with cobalt ions and pamidronate
37	<a href="#">d1rqja</a>	Alignment	not modelled	94.9	20	<b>Fold:</b> Terpenoid synthases <b>Superfamily:</b> Terpenoid synthases <b>Family:</b> Isoprenyl diphosphate synthases
38	<a href="#">c3cp6A</a>	Alignment	not modelled	94.8	16	<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 biposphonate inhibitor
39	<a href="#">c3m0gB</a>	Alignment	not modelled	94.6	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> farnesyl diphosphate synthase; <b>PDBTitle:</b> crystal structure of putative farnesyl diphosphate synthase from2 rhodobacter capsulatus
40	<a href="#">c4jzbA</a>	Alignment	not modelled	94.2	14	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> farnesyl pyrophosphate synthase; <b>PDBTitle:</b> crystal structure of leshmaniasis major farnesyl diphosphate synthase2 in complex with 1-(2-hydroxy-2,2-diphosphonoethyl)-3-3 phenylpyridinium, ipp and ca2+
41	<a href="#">c1wmwA</a>	Alignment	not modelled	94.2	16	<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
42	<a href="#">c2jlpB</a>	Alignment	not modelled	94.0	17	<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
43	<a href="#">c3lomA</a>	Alignment	not modelled	93.7	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> geranyltrantransferase; <b>PDBTitle:</b> crystal structure of geranyltransferase from legionella pneumophila
44	<a href="#">c3ez3A</a>	Alignment	not modelled	93.5	12	<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 pxv_092040 with zoledronate and ipp bound
45	<a href="#">c5nx4A</a>	Alignment	not modelled	93.4	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> pentalenene synthase; <b>PDBTitle:</b> crystal structure of linalool/nerolidol synthase from streptomyces2 clavuligerus
46	<a href="#">d1fpsa</a>	Alignment	not modelled	93.3	12	<b>Fold:</b> Terpenoid synthases <b>Superfamily:</b> Terpenoid synthases <b>Family:</b> Isoprenyl diphosphate synthases
47	<a href="#">c3ucaB</a>	Alignment	not modelled	93.2	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> geranyltrantransferase; <b>PDBTitle:</b> crystal structure of isoprenoid synthase (target efi-501974) from2 clostridium perfringens
48	<a href="#">c5aypA</a>	Alignment	not modelled	92.6	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> farnesyl diphosphate synthase; <b>PDBTitle:</b> crystal structure of bacillus stearothermophilus farnesyl2 pyrophosphate synthase
49	<a href="#">c3lk5A</a>	Alignment	not modelled	92.6	17	<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
50	<a href="#">c1yhlA</a>	Alignment	not modelled	92.2	14	<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
51	<a href="#">d1kiya</a>	Alignment	not modelled	91.5	13	<b>Fold:</b> Terpenoid synthases <b>Superfamily:</b> Terpenoid synthases <b>Family:</b> Trichodiene synthase
						<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> geranyl diphosphate synthase small

52	<a href="#">c3qkcB_</a>	Alignment	not modelled	91.4	13	subunit; <b>PDBTitle:</b> crystal structure of geranyl diphosphate synthase small subunit from <i>Antirrhinum majus</i>
53	<a href="#">c4kkmB_</a>	Alignment	not modelled	91.3	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> polyprenyl synthetase; <b>PDBTitle:</b> crystal structure of a fpp/gfpp synthase (target efi-501952) from <i>Zymomonas mobilis</i> , apo structure
54	<a href="#">c5e8kA_</a>	Alignment	not modelled	91.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> geranylgeranyl pyrophosphate synthase 10, mitochondrial; <b>PDBTitle:</b> crystal structure of polyprenyl pyrophosphate synthase 2 from <i>Arabidopsis thaliana</i>
55	<a href="#">c3p8rA_</a>	Alignment	not modelled	90.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> geranyltranstransferase; <b>PDBTitle:</b> crystal structure of polyprenyl synthase from <i>Vibrio cholerae</i>
56	<a href="#">c2o1oB_</a>	Alignment	not modelled	90.4	11	<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 pyrophosphate synthase2 (cgd4_2550) in complex with risedronate.
57	<a href="#">c2f94F_</a>	Alignment	not modelled	90.0	12	<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
58	<a href="#">c5xn6D_</a>	Alignment	not modelled	90.0	16	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> os02g0668100 protein; <b>PDBTitle:</b> heterodimer crystal structure of geranylgeranyl diphosphate synthases2 1 with ggpps recruiting protein(osgrp) from <i>Oryza sativa</i>
59	<a href="#">c2ogdB_</a>	Alignment	not modelled	89.6	14	<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
60	<a href="#">c3ipiA_</a>	Alignment	not modelled	89.4	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> geranyltranstransferase; <b>PDBTitle:</b> crystal structure of a geranyltranstransferase from the methanosarcina2 mazei
61	<a href="#">c4kk2B_</a>	Alignment	not modelled	88.5	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> monoterpene synthase fds-5, chloroplastic - farnesyl <b>PDBTitle:</b> crystal structure of a chimeric fpp/gfpp synthase (target efi-502313c)2 from <i>Artemisia spiciformis</i> (1-72:gi751454468,73-346:gi75233326), apo3 structure
62	<a href="#">c3oyrA_</a>	Alignment	not modelled	88.0	18	<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 <i>Caulobacter crescentus</i> 2 cb15 complexed with calcium and isoprenyl diphosphate
63	<a href="#">c3n0fA_</a>	Alignment	not modelled	87.8	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> isoprene synthase; <b>PDBTitle:</b> crystal structure of isoprene synthase from grey poplar leaves2 ( <i>Populus x canescens</i> )
64	<a href="#">c1hx9A_</a>	Alignment	not modelled	87.1	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-epi-aristolochene synthase; <b>PDBTitle:</b> crystal structure of teas w273s form 1
65	<a href="#">c2j1oA_</a>	Alignment	not modelled	86.5	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> geranylgeranyl pyrophosphate synthetase; <b>PDBTitle:</b> geranylgeranyl diphosphate synthase from <i>Sinapis alba</i>
66	<a href="#">d1ps1a_</a>	Alignment	not modelled	84.8	17	<b>Fold:</b> Terpenoid synthases <b>Superfamily:</b> Terpenoid synthases <b>Family:</b> Aristolochene/pentalenene synthase
67	<a href="#">c4gaxA_</a>	Alignment	not modelled	82.9	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> amorpha-4,11-diene synthase; <b>PDBTitle:</b> crystal structure of an alpha-bisabolol synthase mutant
68	<a href="#">d5easa2</a>	Alignment	not modelled	82.7	16	<b>Fold:</b> Terpenoid synthases <b>Superfamily:</b> Terpenoid synthases <b>Family:</b> Terpenoid cyclase C-terminal domain
69	<a href="#">c4zq8B_</a>	Alignment	not modelled	82.2	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> isoprenoid synthase; <b>PDBTitle:</b> crystal structure of a terpene synthase from <i>Streptomyces lydicus</i> ,2 target efi-540129
70	<a href="#">c3lsnA_</a>	Alignment	not modelled	82.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> geranyltranstransferase; <b>PDBTitle:</b> crystal structure of putative geranyltranstransferase from <i>Pseudomonas fluorescens</i> pf-5 complexed with magnesium
71	<a href="#">c3p8lB_</a>	Alignment	not modelled	81.5	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> geranyltranstransferase; <b>PDBTitle:</b> crystal structure of polyprenyl synthase from <i>Enterococcus faecalis</i> 2 v583
72	<a href="#">c5a0iA_</a>	Alignment	not modelled	81.0	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> labdane-related diterpene synthase; <b>PDBTitle:</b> crystallographic structure of the bacterial labdane-related diterpene2 synthase lrdc in complex with mg and ppi at 2.57 a resolution.
73	<a href="#">c4okmA_</a>	Alignment	not modelled	78.1	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> terpene synthase metal-binding domain-containing protein; <b>PDBTitle:</b> selinadiene synthase apo and in complex with diphosphate
74	<a href="#">c2forB_</a>	Alignment	not modelled	78.0	18	<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
75	<a href="#">c5i1uB_</a>	Alignment	not modelled	77.2	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> germacradien-4-ol synthase; <b>PDBTitle:</b> crystal structure of germacradien-4-ol synthase from <i>Streptomyces citricolor</i>
76	<a href="#">c6q4sA_</a>	Alignment	not modelled	72.7	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> pentalenene synthase;

						<b>PDBTitle:</b> crystal structure of a-eudesmol synthase
77	<a href="#">c1n20A_</a>	Alignment	not modelled	72.6	12	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> (+)-bornyl diphosphate synthase; <b>PDBTitle:</b> (+)-bornyl diphosphate synthase: complex with mg and 3-aza-2,2,3-dihydrogeranyl diphosphate
78	<a href="#">c5dw7A_</a>	Alignment	not modelled	72.3	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> germacradienol/geosmin synthase; <b>PDBTitle:</b> crystal structure of the unliganded geosmin synthase n-terminal domain2 from streptomyces coelicolor
79	<a href="#">c3g4dB_</a>	Alignment	not modelled	72.2	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> (+)-delta-cadinene synthase isozyme xc1; <b>PDBTitle:</b> crystal structure of (+)-delta-cadinene synthase from gossypium2 arboreum and evolutionary divergence of metal binding motifs for3 catalysis
80	<a href="#">c4f62B_</a>	Alignment	not modelled	71.9	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> geranyltranstransferase; <b>PDBTitle:</b> crystal structure of a putative farnesyl-diphosphate synthase from2 marinomonas sp. med121 (target efi-501980)
81	<a href="#">c2h8oA_</a>	Alignment	not modelled	71.7	19	<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
82	<a href="#">c3kraB_</a>	Alignment	not modelled	69.8	14	<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 in complex with2 magnesium
83	<a href="#">c3p5rB_</a>	Alignment	not modelled	67.3	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> taxadiene synthase; <b>PDBTitle:</b> crystal structure of taxadiene synthase from pacific yew (taxus2 brevifolia) in complex with mg2+ and 2-fluorogeranylgeranyl3 diphosphate
84	<a href="#">c5zzjC_</a>	Alignment	not modelled	64.1	12	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> santalene synthase; <b>PDBTitle:</b> crystal structure of a enzyme from santalum album
85	<a href="#">c2ftzA_</a>	Alignment	not modelled	63.2	19	<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
86	<a href="#">c6o9qA_</a>	Alignment	not modelled	60.7	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> sesquisabinene b synthase 1; <b>PDBTitle:</b> wild-type sasqs1
87	<a href="#">c2mk6A_</a>	Alignment	not modelled	59.5	12	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> adapter protein meca; <b>PDBTitle:</b> structure determination of substrate binding domain of meca
88	<a href="#">c5nx6A_</a>	Alignment	not modelled	59.4	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> pentalenene synthase; <b>PDBTitle:</b> crystal structure of 1,8-cineole synthase from streptomyces2 clavuligerus in complex with 2-fluoroneryl diphosphate
89	<a href="#">c3lg5A_</a>	Alignment	not modelled	58.7	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> epi-isozizaene synthase; <b>PDBTitle:</b> f198a epi-isozizaene synthase: complex with mg, inorganic2 pyrophosphate and benzyl triethyl ammonium cation
90	<a href="#">d1n1ba2</a>	Alignment	not modelled	56.6	14	<b>Fold:</b> Terpenoid synthases <b>Superfamily:</b> Terpenoid synthases <b>Family:</b> Terpenoid cyclase C-terminal domain
91	<a href="#">c3saeA_</a>	Alignment	not modelled	53.3	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-bisabolene synthase; <b>PDBTitle:</b> structure of a three-domain sesquiterpene synthase: a prospective2 target for advanced biofuels production
92	<a href="#">c6emwg_</a>	Alignment	not modelled	50.8	11	<b>PDB header:</b> chaperone <b>Chain:</b> G: <b>PDB Molecule:</b> atp-dependent clp protease atp-binding subunit clpc; <b>PDBTitle:</b> structure of s.aureus clpc in complex with meca
93	<a href="#">c5c05A_</a>	Alignment	not modelled	50.3	12	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative gamma-terpinene synthase; <b>PDBTitle:</b> crystal structure of gamma-terpinene synthase from thymus vulgaris
94	<a href="#">d1di1a_</a>	Alignment	not modelled	48.0	11	<b>Fold:</b> Terpenoid synthases <b>Superfamily:</b> Terpenoid synthases <b>Family:</b> Aristolochene/pentalenene synthase
95	<a href="#">c3v1vA_</a>	Alignment	not modelled	47.4	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-methylisborneol synthase; <b>PDBTitle:</b> crystal structure of 2-methylisborneol synthase from streptomyces2 coelicolor a3(2) in complex with mg2+ and geranyl-s-thiolodiphosphate
96	<a href="#">c6egkB_</a>	Alignment	not modelled	47.0	14	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> cucumene synthase; <b>PDBTitle:</b> t181n cucumene synthase
97	<a href="#">c4mc8A_</a>	Alignment	not modelled	46.0	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative sesquiterpene cyclase; <b>PDBTitle:</b> hedycaryl synthase in complex with hepes
98	<a href="#">c5uv1A_</a>	Alignment	not modelled	45.0	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> (+)-limonene synthase; <b>PDBTitle:</b> crystal structure of (+)-limonene synthase complexed with 2-2 fluorogeranyl diphosphate
99	<a href="#">c2ongA_</a>	Alignment	not modelled	39.9	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 4s-limonene synthase; <b>PDBTitle:</b> crystal structure of of limonene synthase with 2-2 fluorogeranyl diphosphate (fgpp).
100	<a href="#">c4fp4A_</a>	Alignment	not modelled	39.9	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polyprenyl synthetase; <b>PDBTitle:</b> crystal structure of isoprenoid synthase a3mx09 (target efi-501993)2 from pyrobaculum calidifontis
101	<a href="#">c2vf1A_</a>	Alignment	not modelled	38.6	17	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> capsid protein;

101	<a href="#">c2v1tA_</a>	Alignment	not modelled	38.8	17	<b>PDBTitle:</b> x-ray crystallographic structure of the picobirnavirus2 capsid <b>PDB header:</b> transferase
102	<a href="#">c3npkB_</a>	Alignment	not modelled	36.2	16	<b>Chain:</b> B; <b>PDB Molecule:</b> geranyltranstransferase; <b>PDBTitle:</b> the crystal structure of geranyltranstransferase from campylobacter2 jejuni
103	<a href="#">c2j5cB_</a>	Alignment	not modelled	36.1	15	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> 1,8-cineole synthase; <b>PDBTitle:</b> rational conversion of substrate and product specificity in a2 monoterpene synthase. structural insights into the molecular basis of3 rapid evolution.
104	<a href="#">c3llwA_</a>	Alignment	not modelled	34.7	12	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> geranyltranstransferase (ispa); <b>PDBTitle:</b> crystal structure of geranyltransferase from helicobacter pylori 26695
105	<a href="#">c1n0fF_</a>	Alignment	not modelled	32.5	18	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> F; <b>PDB Molecule:</b> protein mraz; <b>PDBTitle:</b> crystal structure of a cell division and cell wall2 biosynthesis protein upf0040 from mycoplasma pneumoniae:3 indication of a novel fold with a possible new conserved4 sequence motif
106	<a href="#">d1q1fa_</a>	Alignment	not modelled	29.9	14	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Globins
107	<a href="#">c2p0tA_</a>	Alignment	not modelled	29.9	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> upf0307 protein pspto_4464; <b>PDBTitle:</b> structural genomics, the crystal structure of a conserved putative2 protein from pseudomonas syringae pv. tomato str. dc3000
108	<a href="#">d2p0ta1</a>	Alignment	not modelled	29.9	17	<b>Fold:</b> PSPTO4464-like <b>Superfamily:</b> PSPTO4464-like <b>Family:</b> PSPTO4464-like
109	<a href="#">d1n0ea_</a>	Alignment	not modelled	29.1	18	<b>Fold:</b> Double-split beta-barrel <b>Superfamily:</b> AbrB/MazE/MraZ-like <b>Family:</b> Hypothetical protein MraZ
110	<a href="#">d1scta_</a>	Alignment	not modelled	27.9	11	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Globins
111	<a href="#">c3s9vD_</a>	Alignment	not modelled	25.3	13	<b>PDB header:</b> lyase, isomerase <b>Chain:</b> D; <b>PDB Molecule:</b> abietadiene synthase, chloroplastic; <b>PDBTitle:</b> abietadiene synthase from abies grandis
112	<a href="#">c2l66B_</a>	Alignment	not modelled	24.4	10	<b>PDB header:</b> transcription regulator <b>Chain:</b> B; <b>PDB Molecule:</b> transcriptional regulator, abrb family; <b>PDBTitle:</b> the dna-recognition fold of sso7c4 suggests a new member of spovt-abrb2 superfamily from archaea.
113	<a href="#">c3riuC_</a>	Alignment	not modelled	24.1	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> translin associated factor x, isoform b; <b>PDBTitle:</b> crystal structure of drosophila hexameric c3po formed by truncated2 translin and trax
114	<a href="#">c2ltuA_</a>	Alignment	not modelled	24.1	2	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> 5'-amp-activated protein kinase catalytic subunit alpha-2; <b>PDBTitle:</b> solution structure of autoinhibitory domain of human amp-activated2 protein kinase catalytic subunit
115	<a href="#">d3sdha_</a>	Alignment	not modelled	22.4	10	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Globins
116	<a href="#">d1oj6a_</a>	Alignment	not modelled	21.2	14	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Globins
117	<a href="#">d1sctb_</a>	Alignment	not modelled	20.9	13	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Globins