Sce1440

Table 1. Sesquiterpene synthase orthologs of sce1440, which were identified in the genomes of myxobacterial strains.

Myxobacterial Strain	NCBI Reference Sequence / Locus Tag	Number of Amino Acid Residues	Sequence Identity [%]	Sequence similarity [%]
Sorangium cellulosum So0157-2	WP_020735216	781	61.8	73.4
Archangium gephyra DSM 2261	WP_047855443	774	59.6	71.6
Cystobacter violaceus Cb vi76	WP_043389732	773	59.5	70.9
Chondromyces crocatus	WP_050434199	760	59.3	72.8
Cystobacter fuscus DSM 2262	WP_043432513	771	58.6	70.1
Hyalangium minutum DSM 14724	WP_044199666	748	58.4	71.0
Myxococcus xanthus DK 1622	WP_011556189	755	57.8	70.7
Myxococcus xanthus DZF1	WP_011556189_	755	57.8	70.7
Myxococcus xanthus DZ2	WP_011556189_	755	57.8	70.7
Myxococcus fulvus HW-1	WP_013938107	755	57.3	69.9
Enhygromyxa salina DSM 15201	KIG18953	787	57.1	68.3.
Myxococcus stipitatus DSM 14675	WP_015352290	750	55.9	69.7
Corallococcus coralloides DSM 2259	WP_014400162	752	55.7	71.4
Haliangium ochraceum DSM 14365	WP_012826426	756	55.6	68.2
Chondromyces apiculatus DSM 436	EYF04694	796	55.5	67.1
Myxococcus virescens DSM 2260	Ga0070493_11424	754	55.1	69.8
Stigmatella aurantiaca DW4/3-1	WP_002611863	704	53.3	65.2

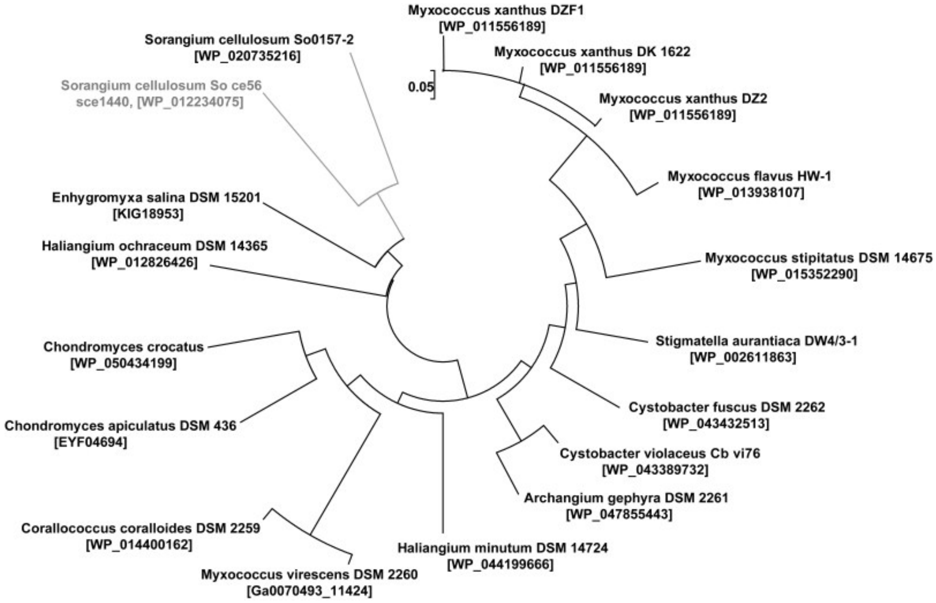


Figure 1. The radial view of an unrooted phylogenetic tree obtained by MEGA4 (version 4.0) analysis for the determination of relatedness of the sce1440 from *Sorangium cellulosum* So ce56 with other myxobacterial terpene synthases. The sce1440 gene from *S. cellulosum* So ce56 is shown in grey branches. Sce 4636 (WP_049876337)

Table 2. Sesquiterpene synthase orthologs of sce4636, which were identified in the genomes of myxobacterial strains.

Myxobacterial Strain	**NCBI Reference Sequence**	**Number of amino acid residues**	**Sequence Identity [%]**	**Sequence similarity [%]**
Cystobacter fuscus DSM 2262	WP_002627525	509	47.6	60.9
Cystobacter violaceus Cb vi76	WP_043411369	513	45.3	60.9
Archangium gephyra DSM 2261	WP_053066483	514	44.3	60.3
Chondromyces apiculatus DSM 436	WP_044234889	519	41.8	53.5
Cystobacter violaceus Cb vi76	WP_043405491	512	41.4	54.2
Archangium gephyra DSM 2261	WP_047856205	512	41.1	54.9
Cystobacter fuscus DSM 2262	EPX58993	531	40.9	53.5
Chondromyces apiculatus DSM 436	WP_052376419	542	29.9	39.6

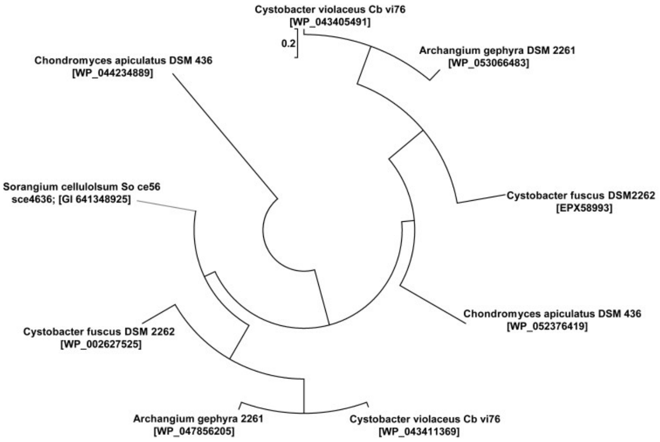


Figure 2. The radial view of an unrooted phylogenetic tree obtained by MEGA4 (version 4.0) analysis for the determination of relatedness of sce4636 from *Sorangium cellulosum* So ce56 with other myxobacterial terpene synthases. The sce4636 gene from *S. cellulosum* So ce56 is shown in grey.

Sce 6369 (CAN96536)

Table 3. Sesquiterpene synthase orthologs of sce6369, which were identified in the genomes of myxobacterial strains.

Myxobacterial Strain	**NCBI Reference Sequence**	**Number of amino acid residues**	**Sequence Identity [%]**	**Sequence similarity [%]**
Chondromyces crocatus	WP_050430829	313	33.2	46.7
Chondromyces apiculatus DSM 436	EYF00967	301	32.1	45.7
Sorangium cellulosum So0157-2	AGP41845	321	31.8	46.8
Hyalangium minutum DSM 14724	WP_044191871	293	29.5	46.2
Sorangium cellulosum So ce56	WP_012241161	315	28.8	44.7
Myxococcus fulvus 124B02	WP_046712537	331	28.4	41.8
Plesiocystis pacifica SIR-1	WP_006972929	364	24.1	38.1

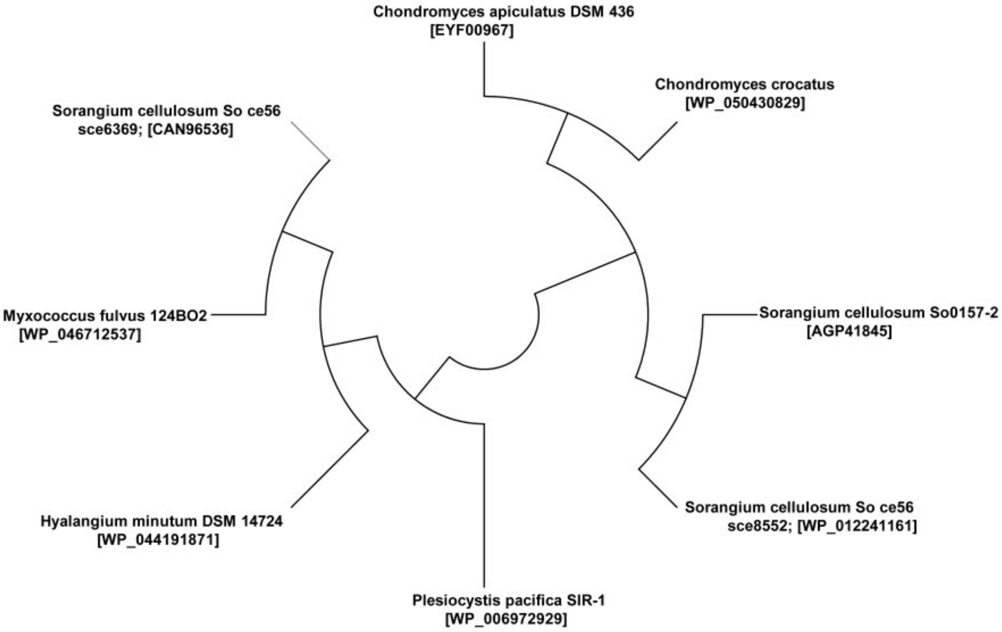


Figure 3. The radial view of an unrooted phylogenetic tree obtained by MEGA4 (version 4.0) analysis for the determination of relatedness of the sce6369 from *Sorangium cellulosum* So ce56 with other myxobacterial terpene synthases. The gene sce6369 from *S. cellulosum* So ce56 is shown in grey.

Sce 8552 (WP_012241161)

Table 4. Sesquiterpene synthase orthologs of sce8552, which were identified in the genomes of myxobacterial strains.

	NCBI Reference Sequence / Locus Tag	**Number of amino acid residues**	**Sequence Identity [%]**	**Sequence similarity [%]**
Sorangium cellulosum So0157-2	AGP41845	321	68.7	81.2
Sorangium cellulosum So ce56	CAN96536	315	28.8	44.7
Nannocystis exedens ATCC 25963	Ga0008035_06483	328	27.9	42.6
Chondromyces crocatus	WP_050430829	313	27.9	46.9
Chondromyces apiculatus DSM 436	EYF00967	301	27.7	45.5
Myxococcus fulvus 124B02	WP_046712537	331	27.4	46.1
Hyalangium minutum DSM 14724	WP_044191871	293	26.8	45.4
Myxococcus stipitatus DSM 14675	WP_044281543	358	25.2	37.0
Cystobacter violaceus Cb vi76	WP_043410615	324	25.2	39.3
Plesiocystis pacifica SIR-1*	WP_006972929	364	24.7	41.0
Plesiocystis pacifica SIR-1	EDM79289	355	24.6	42.6
Archangium gephyra DSM 2261	AKJ08214	343	24.5	39.8
Cystobacter fuscus DSM 2262	WP_002630213	365	22.1	41.4

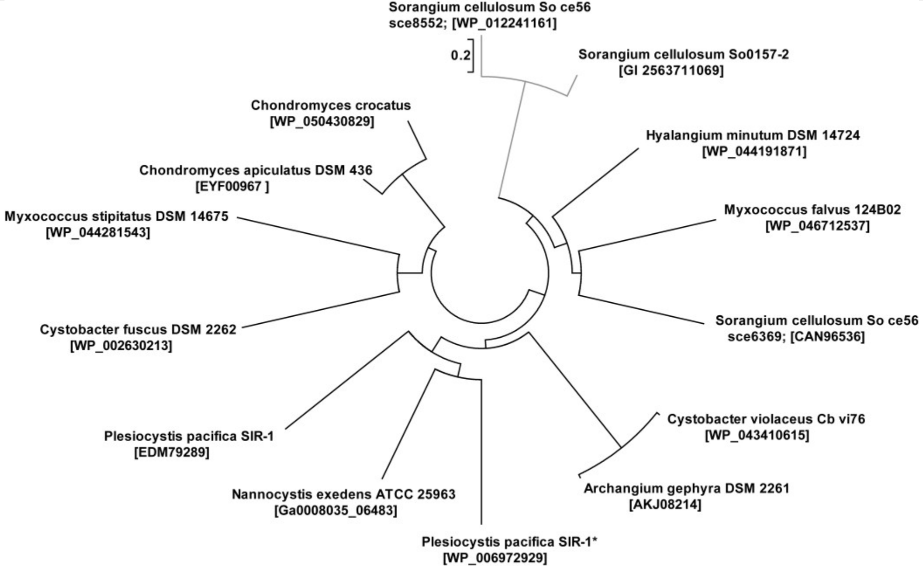
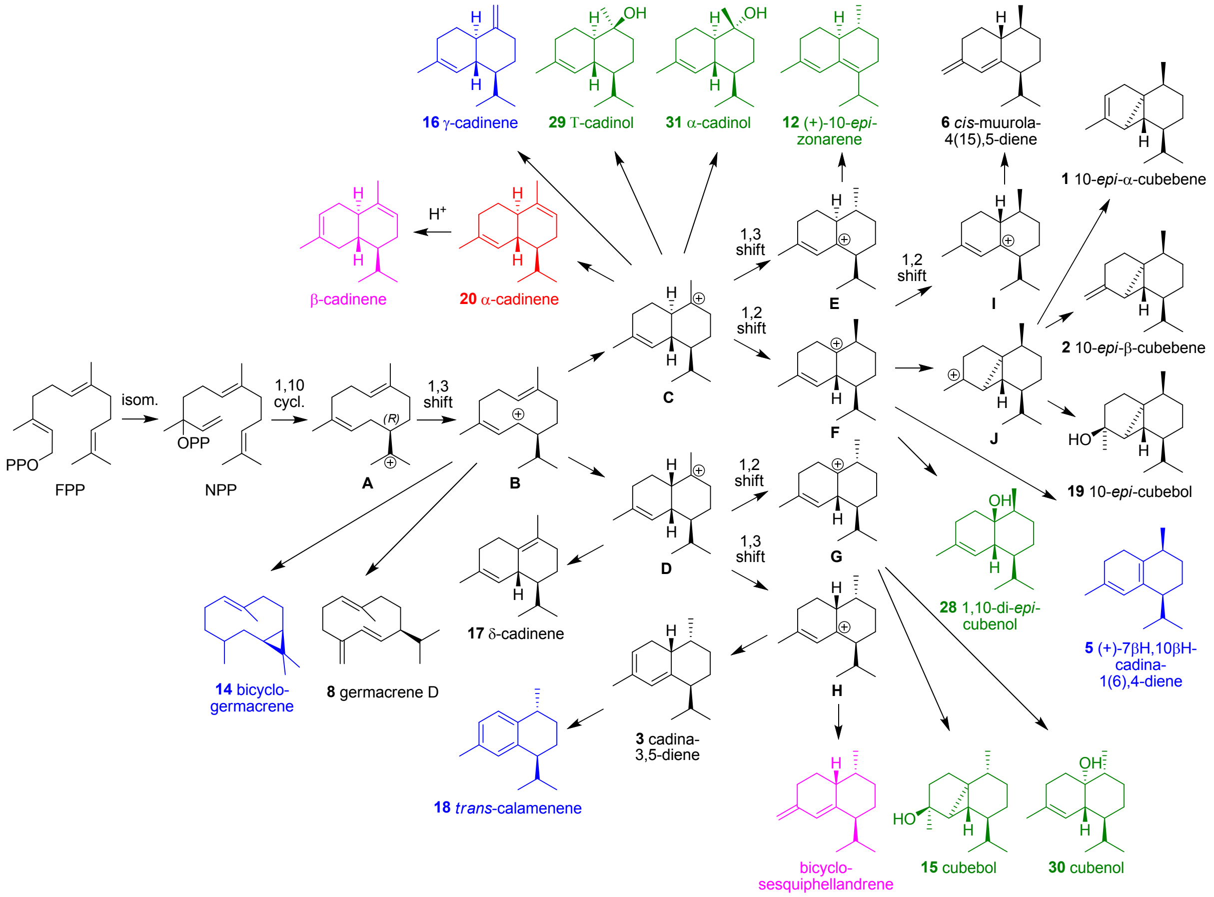
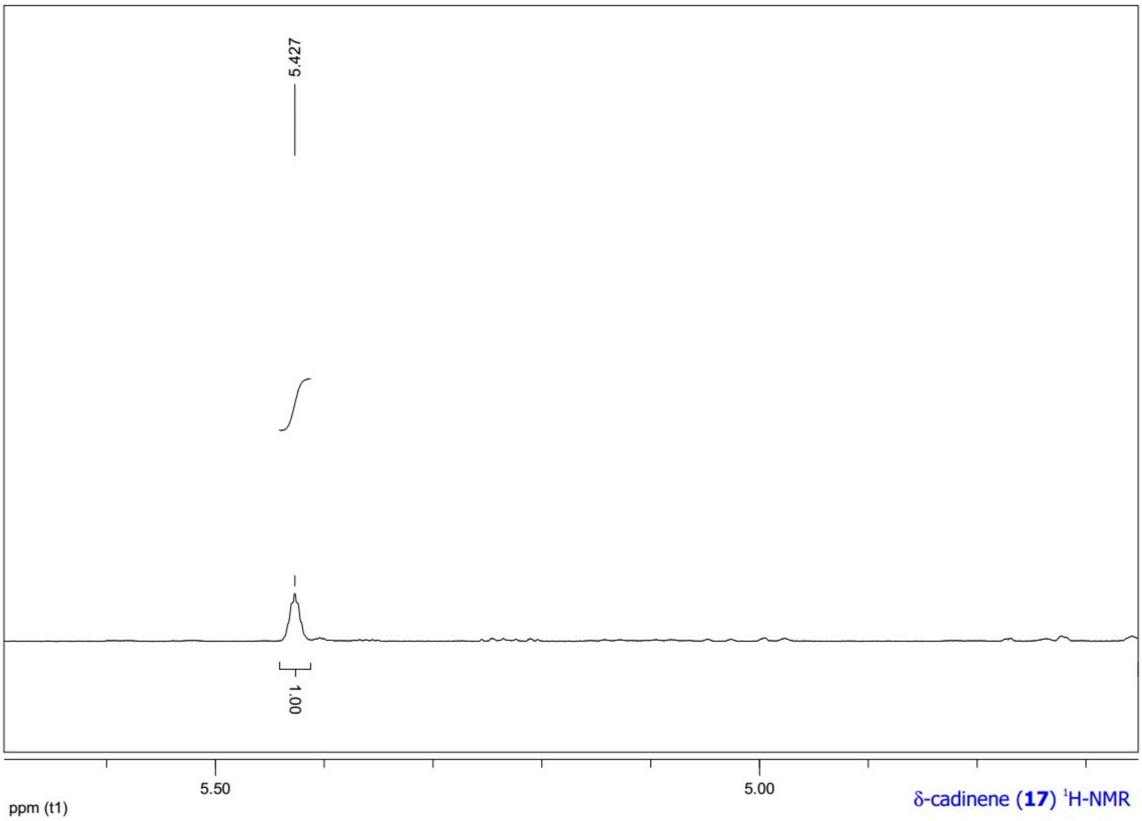


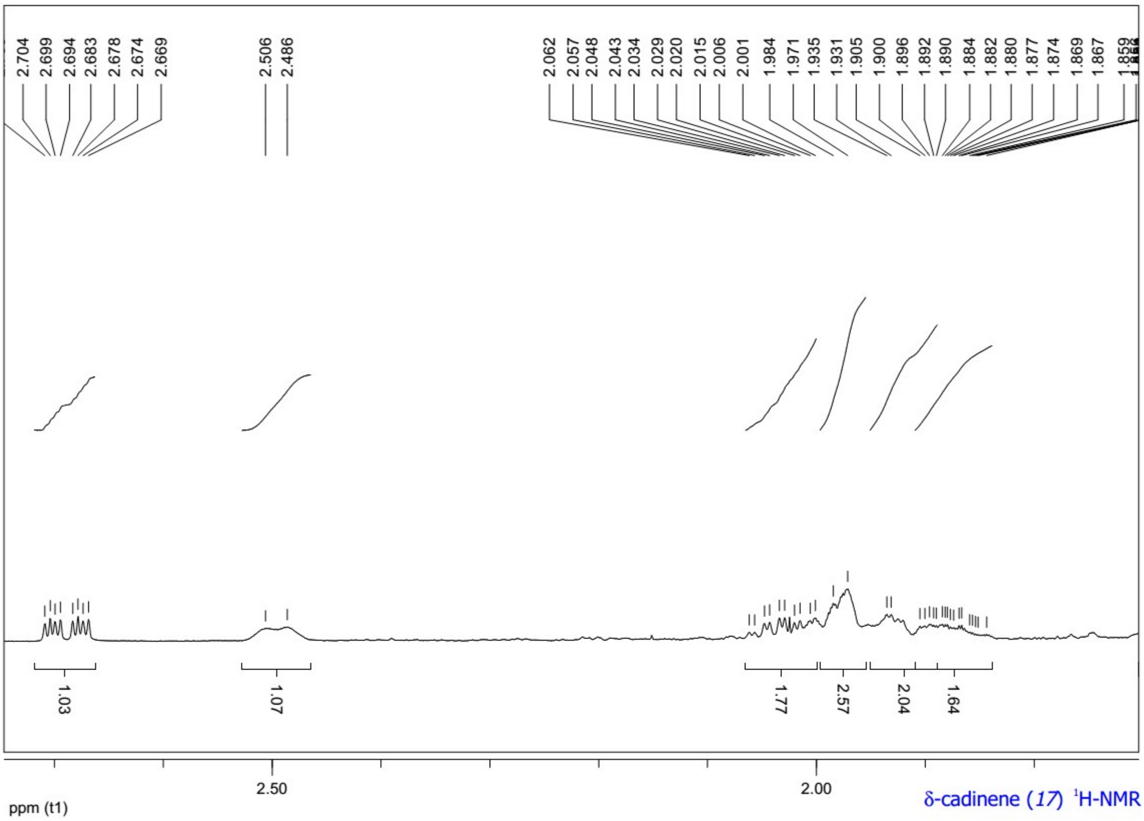
Figure 4. The radial view of an unrooted phylogenetic tree obtained by MEGA4 (version 4.0) analysis for the determination of relatedness of the sce8552 from *Sorangium cellulosum* So ce56 with other myxobacterial terpene synthases. The gene sce8552 from *S. cellulosum* is shown in grey.



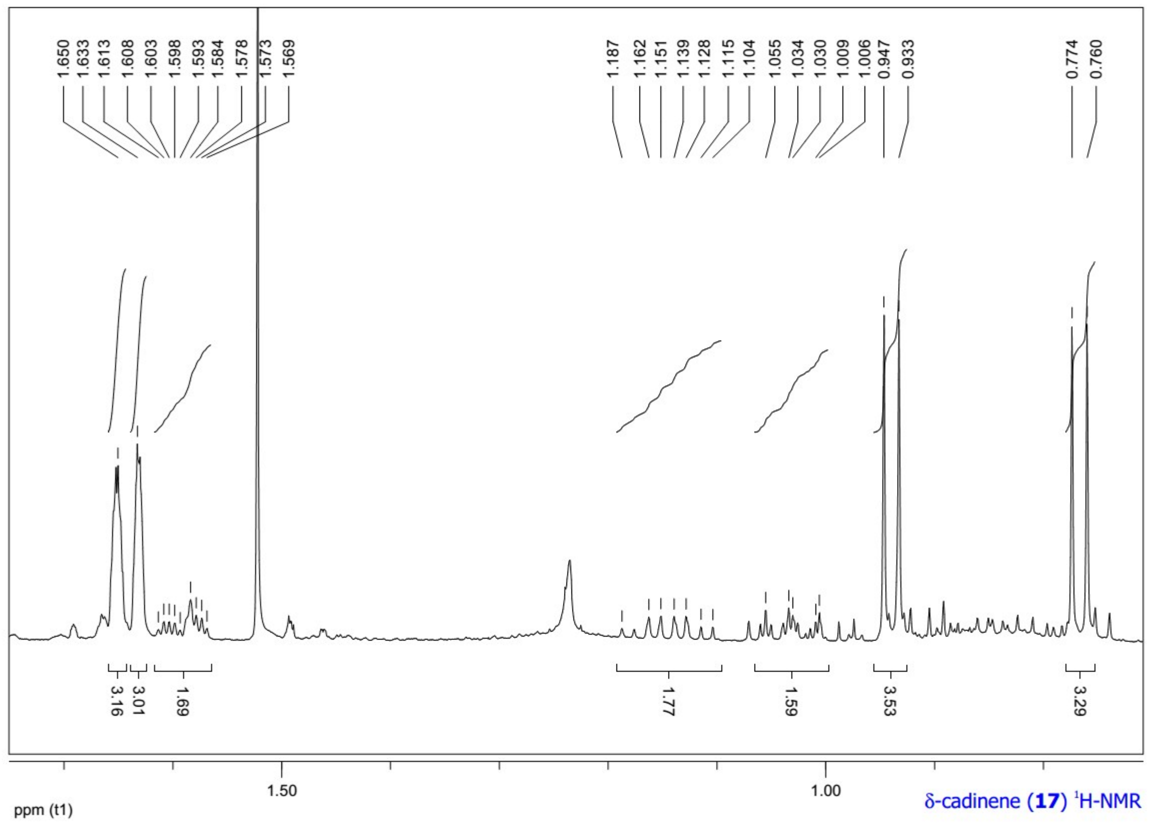
Scheme 1 Proposed alternative mechanism (involving enantiomers of all molecules) for the biosynthesis of cadalane- and cubebane-type sesquiterpenes by sce6369; sesquiterpenes observed in *S. cellulosum* and the sce6369 expressing *E. coli* strain are represented in black; sesquiterpenes observed only in *S. cellulosum* are represented in blue; sesquiterpenes observed only in the sce6369 expressing *E. coli* strain are represented in green; sesquiterpenes observed in *S. cellulosum* and the sce6369 expressing *Streptomyces avermitilis* SUKA22[12] are represented in red; sesquiterpenes observed only in the sce6369 expressing *S. avermitilis* SUKA22[12] are represented in pink; cadina-3,5-diene (**3**) was observed in *S. cellulosum* as well as both *E. coli* and *S. avermitilis* SUKA22 expressing sce6369[12]



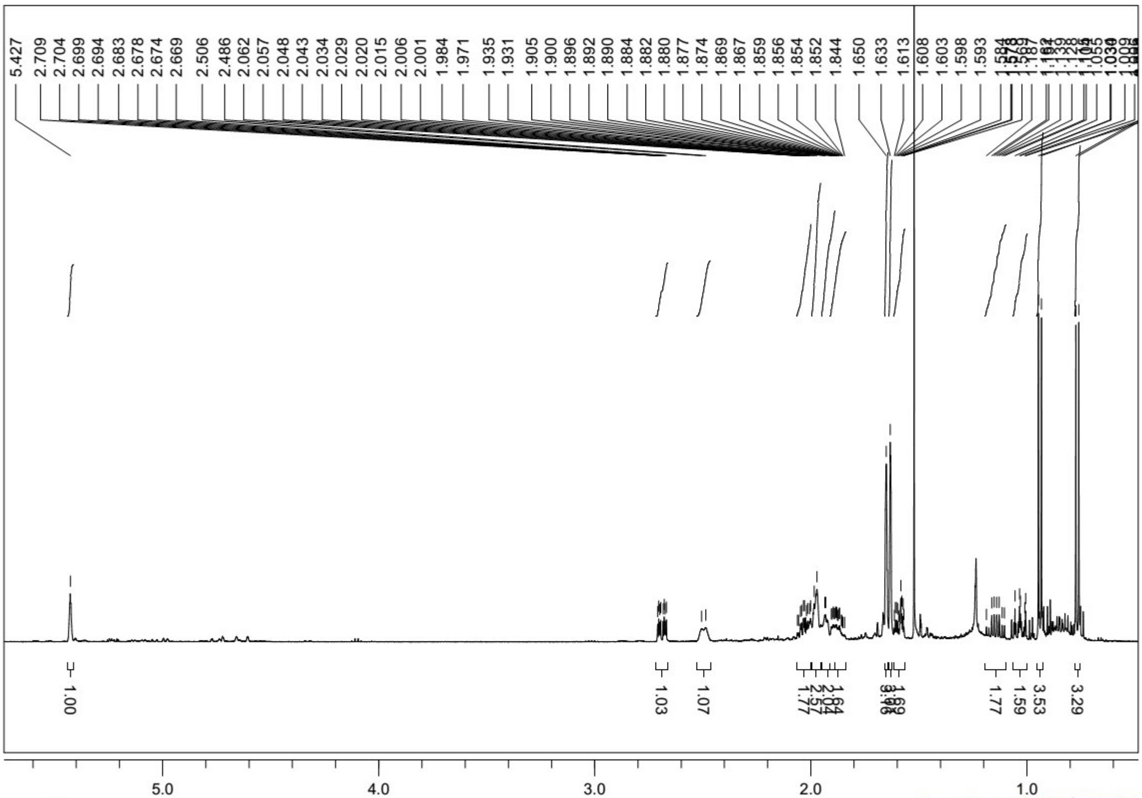
δ-cadinene (**17**) ^{1}H-NMR



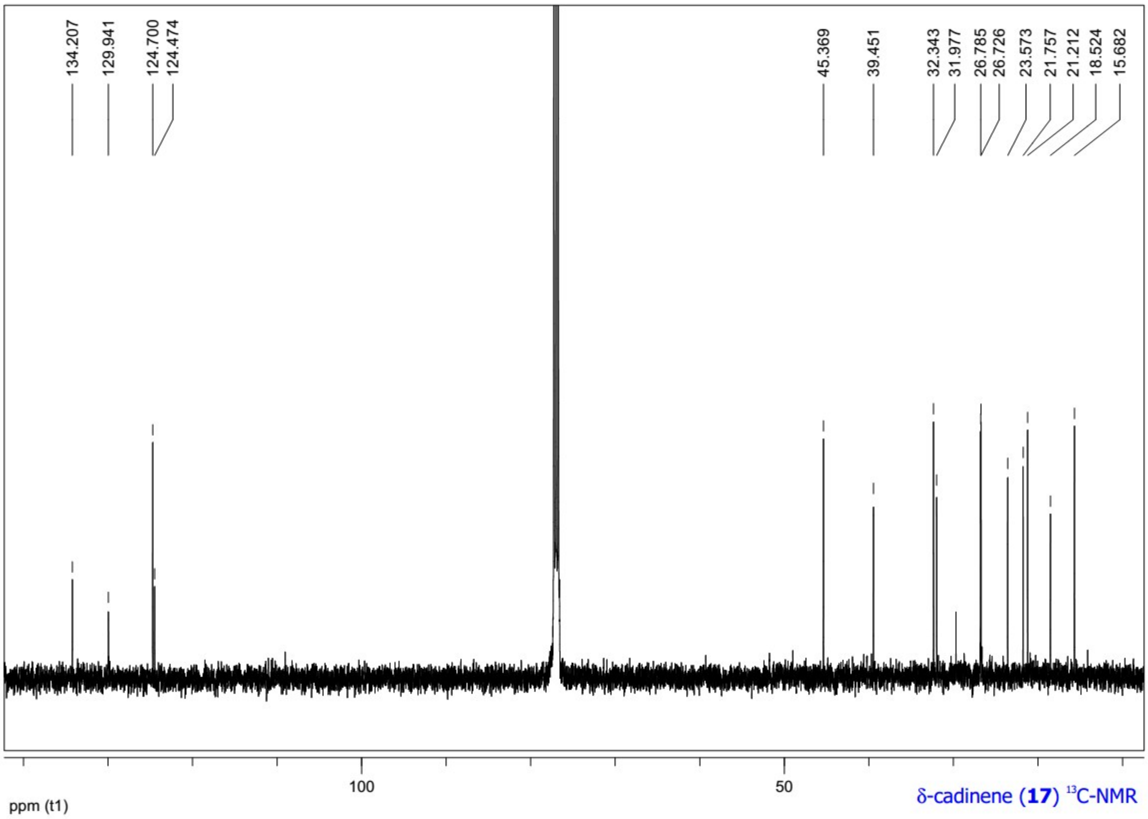
δ-cadinene (*17*) ^{1}H-NMR



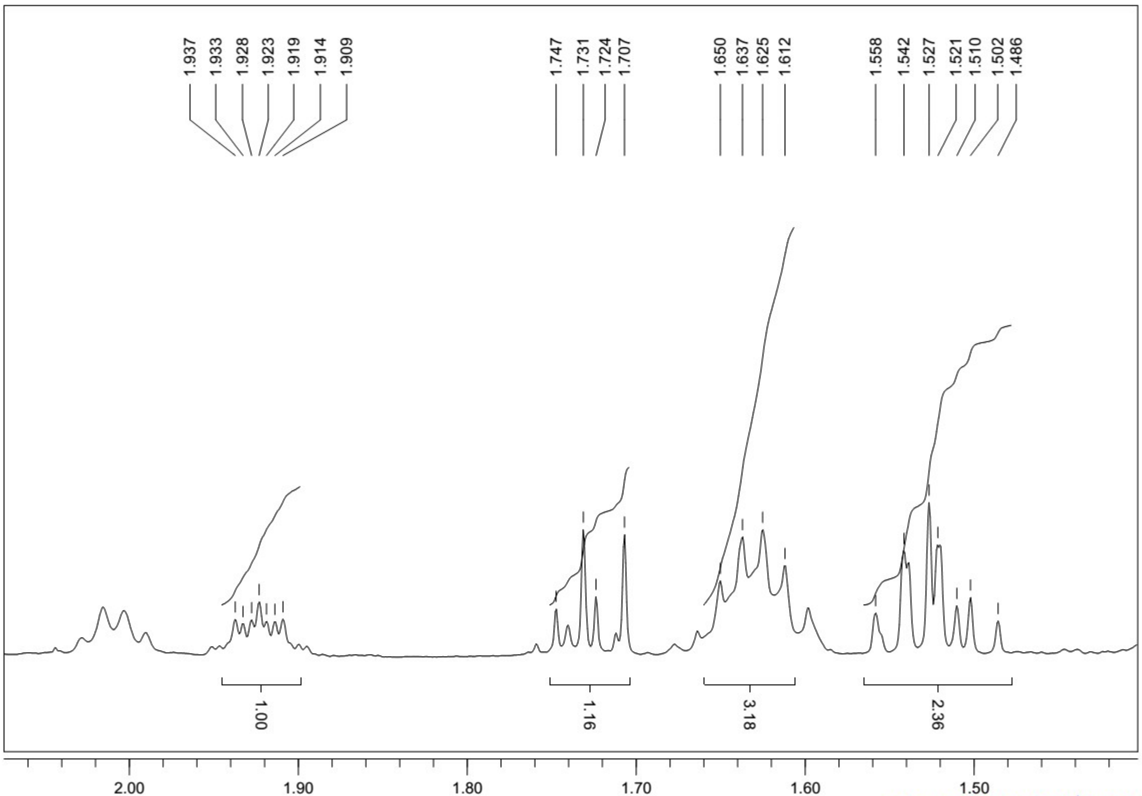
δ-cadinene (**17**) ^{1}H-NMR



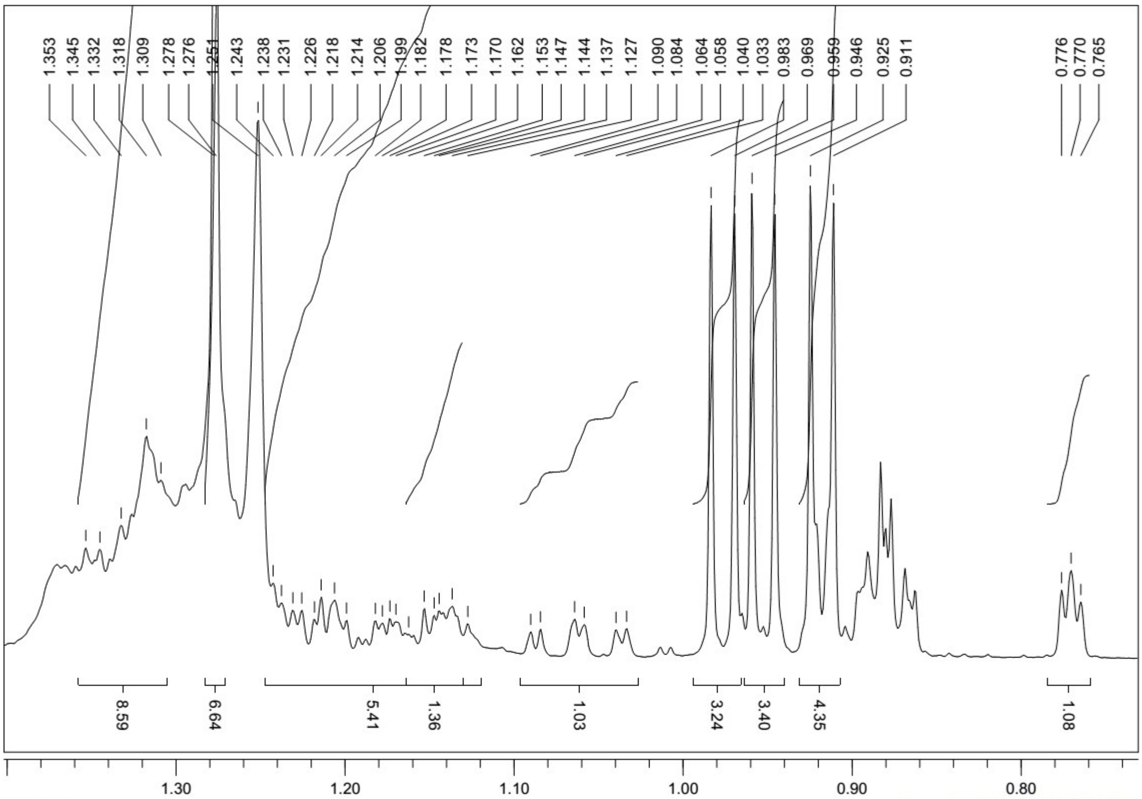
δ-cadinene (**17**) ^{1}H-NMR



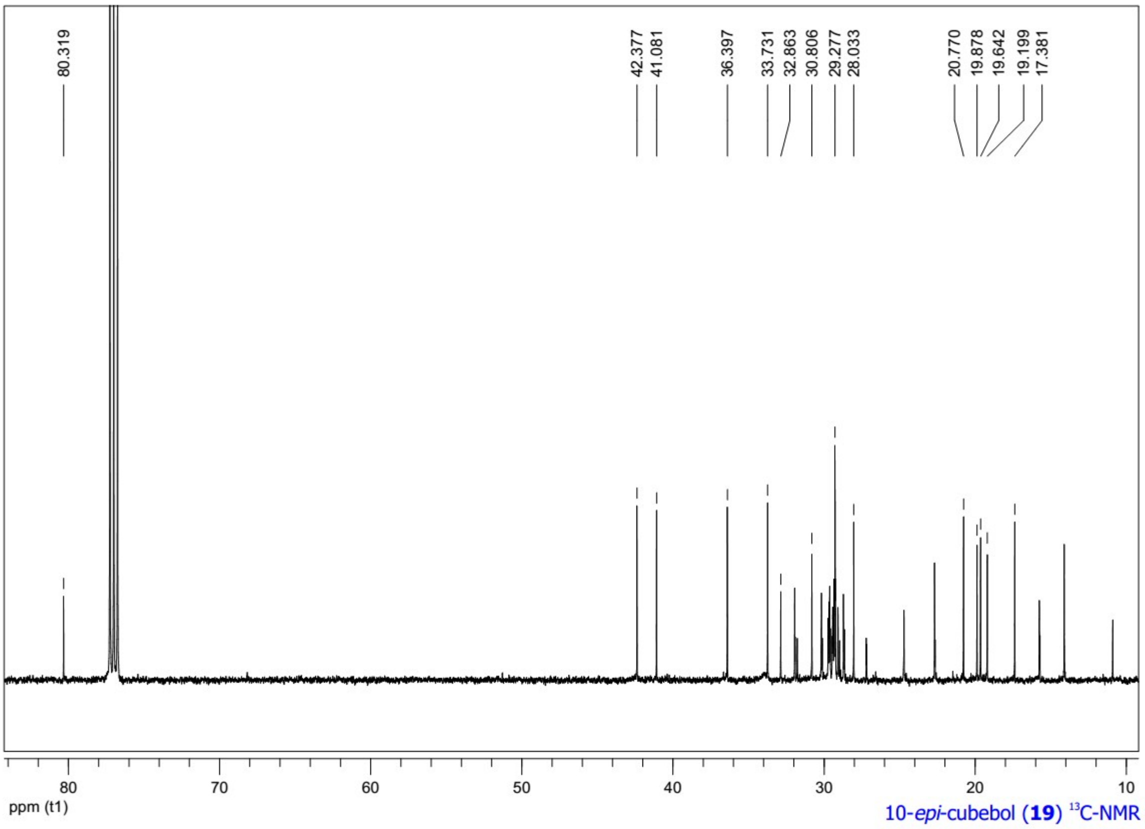
δ-cadinene (**17**) ^{13}C-NMR



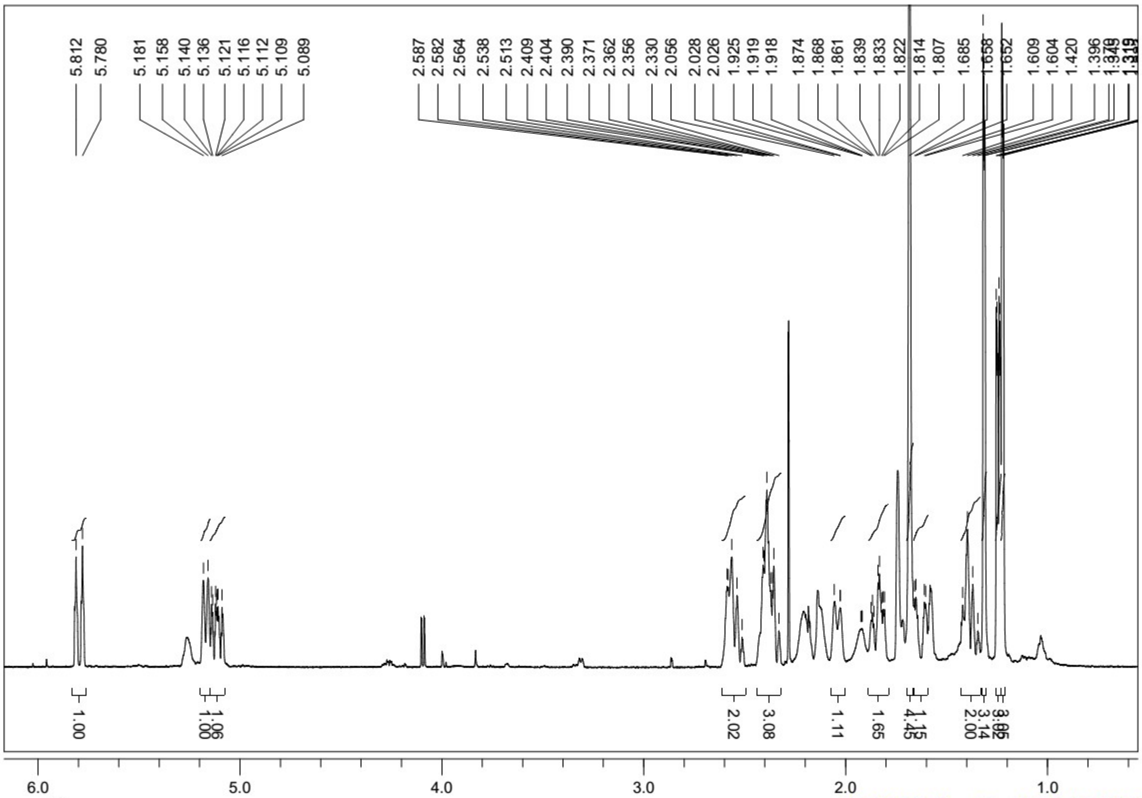
10-*epi*-cubebol (**19**) ^{1}H-NMR



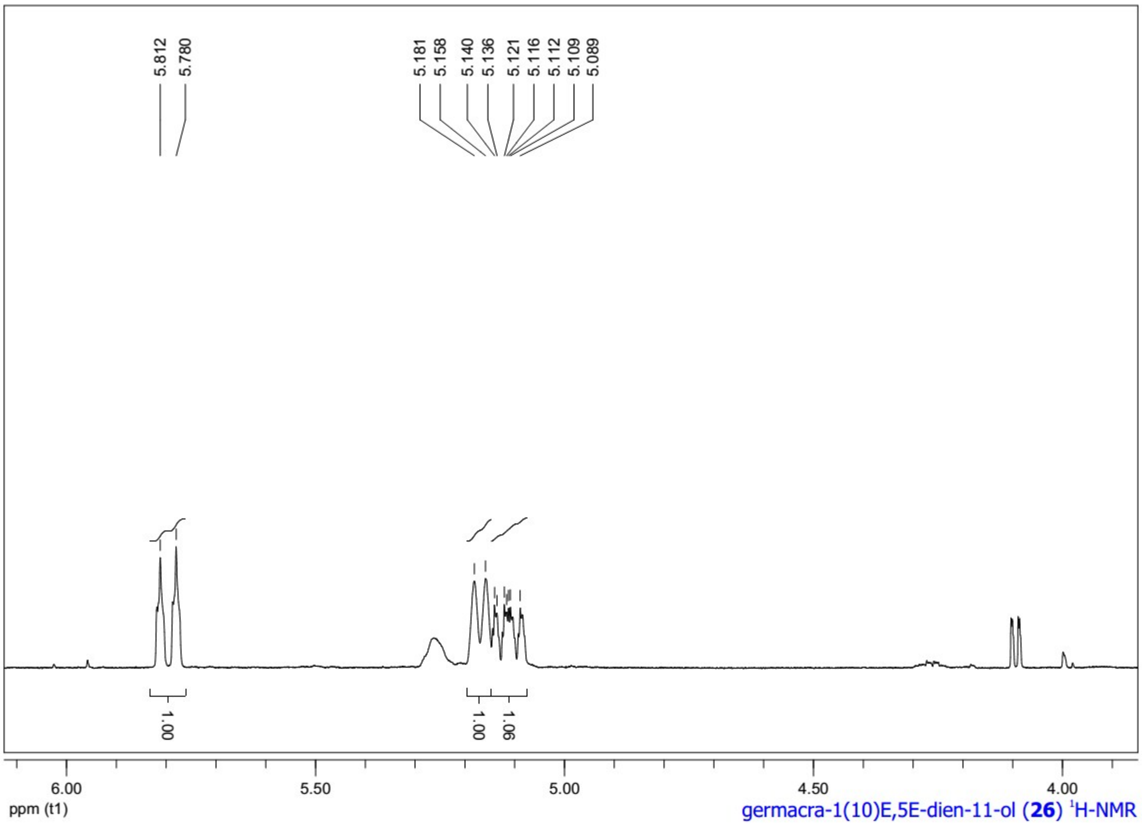
10-*epi*-cubebol (**19**) ^{1}H-NMR



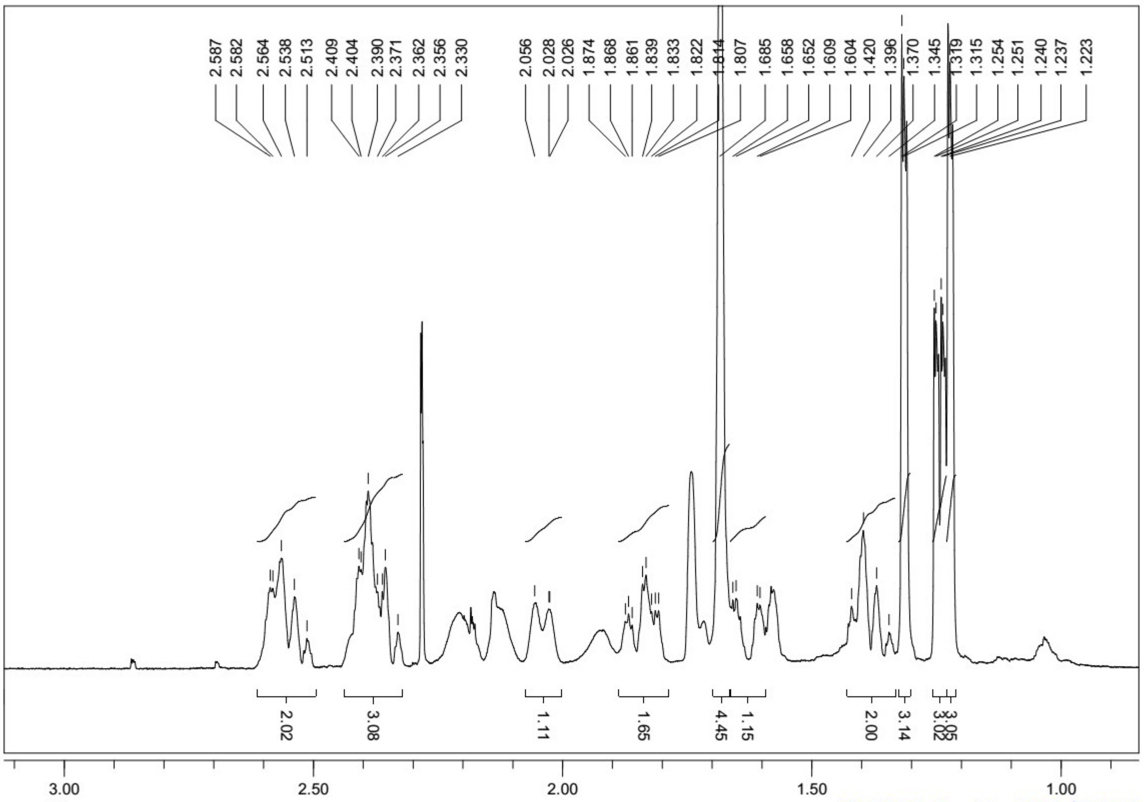
10-*epi*-cubebol (**19**) ^{13}C-NMR



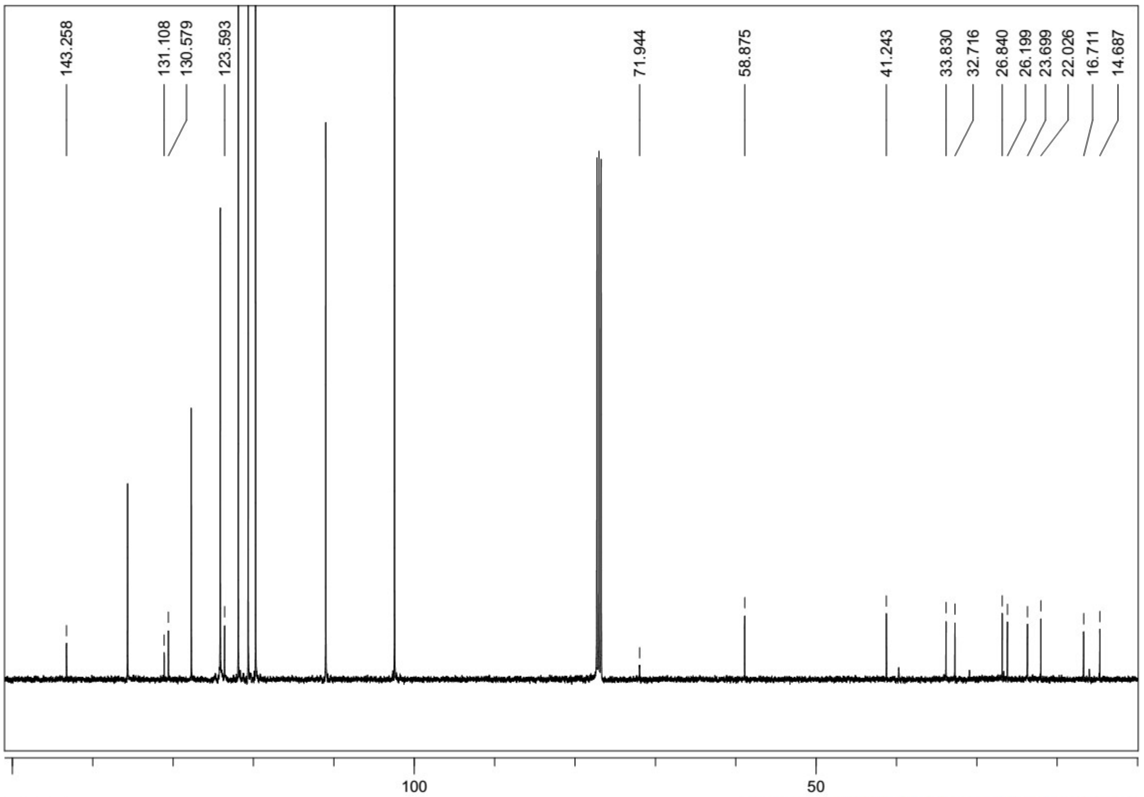
germacra-1(10)E,5E-dien-11-ol (**26**) ^{1}H-NMR



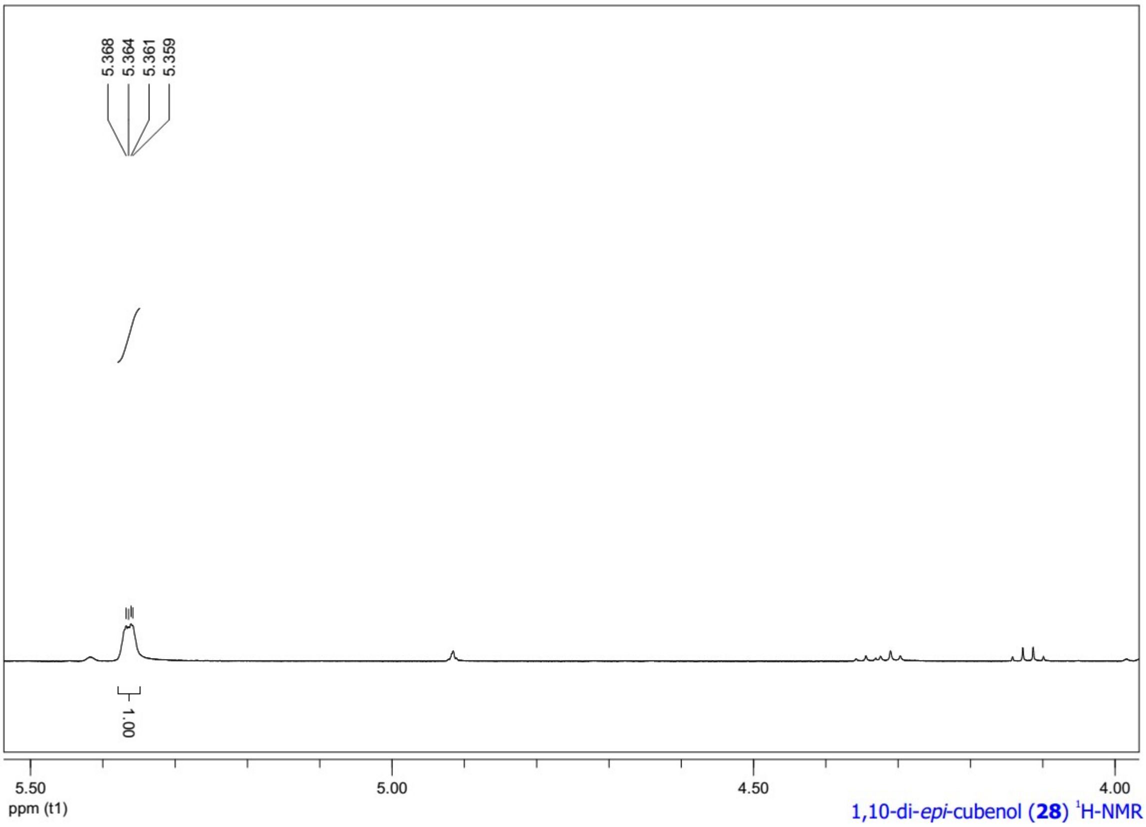
germacra-1(10)E,5E-dien-11-ol (**26**) ^{1}H-NMR



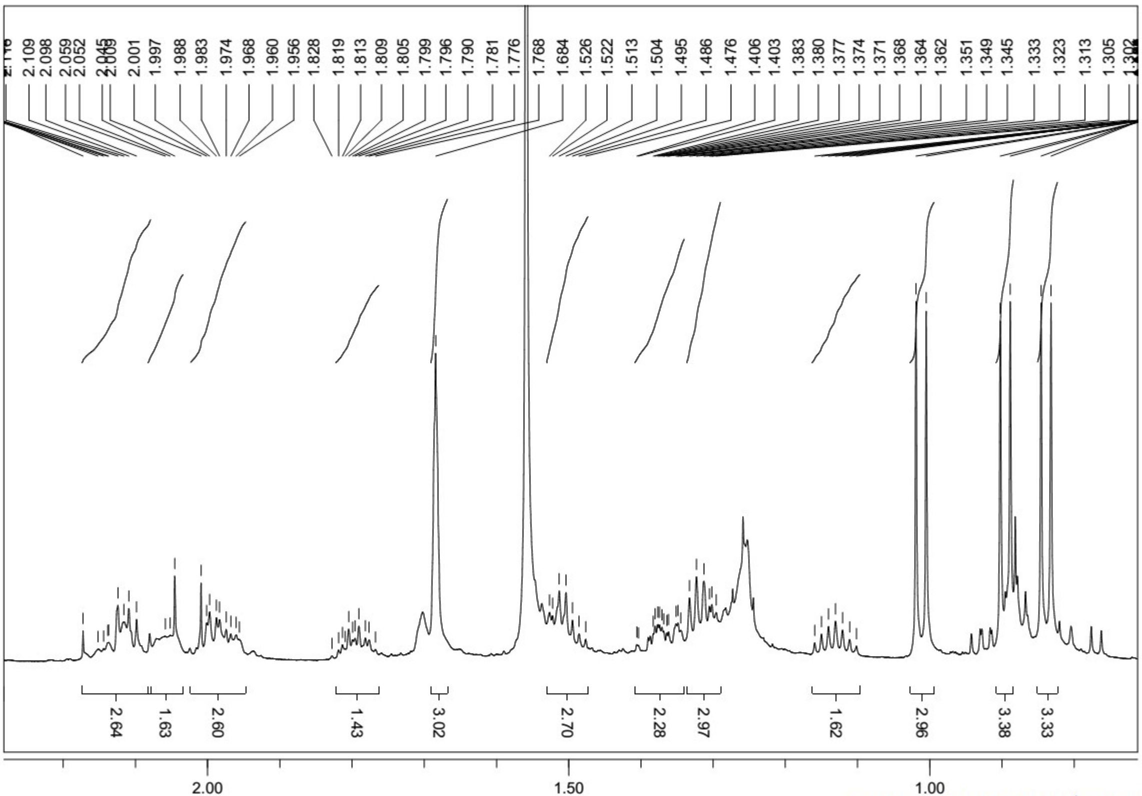
germacra-1(10)E,5E-dien-11-ol (**26**) ^{1}H-NMR



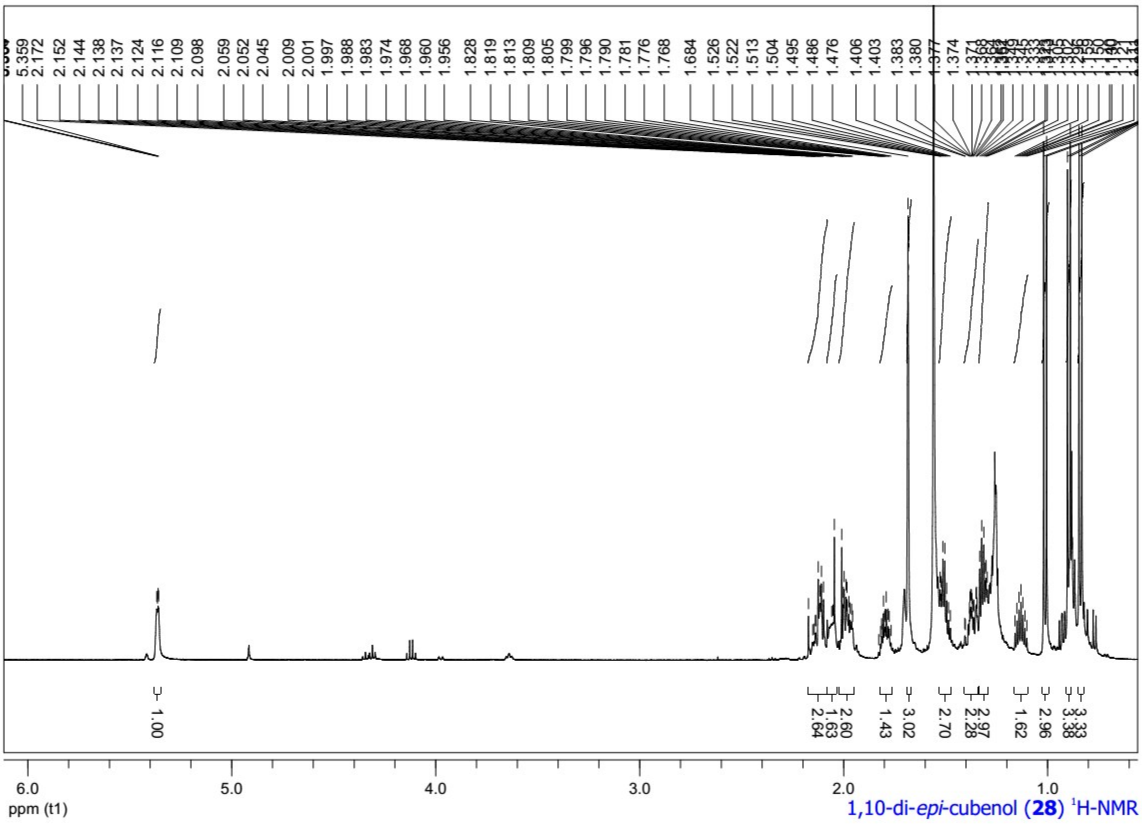
germacra-1(10)E,5E-dien-11-ol (**26**) ^{13}C-NMR



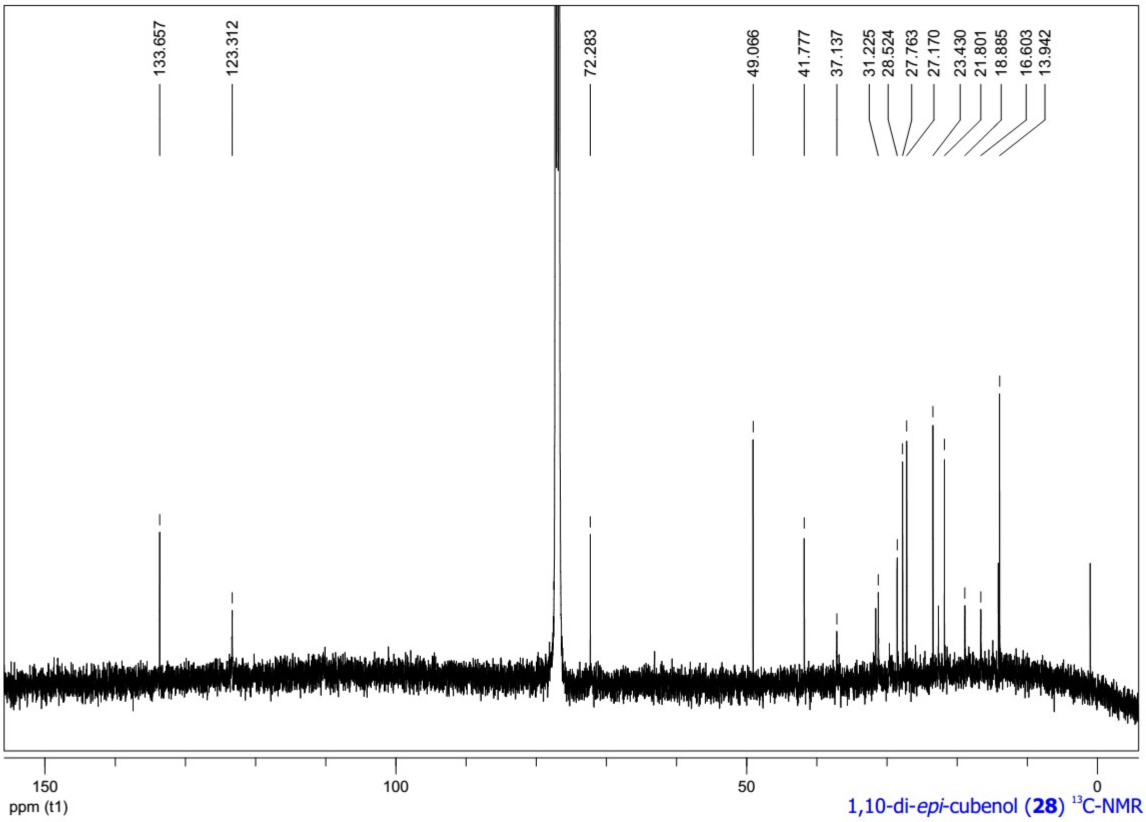
1,10-di-*epi*-cubenol (**28**) ^{1}H-NMR



1,10-di-*epi*-cubenol (**28**) ^{1}H-NMR



1,10-di-*epi*-cubenol (**28**) ^{1}H-NMR



1,10-di-*epi*-cubenol (**28**) ^{13}C-NMR