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Table S1. Sources of plants used in this study.

Table S2. List of Primers used in this study.

Table S3. Index of class I diTPS functional assays by *N. benthamiana* transient expression.

Table S4. Index of class II diTPS functional assays by *N. benthamiana* transient expression.

Table S5. Index of *in-vitro* assays.

Figure S1. An example of skeleton extraction.

Figure S2. Pathway diagram of newly characterized enzyme activities

Figure S3. Class I diTPS *N. benthamiana* assays with (+)-CPP.

Figure S4. Class I diTPS *N. benthamiana* assays with (+)-8-LPP.

Figure S5. Class I diTPS *N. benthamiana* assays with PgPP.

Figure S6. Class I diTPS *N. benthamiana* assays with *ent*-CPP.

Figure S7. (+)-CPP synthase *N. benthamiana* assays.

Figure S8. Other class II diTPS *N. benthamiana* assays.

Figure S9. Comparison of *in-vitro* and *in-vivo* activities for selected combinations.

Figure S10. NMR of trans-abienol [**11**]

Figure S11. NMR of labda-7,13E-dien-15-ol [**21a**]

Figure S12. NMR of labda-7,13(16),14-triene [**22**]

Figure S13. NMR of labda-7,12E,14-triene [**24**]

Figure S14. NMR of (10R)-labda-8,13E-diene-15-ol [**25a**]

Figure S15. NMR of (10R)-labda-8,14-dien-13-ol [**26**]

Figure S16. NMR of trans-biformene [**34**]

Figure S17. NMR of neo-cleroda-4(18),14-dien-13-ol [**37**]

Figure S18. NMR of neo-cleroda-4(18),13E-diene-15-ol [**38a**]

Figure S19. NOESY of (+)-cis-abienol

Figure S20. Phylogenetic tree of all known and candidate diTPSs from Lamiaceae

Figure S21. Activity-determining regions in an alignment of previously known, newly characterized, and candidate TPS-c enzymes from Lamiaceae

Figure S22. An activity-determining region in an alignment of previously known, newly characterized, and candidate TPS-e enzymes from Lamiaceae

Taxon	Subfamily	Source
<i>Ajuga reptans</i> L.	Ajugoideae	Horizon Herbs, Williams, Oregon, USA
<i>Hyptis suaveolens</i> (L.) Poit.	Nepetoideae	Native seeds, Tucson, Arizona, USA
<i>Leonotis leonurus</i> (L.) R.Br.	Lamioideae	Logee's Greenhouses, Danielson, Connecticut, USA
<i>Mentha spicata</i> L.	Nepetoideae	Richters Herbs, Goodwood, Ontario, Canada
<i>Nepeta mussinii</i> Spreng. ex Henckel.	Nepetoideae	Outside Pride, Independence, Oregon, USA
<i>Origanum majorana</i> L.	Nepetoideae	Richters Herbs, Goodwood, Ontario, Canada
<i>Perovskia atriplicifolia</i> Benth.	Nepetoideae	Department of Horticulture, Michigan State University (https://www.canr.msu.edu/hrt/)
<i>Plectranthus barbatus</i>	Nepetoideae	Companion Plants, Athens, Ohio, USA
<i>Pogostemon cablin</i> (Blanco) Benth.	Lamioideae	Richters Herbs, Goodwood, Ontario, Canada
<i>Prunella vulgaris</i> L.	Nepetoideae	WJ Beal Botanical Garden, Michigan State University
<i>Salvia officinalis</i> L.	Nepetoideae	Department of Horticulture, Michigan State University (https://www.canr.msu.edu/hrt/)

Table S1. Sources of plants used in this study.

Name	Sequence	Gene of interest
<i>Amplification of full length genes from cDNA synthesized from plant tissues total RNA</i>		
<i>ZmAN2-F</i>	ATGGTTCTTTCATCGTCTTGCACA	<i>ZmAN2</i>
<i>ZmAN2-R</i>	TTATTTTGC GCGCGGAAACAGGTTCA	
<i>CfTPS2-F</i>	AGATTGAGGATTCCATTGAGTACGTGAAGG	<i>CfTPS2</i>
<i>CfTPS2-R</i>	GAAGTTTAATATCCTTCATTCTTTATTACA	
<i>CfTPS3-F</i>	AGCTCCATTCAACTAGAGTCATGTCGT	<i>CfTPS3</i>
<i>CfTPS3-R</i>	TTCATCTGGCTTAACTAGTTGCTGACAC	
<i>CfTPS16-F</i>	TTAAAGTACTCTCTCAAAGAGTACTTTGG	<i>CfTPS16</i>
<i>CfTPS16-R</i>	GCGACCAACCATCATACTGACT	
<i>LITPS1-F</i>	AATGGCCTCCACTGCATCCACTCTA	<i>LITPS1</i>
<i>LITPS1-R</i>	CCATACTCATTCAACTGGTTCGAACA	
<i>LITPS4-F</i>	AGCCTGTGTACTCGAAATGTC	<i>LITPS4</i>
<i>LITPS4-R</i>	CAAGAGGATGATTCATGTACCAAC	

<i>SoTPS1-F</i>	TCTCTTTCAAGAATATCCCCTCTC	<i>SoTPS1</i>
<i>SoTPS1-R</i>	GGCATTCAATGATTTTGAGTCG	
<i>ArTPS1-F</i>	AAATGGCCTCTTTGTCCACTCTC	<i>ArTPS1</i>
<i>ArTPS1-R</i>	TTACGCAACTGGTTCGAAAAGCA	
<i>ArTPS2-F</i>	TAATGTCATTTGCTTCCCAAGCCA	<i>ArTPS2</i>
<i>ArTPS2-R</i>	GGCCTAGACTACCTTCTCAAACAA	
<i>ArTPS3-F</i>	AATGTCACTCTCGTTCACCATCAA	<i>ArTPS3</i>
<i>ArTPS3-R</i>	ACTTCAAGAGGATGAAGTGTTTAGG	
<i>PaTPS1-F</i>	CTCCAAAACCTCGGGCCGGTAAAT	<i>PaTPS1</i>
<i>PaTPS1-R</i>	TACGTATTTCTCACAATCGAGCA	
<i>PaTPS3-F</i>	CTAGAAATGTTACTTGCGTTCAAC	<i>PaTPS3</i>
<i>PaTPS3-R</i>	GGGTAAGAGTTGAATTTAGATGTCT	
<i>NmTPS1-F</i>	ATGACTTCAATATCCTCTCTAAATTTGAGC	<i>NmTPS1</i>
<i>NmTPS1-R</i>	GAATATAGTAATCAGACGACCGGTCCA	
<i>NmTPS2-F</i>	GCCATATCATGTCTCTTCCGCTCT	<i>NmTPS2</i>
<i>NmTPS2-R</i>	TTATTCATGCACCTTAAAATCCTTGAGAG	
<i>OmTPS1-F</i>	ATGACCGATGTATCCTCTCTTCGT	<i>OmTPS1</i>
<i>OmTPS1-R</i>	AAACACTCACATAACCGGCCCAA	
<i>OmTPS3-F</i>	GTCCTTGCTTTCGGAATACT	<i>OmTPS3</i>
<i>OmTPS3-R</i>	GAAGTGATCTACAAGGATTCATAAA	
<i>OmTPS4-F</i>	TCATTGATTTGCCCTGCATCCAC	<i>OmTPS4</i>
<i>OmTPS4-R</i>	CAAAGCTAGTGCTGCTTCTGATT	
<i>OmTPS5-F</i>	ATGGTATCTGCATGTCTAAAACCTCAA	<i>OmTPS5</i>
<i>OmTPS5-R</i>	CTTTCTCTCTTGTGCATCTTAGT	
<i>MsTPS1-F</i>	ACGTTTCATCTTCAATGAGTTCCA	<i>MsTPS1</i>
<i>MsTPS1-R</i>	TACGTGTATGTCGATCTGTTCCAAT	
<i>PcTPS1-F</i>	CATGTCATTTGCTTCTCAATCAC	<i>PcTPS1</i>
<i>PcTPS1-R</i>	CCCATTATCTAAAAGTCTACATCACC	
<i>HsTPS1-F</i>	TCCTCATAAAGCAATGGCGTATA	<i>HsTPS1</i>
<i>HsTPS1-R</i>	CTAAGATTCAGACAATGGGCTCA	
<i>EpTPS8-F</i>	GCAGACGCCAATCTTTCTTGGT	<i>EpTPS8</i>
<i>EpTPS8-R</i>	TTATGAAGTTAAAAGGAGTGGTTCGTTGAC	
<i>PVTPS1-F</i>	GGAACGAGAAATGTCACTCAC	<i>PVTPS1</i>
<i>PVTPS1-R</i>	TTCTAGTTTCTCACAGAAGTCAA	
<i>LP4-2A Ver.1 sequence</i>	TCAAATGCAGCAGACGAAGTTGCTACTCAACTTTTGAATTTTGACTTGCTGAGTTGGCTGGTGATGTTGAGTCAAACCCTGGACCT	Synthesized by Integrated DNA Technologies, Skokie, Illinois, USA
Cloning of full length diTPS genes into pEAQ-HT for transient expression in <i>N. benthamiana</i>		

<i>pEAQ_Infusion</i> <i>_CfTPS1-F</i>	TTCTGCCCAAATTCGATGGGGTCTCTATCCACTATGA	<i>CfTPS1</i>
<i>pEAQ_Infusion</i> <i>_CfTPS1-R</i>	AGTTAAAGGCCTCGATCAGGCGACTGGTTCGAAAAGTA	
<i>pEAQ_Infusion</i> <i>_SsSCS-F</i>	TTCTGCCCAAATTCGATGTCGCTCGCCTTCAAC	<i>SsSS</i>
<i>pEAQ_Infusion</i> <i>_SsSCS-R</i>	AGTTAAAGGCCTCGATCAAAAGACAAAGGATTTTCATA	
<i>pEAQ_Infusion</i> <i>_ZmAN2-F</i>	TTCTGCCCAAATTCGATGGTTCTTTCATCGTCTTGAC	<i>ZmAN2</i>
<i>pEAQ_Infusion</i> <i>_ZmAN2-R</i>	AGTTAAAGGCCTCGATTATTTGCGGCGGAAACAGGT	
<i>pEAQ_Infusion</i> <i>_CfTPS2-F</i>	TTCTGCCCAAATTCGATGAAAATGTTGATGATCAAAAGT	<i>CfTPS2</i>
<i>pEAQ_Infusion</i> <i>_CfTPS2-R</i>	AGTTAAAGGCCTCGATCAGACCACTGGTTCAAATAGTA	
<i>pEAQ_Infusion</i> <i>_CfTPS3-F</i>	TTCTGCCCAAATTCGATGTCGTCCTCGCCGGCAACCT	<i>CfTPS3</i>
<i>pEAQ_Infusion</i> <i>_CfTPS3-R</i>	AGTTAAAGGCCTCGACTAGTTGCTGACACAACCTCATT	
<i>pEAQ_Infusion</i> <i>_CfTPS16-F</i>	TTCTGCCCAAATTCGATGCAGGCTTCTATGTCATCT	<i>CfTPS16</i>
<i>pEAQ_Infusion</i> <i>_CfTPS16-R</i>	AGTTAAAGGCCTCGATCATACGACTGGTTCAAACATT	
<i>pEAQ_Infusion</i> <i>_LITPS1-F</i>	TTCTGCCCAAATTCGATGGCCTCCACTGCATCC	<i>LITPS1</i>
<i>pEAQ_Infusion</i> <i>_LITPS1-R</i>	AGTTAAAGGCCTCGATCATTCAACTGGTTCGAACAA	
<i>pEAQ_Infusion</i> <i>_LITPS2-F</i>	TTCTGCCCAAATTCGATGATTCCCTAATCCCGAAA	<i>LITPS2</i>
<i>pEAQ_Infusion</i> <i>_LITPS2-R</i>	AGTTAAAGGCCTCGATTACATTGGCAATCCGATGAA	
<i>pEAQ_Infusion</i> <i>_LITPS4-F</i>	TTCTGCCCAAATTCGATGTCGGTGGCGTTCAACCT	<i>LITPS4</i>
<i>pEAQ_Infusion</i> <i>_LITPS4-R</i>	AGTTAAAGGCCTCGATCAAGAGGATGATTCATGTACC	
<i>pEAQ_Infusion</i> <i>_SoTPS1-F</i>	TTCTGCCCAAATTCGATGTCCTCGCCTTCAACG	<i>SoTPS1</i>
<i>pEAQ_Infusion</i> <i>_SoTPS1-R</i>	AGTTAAAGGCCTCGATCATTGCCACTCACATTT	
<i>pEAQ_Infusion</i> <i>_ArTPS1-F</i>	TTCTGCCCAAATTCGATGGCCTCTTTGTCCACTTTCC	<i>ArTPS1</i>
<i>pEAQ_Infusion</i> <i>_ArTPS1-R</i>	AGTTAAAGGCCTCGATCACGCAACTGGTTCGAAAAGA	
<i>pEAQ_Infusion</i> <i>_ArTPS2-F</i>	TTCTGCCCAAATTCGATGTCATTTGCTTCCCAAGCCAC	<i>ArTPS2</i>
<i>pEAQ_Infusion</i> <i>_ArTPS2-R</i>	AGTTAAAGGCCTCGACTAGACTACCTTCTCAAACAATAC	
<i>pEAQ_Infusion</i> <i>_ArTPS3-F</i>	TTCTGCCCAAATTCGATGTCACTCTCGTTCACCATCA	<i>ArTPS3</i>
<i>pEAQ_Infusion</i> <i>_ArTPS3-R</i>	AGTTAAAGGCCTCGATCAAGAGGATGAAGTGTTTAG	

<i>pEAQ_Infusion_PaTPS1-F</i>	TTCTGCCCAAATTCGATGACCTCTATGTCCTCTCTAA	<i>PaTPS1</i>
<i>pEAQ_Infusion_PaTPS1-R</i>	AGTTAAAGGCCTCGATCATACGACCGGTCCAAACAGT	
<i>pEAQ_Infusion_PaTPS3-F</i>	TTCTGCCCAAATTCGATGTTACTTGC GTTCAACATAAGC	<i>PaTPS3</i>
<i>pEAQ_Infusion_PaTPS3-R</i>	AGTTAAAGGCCTCGATTAATTAGGTAGGTAGAGGGGTT	
<i>pEAQ_Infusion_NmTPS1-F</i>	ATATTCTGCCCAAATTCGATGACTTCAATATCCTCTCTAAATTTGAGCAATG	<i>NmTPS1</i>
<i>pEAQ_Infusion_NmTPS1-R</i>	CAGAGTTAAAGGCCTCGATCAGACGACCGGTCCAA	
<i>pEAQ_Infusion_NmTPS2-F</i>	TTCTGCCCAAATTCGATGTCTCTTCCGCTCTCCTCT	<i>NmTPS2</i>
<i>pEAQ_Infusion_NmTPS2-R</i>	GATAAGTTAAAGGCCTCGATTATTCATGCACCTTAAAATCCTTGAGAGC	
<i>pEAQ_Infusion_OmTPS1-F</i>	TTCTGCCCAAATTCGATGACCGATGTATCCTCTCTTC	<i>OmTPS1</i>
<i>pEAQ_Infusion_OmTPS1-R</i>	AGTTAAAGGCCTCGATCACATAACCGGCCCAAACA	
<i>pEAQ_Infusion_OmTPS3-F</i>	TTCTGCCCAAATTCGATGGCGTCGCTCGCGTTCAC	<i>OmTPS3</i>
<i>pEAQ_Infusion_OmTPS3-R</i>	AGTTAAAGGCCTCGACTACAAGGATTCATAAATTAAGGA	
<i>pEAQ_Infusion_OmTPS4-F</i>	TTCTGCCCAAATTCGCGAATGTCACTCGCCTTCAGC	<i>OmTPS4</i>
<i>pEAQ_Infusion_OmTPS4-R</i>	AGTTAAAGGCCTCGAGCTAGGAGCTTAGGGTTTTTCAT	
<i>pEAQ_Infusion_OmTPS5-F</i>	TTCTGCCCAAATTCGATGGTATCTGCATGTCTAAA	<i>OmTPS5</i>
<i>pEAQ_Infusion_OmTPS5-R</i>	AGTTAAAGGCCTCGATCATGAAGGAATTGAAGGAA	
<i>pEAQ_Infusion_MsTPS1-F</i>	TTCTGCCCAAATTCGATGAGTTCCATTCGAAATTTAAGT	<i>MsTPS1</i>
<i>pEAQ_Infusion_MsTPS1-R</i>	AGTTAAAGGCCTCGATCACTTGAGAGGCTCAAACATCAT	
<i>pEAQ_Infusion_PcTPS1-F</i>	TTCTGCCCAAATTCGATGTCATTTGCTTCTCAATCAC	<i>PcTPS1</i>
<i>pEAQ_Infusion_PcTPS1-R</i>	AGTTAAAGGCCTCGACTACATCACCTCTCAAACAATAC	
<i>pEAQ_Infusion_HsTPS1-F</i>	TTCTGCCCAAATTCGATGGCGTATATGATATCTATTTCAAATCTC	<i>HsTPS1</i>
<i>pEAQ_Infusion_HsTPS1-R</i>	AGTTAAAGGCCTCGATCAGACAATGGGCTCAAATAGAAC	
<i>pEAQ_Infusion_EpTPS8-F</i>	TTCTGCCCAAATTCGATGCAAGTCTCTCTCTCCCTCA	<i>EpTPS8</i>
<i>pEAQ_Infusion_EpTPS8-R</i>	AGTTAAAGGCCTCGATTATGAAGTTAAAAGGAGTGGTT	
<i>pEAQ_Infusion_PVTPS1-F</i>	TTCTGCCCAAATTCGCGAATGTCACTCACTTTCAACG	<i>PVTPS1</i>
<i>pEAQ_Infusion_PVTPS1-R</i>	AGTTAAAGGCCTCGAGCTAGTTTCTCACAGAAGTCAA	
Cloning of diTPS genes into pET-28 b (+) for E. coli expression		

<i>pET28_CfTPS1</i> -F	AGGAGATATAACCATGGCCGAGATTTCGAGTTGCCAC	<i>CfTPS1</i>
<i>pET28_CfTPS1</i> -R	GGTGGTGGTGCTCGAAGGCGACTGGTTCGAAAAGTAC	
<i>pET28_SsSS-F</i>	AGGAGATATAACCATGGATTTTCATGGCGAAAATGAAAGAGA	<i>SsSS</i>
<i>pET28_SsSS-R</i>	GGTGGTGGTGCTCGAAAAGACAAAGGATTTTCATAT	
<i>pET28_CfTPS2</i> -F	AGGAGATATAACCATGCAAATTCGTGGAAAGCAAAGATCAC	<i>CfTPS2</i>
<i>pET28_CfTPS2</i> -R	GGTGGTGGTGCTCGAAGACCACTGGTTCAAATAGAACT	
<i>pET28_CfTPS3</i> -F	AGGAGATATAACCATGTCTAAATCATCTGCAGCTGT	<i>CfTPS3</i>
<i>pET28_CfTPS3</i> -R	GGTGGTGGTGCTCGAAGTTGCTGACACAACCTCATT	
<i>pET28_OmTPS</i> 3-F	AGGAGATATAACCATGACCGTCAAATGCTAC	<i>OmTPS3</i>
<i>pET28_OmTPS</i> 3-R	GGTGGTGGTGCTCGAACAAGGATTCATAAATTAAG	
<i>pET28_OmTPS</i> 5-F	AGGAGATATAACCATGACTGTCAAGTGCAGC	<i>OmTPS5</i>
<i>pET28_OmTPS</i> 5-R	GGTGGTGGTGCTCGAATGAAGGAATTGAAG	
<i>pET28_PcTPS</i> 1-F	AGGAGATATAACCATGTTTATGCCCACTTCCATTAAATGTA	<i>PcTPS1</i>
<i>pET28_PcTPS</i> 1-R	GGTGGTGGTGCTCGAACATCACCTCTCAAACAATACTTTGG	
<i>pET28_HsTPS</i> 1-F	AGGAGATATAACCATGGTAGCAAAAAGTGATCGAGAGCCGAGTTA	<i>HsTPS1</i>
<i>pET28_HsTPS</i> 1-R	GGTGGTGGTGCTCGAAGACAATGGGCTCAAATAGAACTTTAAAT	

Table S2. List of synthetic oligonucleotides used in this study.

	CfTPS1 [31]		CfTPS2 [10]		LITPS1 [5]		ZmAN2 [16]		HsTPS1 [21]		PcTPS1 [25]		ArTPS2 [38]		OmTPS1 [31]	
	products	figure	products	figure	products	figure	products	figure	products	figure	products	figure	products	figure	products	figure
<i>ArTPS3</i>	32	S-3A	8	S-4B	1, 2, 3	S-5A	np	S-6B	-		-		-	-	-	
<i>LITPS4</i>	27	S-3A	8	S-4A	1, 2, 3	S-5B	np	S-6A	-		-		-		-	
<i>MsTPS1</i>	27	S-3A	8	S-4C	3	S-5A	np	S-6A	-		-		np	S-8A	-	
<i>NmTPS2</i>	np	S-3D	np	S-4D	np	S-5D	19	S-6A	-		-		np	S-8A	-	
<i>OmTPS3</i>	34	S-3A	11	S-4D,E	1, 2	S-5A	np	S-6A	24	S-8B	-		np	S-8A	34	S-3C
<i>OmTPS4</i>	33	S-3A	8	S-4C	1, 2, 3, 4	S-5D	20	S-6A	-		-		-		33	S-3C
<i>OmTPS5</i>	29	S-3A	8	S-4A	1, 2, 3	S-5A	np	S-6A	-		-		np	S-8A	29	S-3C
<i>PaTPS3</i>	32	S-3B	8	S-4B	1, 2, 3	S-5C	np	S-6B	-		-		-		-	
<i>PvTPS1</i>	32	S-3B	8	S-4B	1, 2, 3	S-5C	np	S-6B	-		-		-		-	
<i>SoTPS1</i>	32	S-3B	8	S-4B	1, 2, 3	S-5D	np	S-6B	-		-		-		-	
<i>CfTPS3</i>	32		8		1, 2, 3		np		22	S-8B	np	S-8C	np		32	S-7D
<i>SsSS</i>	33		-		4		20		23	S-8B	26	S-8C	37	S-8A	-	

Table S3. Index of class I diTPS functional assays by *N. benthamiana* transient expression. Bold umbers refer to compound numbers; “np” indicates that the combination was tested but no product was detected; “-” indicates that the combination was not tested. Blue genes are new to this study.

	Product	Figure
ArTPS1	Copalyl-PP [31]	S-7A
CfTPS16	Copalyl-PP [31]	S-7B
NmTPS1	Copalyl-PP [31]	S-7C
OmTPS1	Copalyl-PP [31]	S-7D
PaTPS1	Copalyl-PP [31]	S-7A
ArTPS2	Neo-cleroda-4(18),13E-dienyl-PP [38]	S-8A
HsTPS1	Labda-7,13E-dienyl-PP [21]	S-8B
LITPS1	Peregrinol-PP [7]	S-5B
PcTPS1	Ent-labda-8,13E-dienyl-PP [25]	S-8C

Table S4. Index of class II diTPS functional assays by *N. benthamiana* transient expression. Blue genes are new to this study.

Class II	Class I	Product	Figure
CfTPS1 [31]	OmTPS3	trans-biformene [34]	S-9C
CfTPS2 [10]	OmTPS3	trans-abienol [11]	S-9D
HsTPS1 [21]	OmTPS3	[24]	S-9B
CfTPS1 [31]	OmTPS5	palustradiene [29]	S-9E
ArTPS2 [38]	SsSS	[37]	5A
HsTPS1 [21]	SsSS	[23]	S-9A
PcTPS1 [25]	SsSS	[26]	5B

Table S5. Index of *in-vitro* assays. Blue genes are new to this study.



Figure S1. An example of skeleton extraction. By deleting all heteroatoms, desaturation, and stereochemistry, the labdane skeleton is extracted from the forskolin structure.

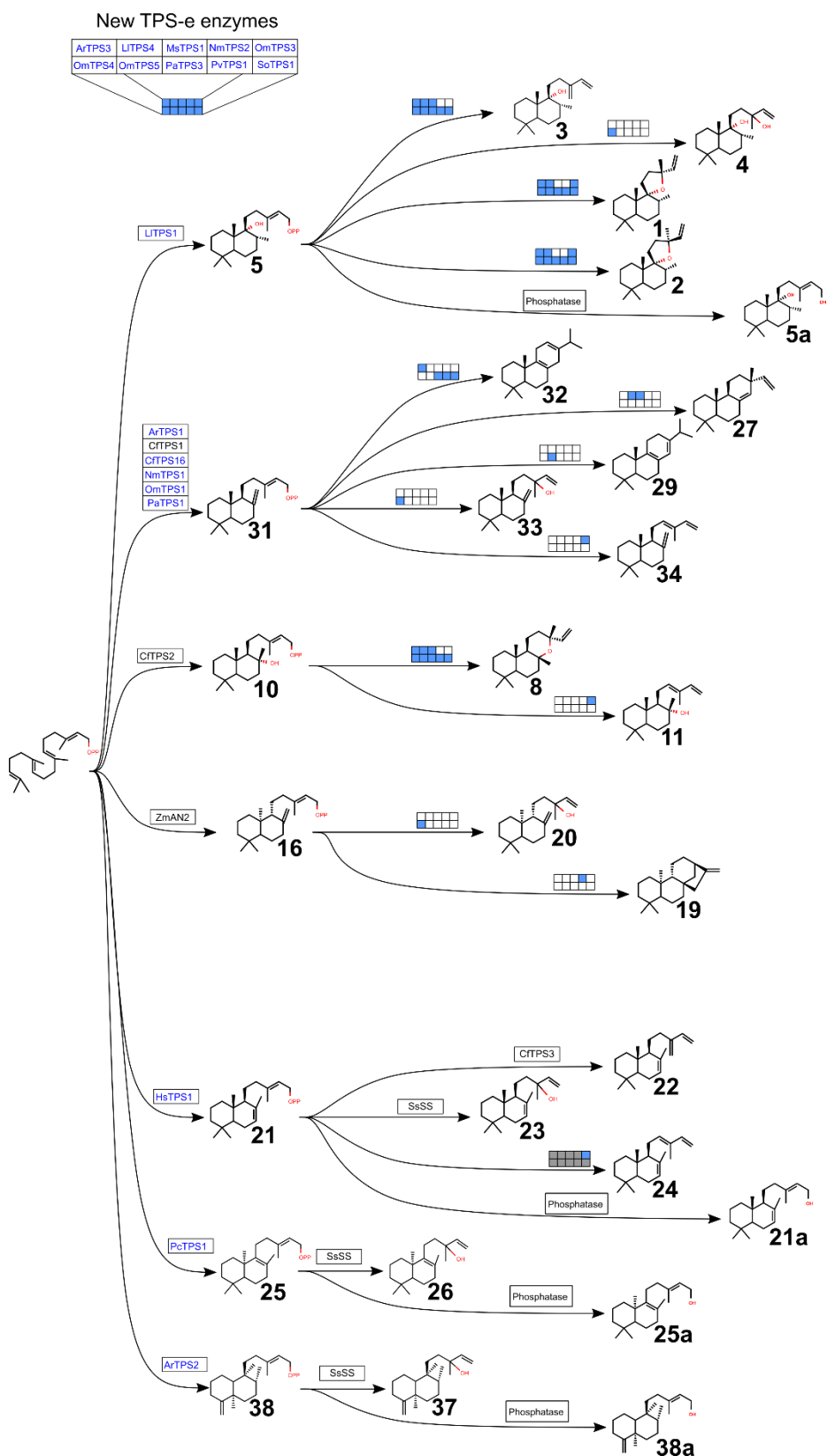


Figure S2. Newly characterized enzyme activities. Blue genes are newly characterized. Blue square: TPS-e from that position on the key catalyzes the shown transformation. White square: corresponding TPS-e does not catalyze the shown activity. Grey square: corresponding TPS-e was not tested on the substrate.

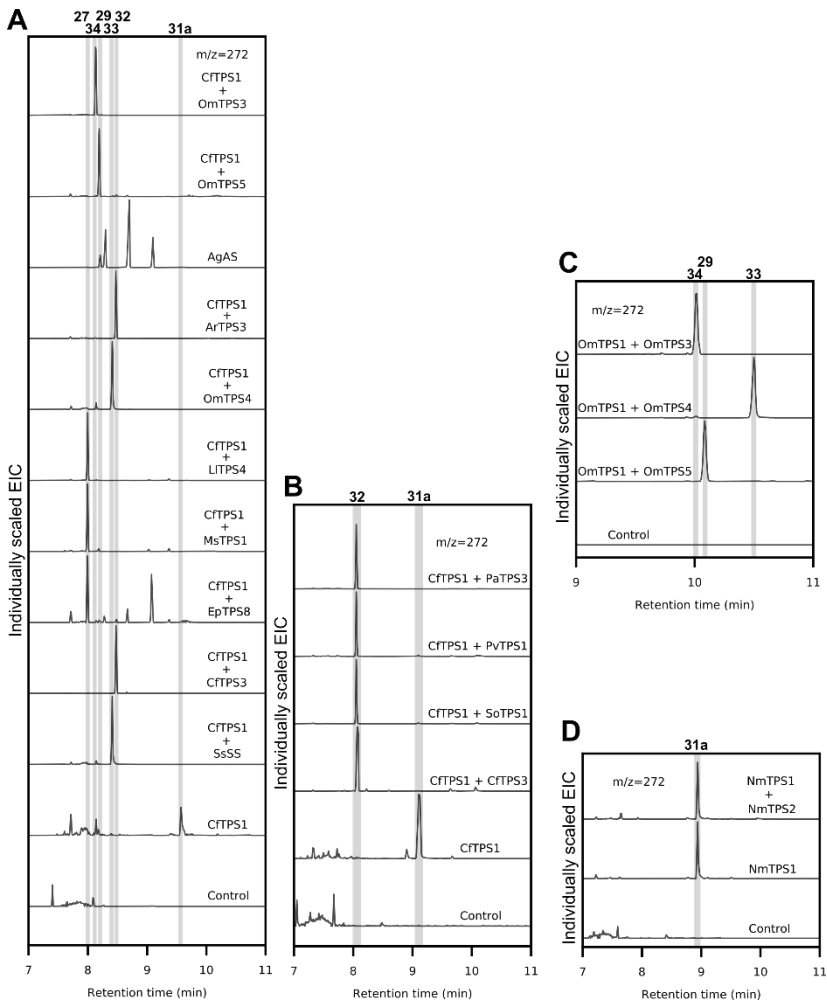


Figure S3. GC-MS chromatograms of hexane extracts from *N. benthamiana* transiently expressing (+)-CPP-producing class II diTPSs along with new class I diTPSs, and reference combinations. AgAS, *Abies grandis* abietadiene synthase; EpTPS8, *Euphorbia peplus* TPS8.

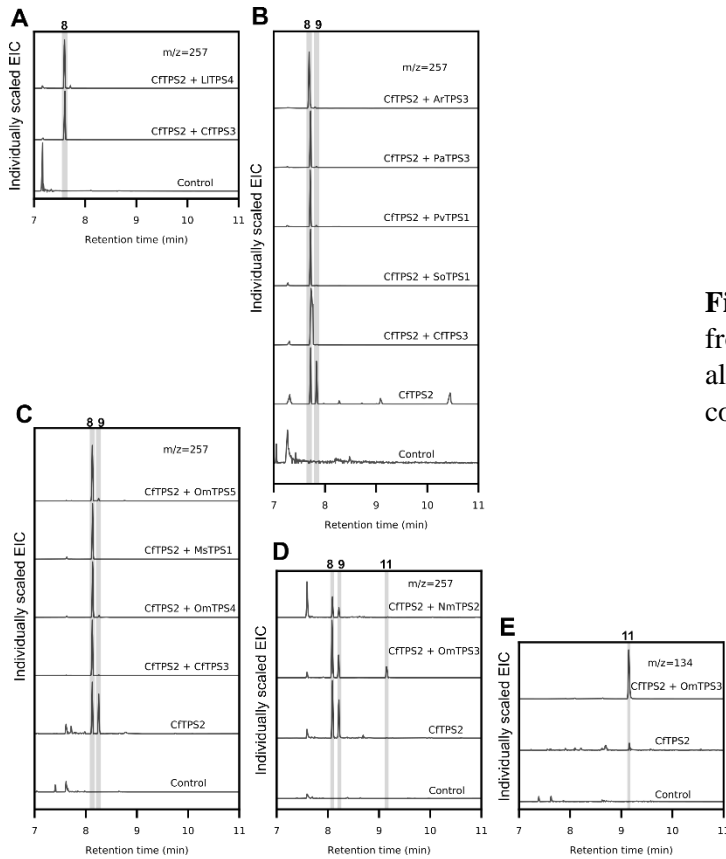


Figure S4. GC-MS chromatograms of hexane extracts from *N. benthamiana* transiently expressing CftPS2 along with new class I diTPSs, and reference combinations.

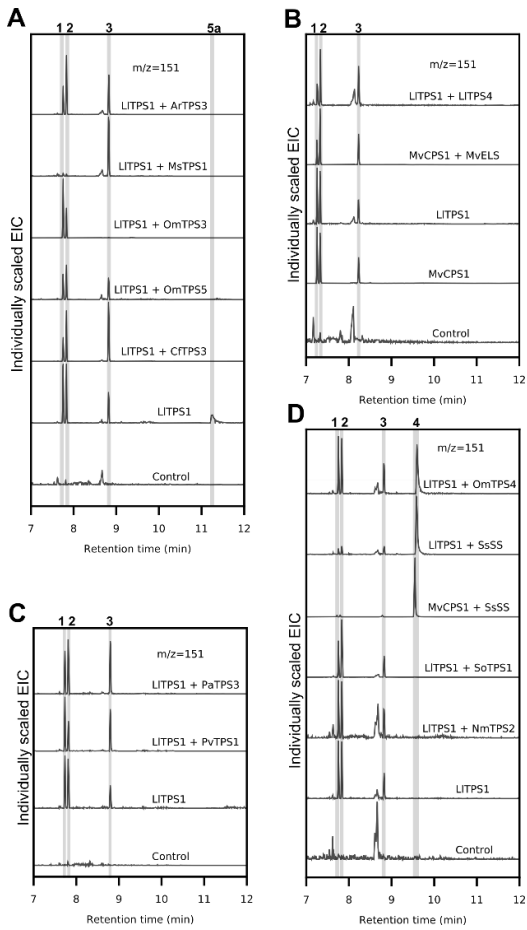


Figure S5. GC-MS chromatograms of hexane extracts from *N. benthamiana* transiently expressing LITPS1 along with new class I diTPSs, and reference combinations.



Figure S6. GC-MS chromatograms of hexane extracts from *N. benthamiana* transiently expressing ZmAN2 along with new class I diTPSs, and reference combinations.

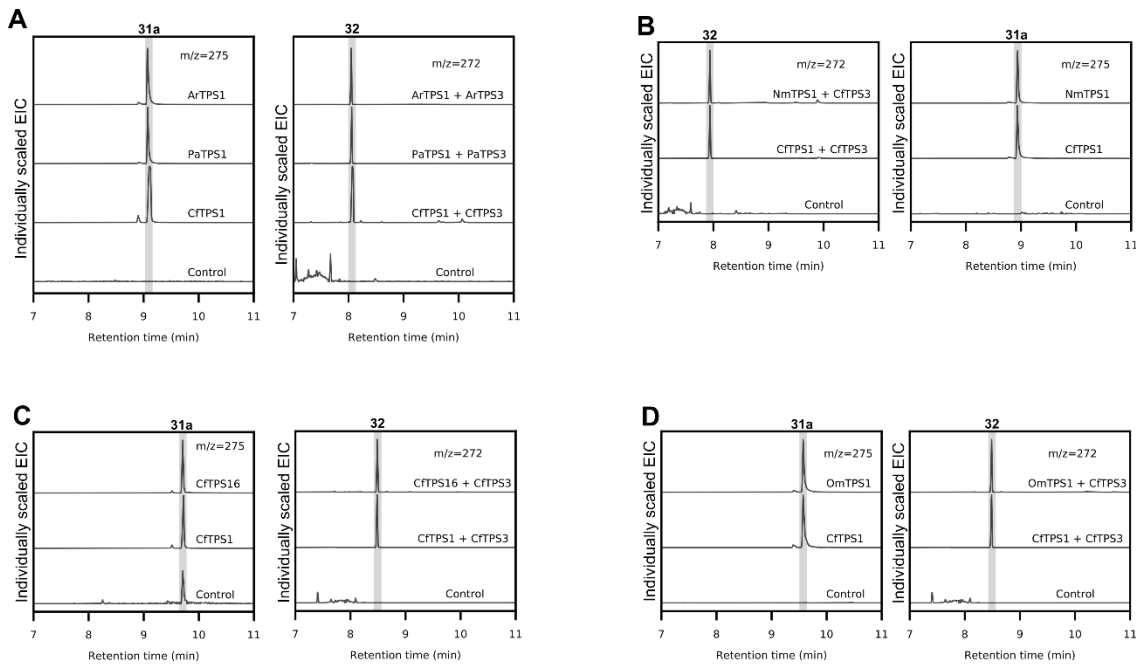


Figure S7. GC-MS chromatograms of hexane extracts from *N. benthamiana* transiently expressing new (+)-CPP synthases along with reference combinations.

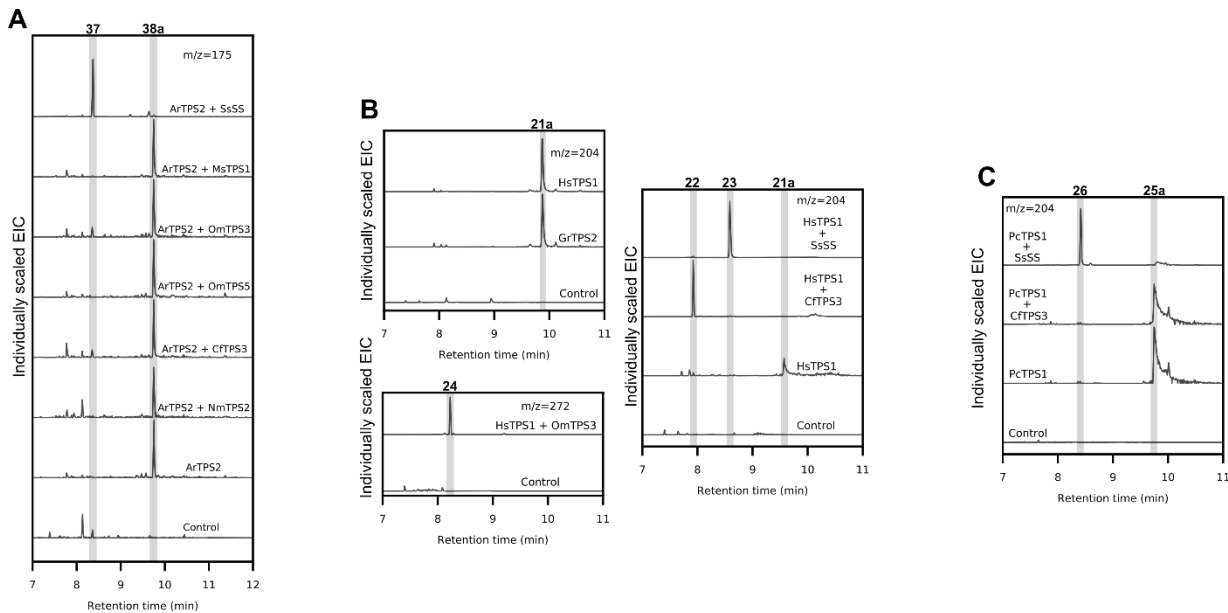


Figure S8. GC-MS chromatograms of hexane extracts from *N. benthamiana* transiently expressing new class II diTPSs, reference combinations, and combinations with new class I diTPSs.

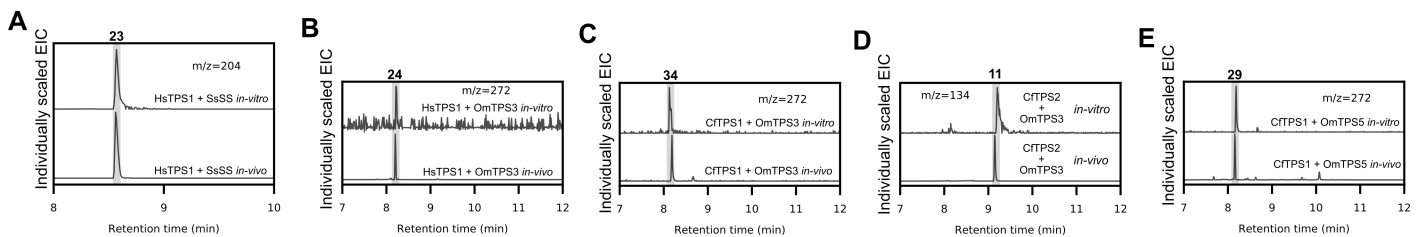


Figure S9. Comparison of GC-MS chromatograms of hexane extracts from *in-vitro* assays of purified diTPSs with extracts from *N. benthamiana* transiently expressing diTPS combinations.

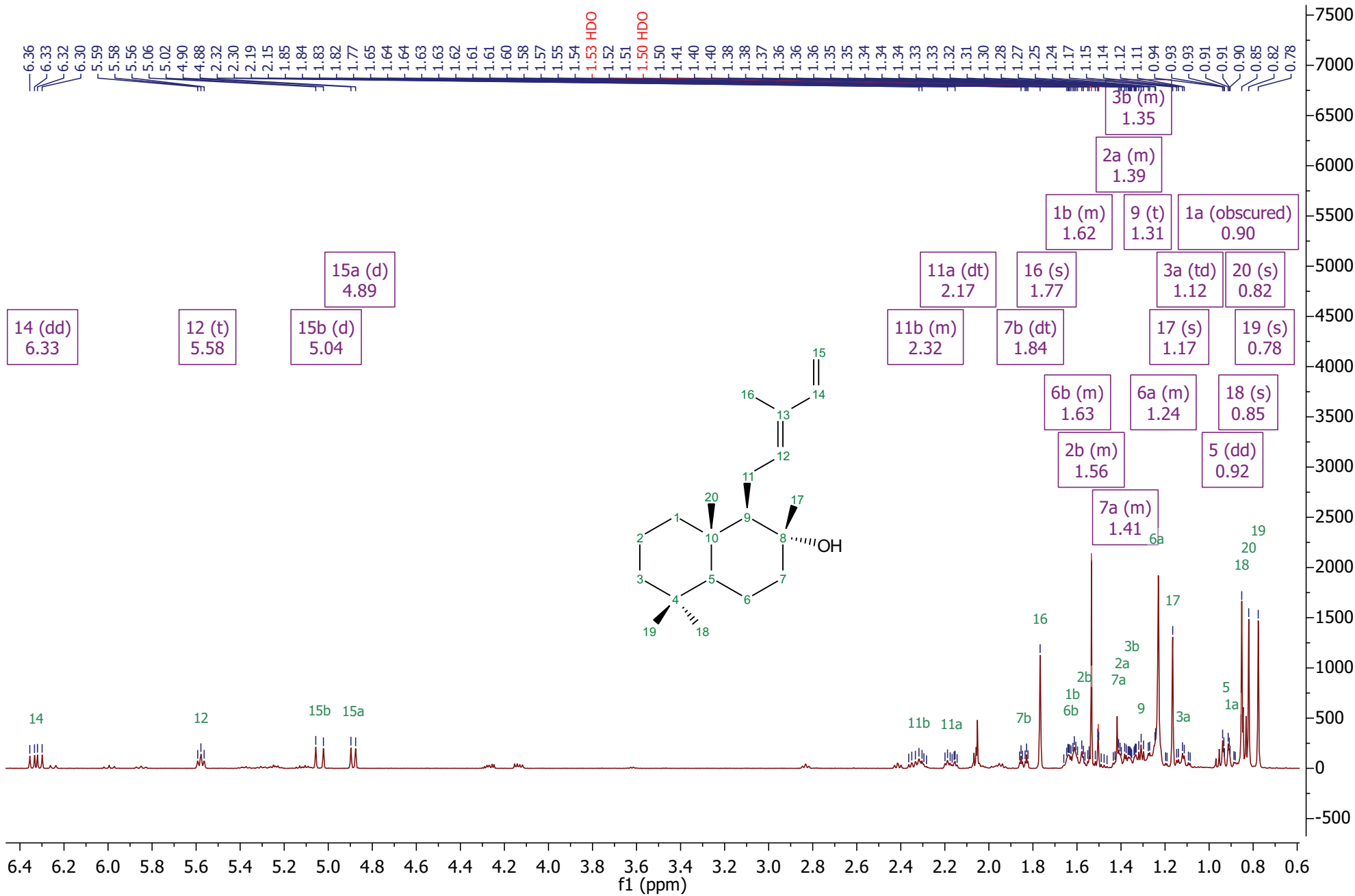


Figure S10-A. ¹H NMR of trans-abienol [11].

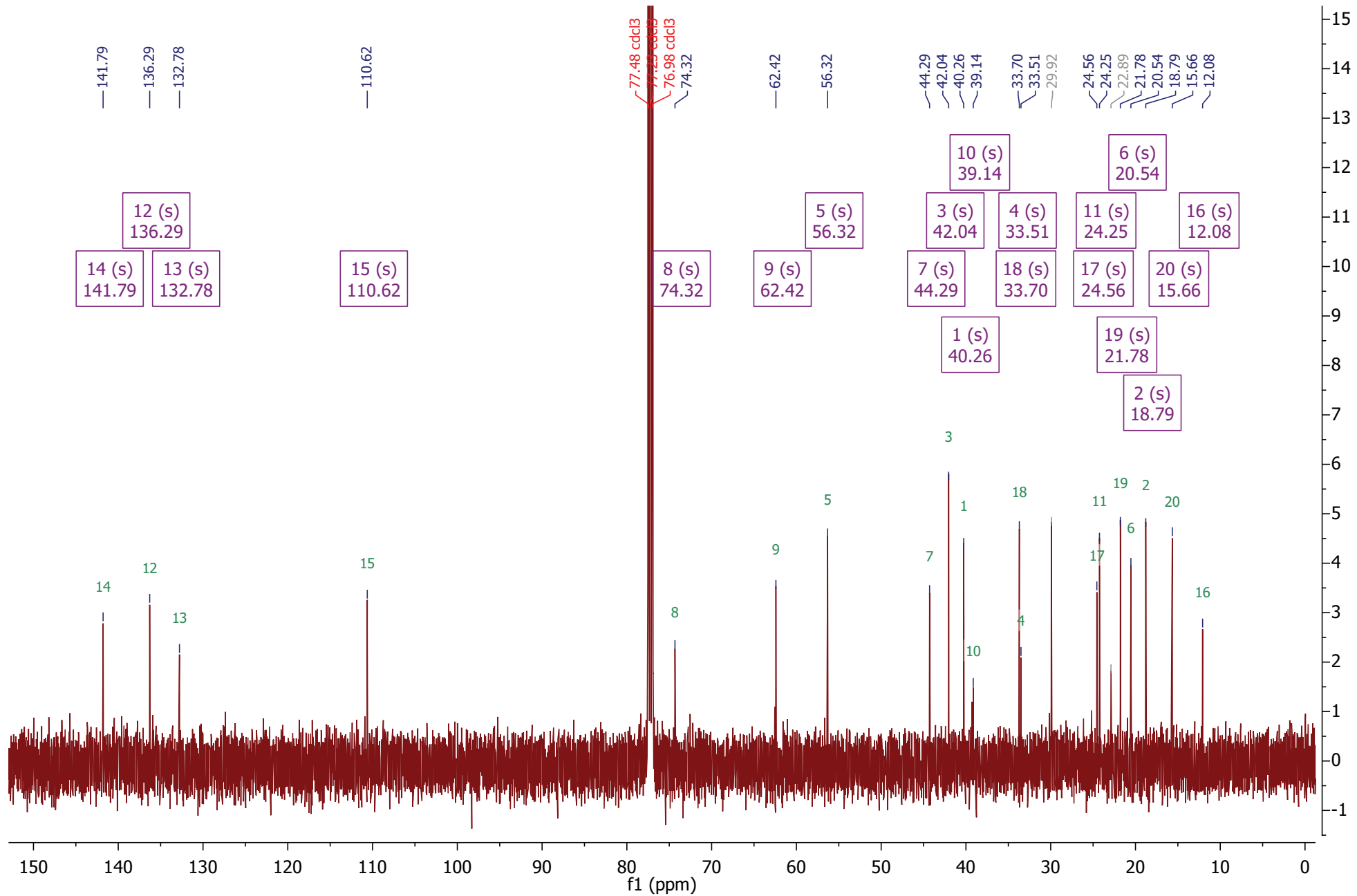


Figure S10-B. ^{13}C NMR of trans-abienol [11].

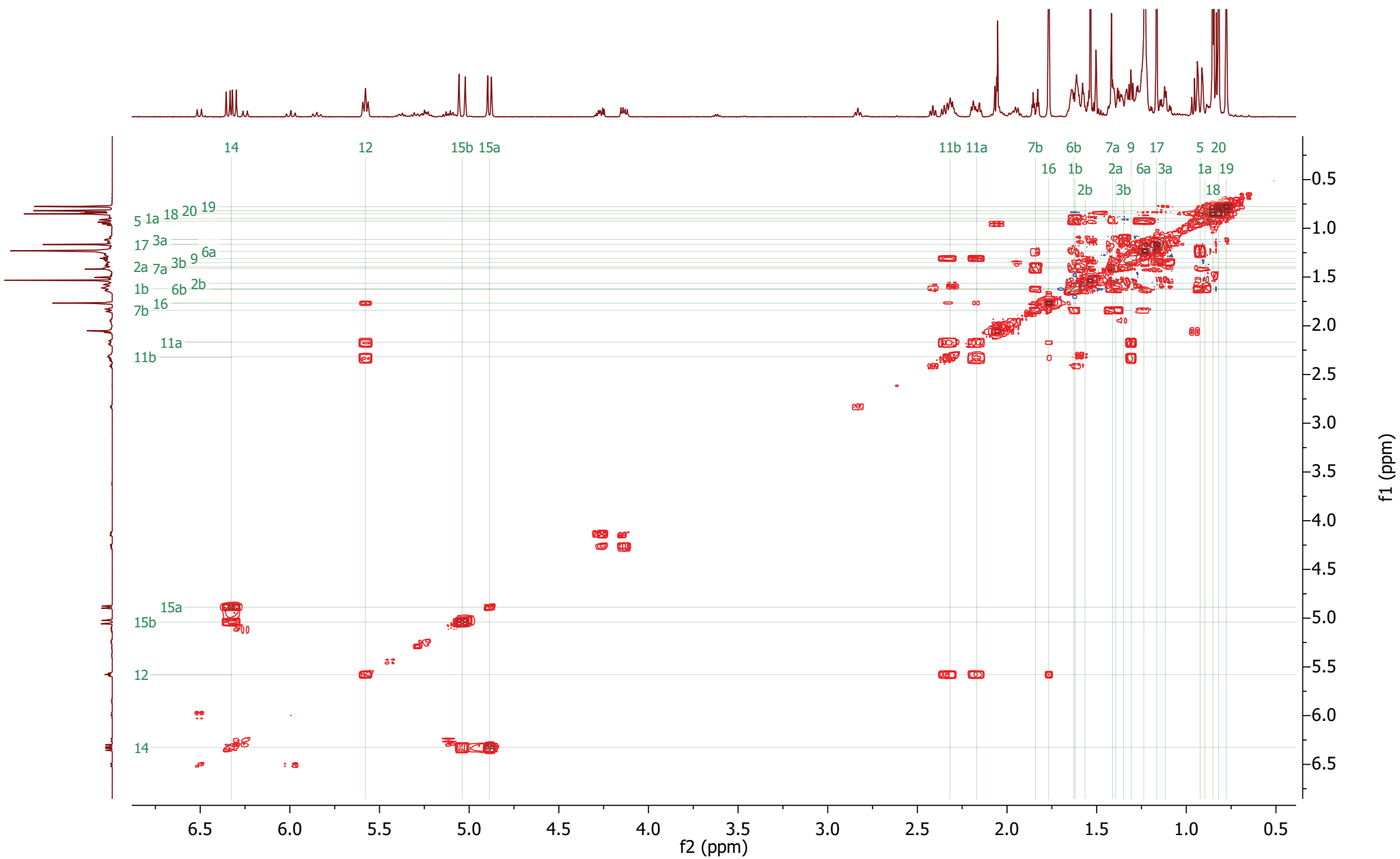


Figure S10-C. ^1H - ^1H COSY of trans-abienol [11].

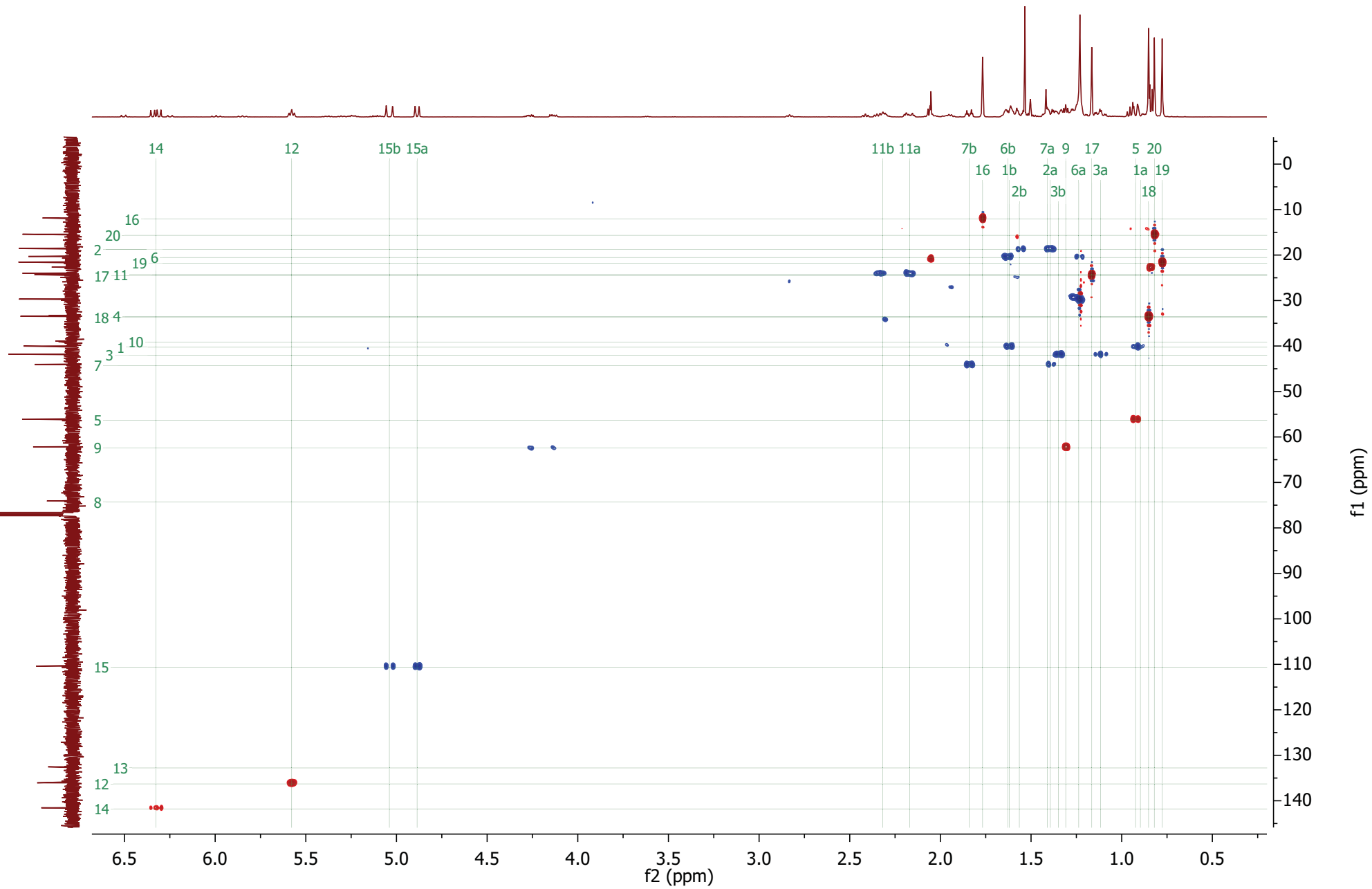


Figure S10-D. ^1H - ^{13}C HSQC of trans-abienol [11].

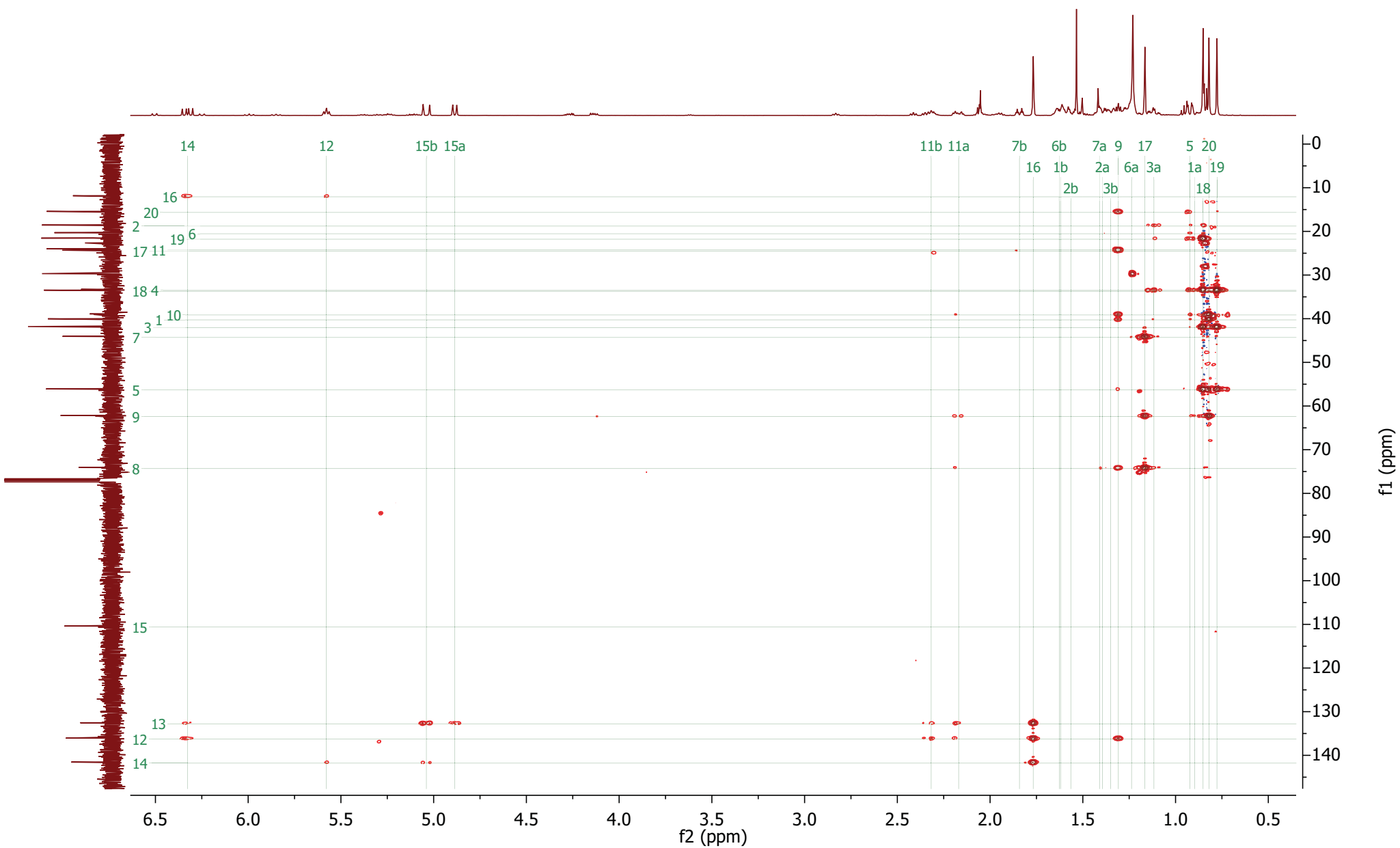


Figure S10-E. ^1H - ^{13}C HMBC of trans-abienol [11].

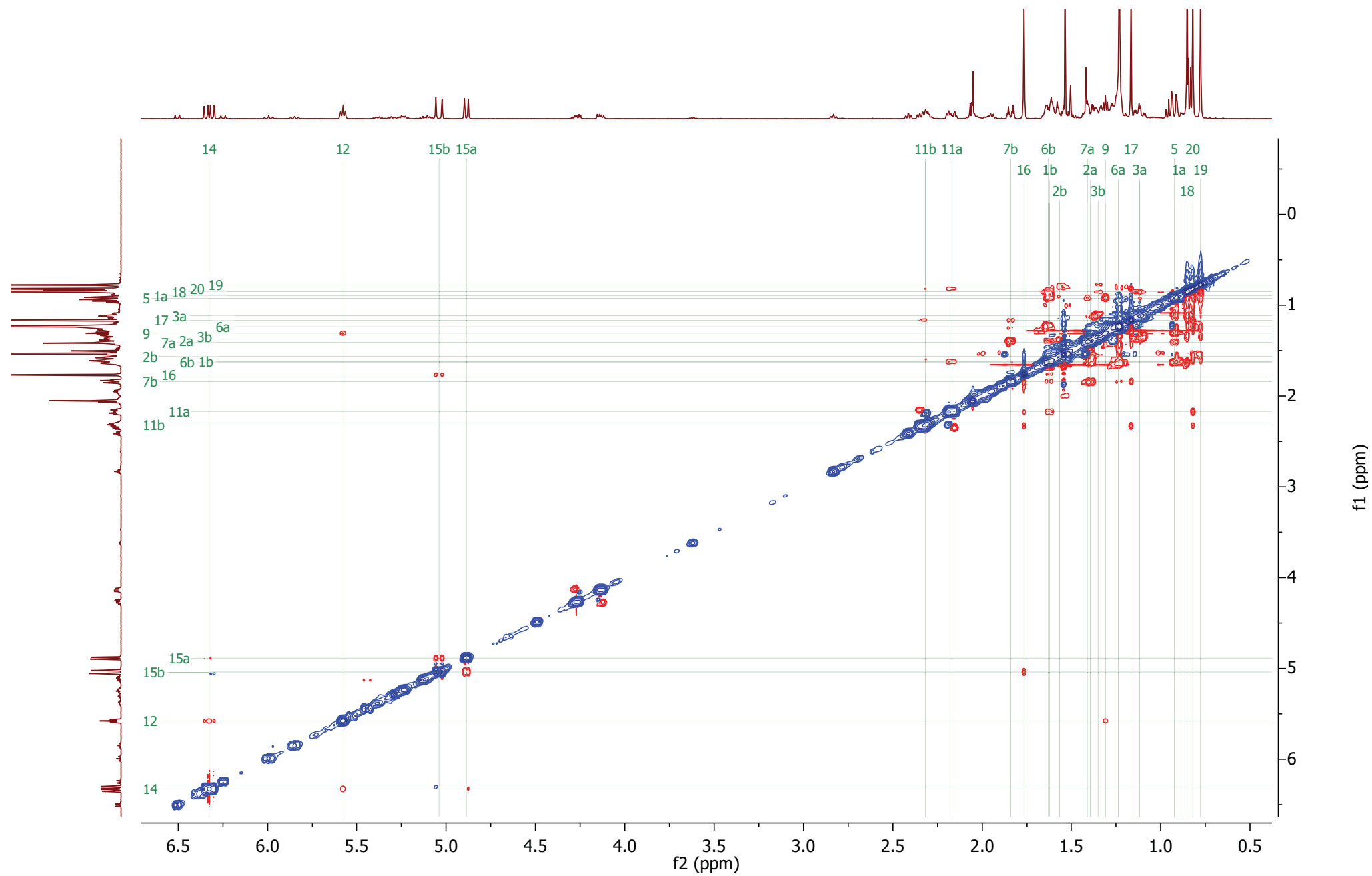


Figure S10-F. ^1H NOESY of trans-abienol [11].

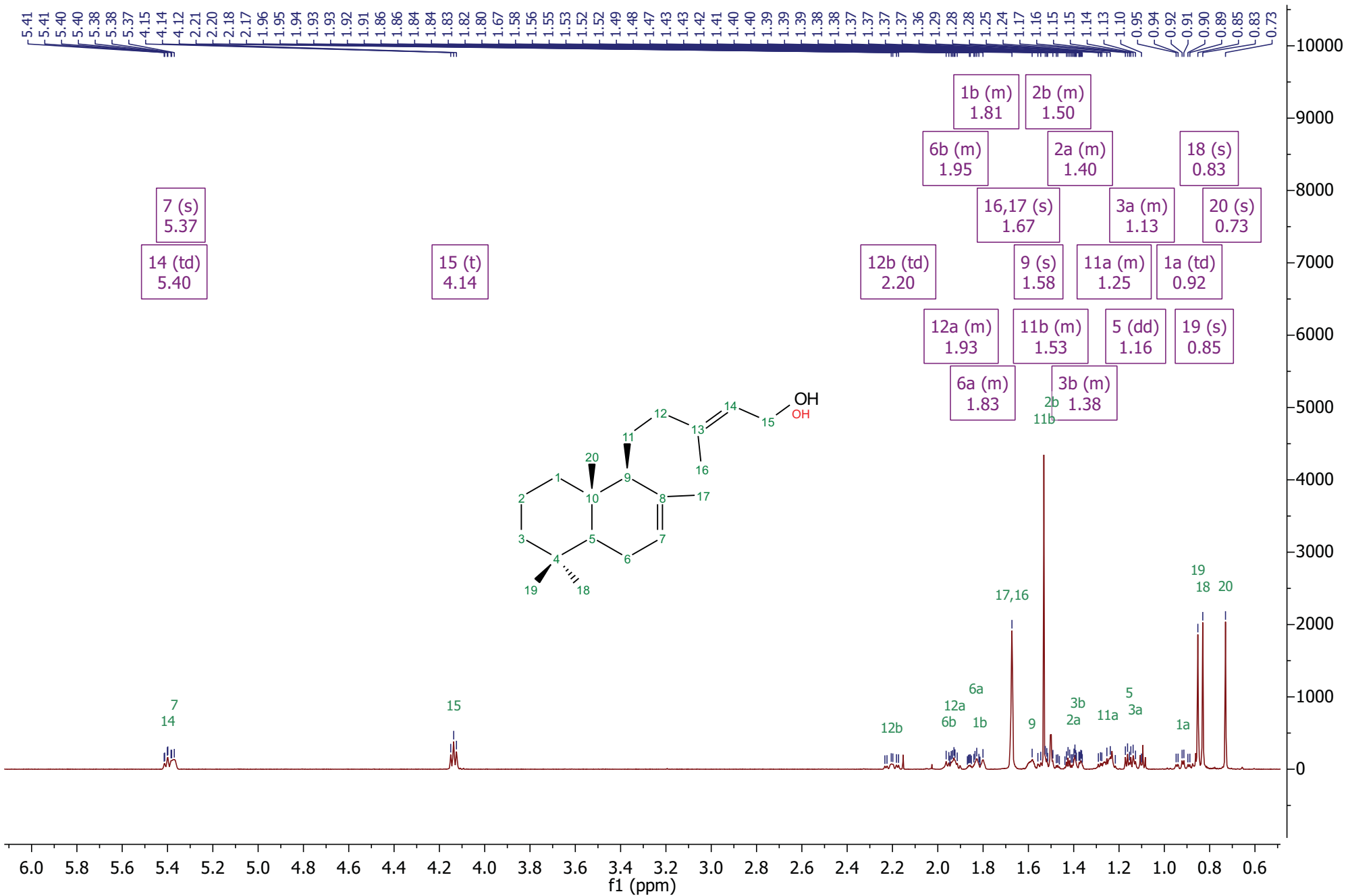


Figure S11-A. ¹H NMR of labda-7,13E-dien-15-ol [21a].

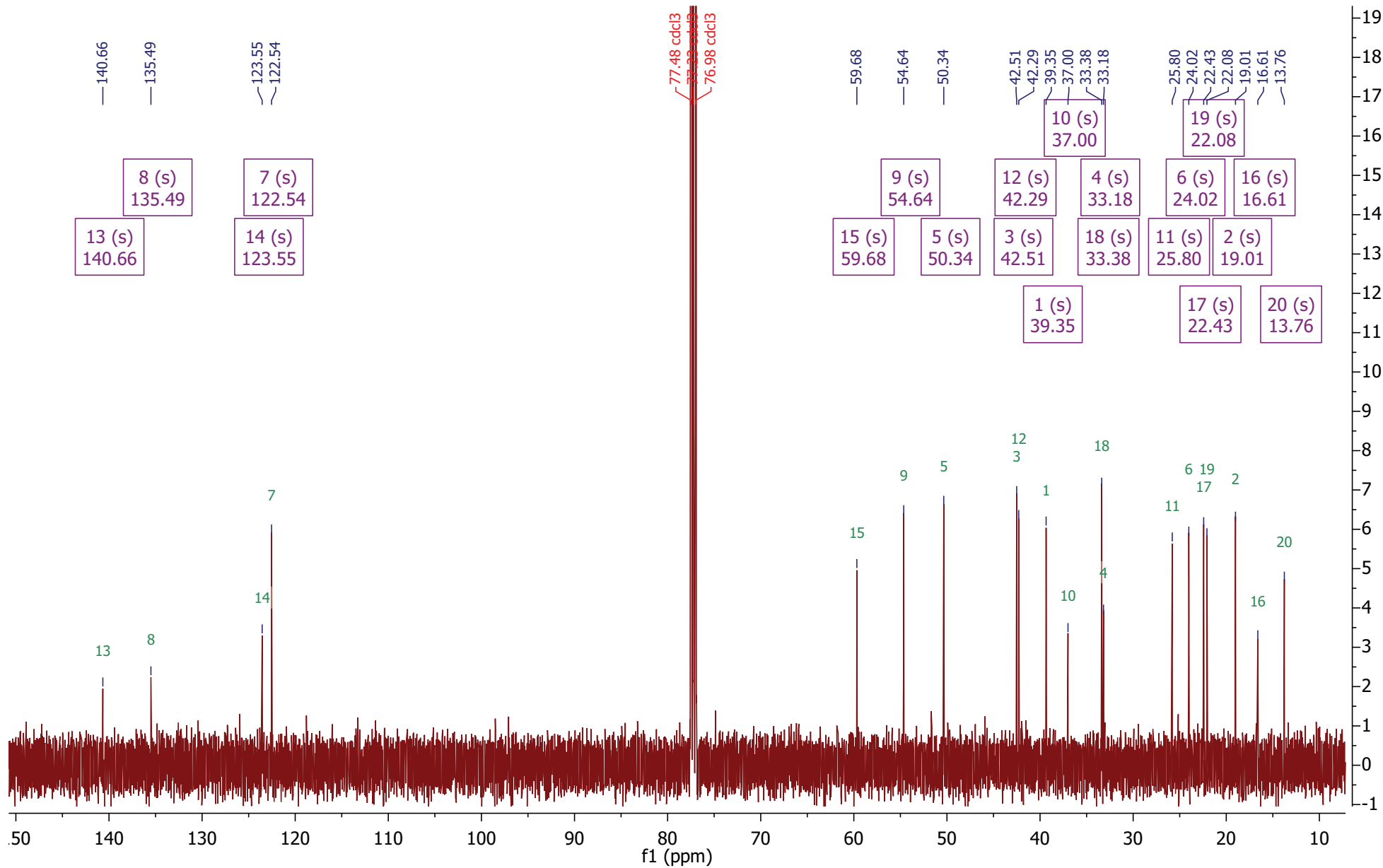
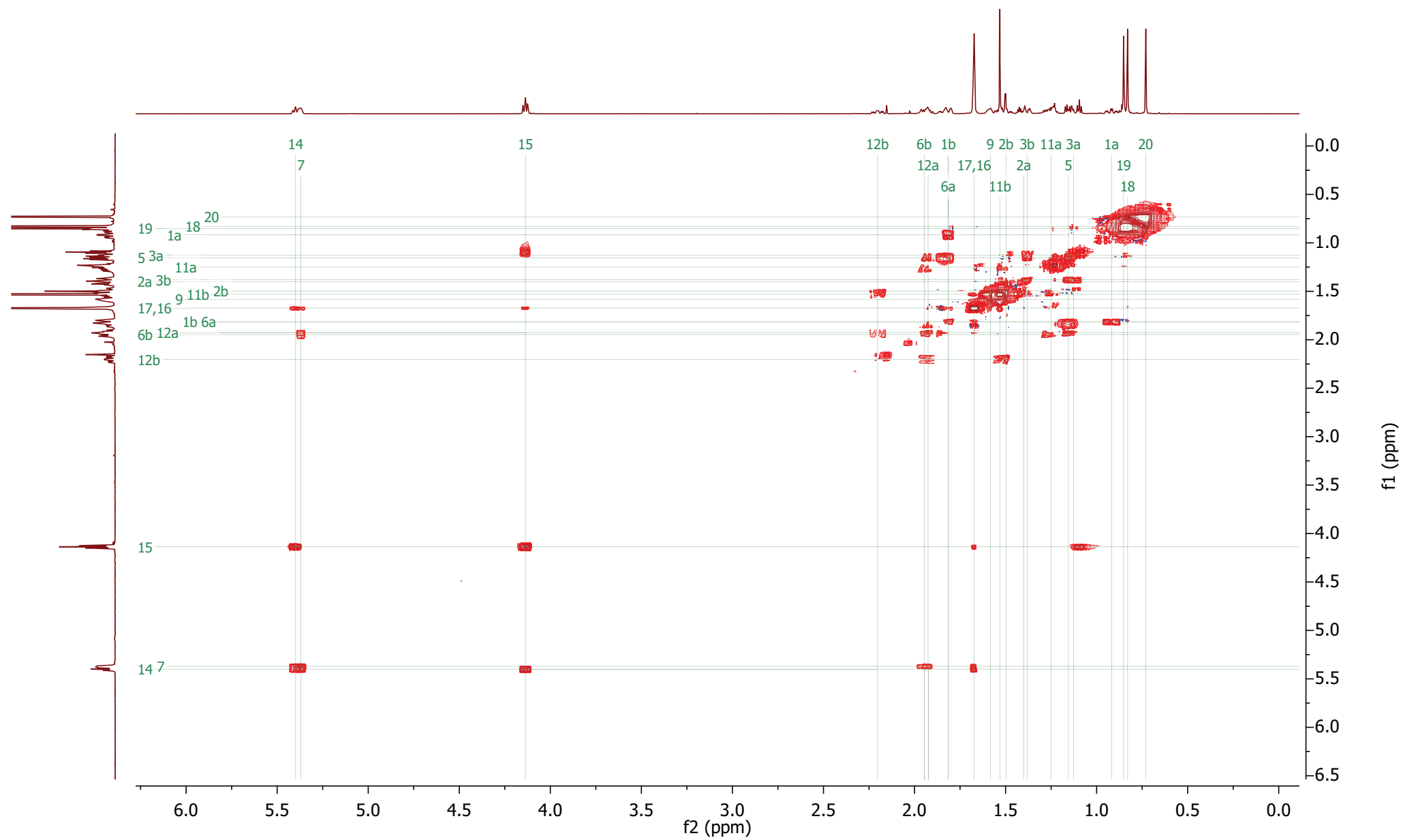
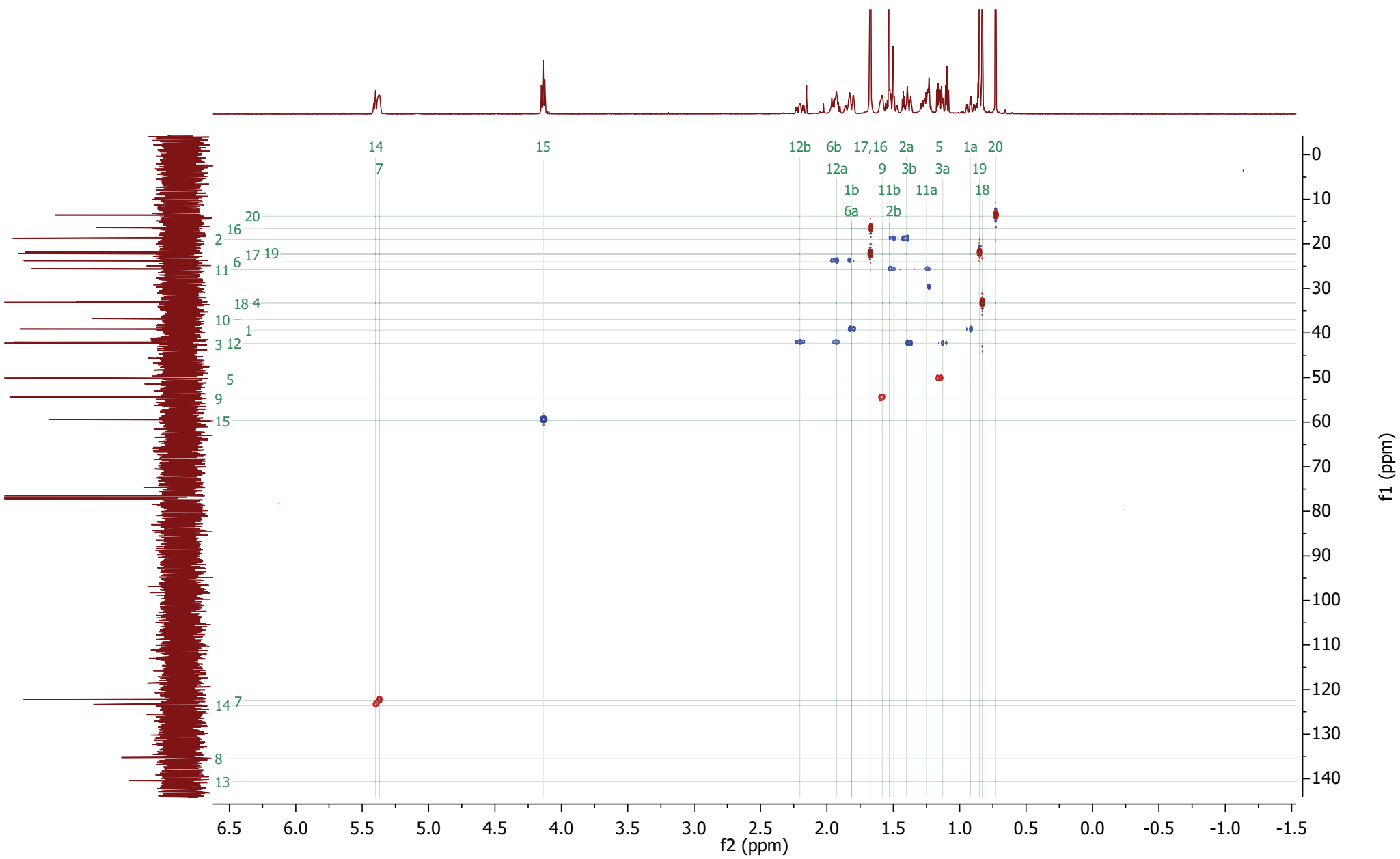


Figure S11-B. ^{13}C NMR of labda-7,13E-dien-15-ol [**21a**].





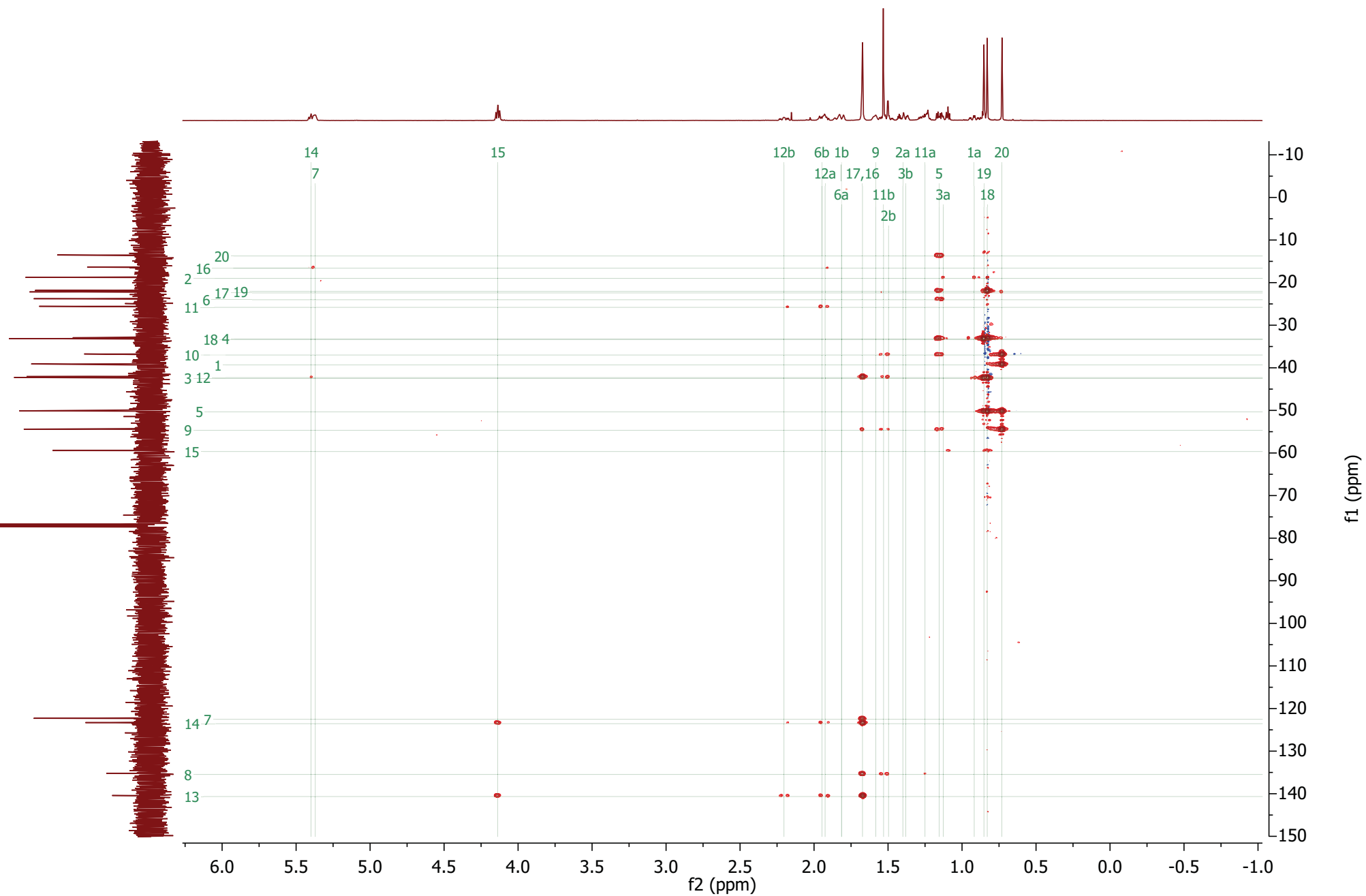


Fig S11-E. ^1H - ^{13}C HMBC of labda-7,13E-dien-15-ol [21a]

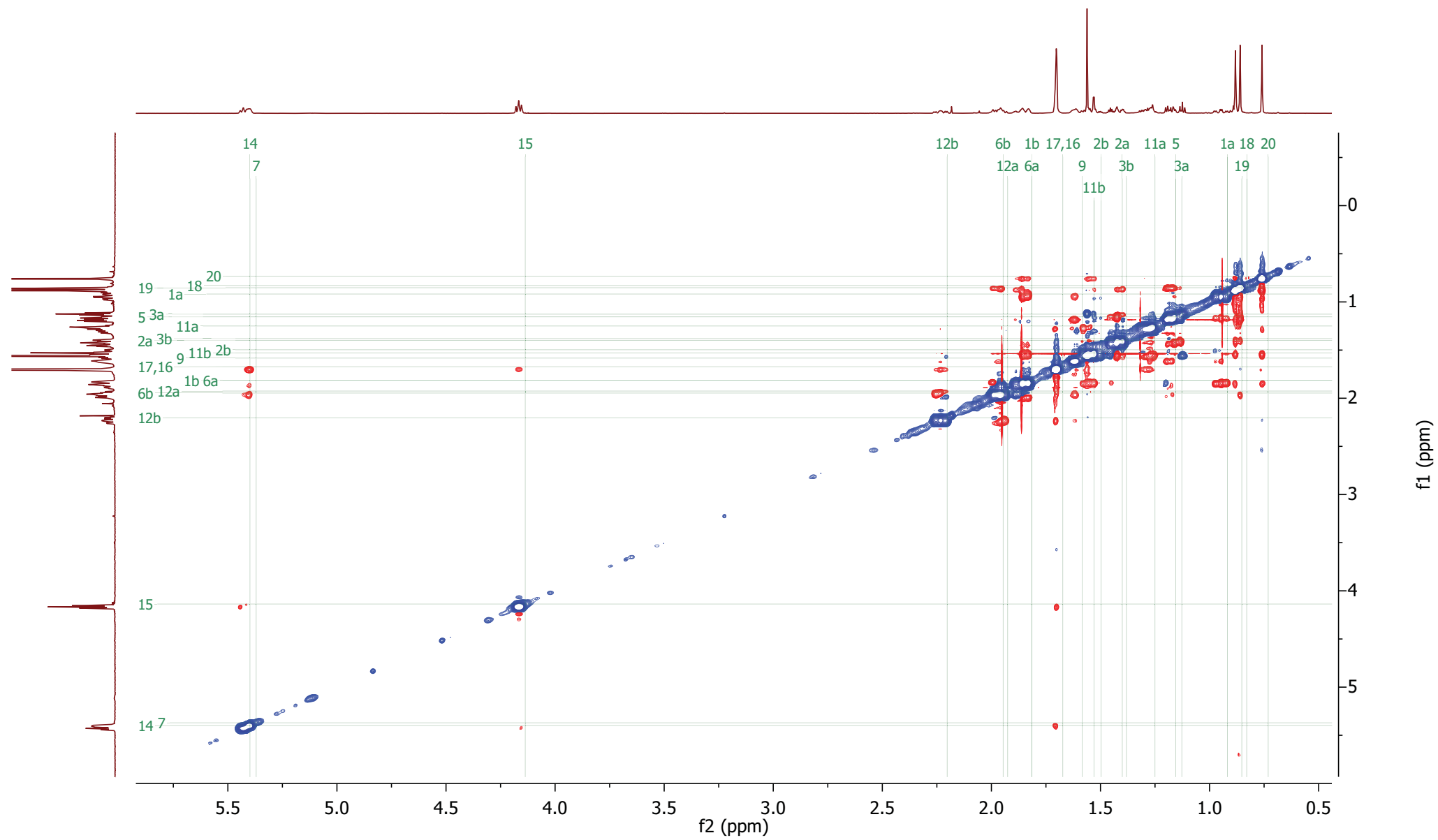


Fig S11-F. ¹H NOESY of lambda-7,13E-dien-15-ol [21a]

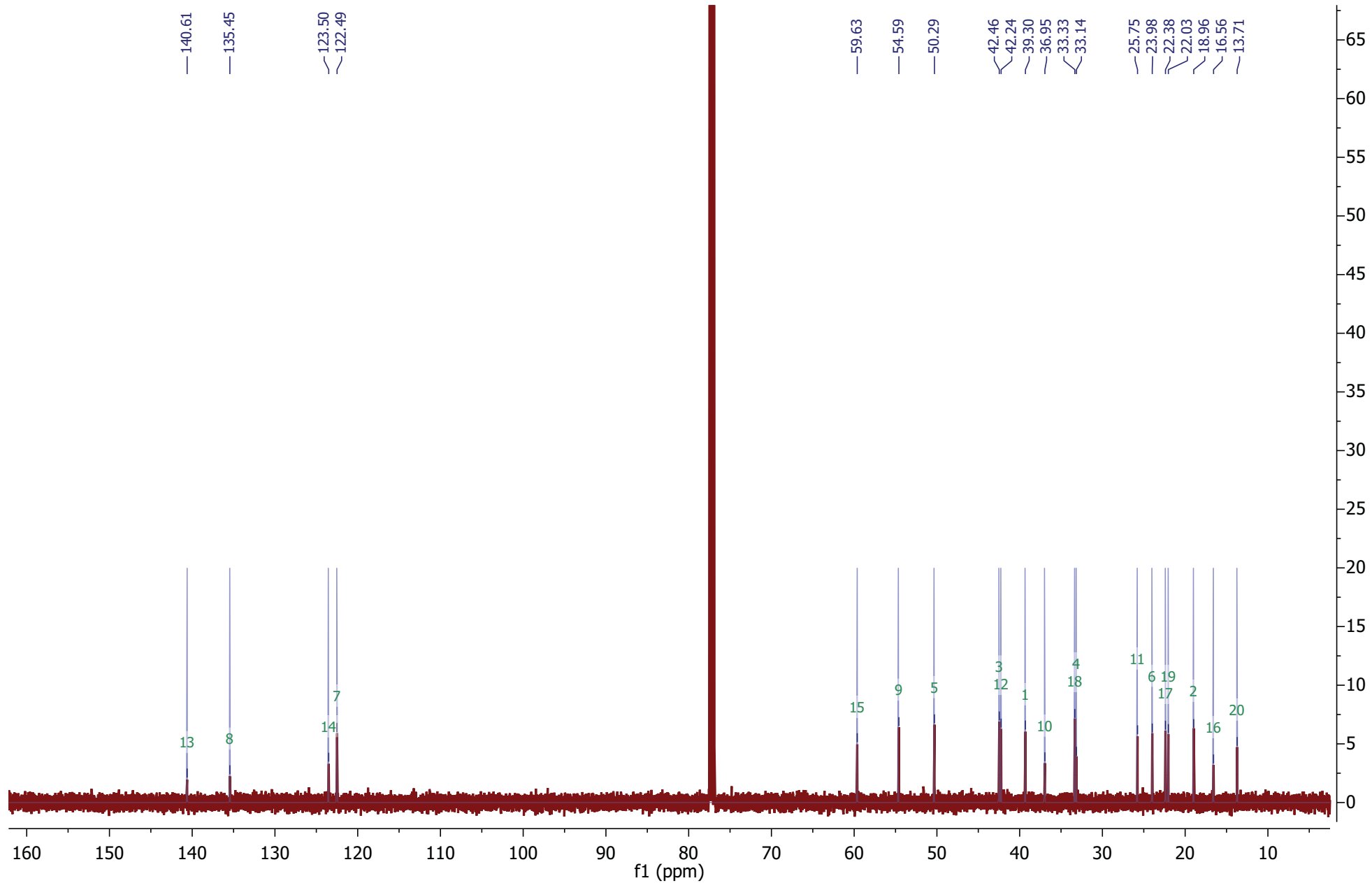


Figure S11-G. Overlay of ^{13}C NMR of labda-7,13E-dien-15-ol [**21a**] (red) with ^{13}C NMR spectrum (blue) reconstructed from shifts reported for the same compound by Mafu et al. (2011) (DOI: 10.1002/cbic.201100336).

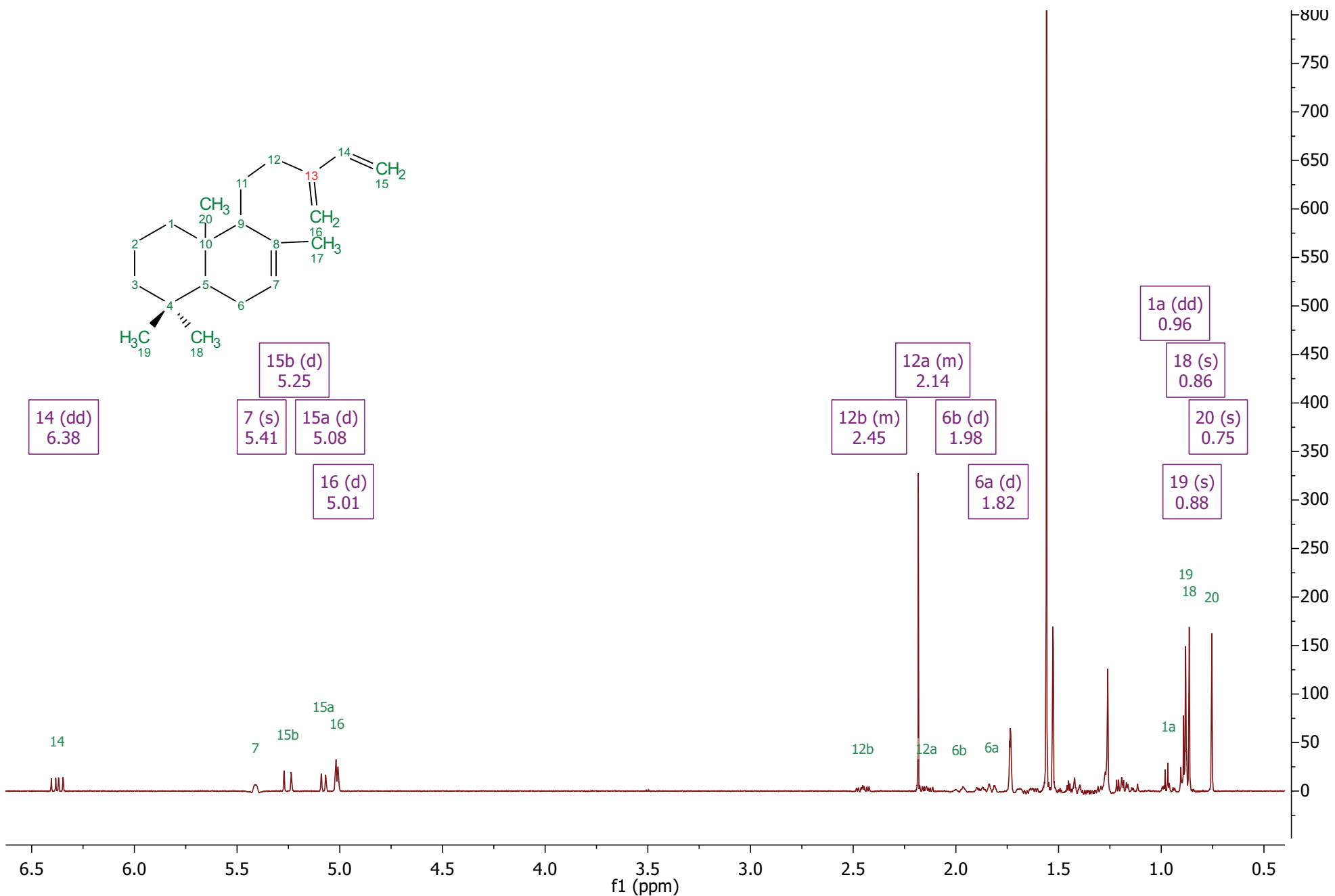


Figure S12-A. ¹H NMR of partially purified labda-7,13(16),14-triene [22].

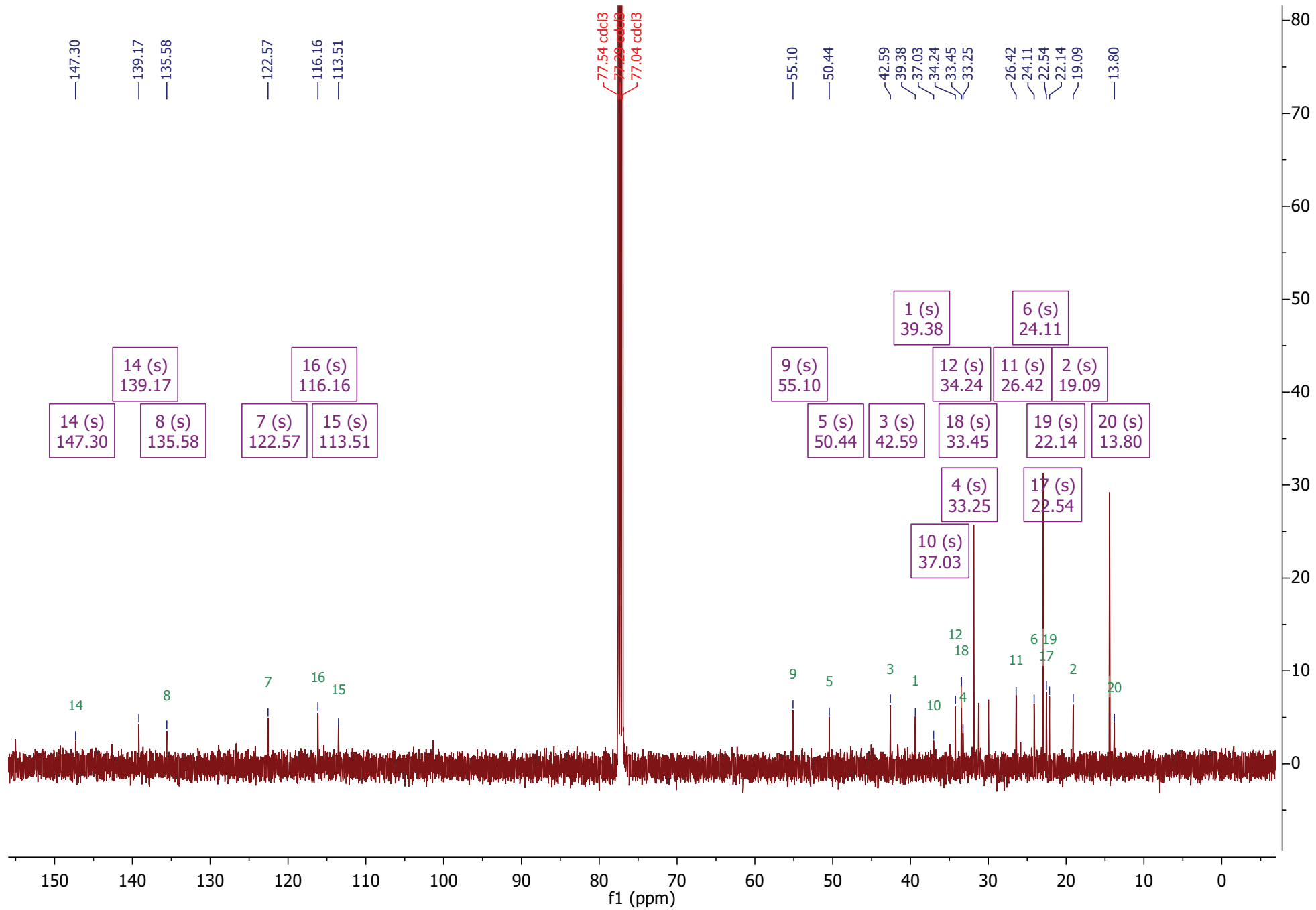


Figure S12-B. ^{13}C NMR of partially purified labda-7,13(16),14-triene [22].

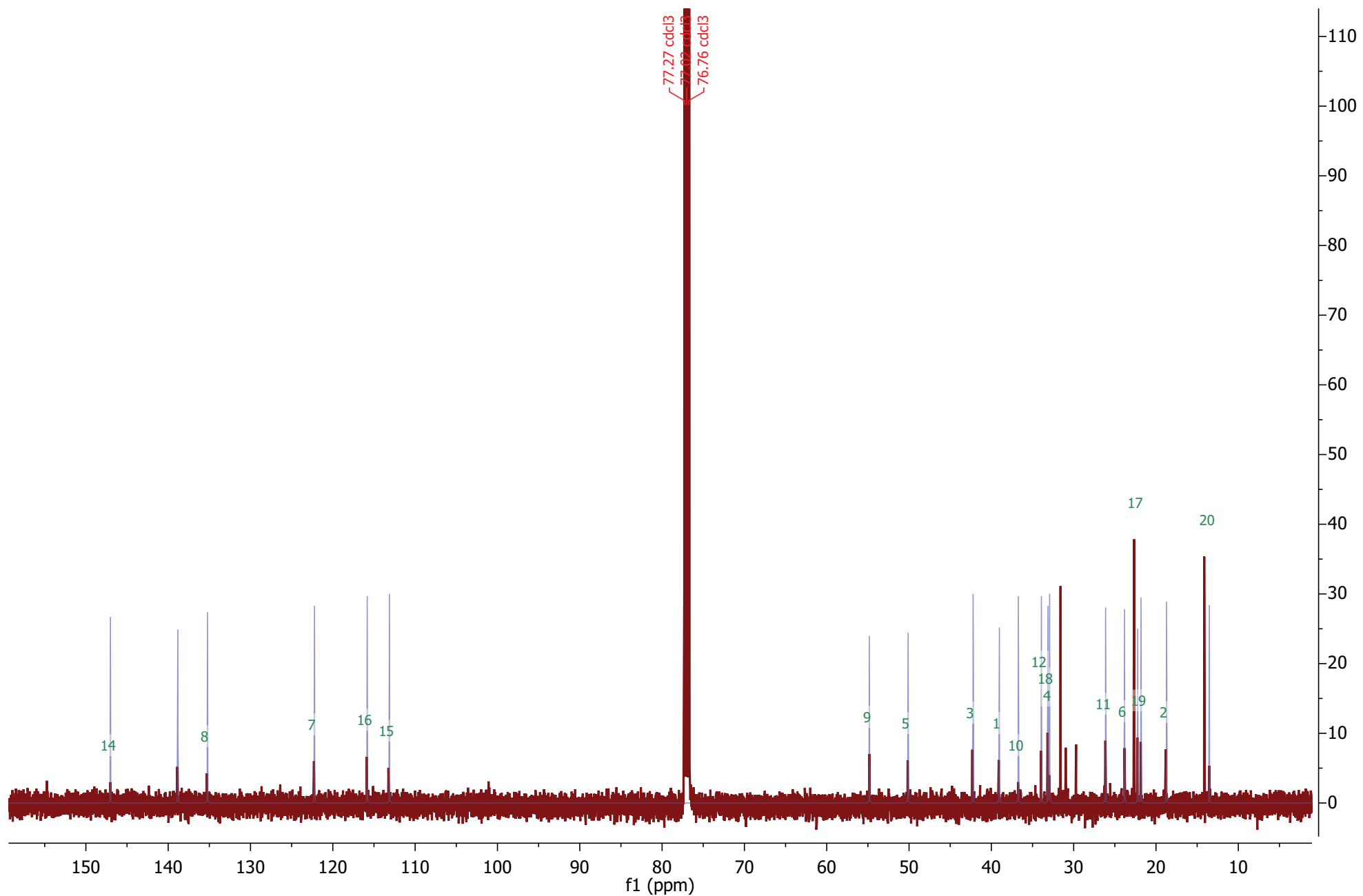


Figure S12-C. Overlay of ^{13}C NMR of partially purified labda-7,13(16),14-triene [**22**] (red) with ^{13}C NMR spectrum (blue) reconstructed from shifts reported for the same compound by Jia et al. (2016) (DOI: 10.1016/j.ymben.2016.04.001).

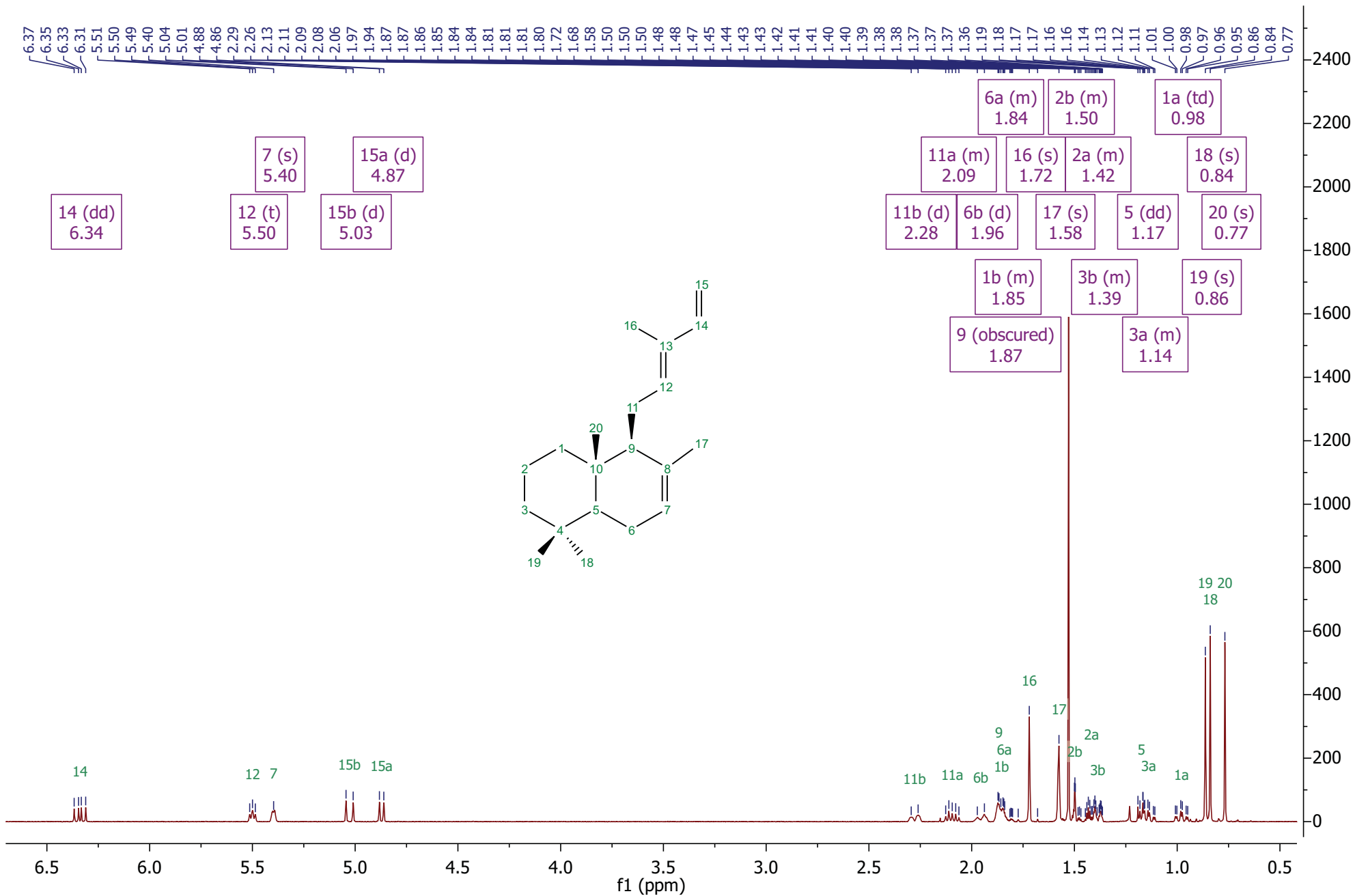


Figure S13-A. ¹H NMR of labda-7,12E,14-triene [24].

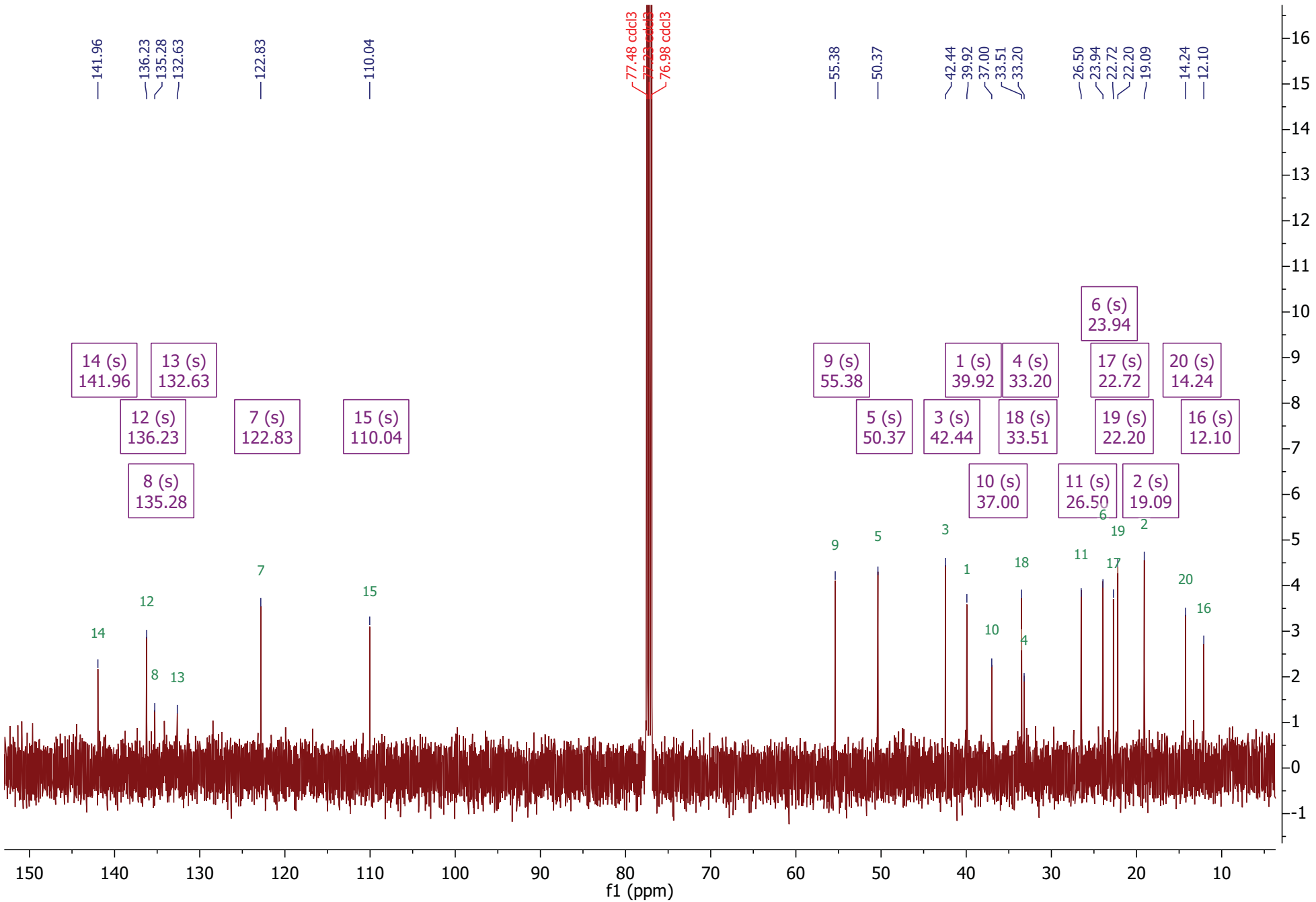


Figure S13-B. ^{13}C NMR of labda-7,12E,14-triene [24].

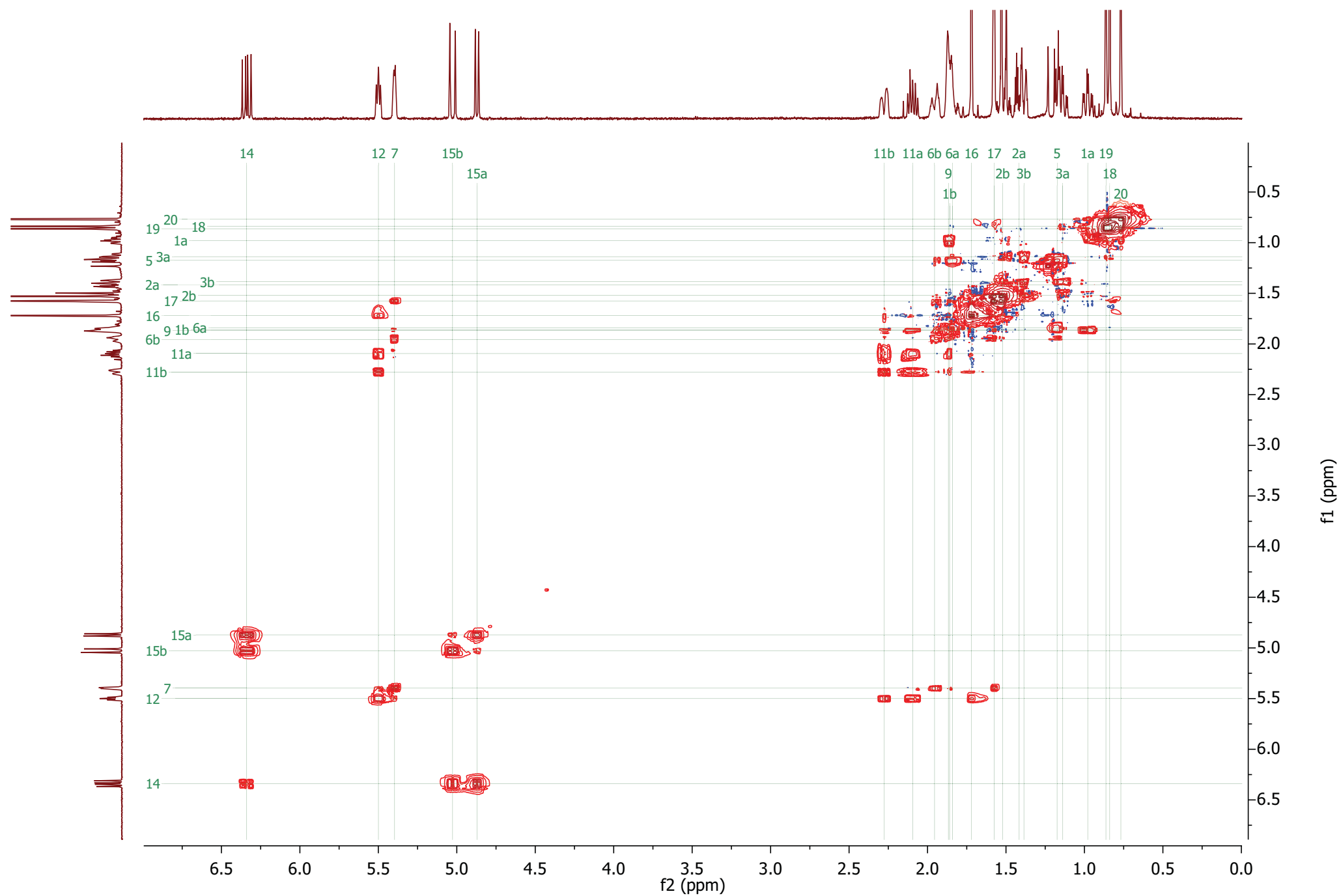


Figure S13-C. ^1H - ^1H COSY of λ -7,12E,14-triene [24].

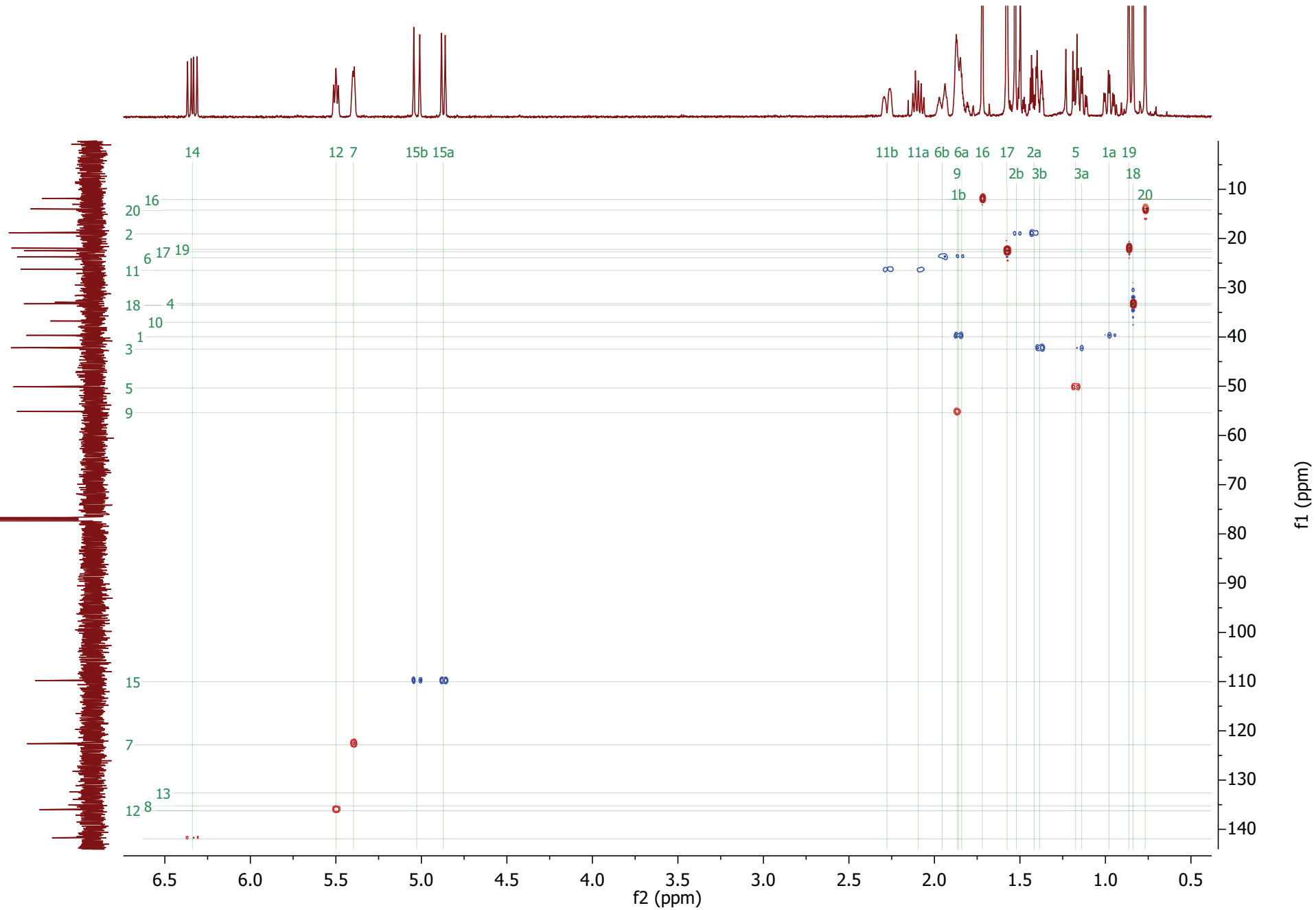


Figure S13-D. ^1H - ^{13}C HSQC of lambda-7,12E,14-triene [24].

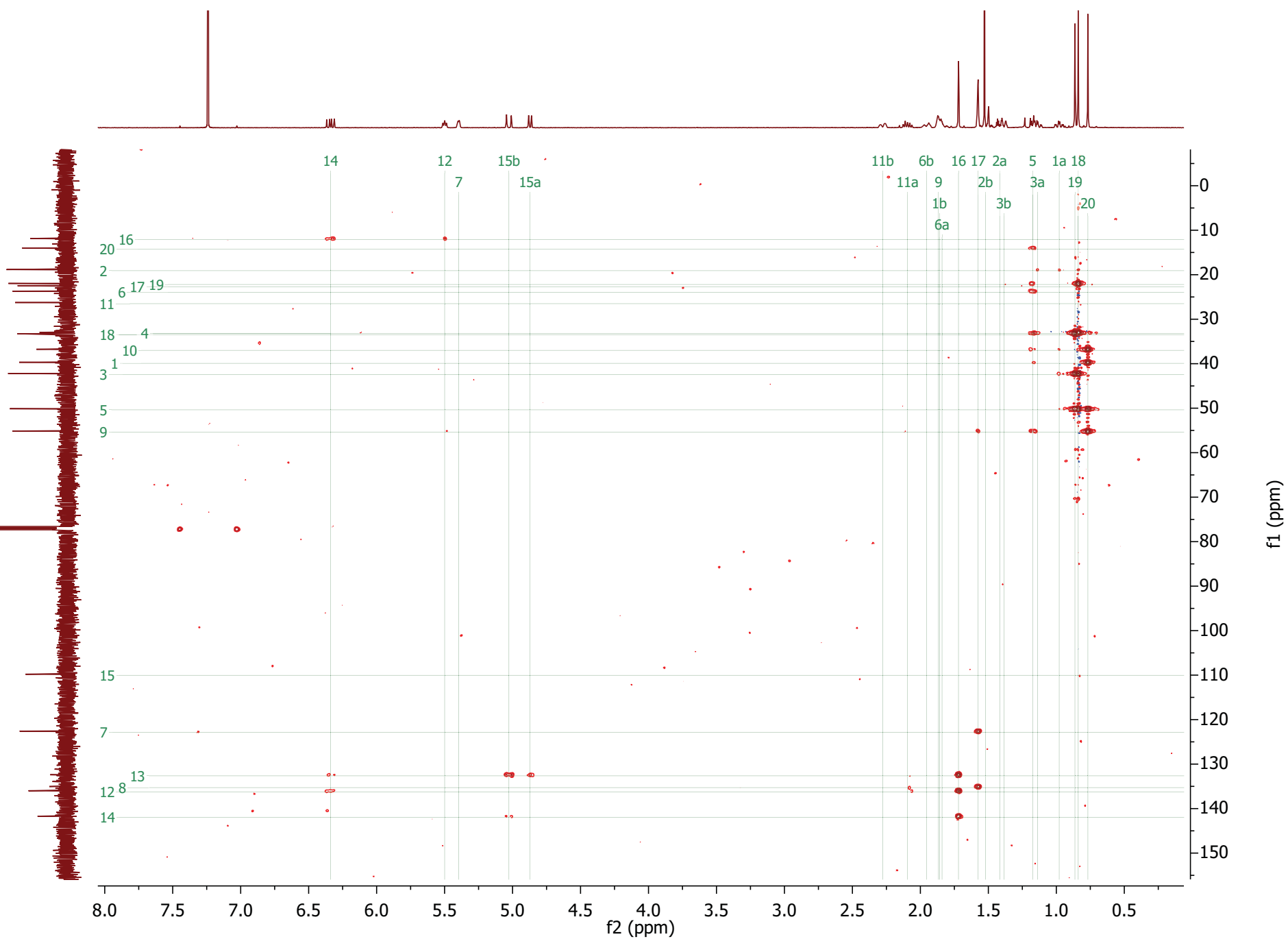


Figure S13-E. ^1H - ^{13}C HMBC of lambda-7,12E,14-triene [24].

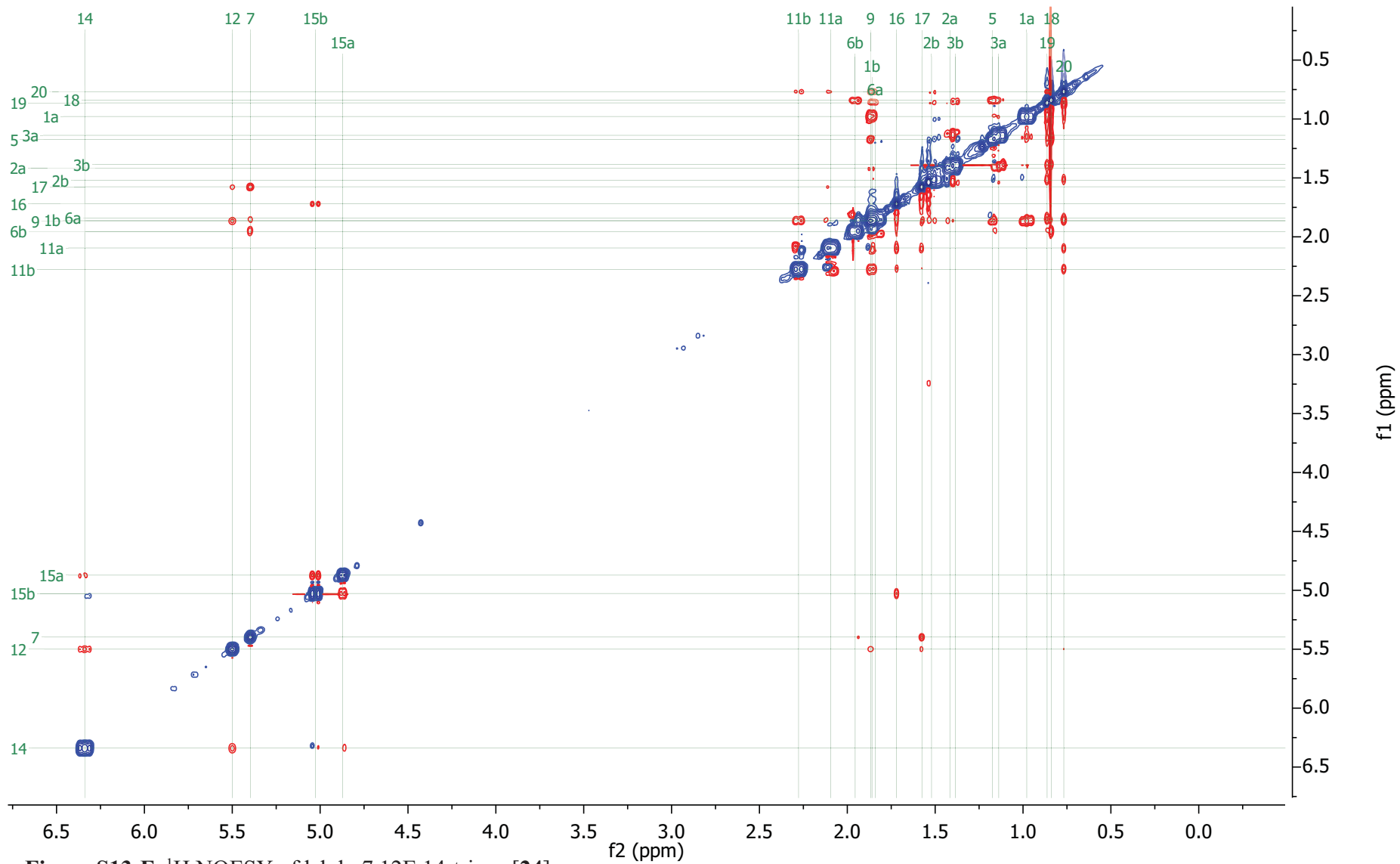


Figure S13-F. ¹H NOESY of labda-7,12E,14-triene [24].

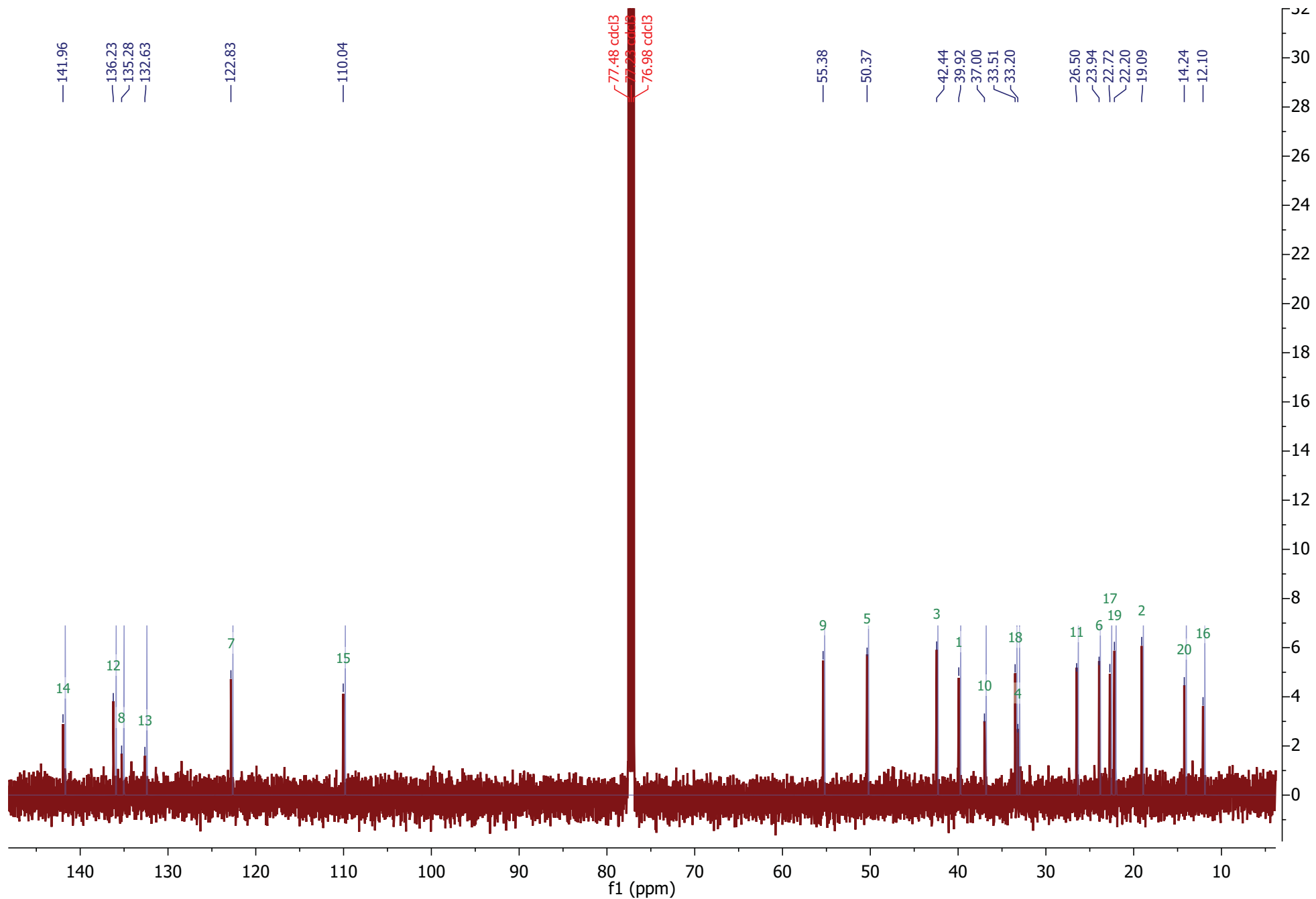


Figure S13-G. Overlay of ^{13}C NMR of λ -7,12E,14-triene [24] (red) with ^{13}C NMR spectrum (blue) reconstructed from shifts reported for the same compound by Roengsumran et al. (1999) (DOI: 10.1016/S0031-9422(98)00604-9).

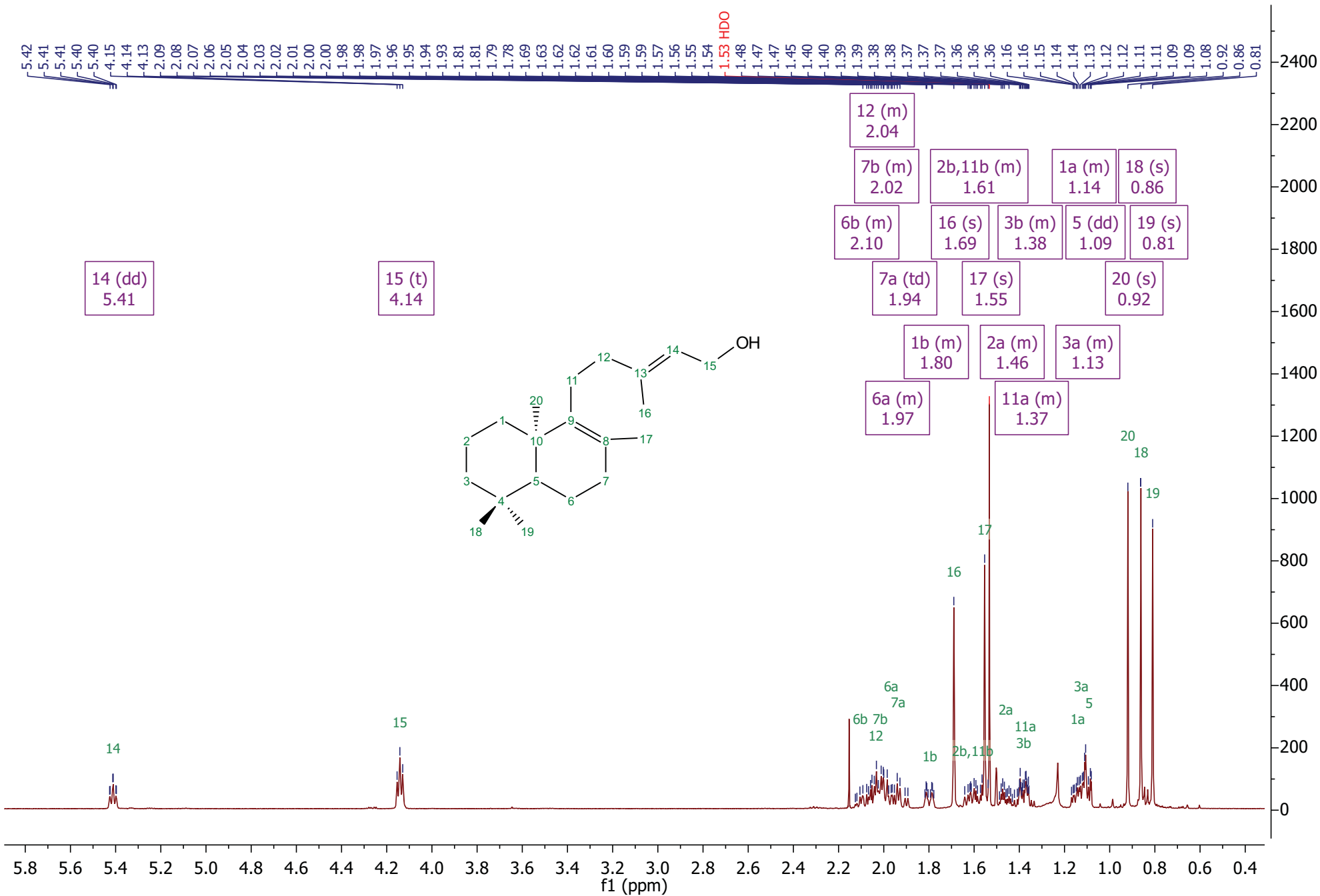


Figure S14-A. ^1H NMR of (10R)-labda-8,13E-diene-15-ol [25a].

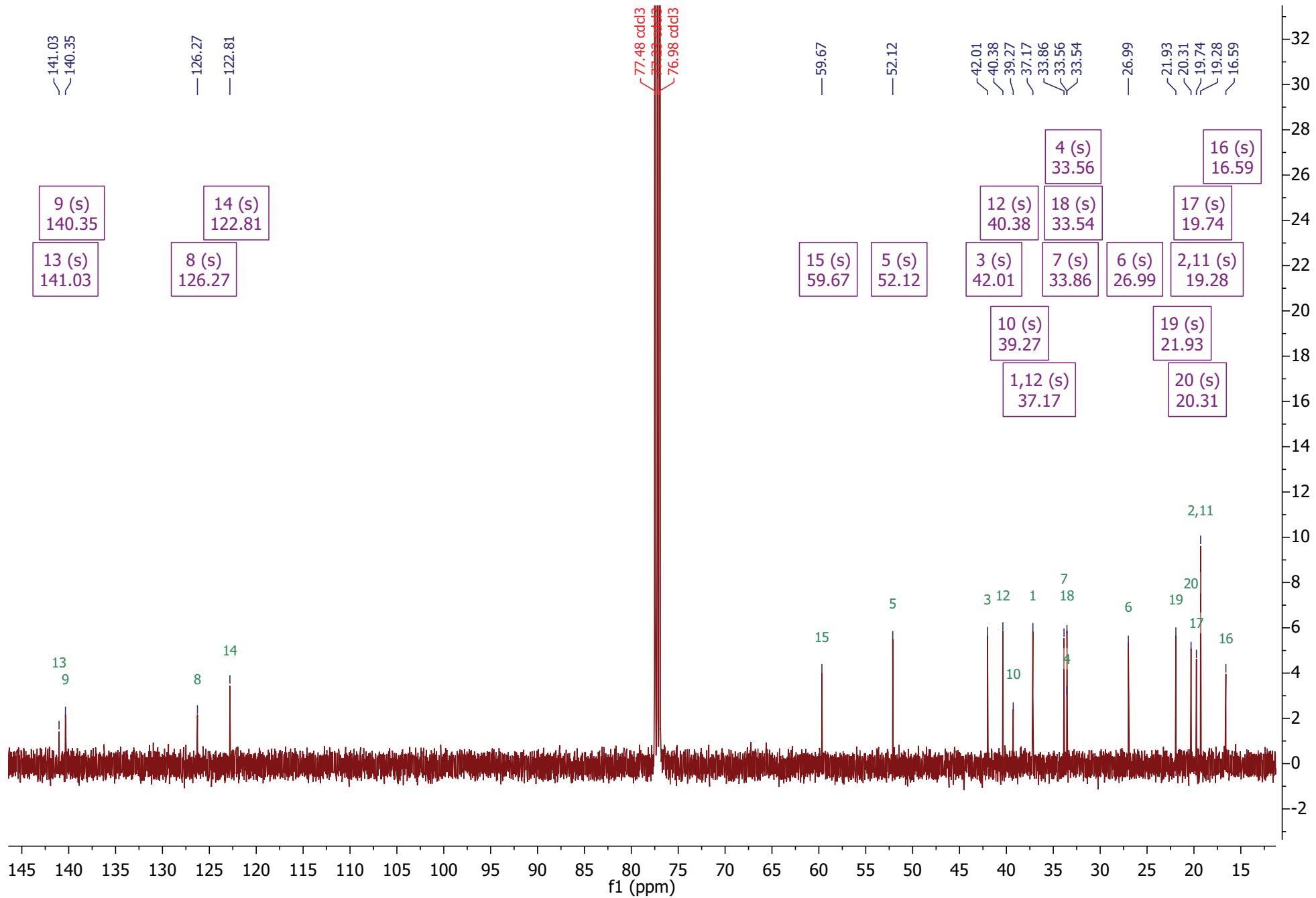


Figure S14-B. ¹³C NMR of (10R)-labda-8,13E-diene-15-ol [25a].

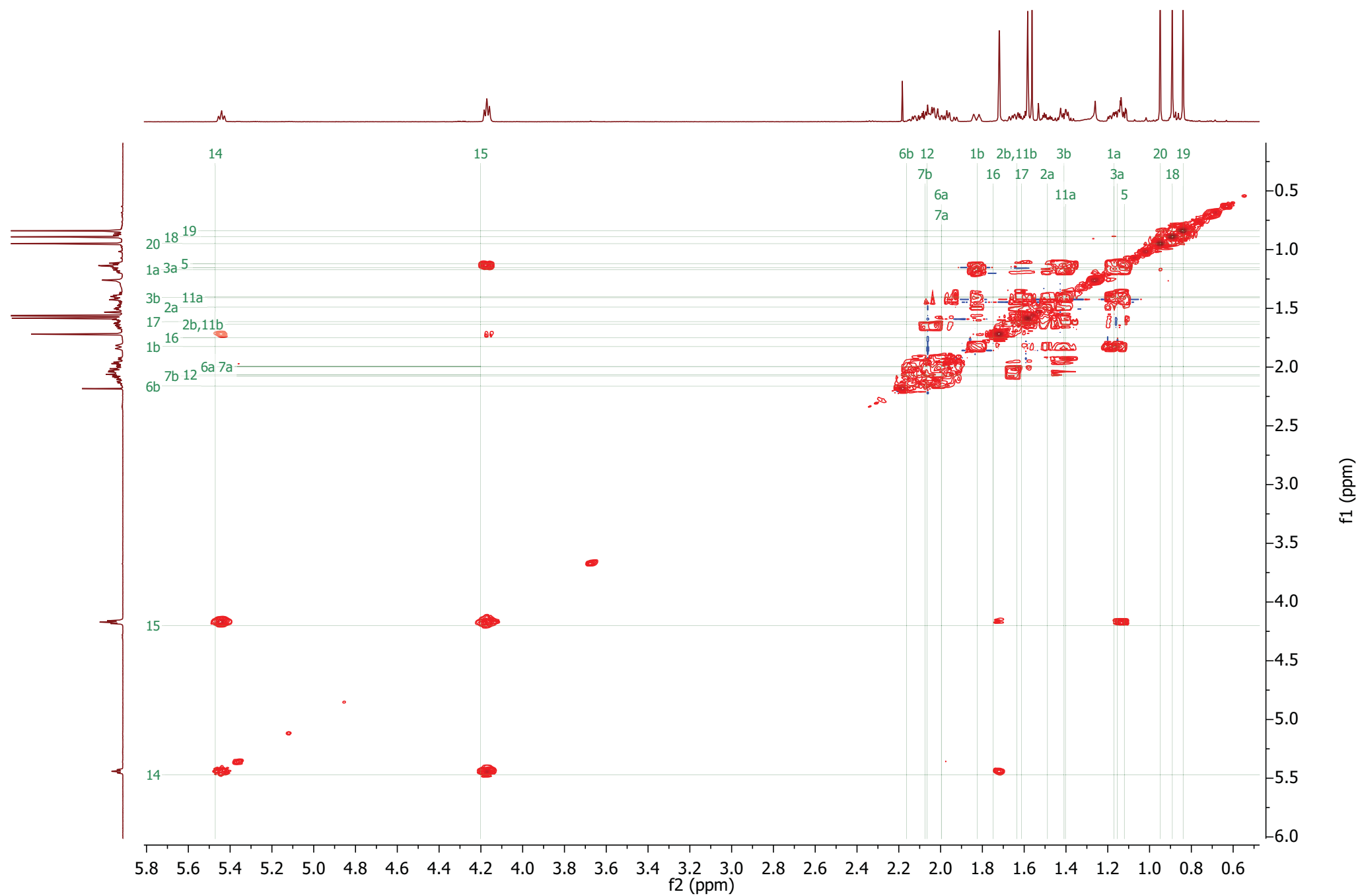


Figure S14-C. ^1H - ^1H COSY of (10R)-labda-8,13E-diene-15-ol [25a].

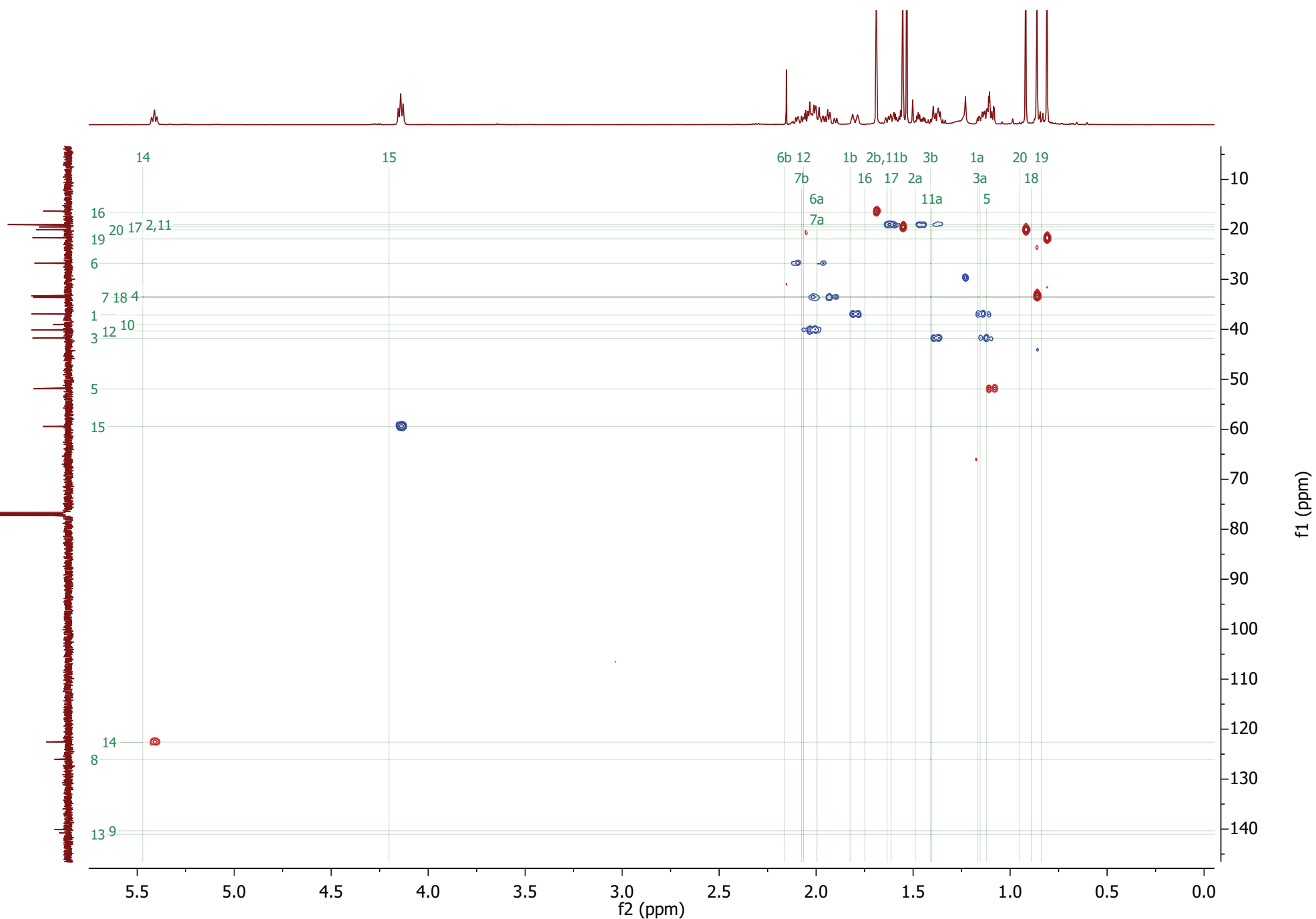


Figure S14-D. ^1H - ^{13}C HSQC of (10R)-labda-8,13E-diene-15-ol [25a].

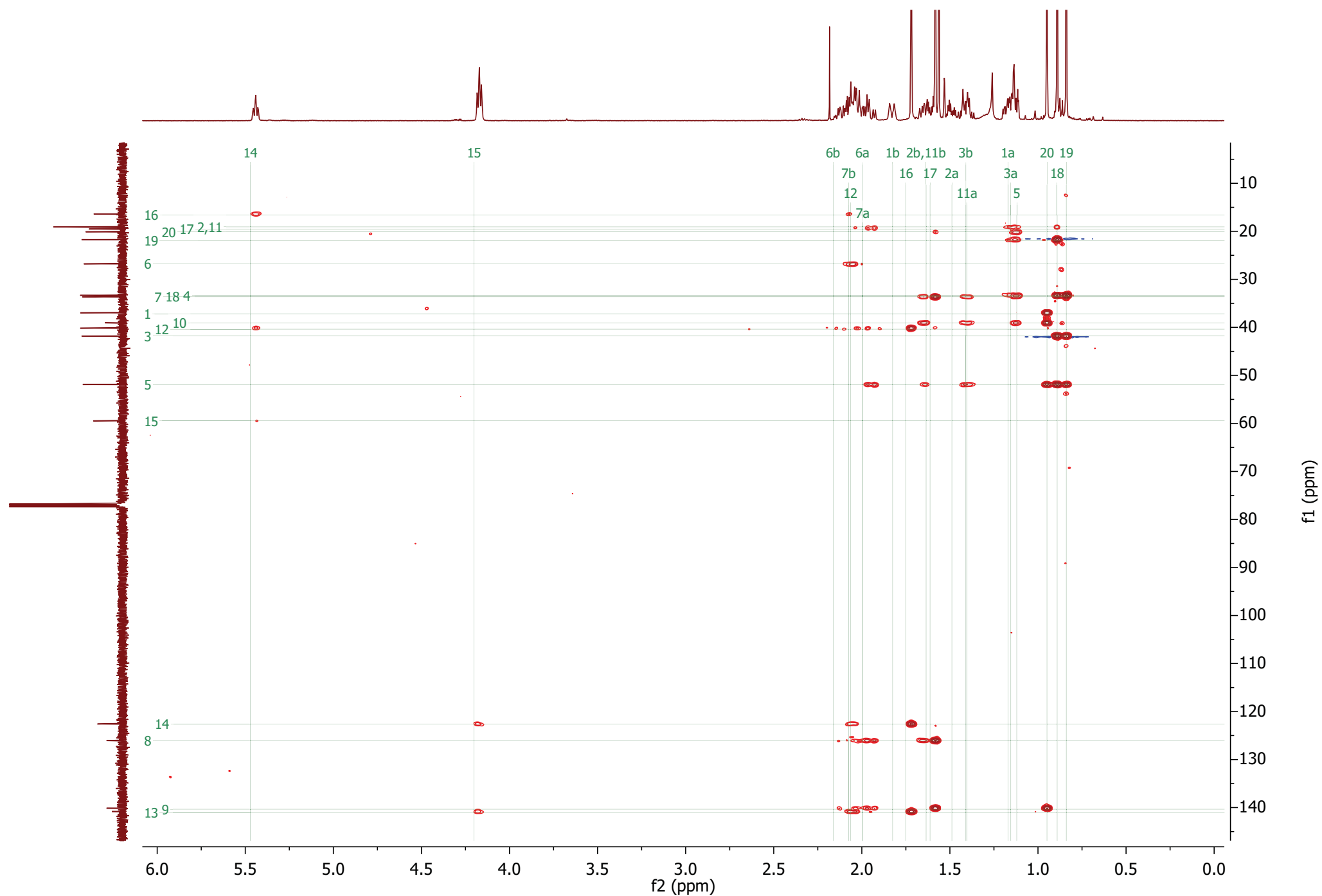


Figure S14-E. ^1H - ^{13}C HMBC of (10R)-labda-8,13E-diene-15-ol [**25a**].

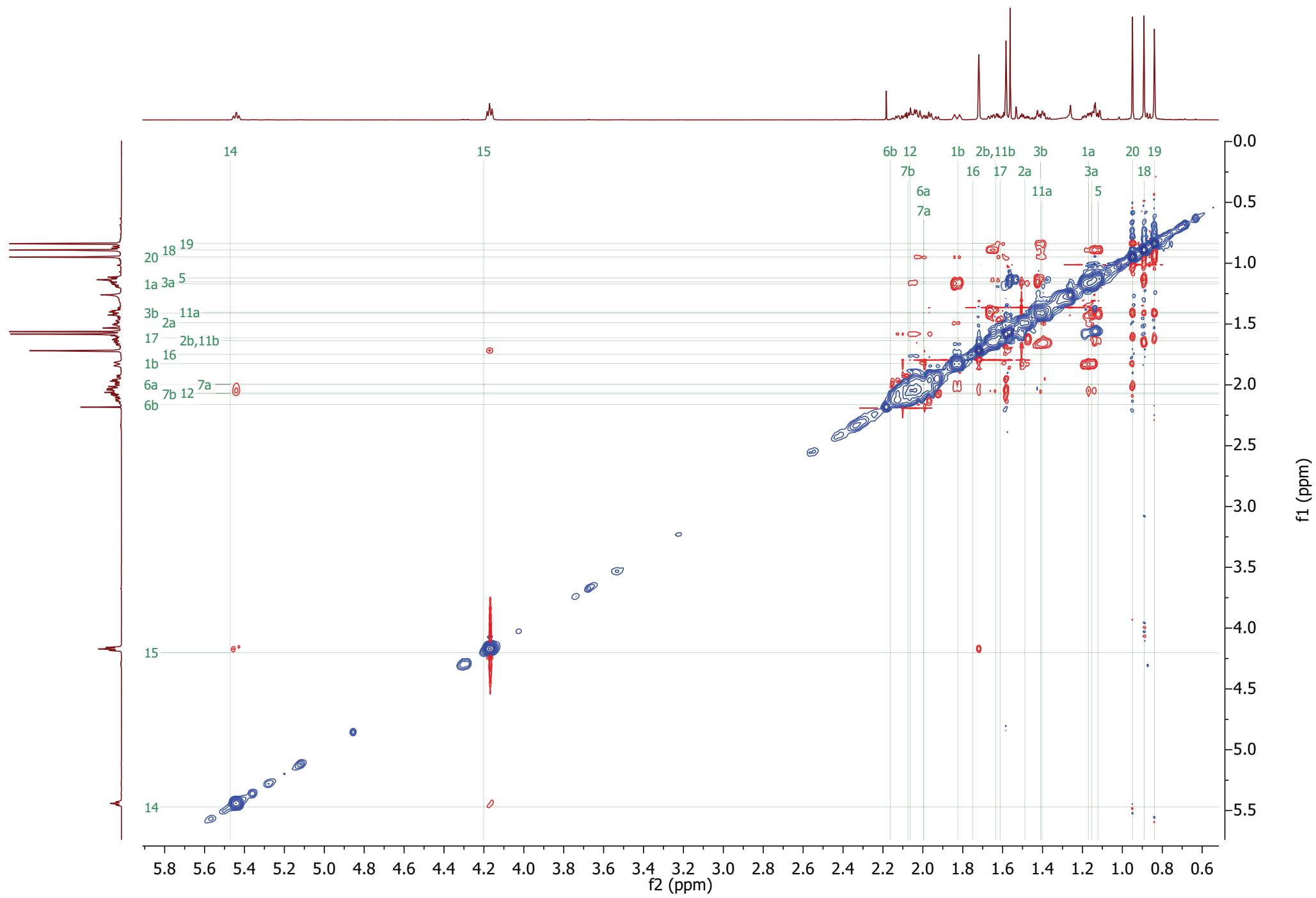


Figure S14-F. ^1H NOESY of (10R)-labda-8,13E-diene-15-ol [25a].

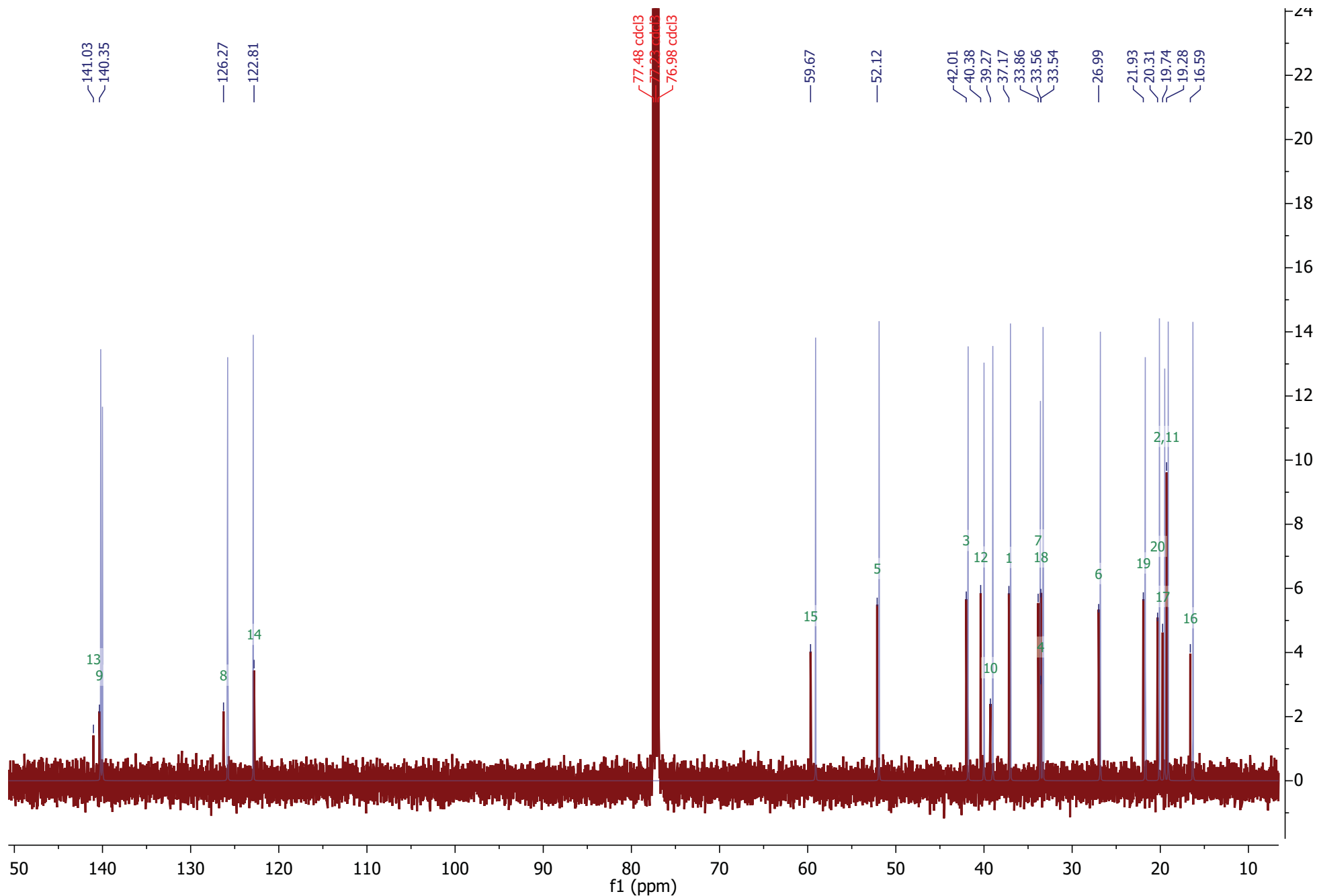


Figure S14-G. Overlay of ¹³C NMR of (10R)-labda-8,13E-diene-15-ol [**25a**] (red) with ¹³C NMR spectrum (blue) reconstructed from shifts reported for the same compound by Suzuki et al. (1983) (DOI: 10.1016/0031-9422(83)80249-0).

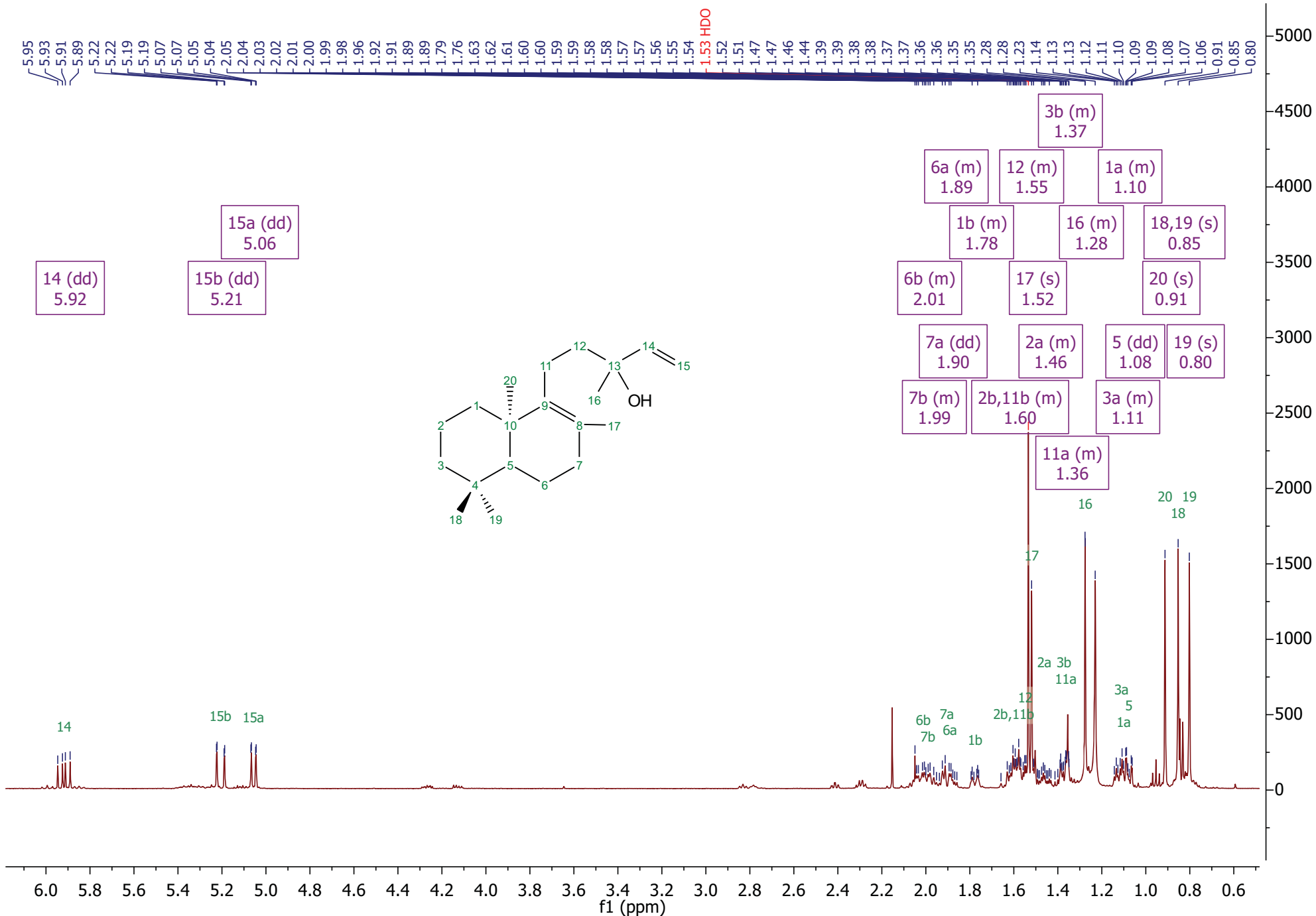


Figure S15-A. ¹H NMR of (10R)-labda-8,14-dien-13-ol [26].

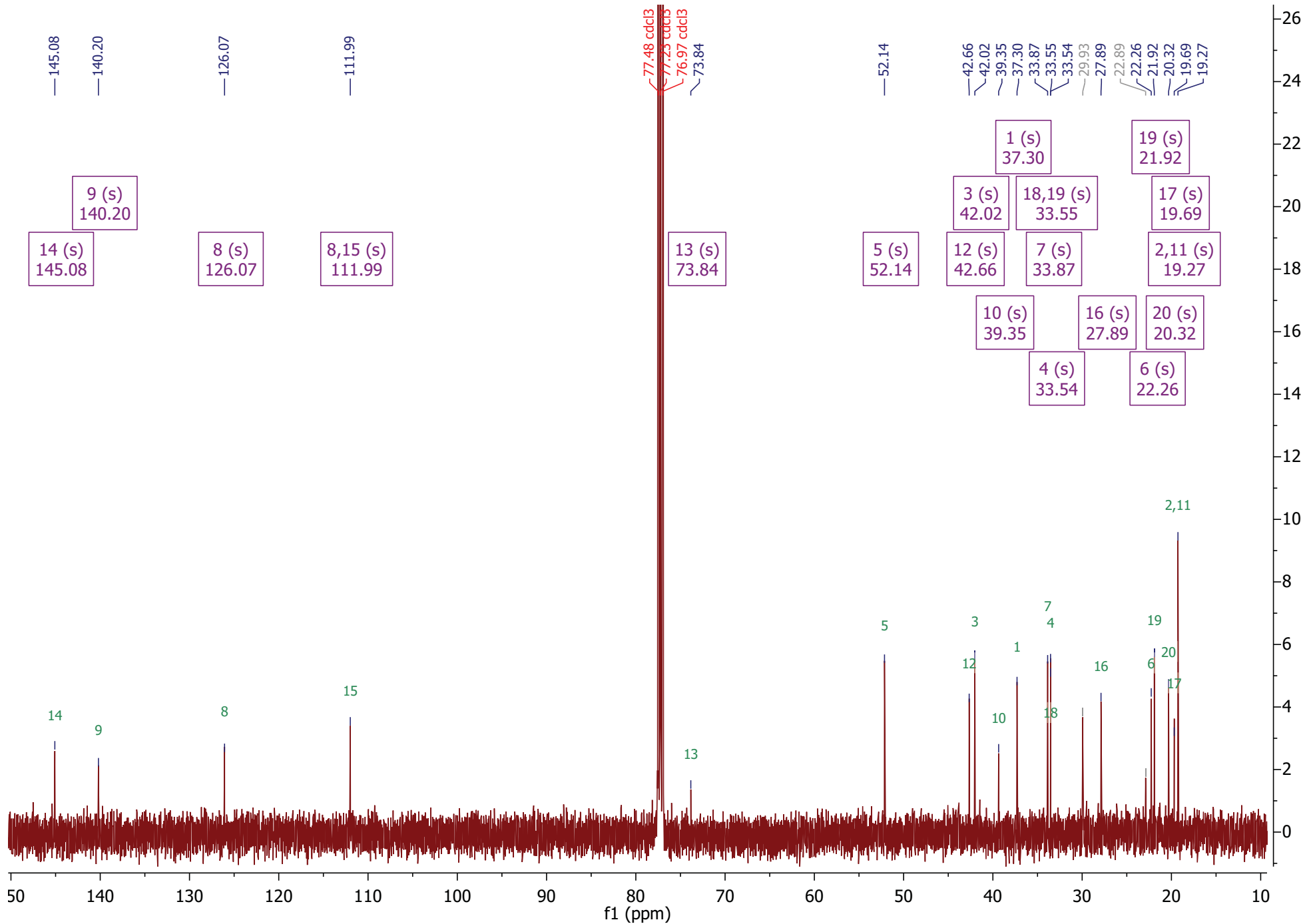


Figure S15-B. ^{13}C NMR of (10R)-labda-8,14-dien-13-ol [26].

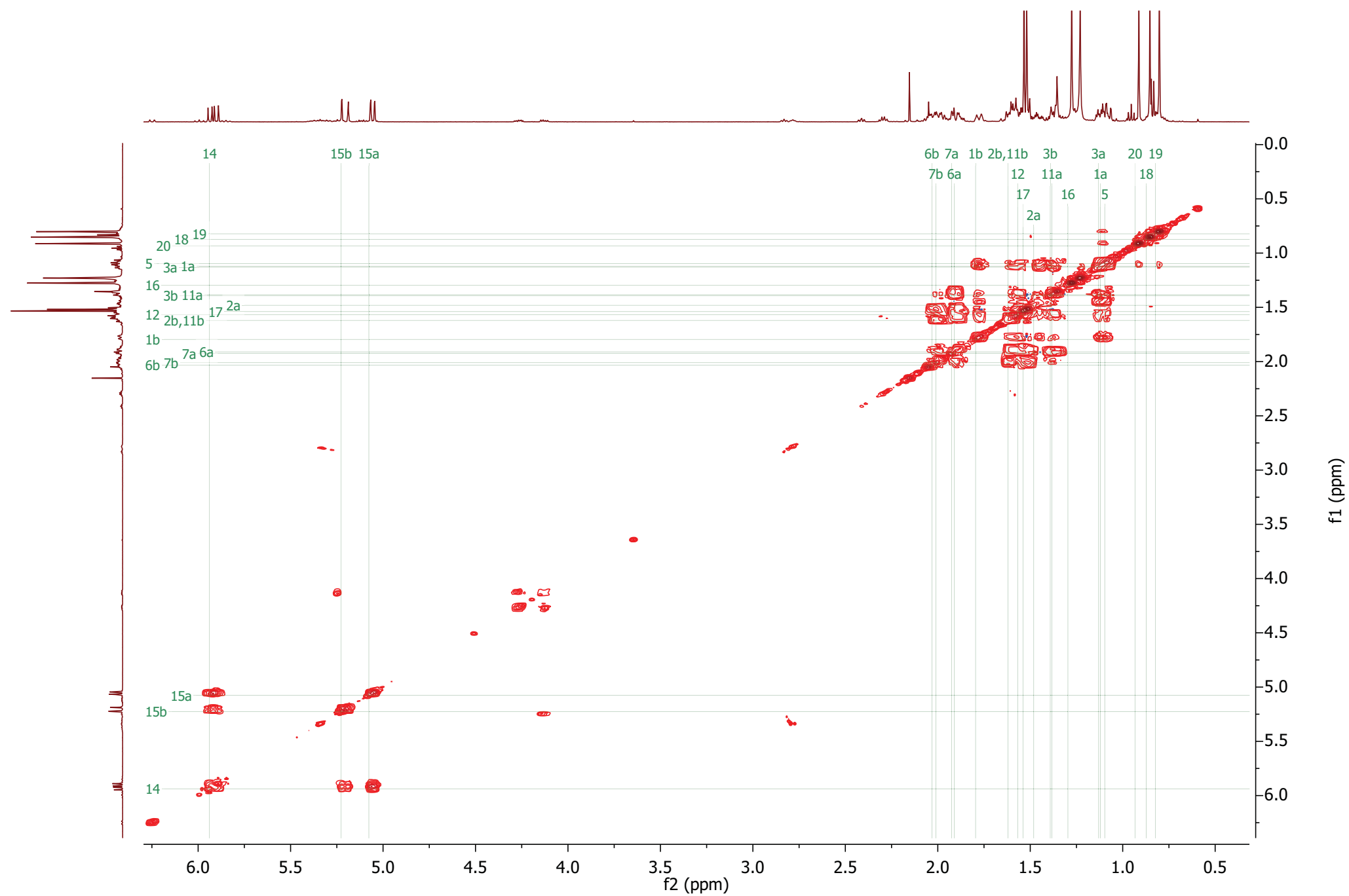
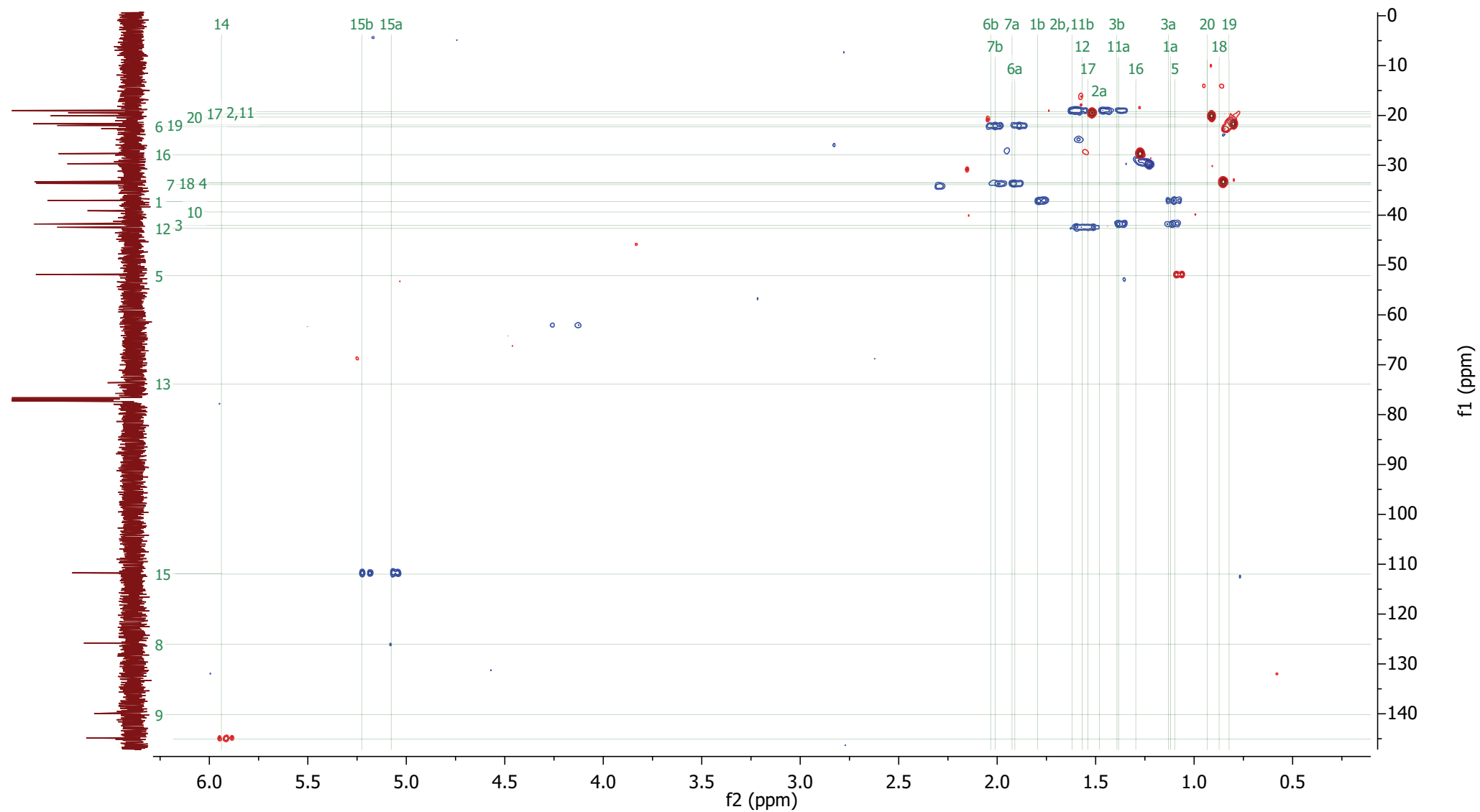


Figure S15-C. ^1H - ^1H COSY of (10R)-labda-8,14-dien-13-ol [26].



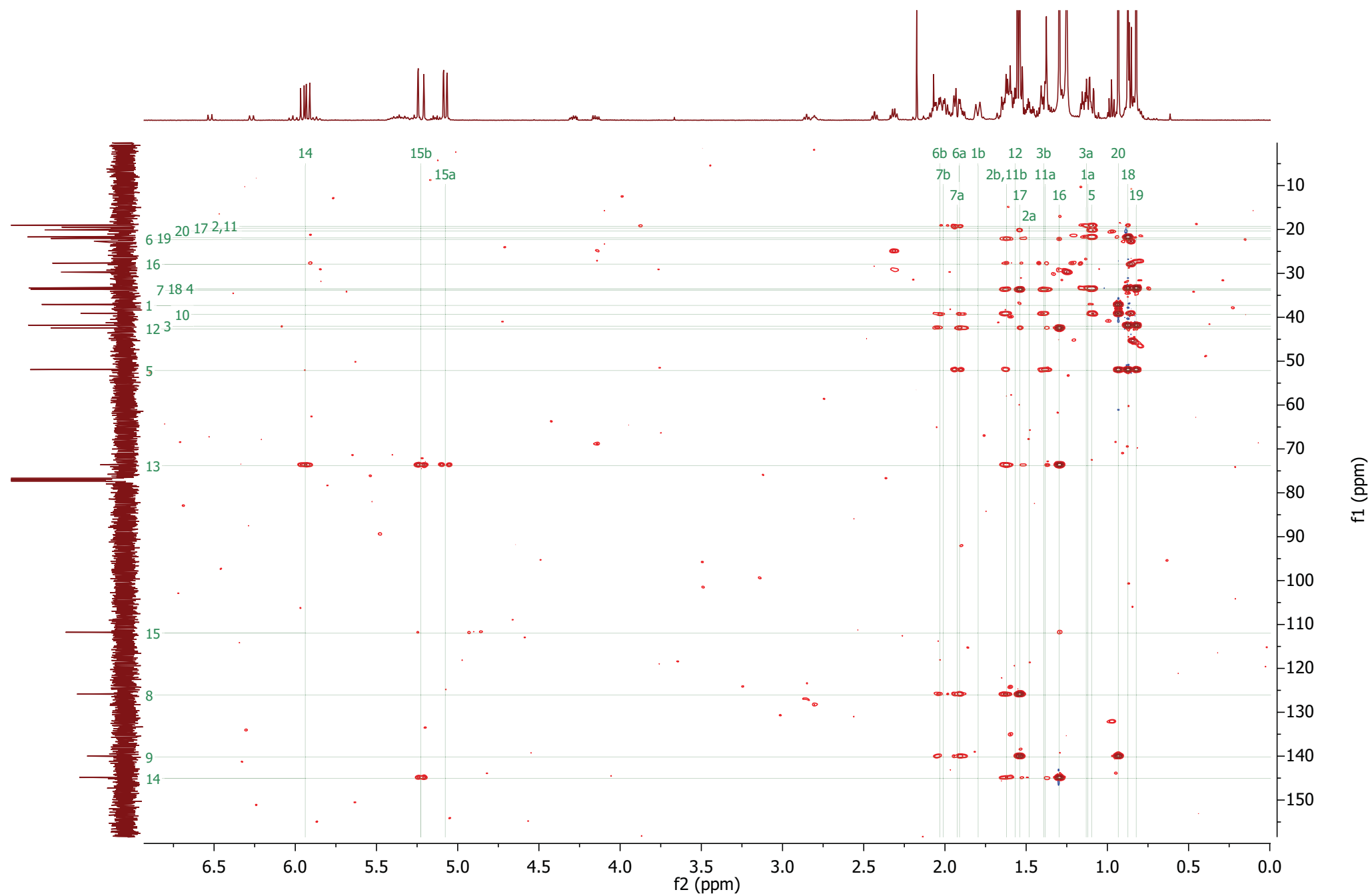


Figure S15-E. ^1H - ^{13}C HMBC of (10R)-labda-8,14-dien-13-ol [26].

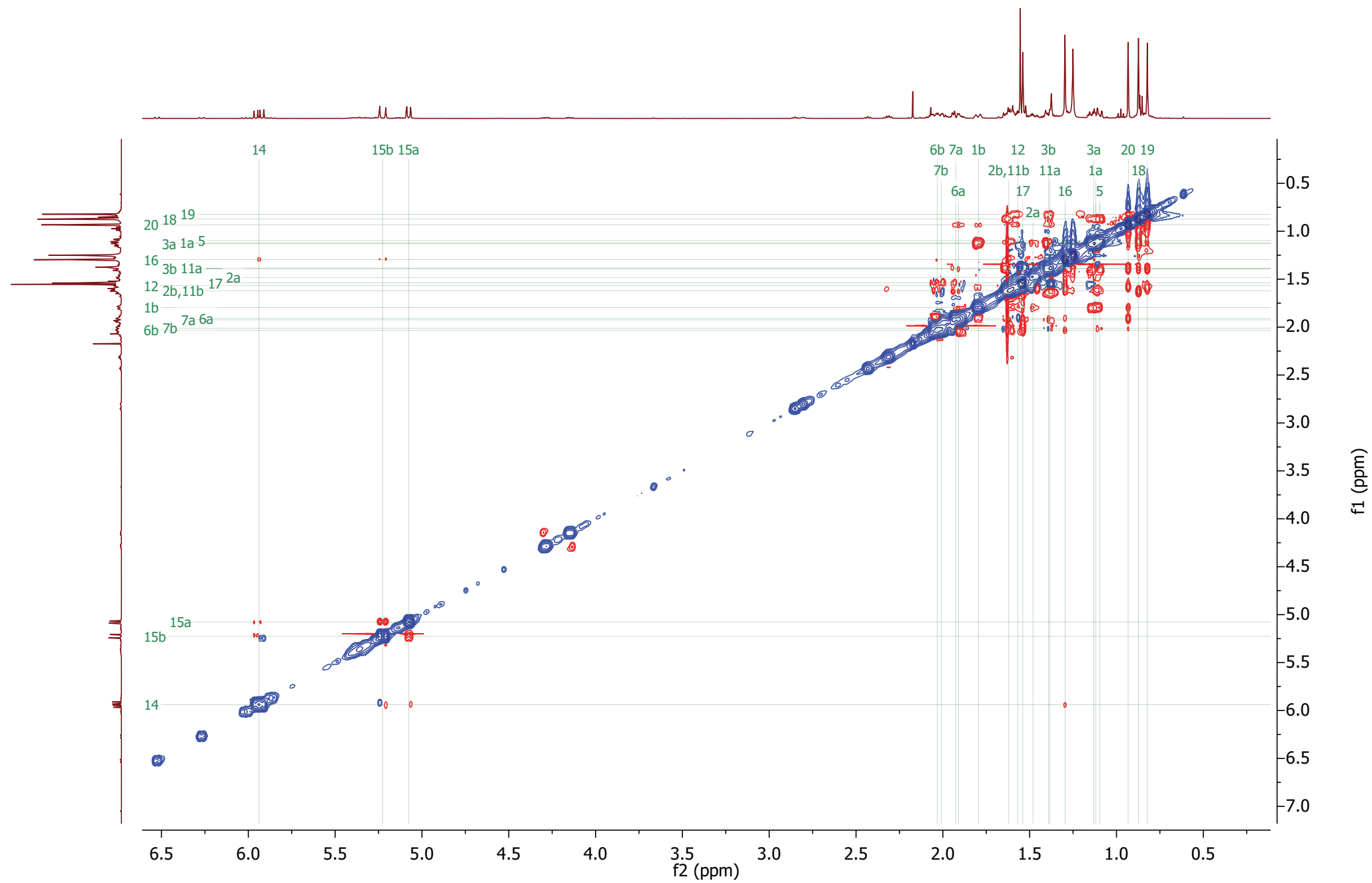


Figure S15-F. ^1H NOESY of (10R)-labda-8,14-dien-13-ol [26].

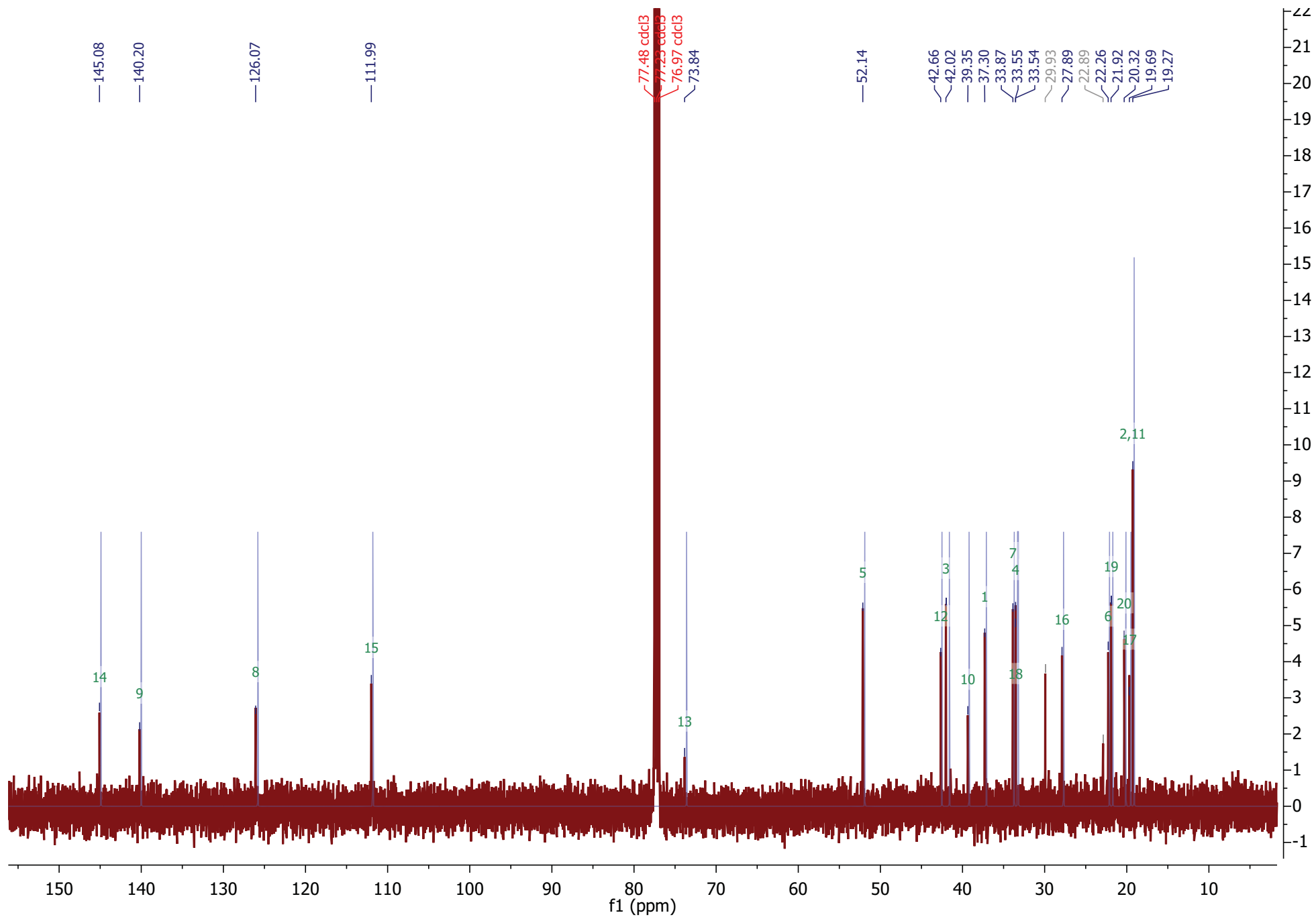


Figure S15-G. Overlay of ^{13}C NMR of (10R)-labda-8,14-dien-13-ol [**26**] (red) with ^{13}C NMR spectrum (blue) reconstructed from shifts reported for the same compound by Wu and Lin (1997) (DOI: 10.1016/S0031-9422(96)00519-5).

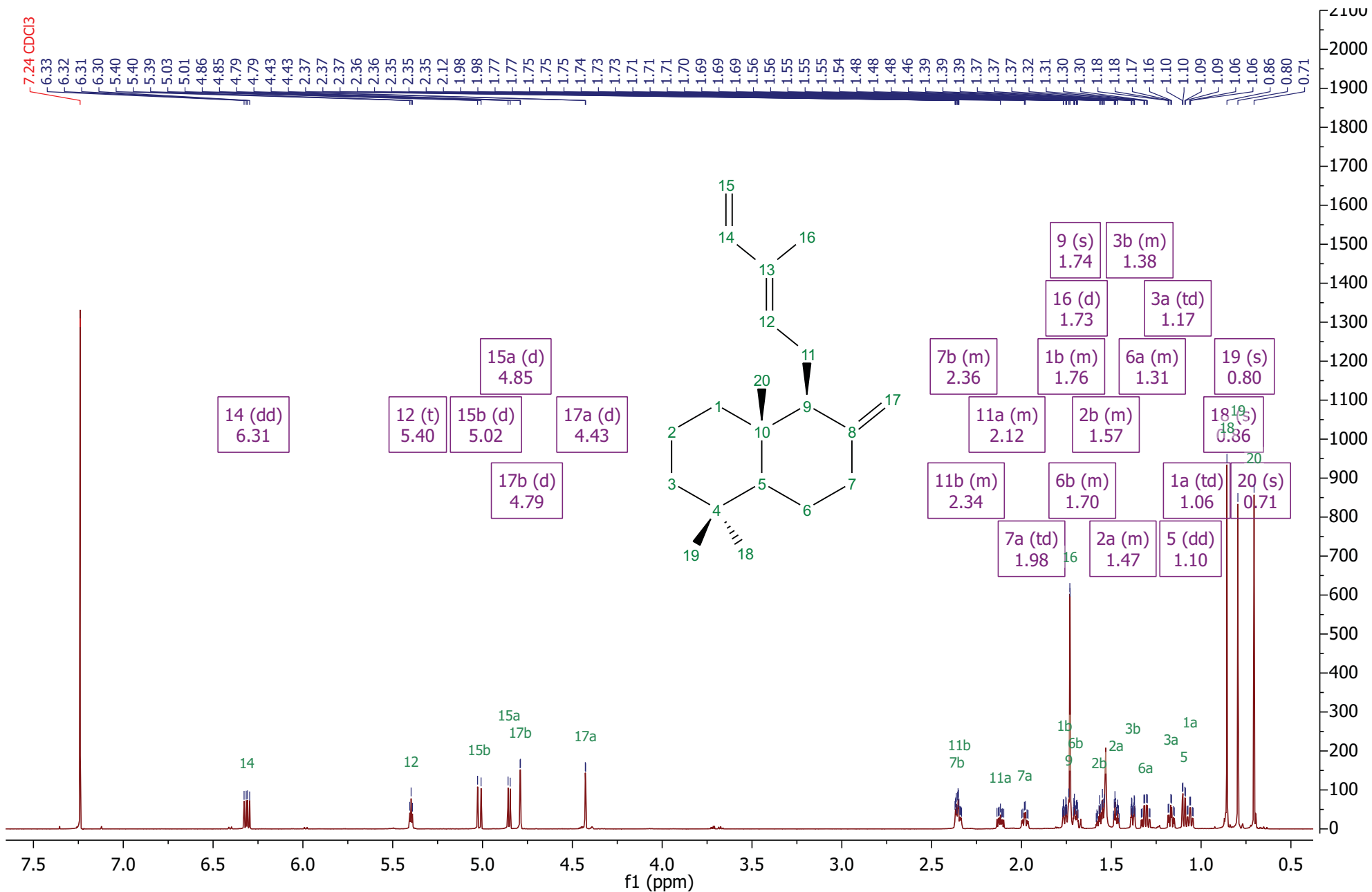


Figure S16-A. ¹H NMR of trans-biformene [34].

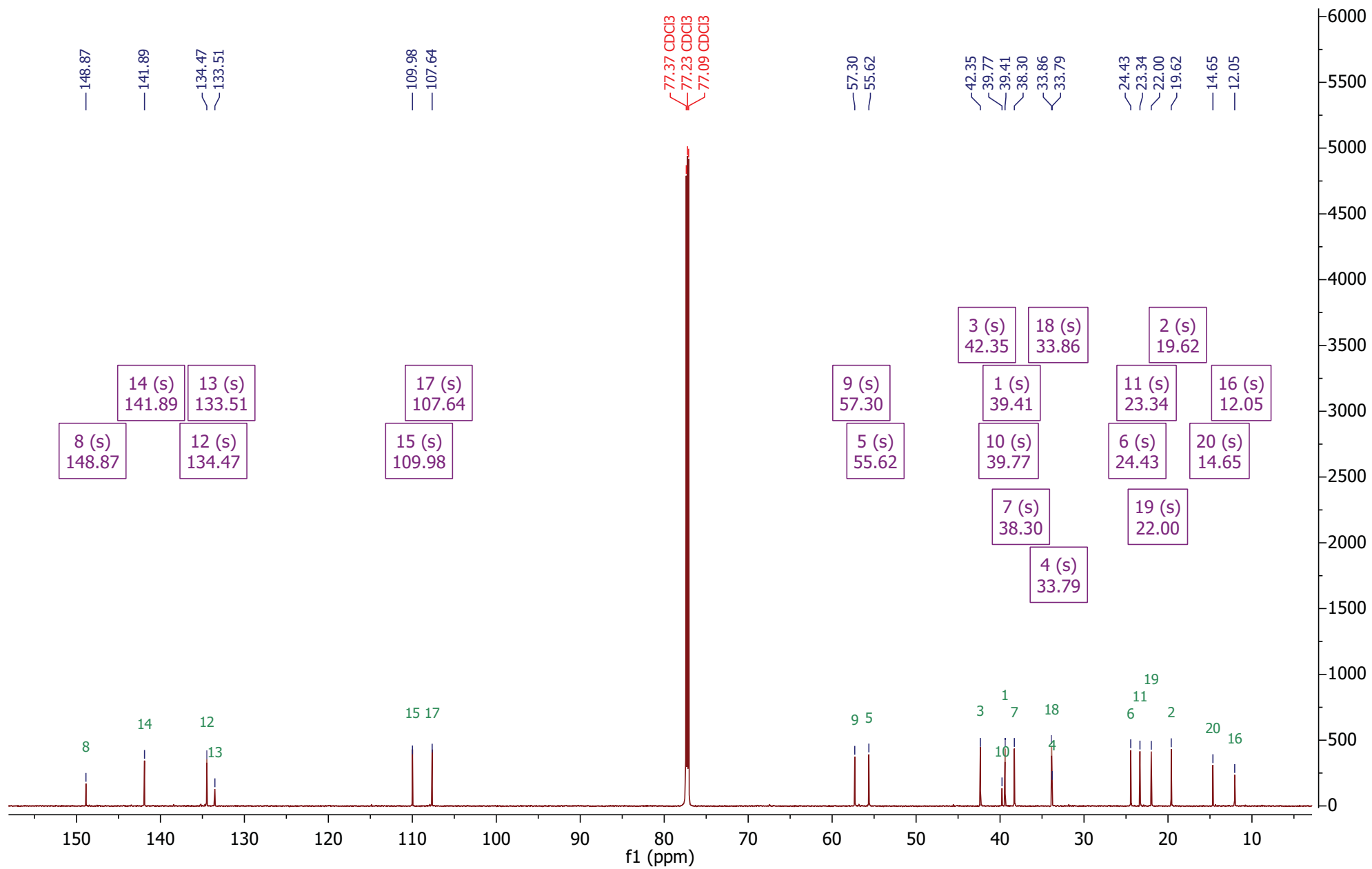


Figure S16-B. ¹³C NMR of trans-biformene [34].

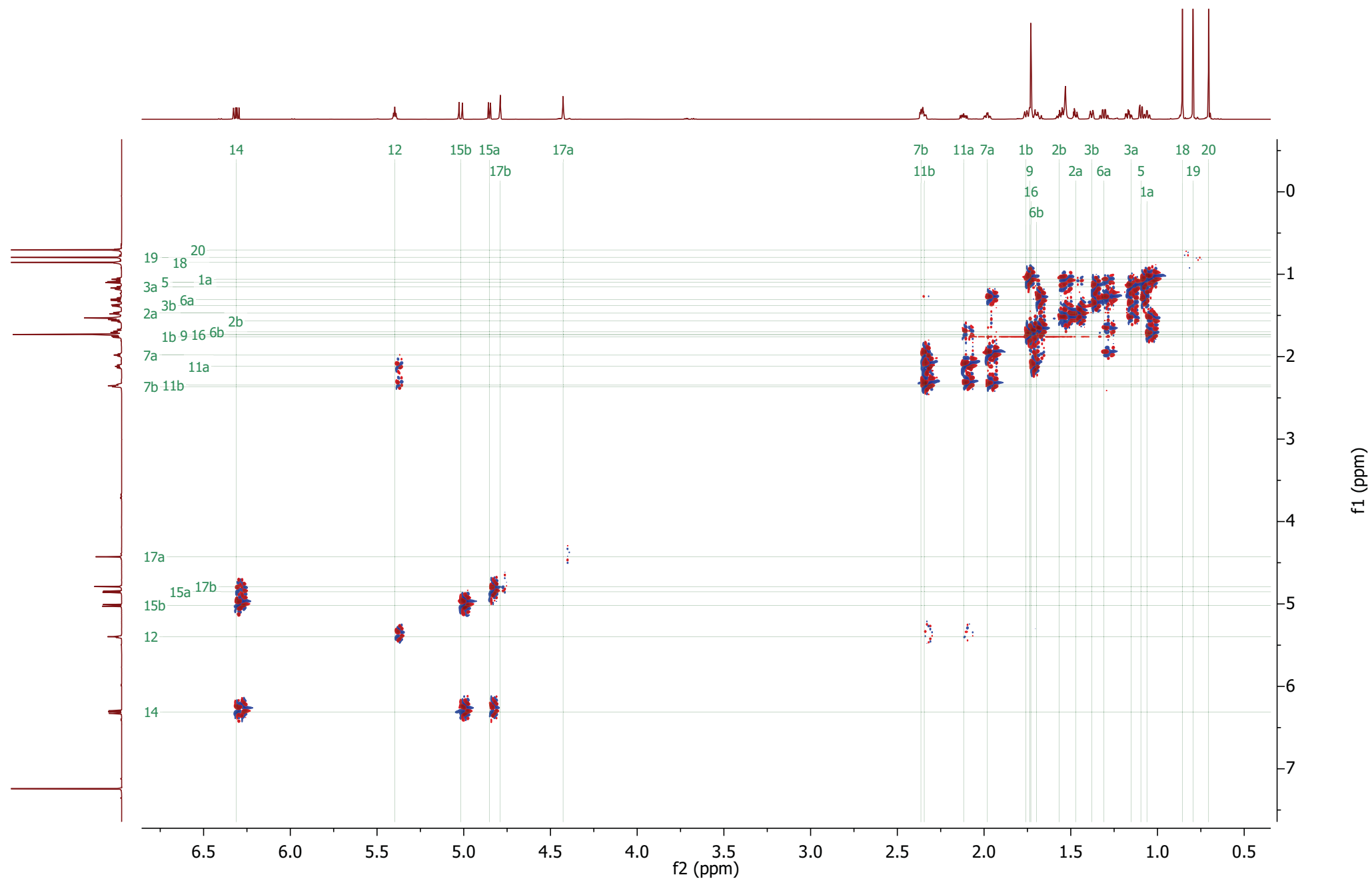


Figure S16-C. ^1H - ^1H COSY of trans-biformene [34].

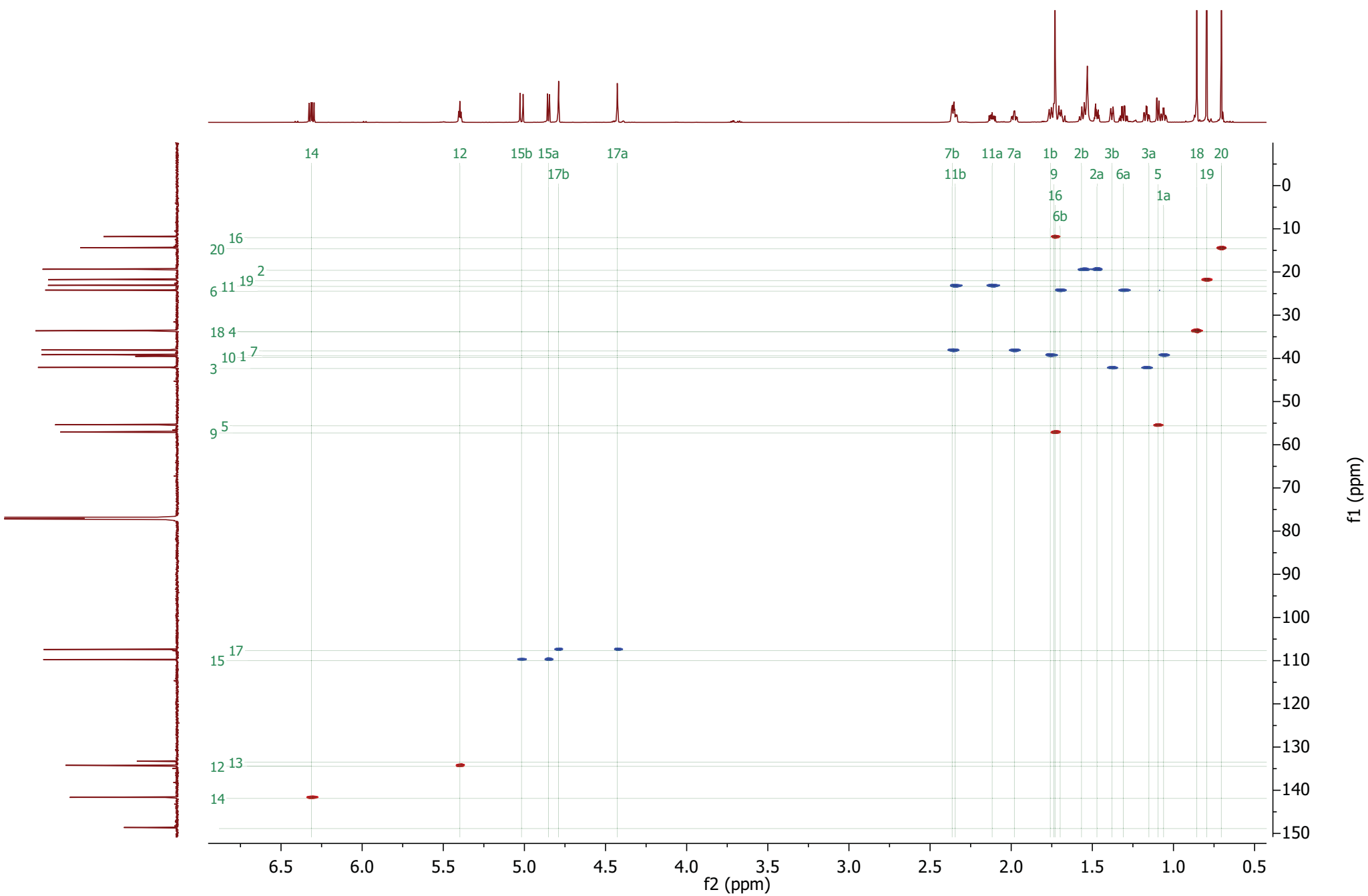


Figure S16-D. ^1H - ^{13}C HSQC of trans-biformene [34].



Figure S16-E. ^1H - ^{13}C HMBC of trans-biformene [34].

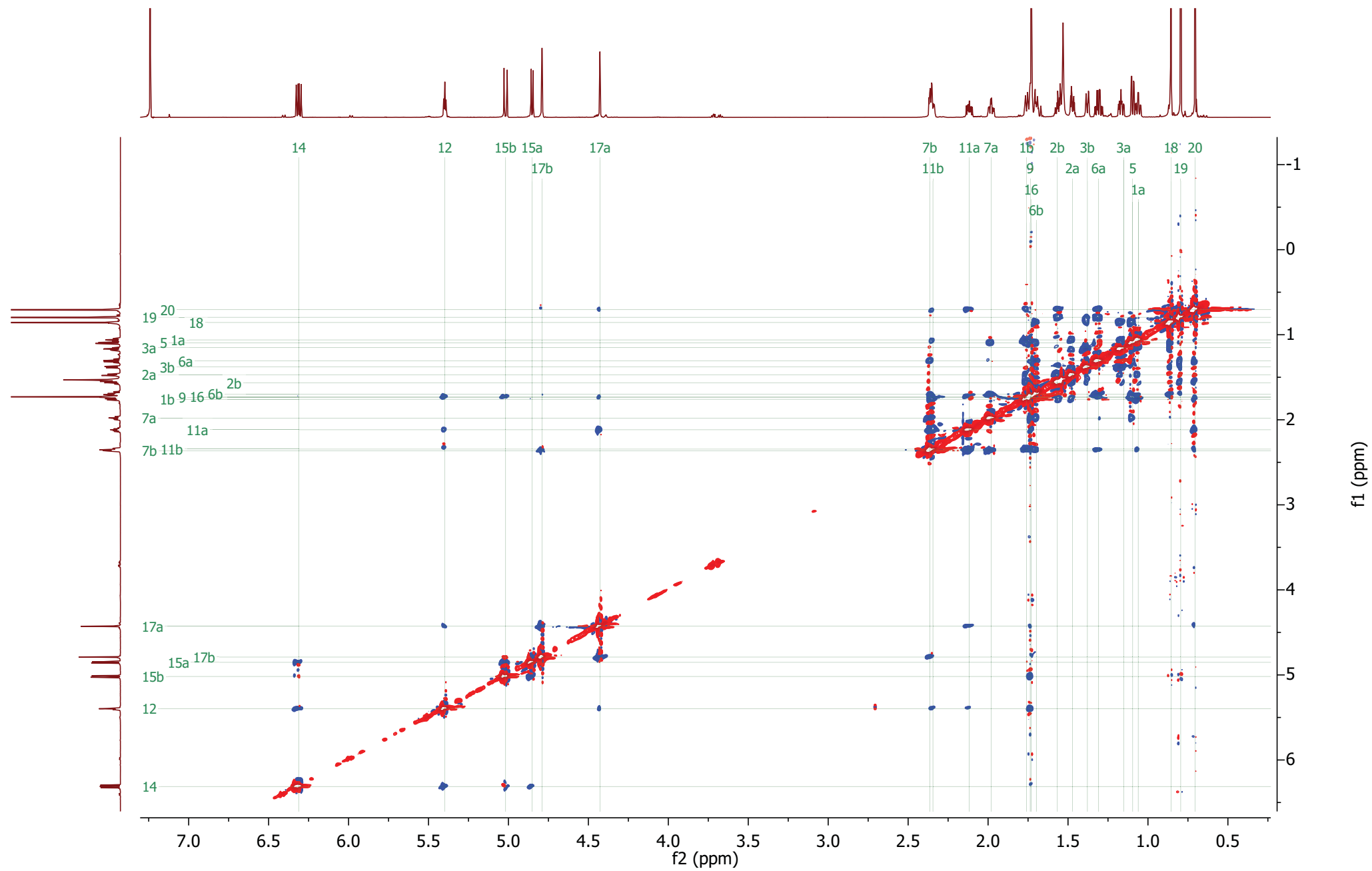


Figure S16-F. ^1H NOESY of trans-biformene [34].

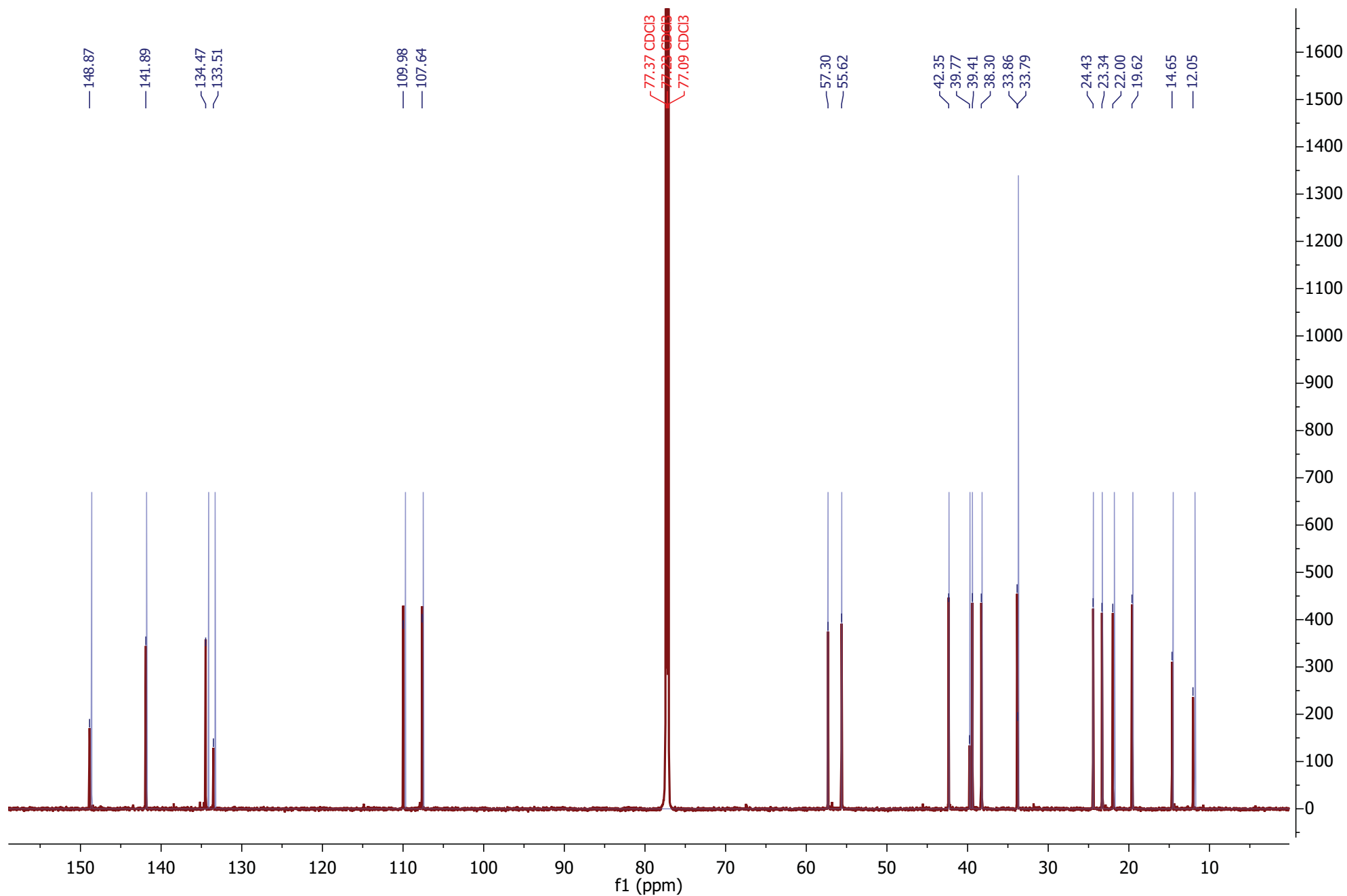


Figure S16-G. Overlay of ^{13}C NMR of trans-biformene [34] (red) with ^{13}C NMR spectrum (blue) reconstructed from shifts reported for the same compound by Bohlmann and Czerson (1979) (DOI: 10.1016/S0031-9422(00)90926-9).

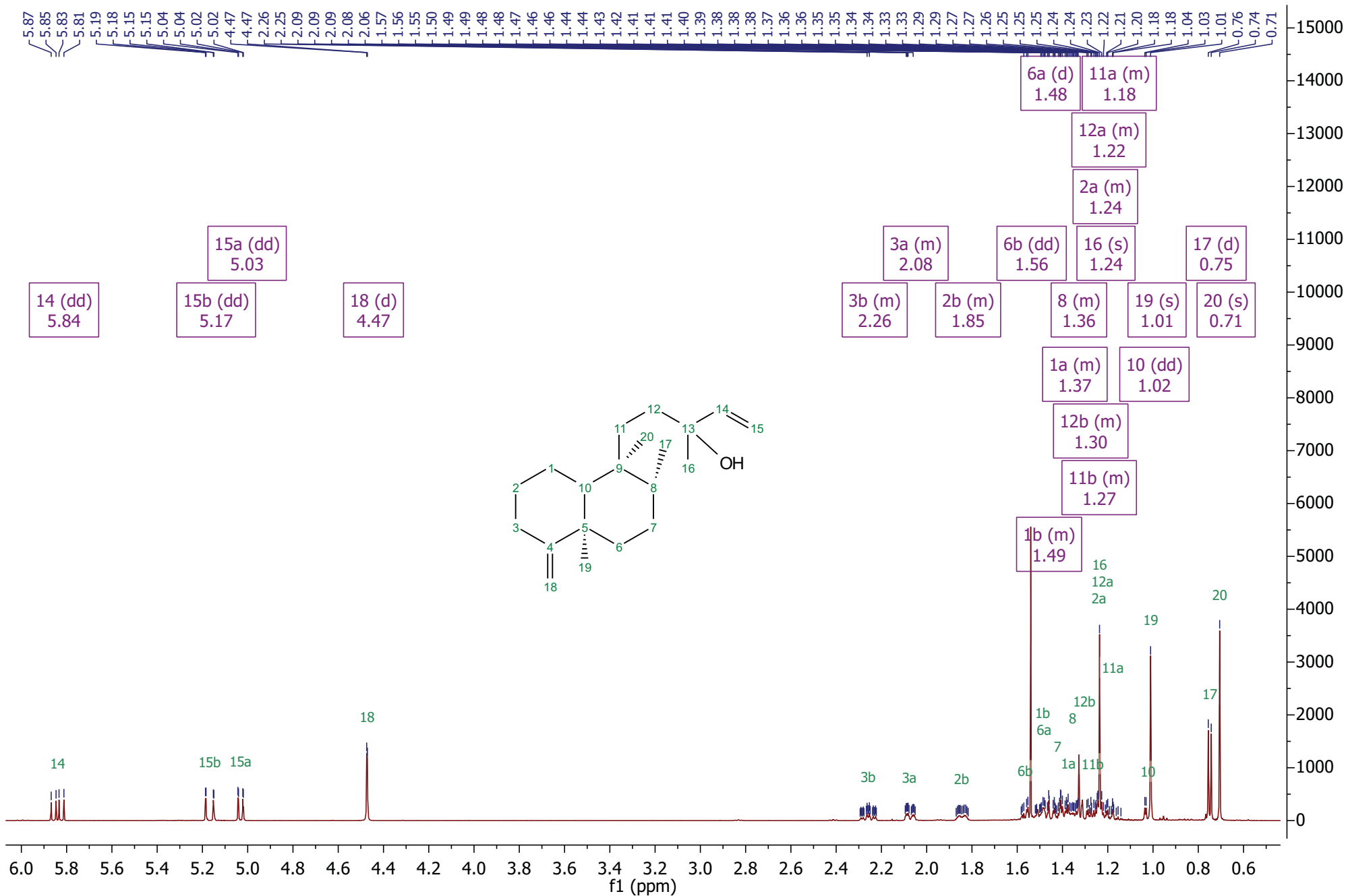


Figure S17-A. ¹H NMR of neo-cleroda-4(18),14-dien-13-ol [37].

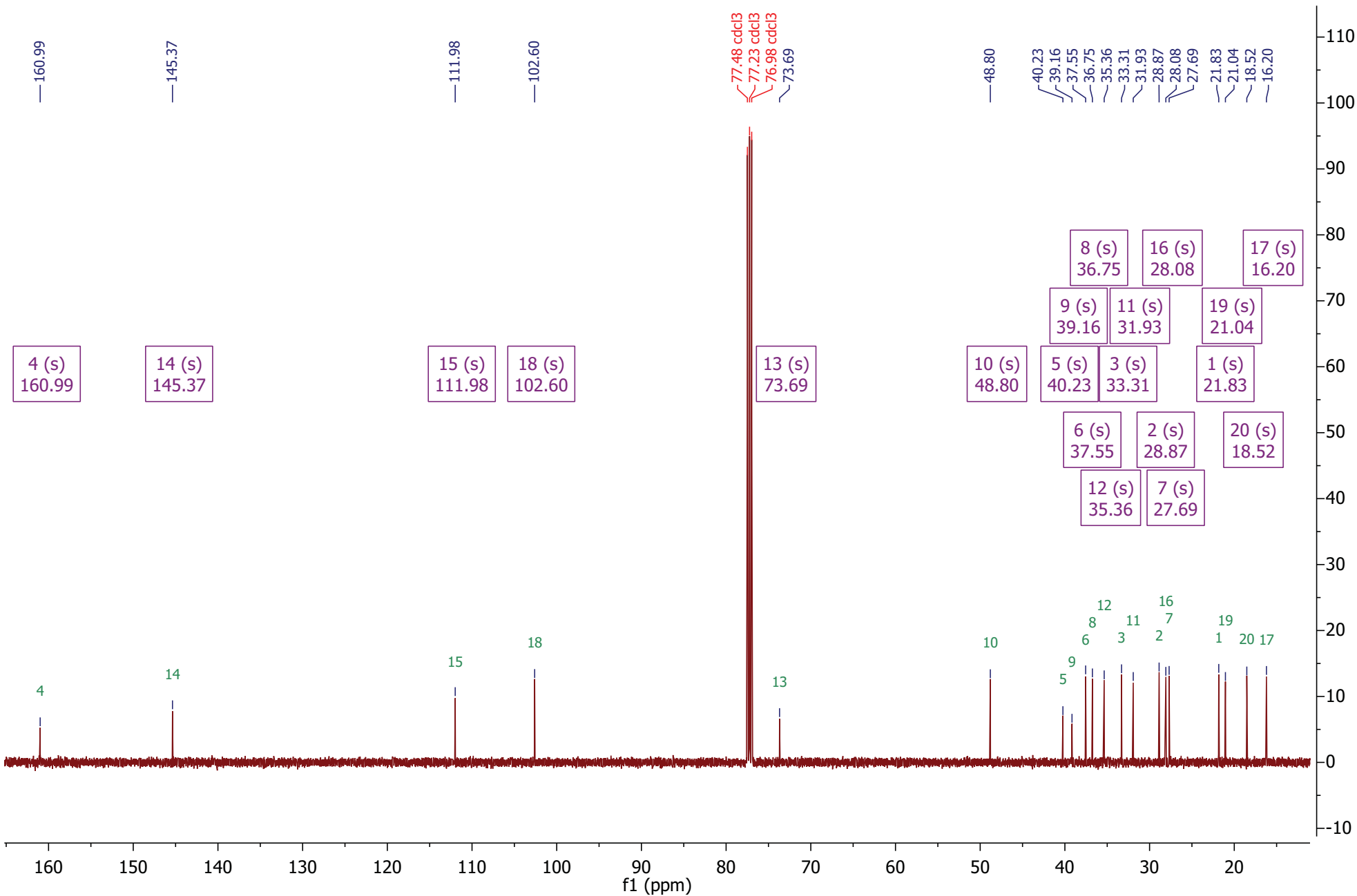


Figure S17-B. ^{13}C NMR of neo-cleroda-4(18),14-dien-13-ol [37].

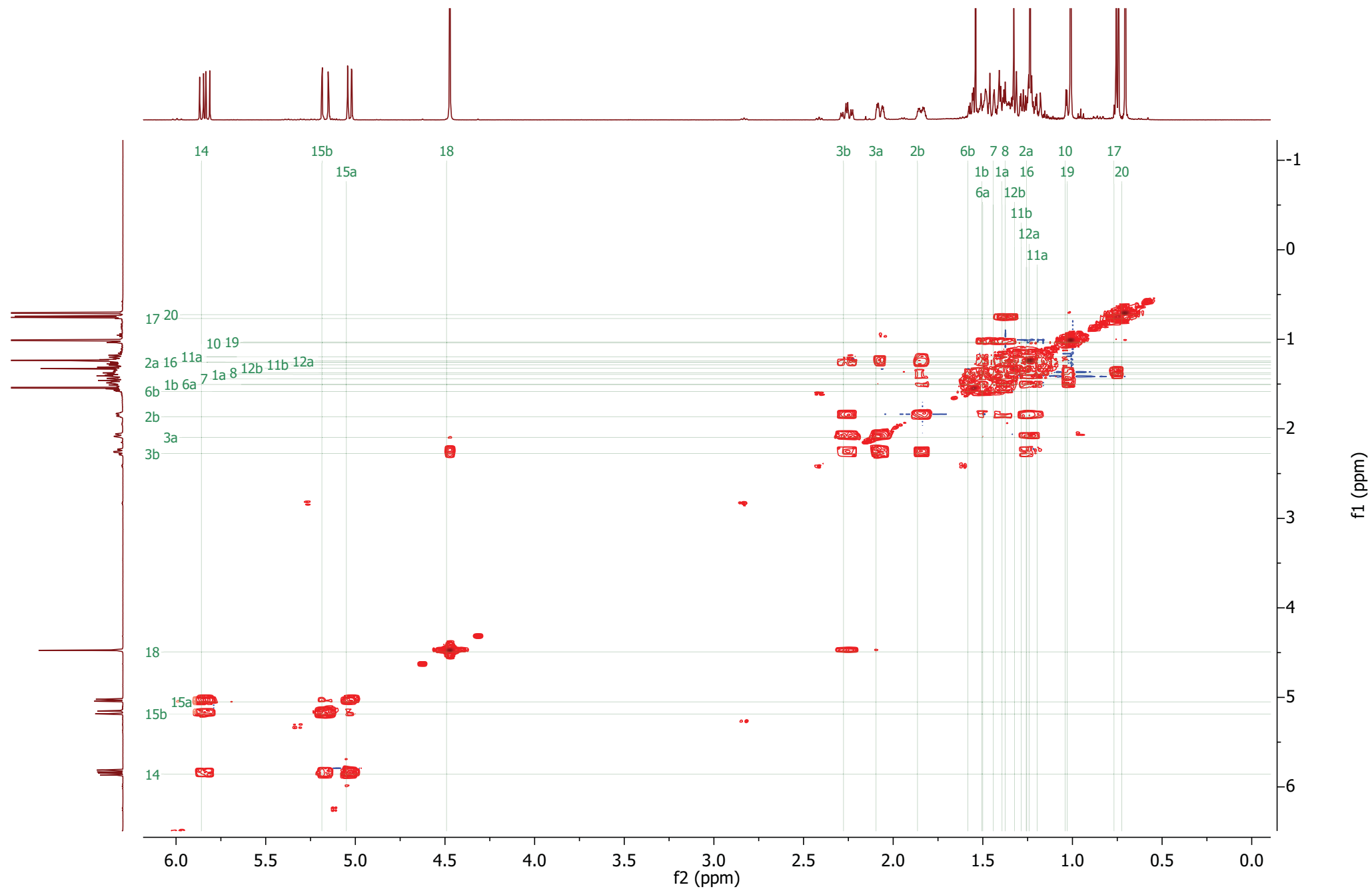


Figure S17-C. ^1H - ^1H COSY of neo-cleroda-4(18),14-dien-13-ol [37].

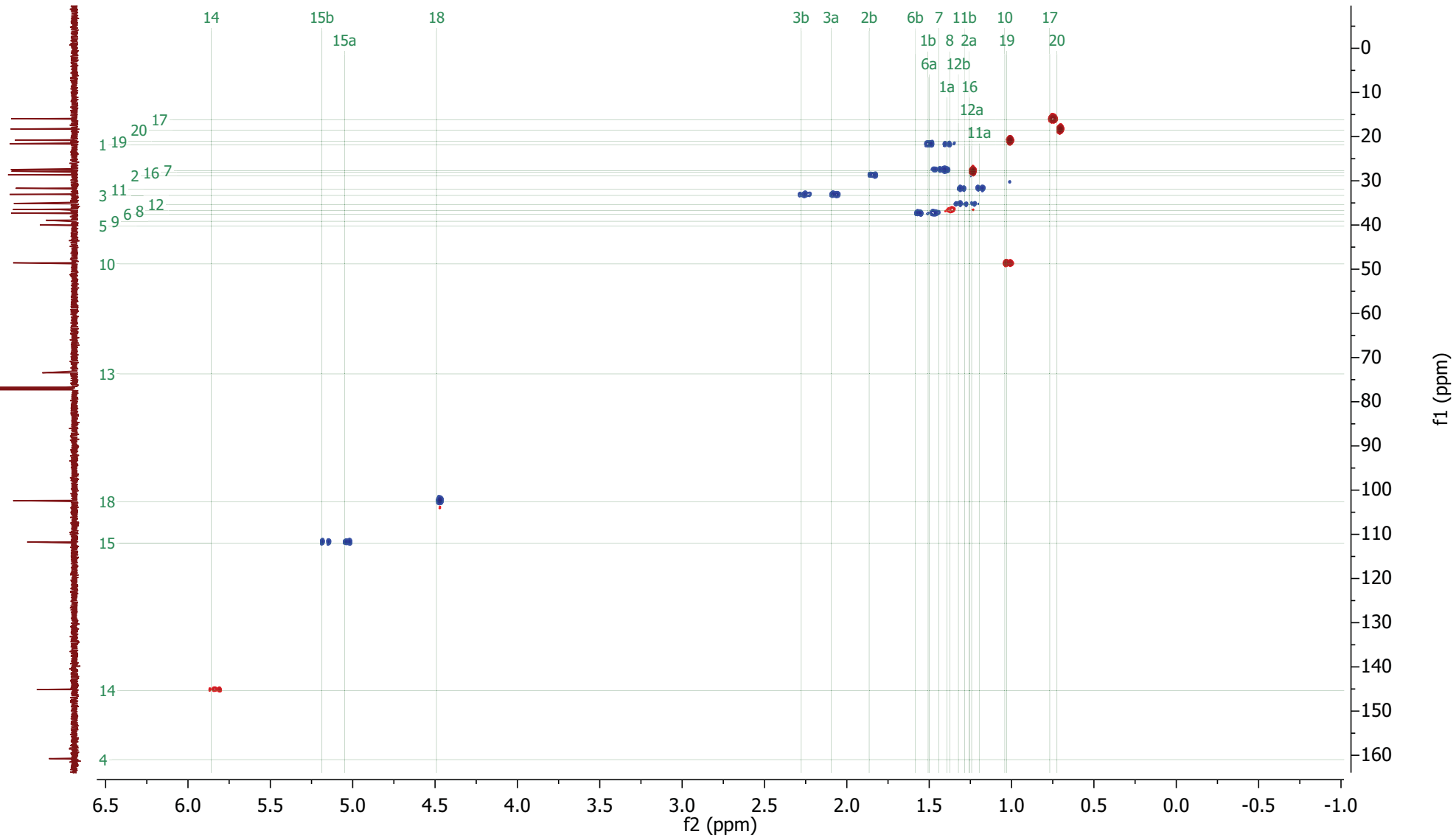
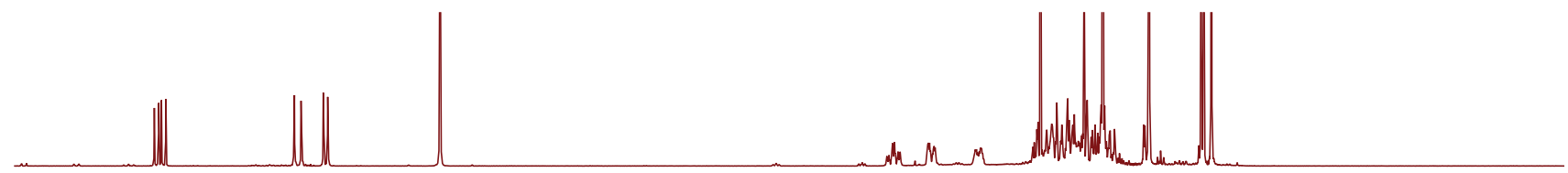
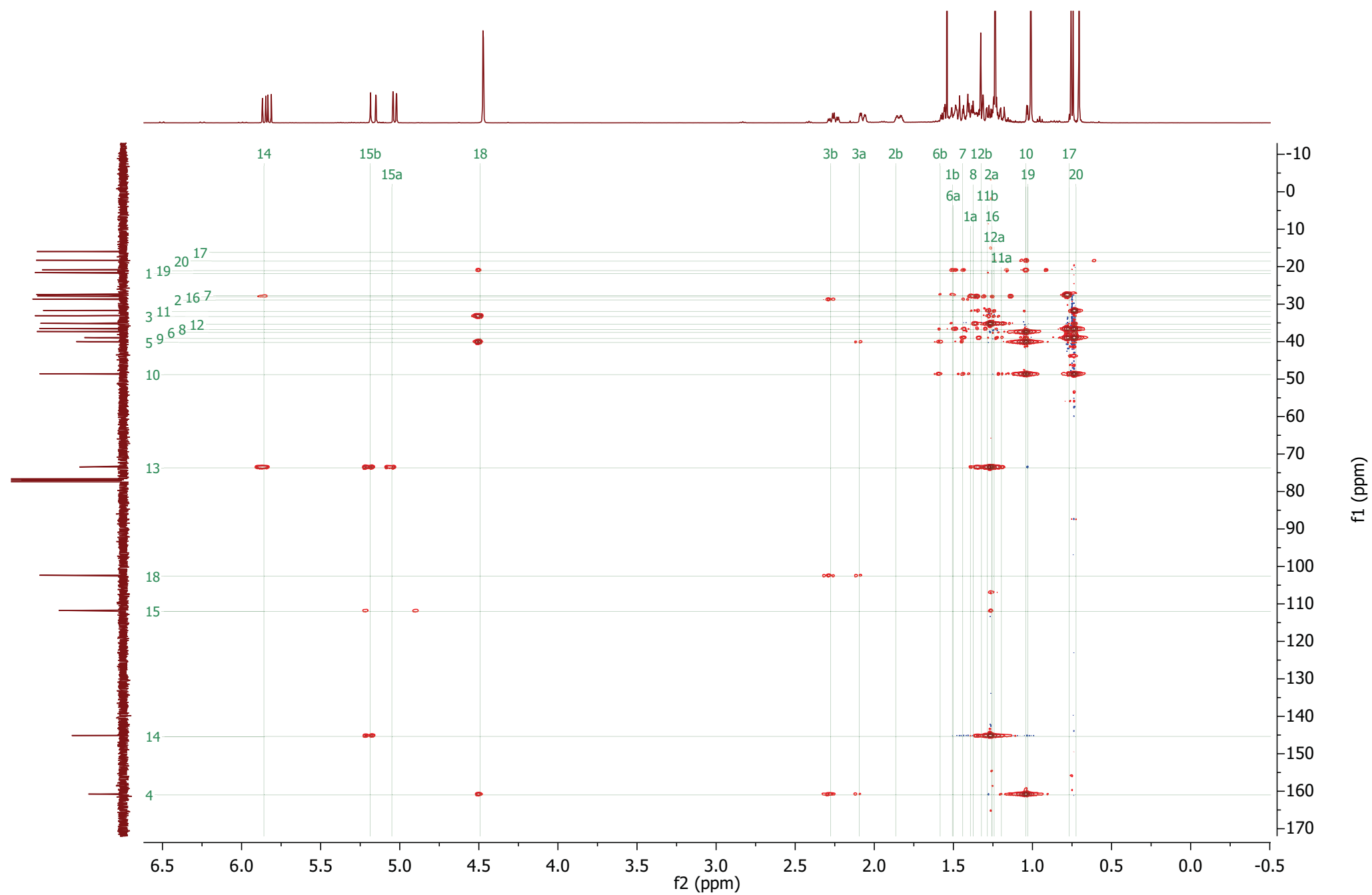


Figure S17-D. ^1H - ^{13}C HSQC of neo-cleroda-4(18),14-dien-13-ol [37].



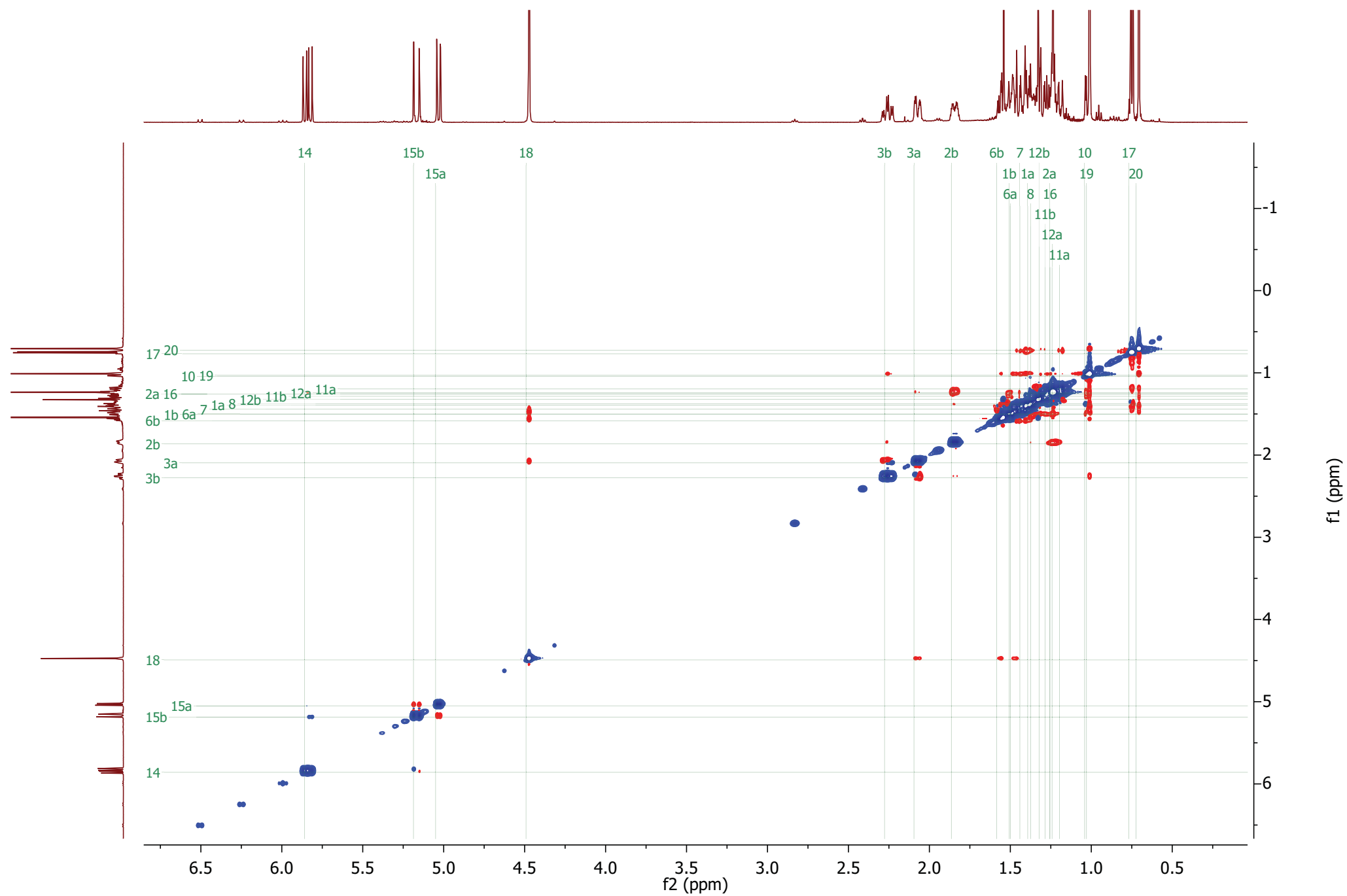


Figure S17-F. ^1H NOESY of neo-cleroda-4(18),14-dien-13-ol [37].

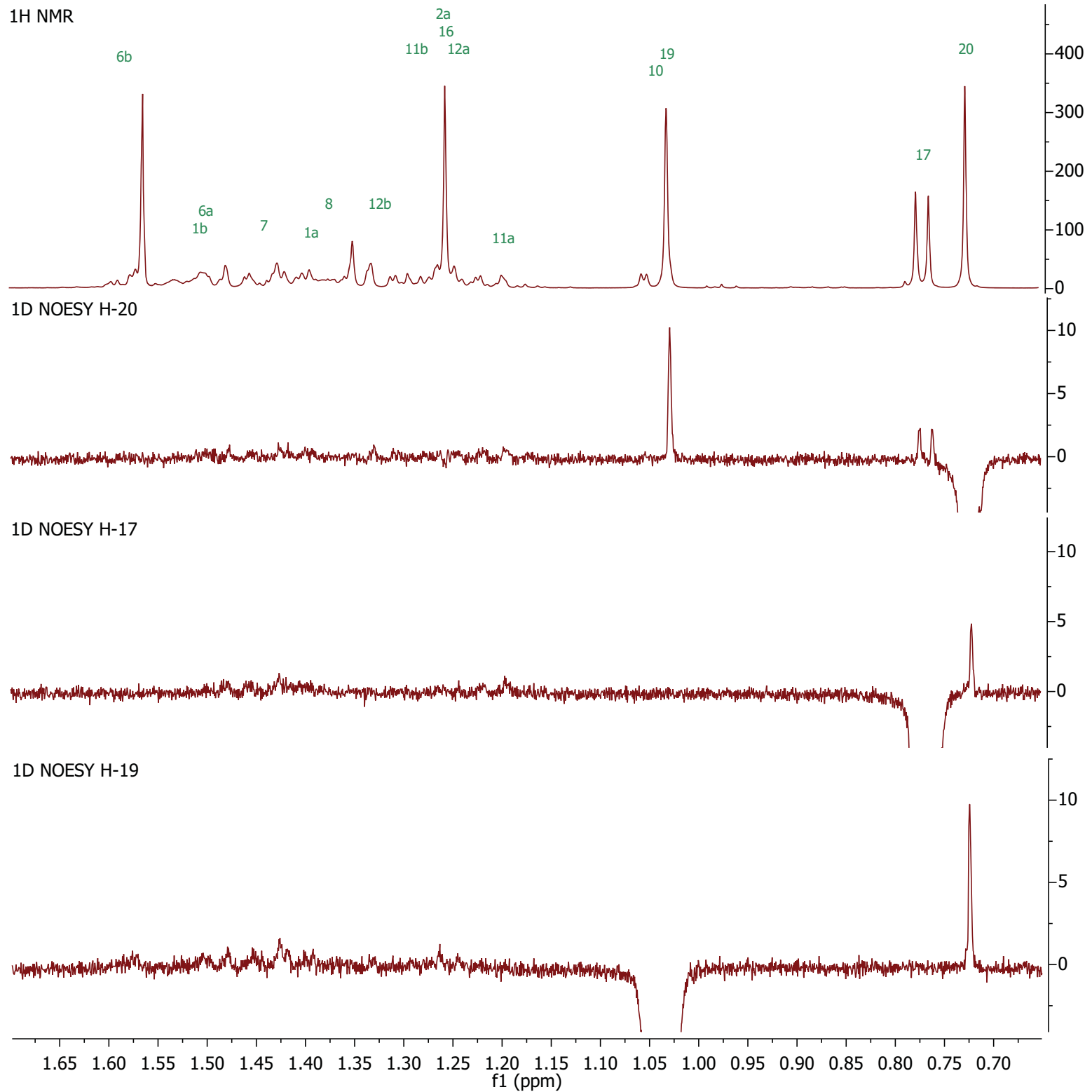


Figure S17-G. ^1H 1D-NOESY of neo-cleroda-4(18),14-dien-13-ol [37].

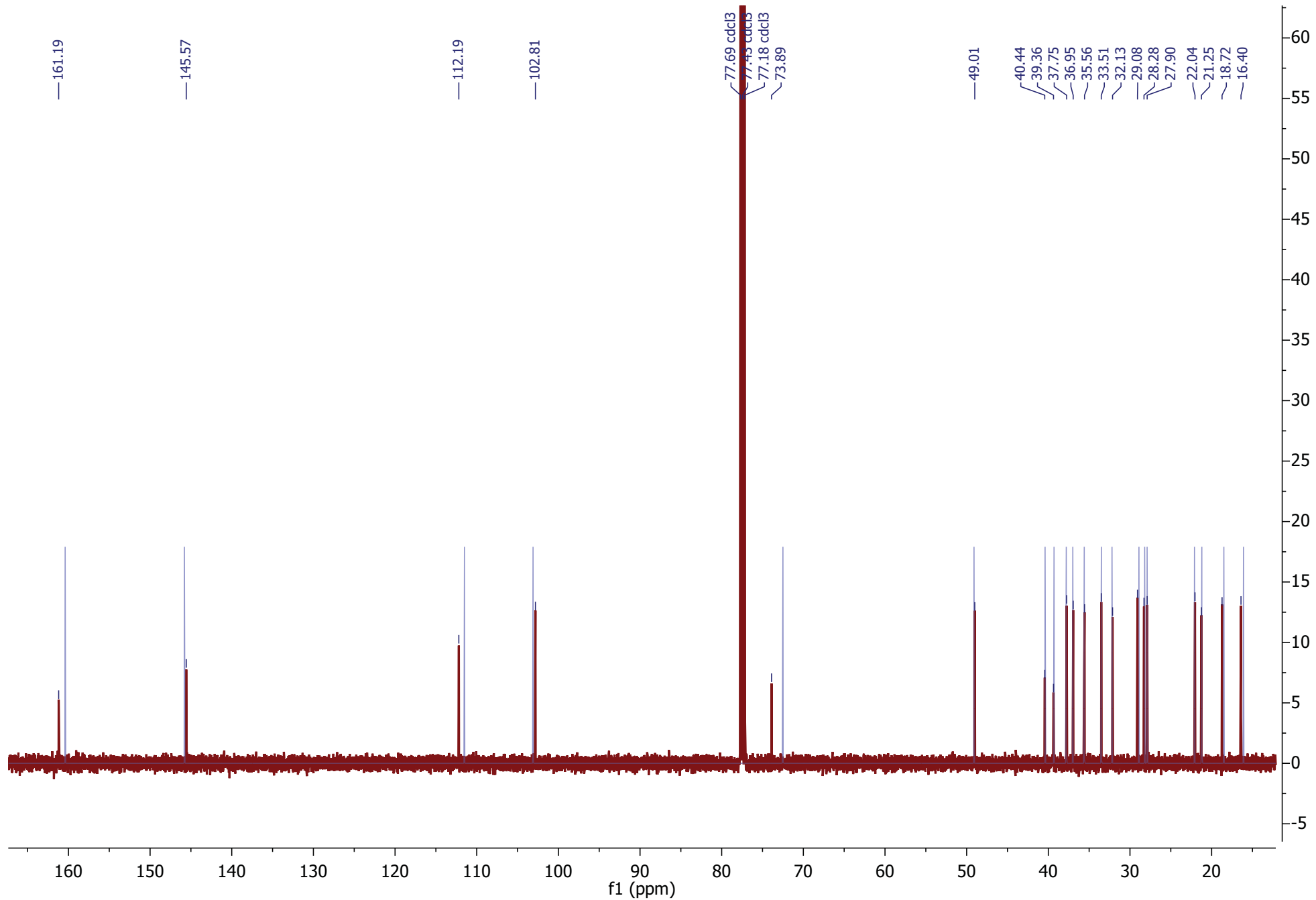


Figure S17-H. Overlay of ^{13}C NMR of neo-cleroda-4(18),14-dien-13-ol [37] (red) with ^{13}C NMR spectrum (blue) reconstructed from shifts reported for the same compound by Rudi and Kashman (1992) (DOI: 10.1021/np50088a004).

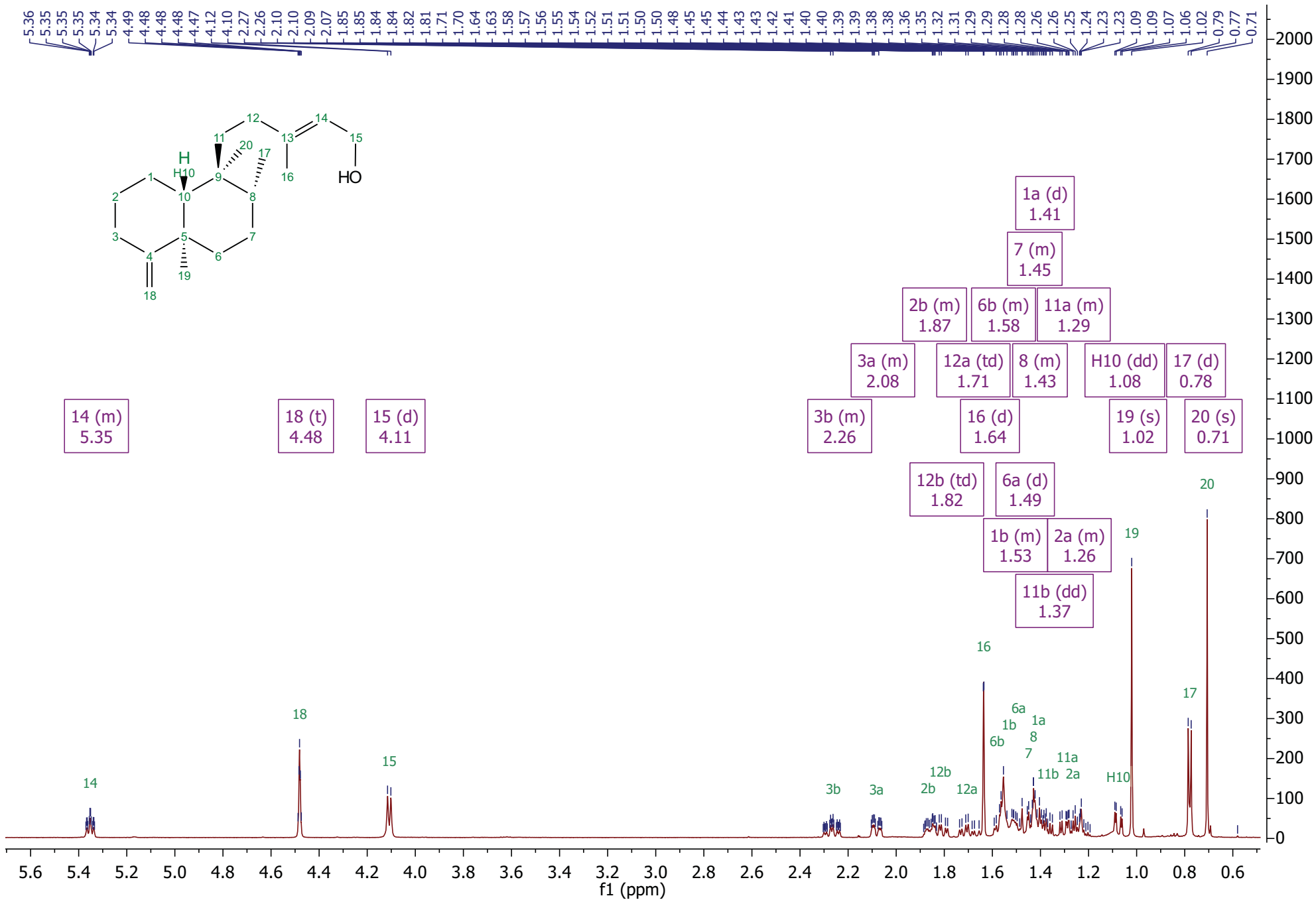


Figure S18-A. ^1H NMR of neo-cleroda-4(18),13E-diene-15-ol [38a].

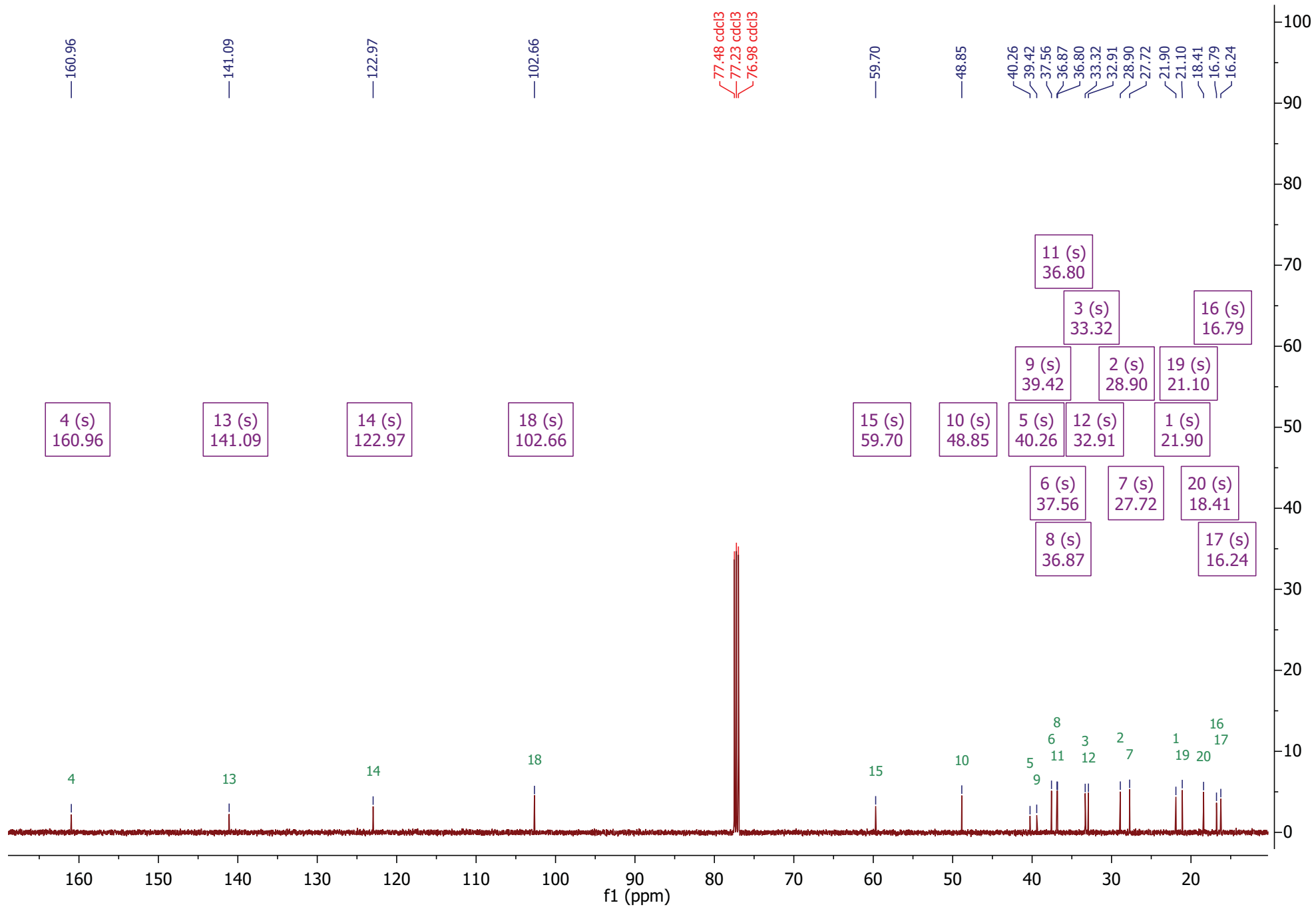


Figure S18-B. ^{13}C NMR of neo-cleroda-4(18),13E-diene-15-ol [**38a**].

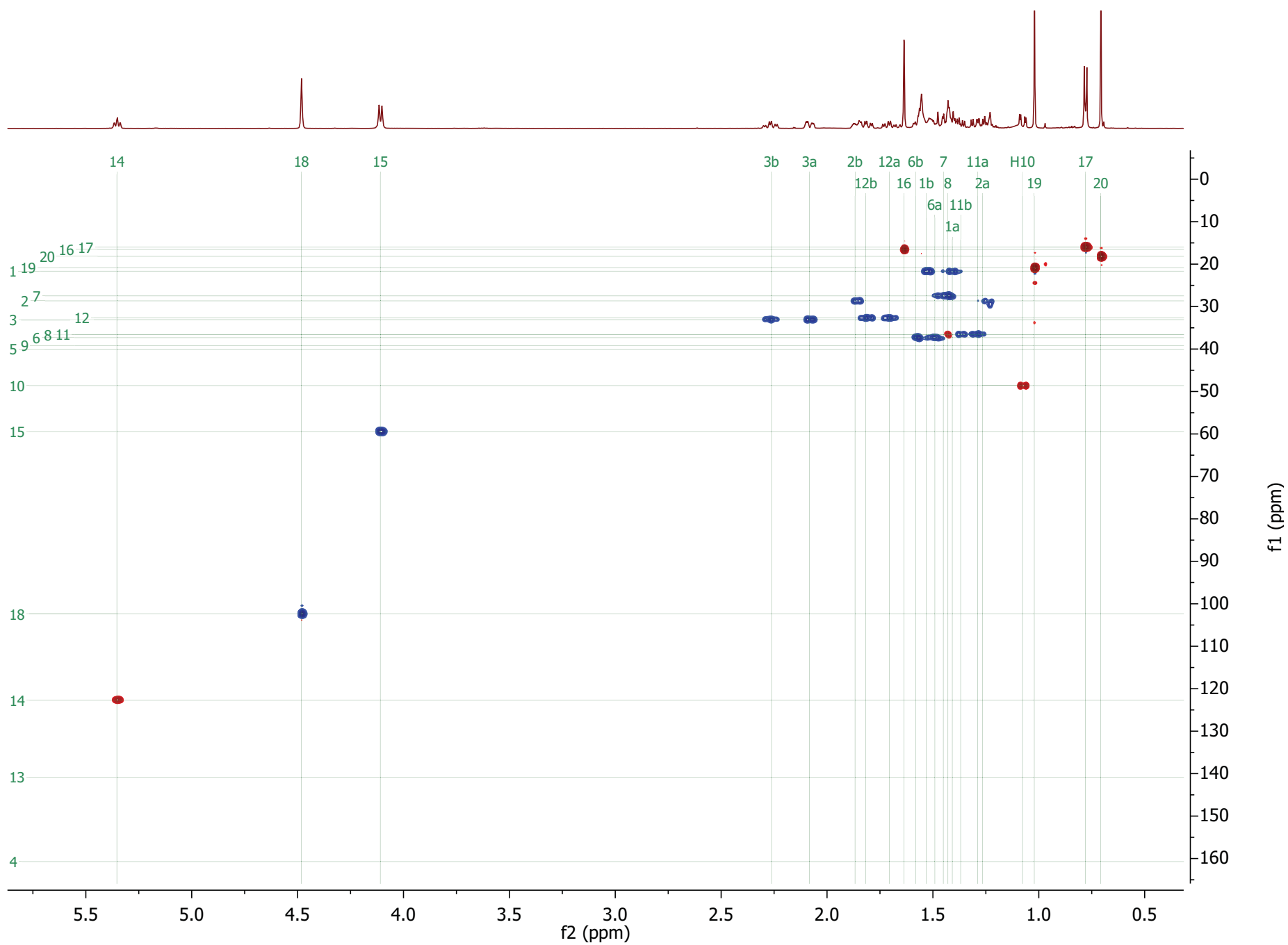


Figure S18-D. ^1H - ^{13}C HSQC of neo-cleroda-4(18),13E-diene-15-ol [**38a**].

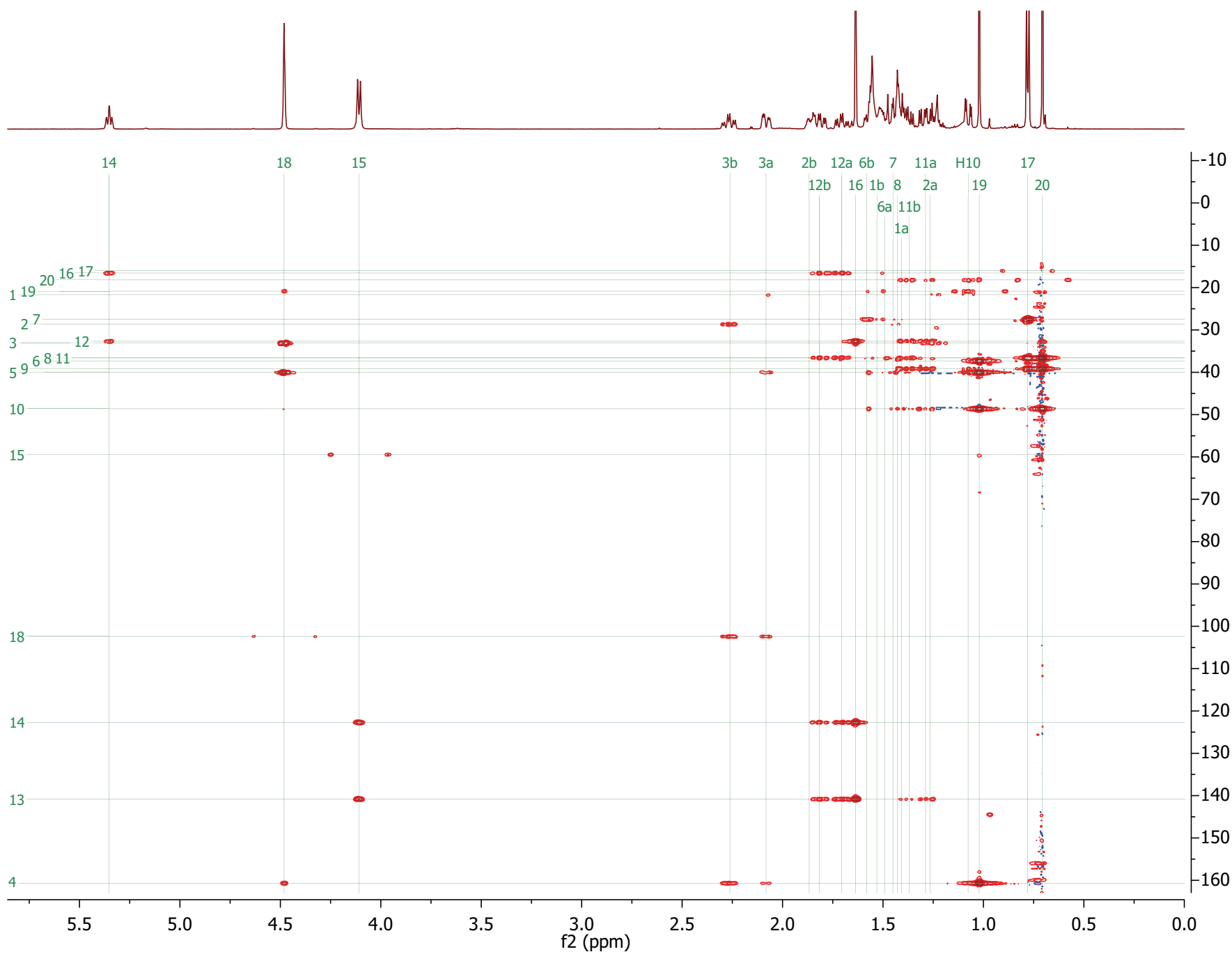


Figure S18-E. ^1H - ^{13}C HMBC of neo-cleroda-4(18),13E-diene-15-ol [38a].

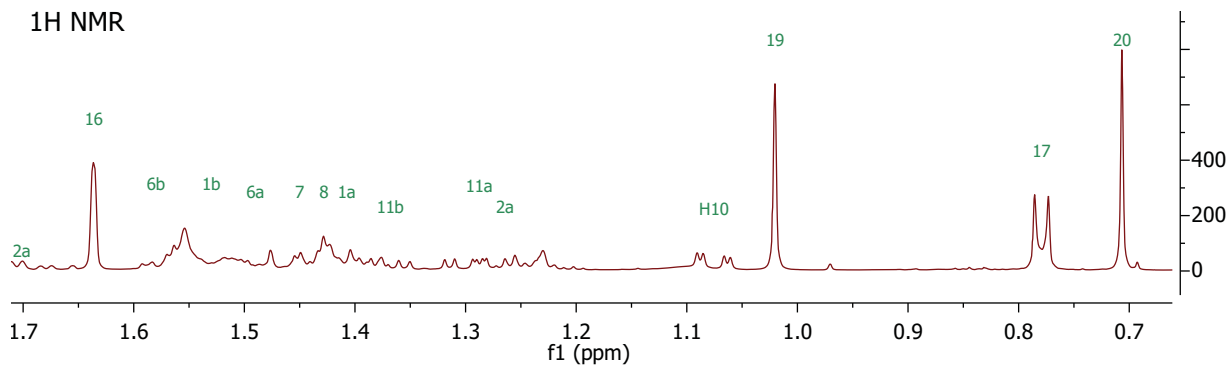
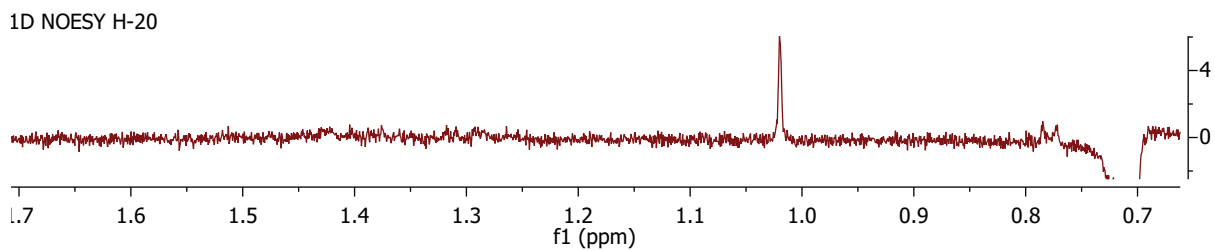
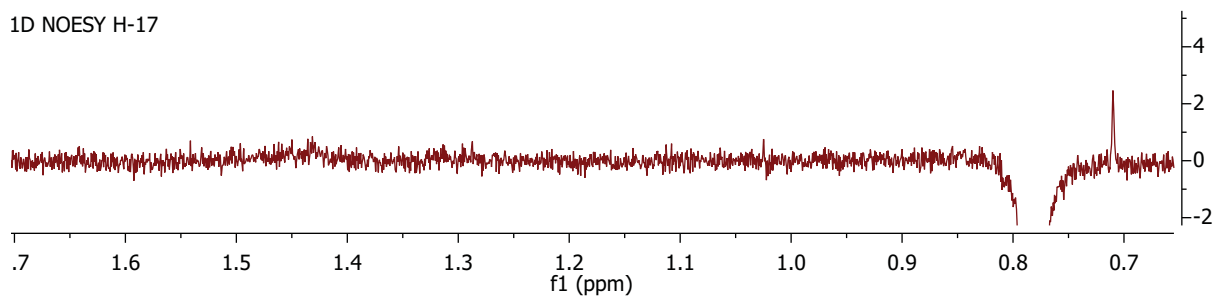
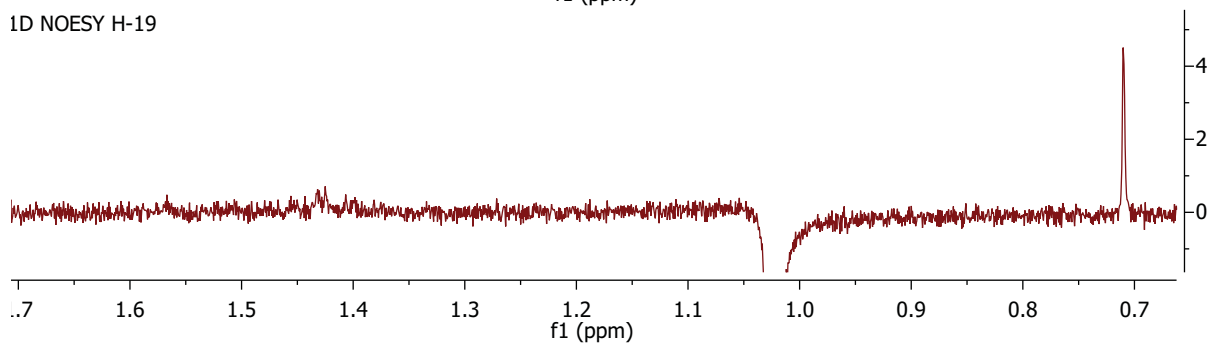
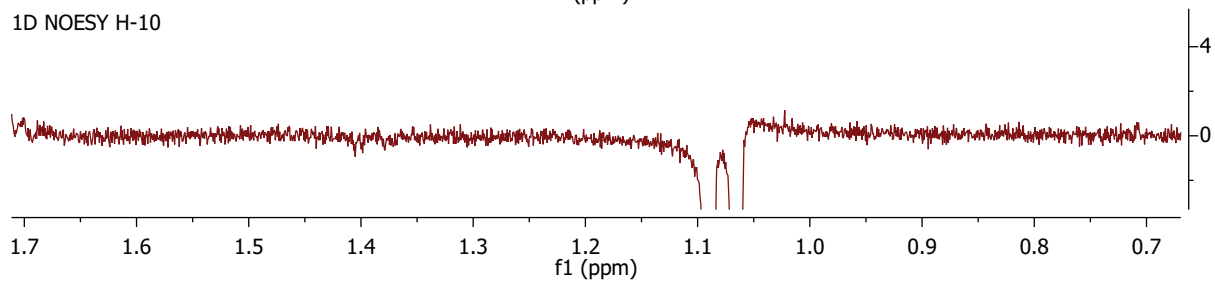


Figure S18-F. ¹H 1D-NOESY of neo-cleroda-4(18),13E-diene-15-ol [**38a**].



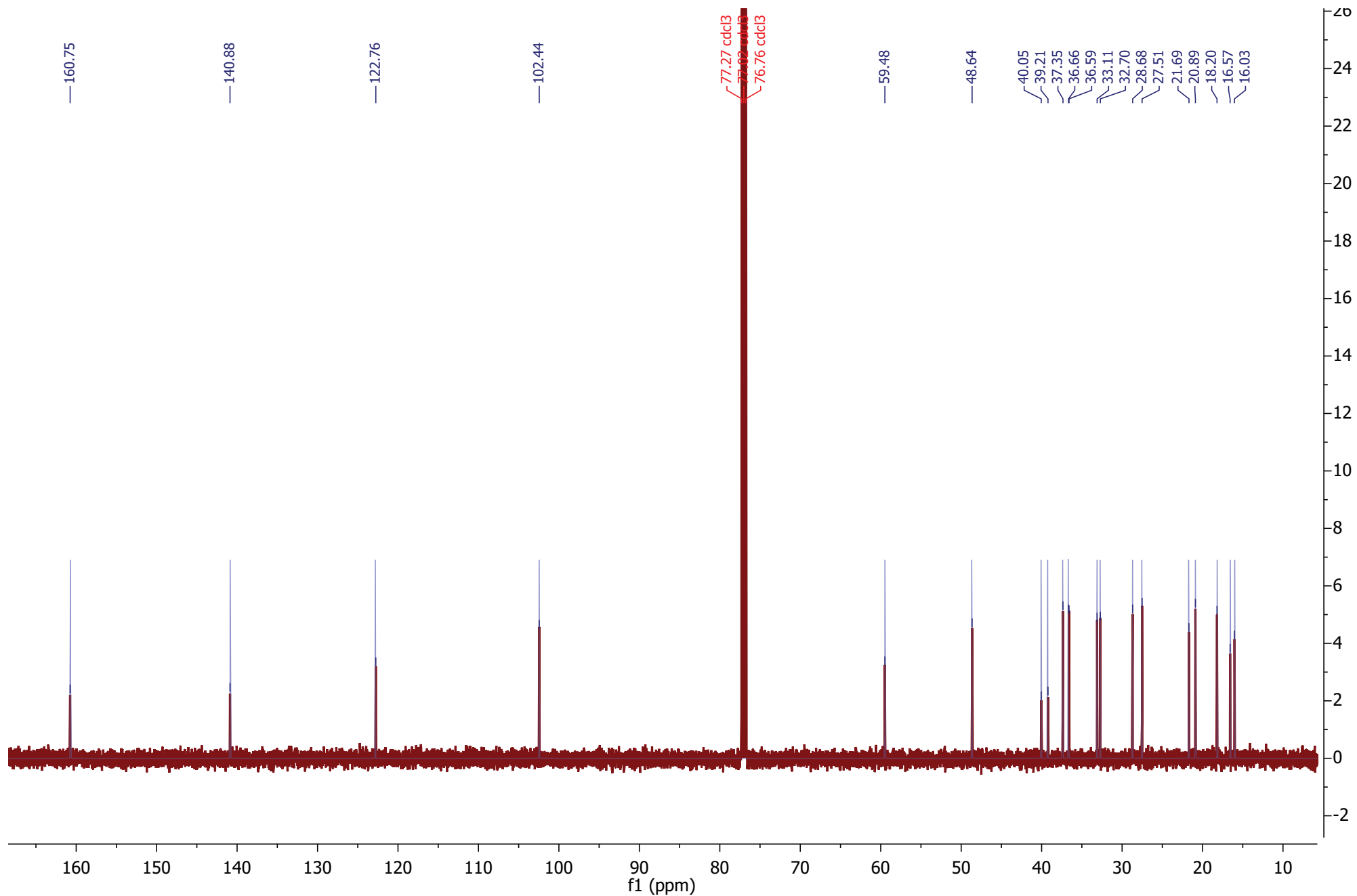


Figure S18-G. Overlay of ^{13}C NMR of neo-cleroda-4(18),13E-diene-15-ol [**38a**] (red) with ^{13}C NMR spectrum (blue) reconstructed from shifts reported for the same compound by Ohsaki (1994) (DOI: 10.1016/S0960-894X(01)80834-9).

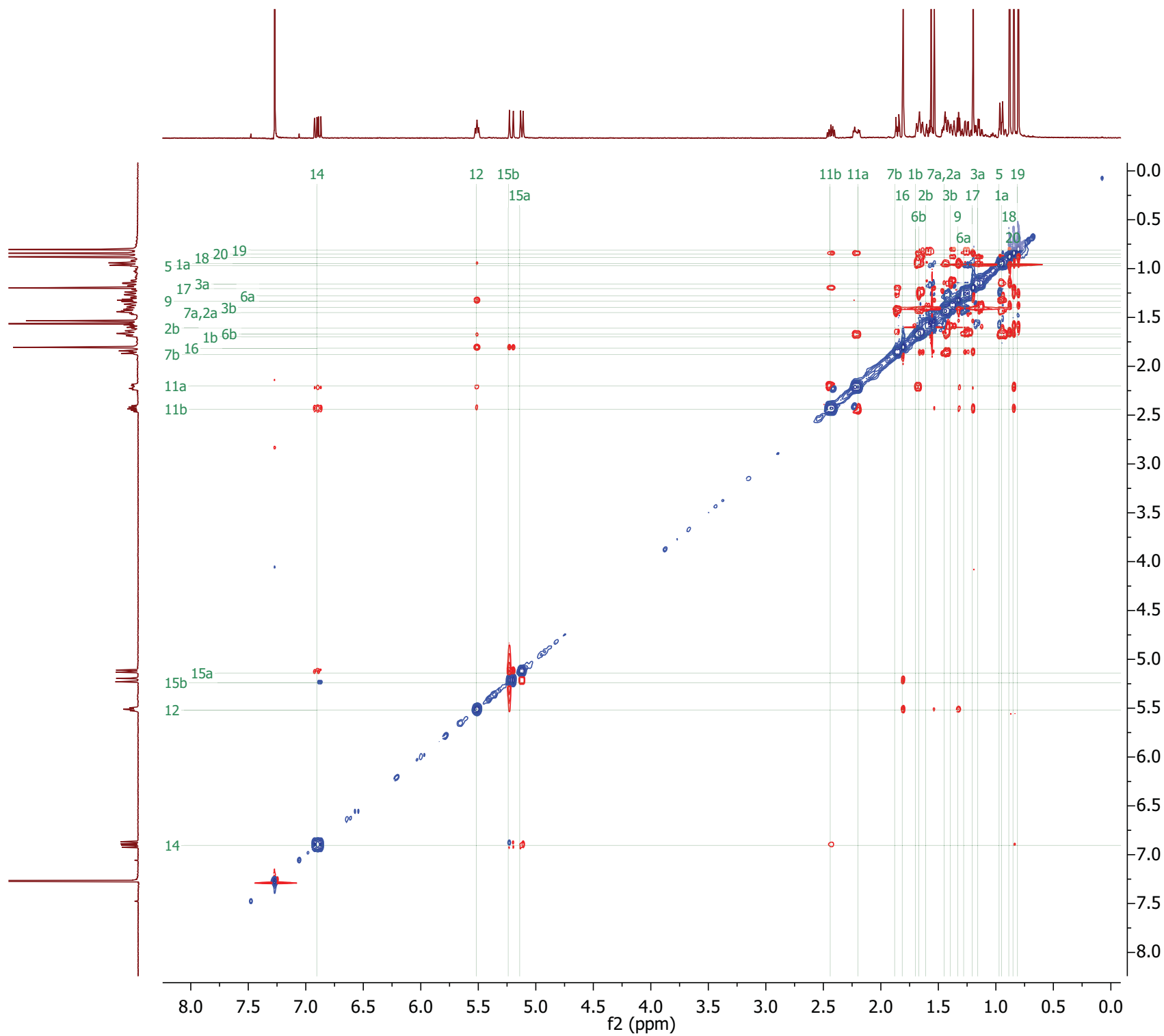


Figure S19. NOESY of (+)-cis-abienol.

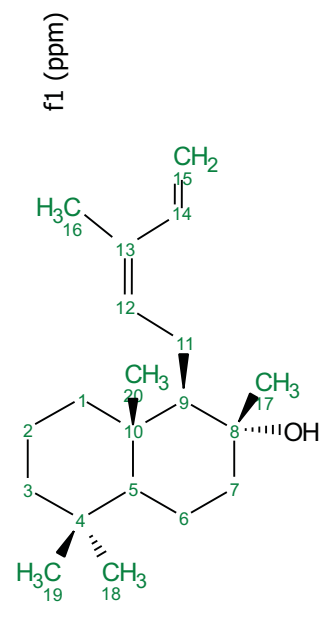




Figure S20. Maximum likelihood tree of all diTPS candidates from the transcriptome datasets (grey), functionally characterized from previous literature (black), and functionally characterized in the current work (blue). Beside each characterized enzyme are its reported activities, with substrates (green) and products (black) corresponding to compound names in Fig. 3. Branches with less than 50% bootstrap support have been merged. We have assigned a hierarchical numbering scheme to selected branches. Scale bar is substitutions per site.

	SmCPS5	247	D I L H O M P T T L L S L S L E	261	313	G G V P V Y P V D L F E H W A V D R	332
	hCPS5	152	D I M H O V P T T L L S L S L E	99	151	G G V P V Y P V D L F E H W A V D R	170
	hCPS1	85	D I M H O V P T T L L S L S L E	166	216	G G V P V Y P V D L F E H W A V D R	237
	LECA_c10585_g1_f1_len_988		
	MAVU_c17503_g1_f1_len_979		
	STOF_c3038_g1_f1_len_1374		
	BAPS_c38975_g1_f1_len_1429		
	GMPH_c28201_g1_f1_len_1294		
	LELE_c34086_g1_f1_len_2568		
	ROMY_c82858_g1_f2_len_2754		
	FLBA_c43822_g1_f3_len_2365		
	SCBA_c36900_g1_f1_len_2503		
	COTO_c42838_g1_f1_len_2629		
	POCA_c40441_g1_f4_len_1907		
	HYOF_c37586_g1_f3_len_2383		
	PEFR_c45278_g1_f8_len_2504		
	GLHE_c57550_g1_f2_len_2480		
	MODI_c38179_g1_f1_len_2041		
	MESP_c38956_g1_f1_len_2158		
	ORVU_c47333_g1_f1_len_1951		
	NEMU_c38266_g1_f2_len_1931		
	HOSA_c37880_g1_f2_len_1881		
	OCBA_c37766_g3_f2_len_2263		
	SAOF_c30355_g1_f1_len_2263		
	SAOF_c30355_g1_f4_len_2316		
	VIAG_c38645_g1_f1_len_1665		
	STOF_c59939_g1_f3_len_2315		
	POCA_c38632_g1_f1_len_2524		
	MAVU_c26355_g1_f1_len_2031		
	STOF_c59939_g1_f1_len_1968		
	PEBA_c25813_g1_f1_len_3431		
	PRMI_c45899_g1_f2_len_2156		
	RcTPS1	246	D I L H S V P T T L L S L S L E	262	317	G G V P V Y P V D L F E H W A V D R	336
	SmCPS4	233	D L L H K E P T S L L S L S L E	247	298	G G V P S T Y P V D M F E H W A V D R	317
	SdCPS	244	D L M H K K P T S L L S L S L E	258	309	G G V P N A Y P V D M F E H W S V D R	328
	SdCPS2	244	D L M H K K P T S L L S L S L E	258	309	G G V P N A Y P V D M F E H W S V D R	328
	hCPS2	245	D L L H K K P T S L L S L S L E	259	310	G G V P N A Y P V D M F E H W S V D R	329
	hTPS5	247	E L L H K K P T S L L S L S L E	261	312	G G V P V Y P V D M F E H W C V D R	331
	hCPS4	247	E L L H K K P T S L L S L S L E	261	312	G G V P N A Y P V D M F E H W C V D R	331
	VacTPS5	251	D L L H K M P T S L L S L S L E	265	316	G G V P N A Y P V D M F E H W S V D R	335
	HYOF_c31998_g1_f1_len_1666		
	AJRE_c45174_g1_f1_len_1668		
	TECA_c19929_g1_f1_len_2476		
	AJRE_c45174_g1_f1_len_2599		
	HOSA_c51370_g1_f1_len_2884		
	SAOF_c14142_g1_f1_len_2823		
	FLBA_c32662_g1_f3_len_2623		
	HYSU_c32723_g3_f2_len_2950		
	SAHI_c23896_g1_f2_len_2514		
	AtTPS2	251	D I L H K M P T L L S L S L E	265	316	G G V P N A F P V D L F O R N Y T V D R	335
	VacTPS3	255	E L L H K V P T C L L H N L E	269	327	G G A P T Y P V D I Y A R W A V D R	346
	LELE_c29933_g1_f4_len_1316		
	MEOF_c10891_g1_f1_len_1225		
	GLHE_c33069_g1_f1_len_1370		
	TECA_c29692_g2_f3_len_1717		
	LAAL_c35372_g1_f6_len_1290		
	PRMI_c42137_g1_f2_len_1091		
	OCBA_c47569_g1_f1_len_2099		
	GMPH_c33245_g1_f3_len_970		
	OCBA_c47569_g1_f4_len_2198		
	AJRE_c45070_g1_f1_len_2433		
	PEBA_c45402_g1_f3_len_2781		
	HOSA_c47203_g1_f1_len_2442		
	ROMY_c81198_g2_f2_len_2017		
	VIAG_c32650_g1_f3_len_2627		
	hCPS2	249	D M I Y Q T P T L L S L S L E	263	315	G G A P T Y P V D V F A R W A I D R	334
	PEAT_c33246_g1_f3_len_2607		
	HYSU_c33333_g1_f3_len_2503		
	FLBA_c40811_g2_f2_len_2549		
	CTPS16	261	D M I Y K P T L L S L S L E	281	335	G G A P T Y P V D V F A R W A V D R	354
	LYAM_c35560_g1_f1_len_2678		
	GLHE_c59273_g1_f1_len_1937		
	SdCPS	249	D M I Y Q T P T L L S L S L E	261	315	G G A P T Y P V D V F A R W A V D R	332
	PaTPS1	249	D M I Y Q T P T L L S L S L E	263	315	G G A P T Y P V D V F A R W A I D R	334
	RcCPS1	250	D M I Y Q K P T L L S L S L E	264	316	G G A P T Y P V D V F A R W A V D R	335
	ROOF_c45565_g1_f2_len_2515		
	GLHE_c59273_g1_f1_len_1653		
	hCPS5	129	E I M H K V P T S L L S L S L E	143	195	G G A P T Y P V D V F A R W A I D R	214
	SmCPS2	248	D M I Y Q T P T L L S L S L E	262	314	G G V P T Y P V D V F A R W A V D R	333
	OmTPS1	246	D L I Y K L P T L L S L S L E	260	312	G G A P T Y P V D V F A R W A V D R	331
	ORMA_c54314_g1_f2_len_2574		
	NEMU_c35579_g1_f1_len_2522		
	hMTPS1	161	D F I Y Q L P T L L S L S L E	175	227	G G V P H T Y P V D V F A R W A V D R	246
	CTPS2	233	G M I Y E S P T S L L S L S L E	247	299	G G V P T Y P V D I F A R W A V D R	318
	LAAN_c34939_g1_f2_len_1800		
	SaTPS9	247	D L V Y Q M P T N L L S L S L E	261	313	G G A P T Y P V D I F S R W A I D R	332
	SaTPS3	247	D L V Y Q M P T N L L S L S L E	261	313	G G A P T Y P V D I F S R W A I D R	332
	SdCPS	247	D L V Y Q M P T N L L S L S L E	261	313	G G A P T Y P V D I F S R W A I D R	332
	SaTPS1	247	D L V Y Q M P T N L L S L S L E	261	313	G G A P T Y P V D I F S R W A I D R	332
	hTPS3	258	E M M H K V P T S L L S L S L E	272	324	G G A P T Y P V D V F G R W A V D R	343
	HYSU_c13756_g1_f1_len_1339		
	TECA_c34302_g1_f1_len_1099		
	VIAG_c37219_g2_f1_len_1173		
	CTPS1	251	E M M H K V P T S L L S L S L E	265	317	G G A P T Y P V D V F G R W A I D R	336
	FLBA_c39643_g1_f2_len_2593		
	PEAT_c32259_g1_f2_len_1304		
	LAAN_c38531_g1_f2_len_2542		
	OCBA_c37312_g1_f1_len_2648		
	CAAM_c2515_g1_f1_len_2714		
	MESP_c38573_g1_f3_len_1898		
	HYOF_c42573_g1_f1_len_2614		
	WEFR_c42740_g1_f1_len_2690		
	ORMA_c38919_g1_f1_len_2152		
	ROOF_c48395_g1_f1_len_2519		
	SmCPS1	245	E I M H K I P T S L L S L S L E	259	311	G G A P T Y P V D V F G R W A I D R	330
	SmCPS1	245	E I M H K M P T S L L S L S L E	259	311	G G A P T Y P V D V F G R W A I D R	330
	SAHI_c16498_g1_f1_len_2488		
	CLBI_c50557_g1_f2_len_2607		
	SdCPS1	247	E I M H K M P T S L L S L S L E	262	314	G G A P T Y P V D V F G R W A V D R	332
	PRLA_c89704_g1_f1_len_2472		
	VacTPS1	250	E V L H E R S T S I L Y G M E	264	318	G A R V Y P V D L F A R W A V D R	337
	SCBA_c41634_g1_f1_len_2686		
	TECA_c34302_g2_f1_len_2744		
	VIAG_c37219_g1_f2_len_2543		
	AtTPS1	250	E M M H K V P T S L L S L S L E	264	316	G G A P T Y P V D V F G R W A V D R	335
	AJRE_c45774_g1_f2_len_2689		
	MAVU_c27584_g1_f1_len_2109		
	MvCPS1	245	E V V H K V A T S L L S L S L E	259	311	G G A P T Y P V D I F G R W A V D R	330
	CTOF_c59840_g1_f1_len_2078		
	OCBA_c41727_g1_f4_len_1501		
	BAPS_c40929_g1_f1_len_2571		
	MAVU_c24673_g2_f1_len_2610		
	MvCPS1	245	K M M E K E T S L M Y A A E	259	317	G G A P N Y P V D L W S R W A T D R	331
	LECA_c13964_g1_f1_len_2659		
	LELE_c30509_g1_f1_len_2647		
	LTPS1	245	K M M E K E T S L M Y A A E	259	312	G G A P N Y P I D L W S R W A T D R	331
	HsTPS1	241	E V M H O V T T L L S L S L E	255	307	G G A P N Y P I D I F A R W A V D R	326
	HYSU_c34362_g1_f2_len_2759		

Figure S21: Activity-determining regions in an alignment of previously known (black), newly characterized (blue), and candidate (grey) TPS-c enzymes from Lamiaceae. Red stars indicate residues previously implicated in catalytic specificity. Histidine at the first position and asparagine at the second position have been associated with *ent*-CPP synthase activity. Red hash indicates residue previously implicated in Mg²⁺ driven inhibition. A histidine in this position leads to sensitivity to Mg²⁺ inhibition, which is characteristic of *ent*-CPP synthases involved in gibberellin biosynthesis, whereas enzymes of specialized metabolism lacking the histidine showed no susceptibility to Mg²⁺ inhibition. Positions are colored to indicate conservation within each subgroup.

e.1
 LAAN_c45824.g1_i1_len_1972
 GLHE_c51663.g1_i1_len_1889
 IrKSL4
 LAAN_c49734.g1_i6_len_2679
 CTPS14
 IrKSL5
 HYSU_c32023.g1_i3_len_2593
 COCA_c71711.g1_i7_len_2445
 SAHI_c21045.g1_i1_len_2518
 ROOF_c44360.g1_i1_len_1554
 SmKSL2
 SAOF_c36508.g2_i2_len_2830
 PEAT_c42177.g1_i7_len_2662
 PEAT_c42177.g1_i1_len_2596
 MESP_c41204.g1_i6_len_2514
 THVU_c71799.g1_i1_len_2928
 ORVU_c48016.g1_i3_len_2871
 NEMU_c39161.g1_i3_len_2854
 NmTPS2
 LYAM_c36163.g1_i7_len_2644
 LYAM_c36163.g1_i6_len_2758
 HYOF_c40018.g1_i5_len_2592
 AGFO_c19795.g1_i2_len_2660
 POCA_c42029.g1_i1_len_2012
 LELE_c30109.g1_i2_len_2390
 MvEKS
 BAPS_c42988.g1_i1_len_2902
 LAAL_c31822.g1_i5_len_2621
 LECA_c32943.g1_i1_len_2385
 TECA_c30529.g1_i4_len_2666
 ROMY_c72568.g1_i1_len_1551
 HOSA_c49137.g1_i8_len_3068
 PRLA_c67476.g1_i3_len_2691
 SCBA_c41959.g1_i1_len_2133
 VacTPS4
 VIAG_c37546.g1_i6_len_2188
 PEBA_c45575.g1_i4_len_2870
 PRMI_c46179.g2_i1_len_2617
 WEFR_c42053.g1_i7_len_2877
 CAAM_c41278.g1_i3_len_2720
 LELE_c33431.g1_i1_len_1645
 LITPS4
 MvELS
 LECA_c29768.g1_i1_len_2003
 VacTPS6
 VIAG_c47887.g2_i4_len_2207
 VacTPS2
 VIAG_c47887.g2_i7_len_1591
 TECA_c17711.g1_i2_len_2085
 CLBU_c25642.g1_i1_len_2183
 AJRE_c43836.g1_i1_len_2029
 ArTPS3
 WEFR_c37115.g1_i1_len_2120
 PRLA_c63813.g1_i2_len_2643
 CAAM_c38810.g1_i2_len_1928
 SCBA_c32374.g1_i1_len_2023
 HOSA_c47306.g1_i1_len_2051
 TEGR_c39285.g1_i2_len_1630
 PRMI_c37955.g1_i1_len_1395
 SoTPS1132
 SaSS
 ORMA_c53741.g1_i3_len_1957
 OmTPS4
 PEFR_c47770.g1_i2_len_1580
 COCA_c63234.g1_i3_len_1994
 ORMA_c64446.g1_i1_len_1844
 OmTPS3
 SIKSL
 SpMIS
 RoKSL2
 PEAT_c41289.g2_i5_len_2060
 PaTPS3
 ORVU_c50768.g6_i2_len_1826
 CTPS4
 PLBA_c46055.g1_i5_len_2229
 CTPS3
 IrKSL1
 IrTPS4
 LAAN_c45623.g1_i3_len_1948
 MODL_c42947.g1_i2_len_2424
 MESP_c37832.g1_i1_len_1413
 PRVU_c29609.g1_i1_len_1853
 PvTPS1
 HYOF_c42605.g3_i2_len_2025
 GLHE_c55533.g1_i1_len_1649
 SdkSL1
 SmKSL
 RoKSL1
 ROOF_c50490.g1_i1_len_2583
 SAOF_c18770.g1_i1_len_2004
 SoTPS1
 HYSU_c32723.g2_i3_len_2570
 HYSU_c32723.g2_i2_len_1796
 ORMA_c52272.g2_i10_len_2153
 OmTPS5
 IrKSL6
 ORVU_c50288.g1_i1_len_2379
 IrKSL3
 IrTPS2
 WEFR_c48613.g1_i10_len_2048
 SCBA_c35286.g1_i4_len_1913
 VIAG_c45016.g1_i1_len_2531
 VIAG_c45016.g1_i3_len_2443
 MEOF_c18730.g1_i2_len_2471
 LYAM_c30491.g1_i2_len_2428
 MESP_c85932.g1_i1_len_2434
 MsTPS1

412 IGRVILSAI 420
 406 IGRNVLPAL 414
 660 IGPVLPAL 668
 649 IGPVLPAL 657
 647 IGPVLPAL 655
 647 IGPVLPAL 655
 651 IGPVLPAL 659
 666 IGPVLPAL 674
 648 IGPVLPAL 656
 283 IGPVLPAL 291
 650 IGPVLPAL 658
 651 IGPVLPAL 659
 649 IGPVLPAL 657
 645 I--I--ICRGI 650
 652 IGPVLPAL 660
 653 IGPVLPAL 661
 647 IGPVLPAL 655
 697 IGPVLPAL 705
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 611 IGPVLPAL 619
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 649 IGPVLPAL 657
 649 IGPVLPAL 657
 424 IGPVLPAL 432
 638 IGPVLPAL 646
 611 IGPVLPAL 619
 560 IGPVLPAL 568
 645 IGPVLPAL 653
 641 IGPVLPAL 649
 646 IGPVLPAL 654
 283 IGPVLPAL 291
 650 IGRVLPAL 658
 646 IGPVLPAL 654
 427 IGPVLPAL 435
 644 IGPVLPAL 652
 494 IGPVLPAL 502
 642 IGPVLPAL 650
 667 IGPVLPAL 675
 664 IGPVLPAL 672
 647 IGPVLPAL 655
 374 CRCLTEINSL 382
 423 CRCLTEINSL 431
 426 CRCLTEINSL 434
 441 CRCLTEINSL 449
 434 CRVOTLTAL 442
 434 CRVOTLTAL 442
 432 SRINLETSL 440
 433 SRINLETSL 441
 468 CRLOSINSL 476
 433 CRLOTINSL 441
 438 CRLOSINSL 446
 438 CRLOSINSL 446
 442 CRCLITSM 450
 439 CRCLITSM 447
 434 CRCLITSM 442
 434 CRCLITSM 442
 475 CRCLINSL 483
 308 CRCLITSM 316
 259 CRCLITSM 267
 433 SRLTGLTLM 441
 433 SRLTGLTLM 441
 429 CRVSVVTTM 437
 426 CRVSVVTTM 434
 431 CRCLITSM 439
 480 CRCLITSM 488
 434 CRCLIVSM 442
 434 CRCLIVSM 442
 438 CRCLIMSM 446
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 437 CRCLIMSM 445
 448 CRCLIMSM 456
 439 CRCLIMSM 447
 443 CRCLIVSM 451
 435 CRCLIMSM 443
 435 CRCLIMSM 443
 434 CRCLISM 442
 433 CRCLISM 441
 433 CRCLISM 441
 405 CRCLIMSM 413
 437 CRCLIVAM 445
 312 CRCLIVSM 320
 454 CRCLIMSM 462
 433 CRCLIMSM 441
 483 CRCLIMSM 491
 308 CRCLIMSM 316
 433 CRCLIMSM 441
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 475 CRCLIMSM 483
 433 CRCLIMSM 441
 553 SVIICSLSV 561
 467 CRCLIAI 475
 455 CRCLIAI 463
 629 CSLIIPSL 637
 626 CRCLIVSI 634
 631 CELCVLTA 639
 632 CKLCVLTAV 640
 357 AKVIFSVI 365
 362 GNMIFLMSI 370
 360 CDLCVLTSI 368
 643 CDLCVLTSI 651
 561 SKVYIMASSI 569
 543 CKTCVMTSI 551
 623 CKLCVLTSV 631
 607 CKLCVLTSV 615

Figure S22: An activity-determining region in an alignment of previously known (black), newly characterized (blue), and candidate (grey) TPS-e enzymes from Lamiaceae. Red stars indicate residues previously implicated in catalytic specificity. The combination of leucine and isoleucine has been implicated in contributing to *ent*-kaurene synthase activity. Positions are colored to indicate conservation within each subgroup.