

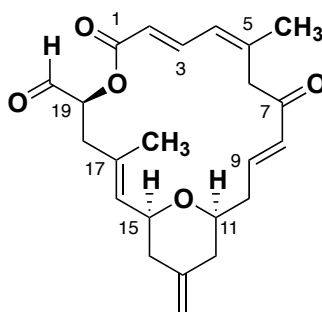
CONFORMATIONAL PREFERENCES OF ZAMPANOLIDE AND DACTYLOLIDE

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Supporting Information: Modeling and Spectral Data

NMR Data



(-)-dactylolide **3**

^1H and ^{13}C NMR Signals of Natural¹ and Synthetic (-)-dactylolide in CDCl_3

$^1\text{H}/^{13}\text{C}$ No.	Natural* ^{13}C , 150 MHz, ppm	Synthetic ^{13}C , 150 MHz, ppm	Natural* ^1H , 600 MHz, (Hz)	Synthetic ^1H , 500 MHz, (Hz)
1	166.0	166.5	-	-
2	120.0	119.9	5.96 d (15.1)	5.96 d (15.0)
3	140.7	140.6	7.62 dd (15.1, 11.6)	7.63 dd (15.0, 11.5)
4	125.7	125.7	6.15 d (11.6)	6.15 d (11.5)
5	144.4	144.2	-	-
5a	23.6	24.3	1.85 s	1.86 s
6	44.8	45.0	3.94 d (14.5) 3.23 d (14.5)	3.95 d (14.5) 3.23 d (14.5)
7	197.0	197.6	-	-
8	131.3	131.6	6.0 d (16.0)	6.0 d (16.5)
9	146.8	146.2	6.84 ddd (5.9, 8.5, 16.0)	6.84 ddd (5.5, 8.7, 16.5)
10	40.1	39.9	2.35 m 2.28 m	2.36 m 2.28 m
11	76.7	76.6	3.31 dddd (2.6, 2.6, 9.6, 12.3)	3.32 dddd (2.3, 2.3, 10.5, 11.5)
12	40.8	41.0	2.16 m 1.95 t (12.3)	2.17 dd (1.6, 13.0) 1.96 m
13	143.4	143.6	-	-
13a	109.0	109.5	4.73 bs	4.74 d (1.2) 4.75 d (1.2)
14	40.4	40.6	2.10 m 1.95 m	2.11 dd (2.1, 13.0) 1.96 m
15	76.1	75.9	3.96 ddd (2.6,	3.96 ddd (2.7, 8.0,

¹ Cutignano, A.; Bruno, I.; Bifulco, G.; Casapullo, A.; Cécile, D.; Gomez-Paloma, L.; Riccio, R. *Eur. J. Org. Chem.* **2001**, 775-778.

			8.3, 10.9)	11.5)
16	130.8	130.7	5.24 d (8.3)	5.24 d (8.0)
17	131.3	131.1	-	-
17a	16.2	16.2	1.70 s	1.71 s
18	39.6	39.9	2.53 brd (14.0) 2.31 brd (14.0)	2.54 brd (14.0) 2.31 dd (11.0, 14.0)
19	75.5	75.5	5.31 dd (11.2, 2.2)	5.31 dd (11.0, 2.5)
19a	199.7	199.3	9.66 s	9.66 s

* Natural dactylolide is reported to be (+)-dactylolide

¹H NMR signals and *J*-coupling constants of synthetic (–)-dactylolide and natural (–)-zampanolide in DMSO-_d6²

¹ H/ ¹³ C No.	Synthetic (–)-dactylolide ¹ H (600 MHz), Hz	Natural (–)-zampanolide ¹ H (500 MHz), Hz
1	-	-
2	5.97 d (15.1)	5.93 d (15.0)
3	7.42 dd (15.1, 11.6)	7.52 dd (15.0, 11.6)
4	6.25 d (11.6)	6.20 d (11.6)
5	-	-
5a	1.82 s	1.75 s
6	3.30 d (15.5) 3.86 d (15.5)	3.01 d (14.4) 4.12 d (14.4)
7	-	-
8	6.02 d (16.1)	5.95 d (15.3)
9	6.79 dt (16.1, 7.2, 7.2)	6.74 ddd (15.3, 8.6, 5.5)
10	2.40 dddd (14.5, 7.5, 2.6, 1.2) 2.26 dddd (14.5, 10.0, 6.9, 1.5)	2.30 m
11	3.34 dddd (11.4, 10.6, 2.6, 2.0)	3.27 m
12	1.85 m 2.21 dd (13.0, 1.6)	1.84 m 2.17 brd (12.8)
13	-	-
13a	4.73 d (1.7) 4.74 d (1.7)	4.73 s
14	1.86 m 2.11 dd (13.1, 2.1)	1.88 m 2.07 m
15	3.93 ddd (10.6, 7.9, 2.4)	3.87 ddd (11.3, 7.6, 2.7)
16	5.20 d (7.9)	5.10 d (7.6)
17	-	-
17a	1.65 d (1.1)	1.61 s

² Tanaka, J.; Higa, T.; *Tetrahedron Lett.* **1996**, 37, 5535-5538.

18	2.30 dd (14.1, 11.2) 2.53 d (14.5)	2.09 m 2.33 m
19	5.29 dd (11.2, 2.7)	4.96 ddd (10.0, 6.0, 1.8)
19a	9.56 s	-

ROESY-derived interproton distances used in DISCON calculations

H1	H2	Peak Volume	Interproton distance (Å)
10proR	10proS	1.00	1.78
16	14proR	0.11	2.65
18proR	16	0.27	2.32
10proR	8	0.06	2.94
3	9	0.07	2.81
9	11	0.09	2.79
2	4	0.14	2.65
3	6proS	0.27	2.30
3	6proR	0.13	2.56
6proS	9	0.12	2.69
17Me	15	0.29	2.22
17Me	19	0.18	2.42

¹H NMR coupling constants used in DISCON calculations

H1	H2	<i>J</i> (Hz)
10proS	9	7.5
10proS	11	2.5
19	18proR	11.2
19	18proS	2.7
10proR	11	10.0
10proR	9	6.9

Conformational Searches

Conformer libraries were generated using the Batchmin package and the MM3, MMFF, and OPLS2005 force fields as implemented in MacroModel 9.0. Solvation was simulated using the GB/SA continuum model for water. Conformational searches were performed with the MCMM torsional sampling, typically using 50,000 Monte Carlo steps per run. Structures within a 20 kJ/mol window were saved and minimized for complete convergence using the Polak-Ribiere conjugate gradient method (5000 steps, convergence threshold of 0.05). The three libraries generated were combined and the redundant conformers were eliminated based on comparison of maximum atom deviation (threshold of 0.5 Å) to yield a single library.

Polar Maps

Backbone dihedral angles were extracted from the conformers using Maestro 9.2 and converted to 0-360° scale before being plotted onto polar coordinate maps using Microsoft Excel 2007 with the Polar Plot2³ add-in.

DISCON

DISCON is a Windows/Mac/Linux application developed by the Amos Smith laboratory for calculating the distribution of solution conformations of a flexible organic molecule by using NOE cross-peak volumes, coupling constants, and a pre-generated library of conformers. The program uses a similar approach to the NAMFIS methodology with the additional steps of using NMR variables to initially cluster compounds and the use of a genetic algorithm to assist with deconvolution, which are beneficial in identifying representative structures while avoiding overfitting. Additional information on DISCON, including software binaries, test files and program documentation, may be found at <http://discon.sourceforge.net> and in selected publications from the Smith lab⁴.

Evaluation of the dactylolide conformer library with DISCON was initially undertaken with the aim of determining the proper clustering level. After examining a wide range, a level of 10 was found to provide an RMS deviation lower than any of the individual structures while still retaining them into distinctive conformational families. Additional testing with different genetic algorithm parameters and random selection of representative structures from individual clusters eventually led to the determination of the major conformers from their respective families.

Coordinates for Solution Conformations

Conformer A

56 57 0 0 1 0 999 V2000

³ <http://www.andypope.info/charts/polarplot3.htm>

⁴ Smith, A. B.; Atasoylu, O.; Risatti, C.; Bennett, C. S.; Liu, J.; Cheng, H.; TenDyke, K.; Xu, Q. *J. Am. Chem. Soc.* **2011**, *133*, 14042-14053.

1.6625	7.7373	15.8925	C	0	0	1	0	0	0
0.6574	8.7333	15.7041	O	0	0	0	0	0	0
1.1734	10.0584	15.8684	C	0	0	2	0	0	0
1.6173	10.2332	17.3270	C	0	0	0	0	0	0
2.1484	7.7878	17.3473	C	0	0	0	0	0	0
2.5092	7.9224	15.1982	H	0	0	0	0	0	0
2.0405	10.2199	15.1876	H	0	0	0	0	0	0
2.0380	11.2526	17.4788	H	0	0	0	0	0	0
0.7427	10.1375	18.0099	H	0	0	0	0	0	0
1.3169	7.5240	18.0402	H	0	0	0	0	0	0
2.9534	7.0352	17.5062	H	0	0	0	0	0	0
0.9947	6.4224	15.5719	C	0	0	0	0	0	0
1.4591	5.4347	14.7858	C	0	0	0	0	0	0
0.6179	4.2019	14.5147	C	0	0	0	0	0	0
1.2615	3.3040	14.6586	H	0	0	0	0	0	0
-0.1824	4.1134	15.2824	H	0	0	0	0	0	0
-0.7840	5.3390	12.8721	O	0	0	0	0	0	0
-2.7239	6.7907	13.3300	C	0	0	0	0	0	0
-2.2795	7.8030	12.5751	C	0	0	0	0	0	0
-3.0726	9.0272	12.3814	C	0	0	0	0	0	0
-2.6333	10.1533	11.7924	C	0	0	0	0	0	0
-1.2368	10.3846	11.2545	C	0	0	0	0	0	0
-0.5497	9.5505	11.5093	H	0	0	0	0	0	0
-1.2980	10.3822	10.1418	H	0	0	0	0	0	0
-0.1925	11.8445	13.1227	C	0	0	0	0	0	0
-0.3719	10.9063	14.0599	C	0	0	0	0	0	0
0.0622	11.0484	15.4975	C	0	0	0	0	0	0
-0.8217	10.8958	16.1582	H	0	0	0	0	0	0
0.4186	12.0872	15.6832	H	0	0	0	0	0	0
3.8571	9.4459	18.1578	C	0	0	0	0	0	0
2.6377	9.1777	17.6757	C	0	0	0	0	0	0
4.1794	10.4812	18.3579	H	0	0	0	0	0	0
4.5782	8.6400	18.3731	H	0	0	0	0	0	0
0.0042	6.2926	16.0444	H	0	0	0	0	0	0
-0.8489	9.9455	13.8085	H	0	0	0	0	0	0
0.2900	12.8015	13.3858	H	0	0	0	0	0	0
-3.6970	6.8510	13.8441	H	0	0	0	0	0	0
-1.2983	7.7061	12.0826	H	0	0	0	0	0	0
-4.1176	9.0113	12.7425	H	0	0	0	0	0	0
2.7854	5.4741	14.0618	C	0	0	0	0	0	0
3.4824	6.2327	14.4752	H	0	0	0	0	0	0
3.3086	4.4952	14.1335	H	0	0	0	0	0	0
2.6463	5.7027	12.9824	H	0	0	0	0	0	0
-3.5716	11.3223	11.6023	C	0	0	0	0	0	0
-3.6163	11.6279	10.5336	H	0	0	0	0	0	0
-4.6121	11.0895	11.9182	H	0	0	0	0	0	0

-3.2425	12.2049	12.1934 H	0	0	0	0	0	0	0
-1.9507	5.5471	13.5235 C	0	0	0	0	0	0	0
-2.3810	4.6991	14.2724 O	0	0	0	0	0	0	0
-0.6010	11.6963	11.7080 C	0	0	0	0	0	0	0
-0.4106	12.6082	10.9305 O	0	0	0	0	0	0	0
0.0025	4.1715	13.1062 C	0	0	2	0	0	0	0
0.8390	4.1845	12.3698 H	0	0	0	0	0	0	0
-1.6011	2.9621	12.0679 H	0	0	0	0	0	0	0
-0.7729	2.8913	12.8187 C	0	0	0	0	0	0	0
-0.5265	1.8116	13.3109 O	0	0	0	0	0	0	0
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1	5	1	0	0	0				
1	6	1	0	0	0				
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Conformer B

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1.6624 7.7374 15.8614 C	0 0 1 0 0 0
0.6645 8.7528 15.7717 O	0 0 0 0 0 0
1.1910 10.0617 16.0083 C	0 0 2 0 0 0
1.6803 10.1407 17.4597 C	0 0 0 0 0 0
2.1888 7.6933 17.3025 C	0 0 0 0 0 0
2.4874 7.9507 15.1479 H	0 0 0 0 0 0
2.0380 10.2639 15.3131 H	0 0 0 0 0 0
2.1144 11.1455 17.6623 H	0 0 0 0 0 0
0.8269 10.0069 18.1626 H	0 0 0 0 0 0
1.3732 7.3928 17.9994 H	0 0 0 0 0 0
2.9900 6.9256 17.3932 H	0 0 0 0 0 0
0.9592 6.4561 15.4773 C	0 0 0 0 0 0
1.4817 5.3959 14.8361 C	0 0 0 0 0 0
0.6238 4.1873 14.5224 C	0 0 0 0 0 0
1.0550 3.3128 15.0623 H	0 0 0 0 0 0
-0.3949 4.3323 14.9503 H	0 0 0 0 0 0
-0.0028 4.9973 12.3426 O	0 0 0 0 0 0
-0.4571 6.1107 10.1796 C	0 0 0 0 0 0
-0.8533 7.2809 10.6944 C	0 0 0 0 0 0
-1.4182 8.3380 9.8397 C	0 0 0 0 0 0
-1.5601 9.6232 10.2038 C	0 0 0 0 0 0

-1.0896	10.1984	11.5247 C	0	0	0	0	0	0	0
-0.1706	9.6564	11.8415 H	0	0	0	0	0	0	0
-0.7796	11.2555	11.3621 H	0	0	0	0	0	0	0
-1.6530	10.3962	14.0223 C	0	0	0	0	0	0	0
-0.4505	10.9078	14.3156 C	0	0	0	0	0	0	0
0.0640	11.0635	15.7258 C	0	0	0	0	0	0	0
-0.7640	10.9150	16.4556 H	0	0	0	0	0	0	0
0.4329	12.1045	15.8696 H	0	0	0	0	0	0	0
3.9374	9.2825	18.1636 C	0	0	0	0	0	0	0
2.7006	9.0559	17.7051 C	0	0	0	0	0	0	0
4.2760	10.2999	18.4206 H	0	0	0	0	0	0	0
4.6573	8.4588	18.3020 H	0	0	0	0	0	0	0
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2.9237	5.2979	14.3974 C	0	0	0	0	0	0	0
3.0112	5.3666	13.2909 H	0	0	0	0	0	0	0
3.5618	6.0976	14.8286 H	0	0	0	0	0	0	0
3.3702	4.3291	14.7122 H	0	0	0	0	0	0	0
-2.2101	10.6260	9.2815 C	0	0	0	0	0	0	0
-1.4920	11.4237	8.9889 H	0	0	0	0	0	0	0
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-3.0788	11.1173	9.7727 H	0	0	0	0	0	0	0
0.0910	5.0063	10.9924 C	0	0	0	0	0	0	0
0.6172	4.0725	10.4281 O	0	0	0	0	0	0	0
-2.1260	10.1451	12.6435 C	0	0	0	0	0	0	0
-3.2935	9.8837	12.4444 O	0	0	0	0	0	0	0
0.4809	3.8436	13.0331 C	0	0	2	0	0	0	0
1.4838	3.5546	12.6440 H	0	0	0	0	0	0	0
-1.2184	2.7299	12.0202 H	0	0	0	0	0	0	0
-0.4624	2.6571	12.8428 C	0	0	0	0	0	0	0
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1 5	1 0 0 0								
1 6	1 0 0 0								
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2 3	1 0 0 0								
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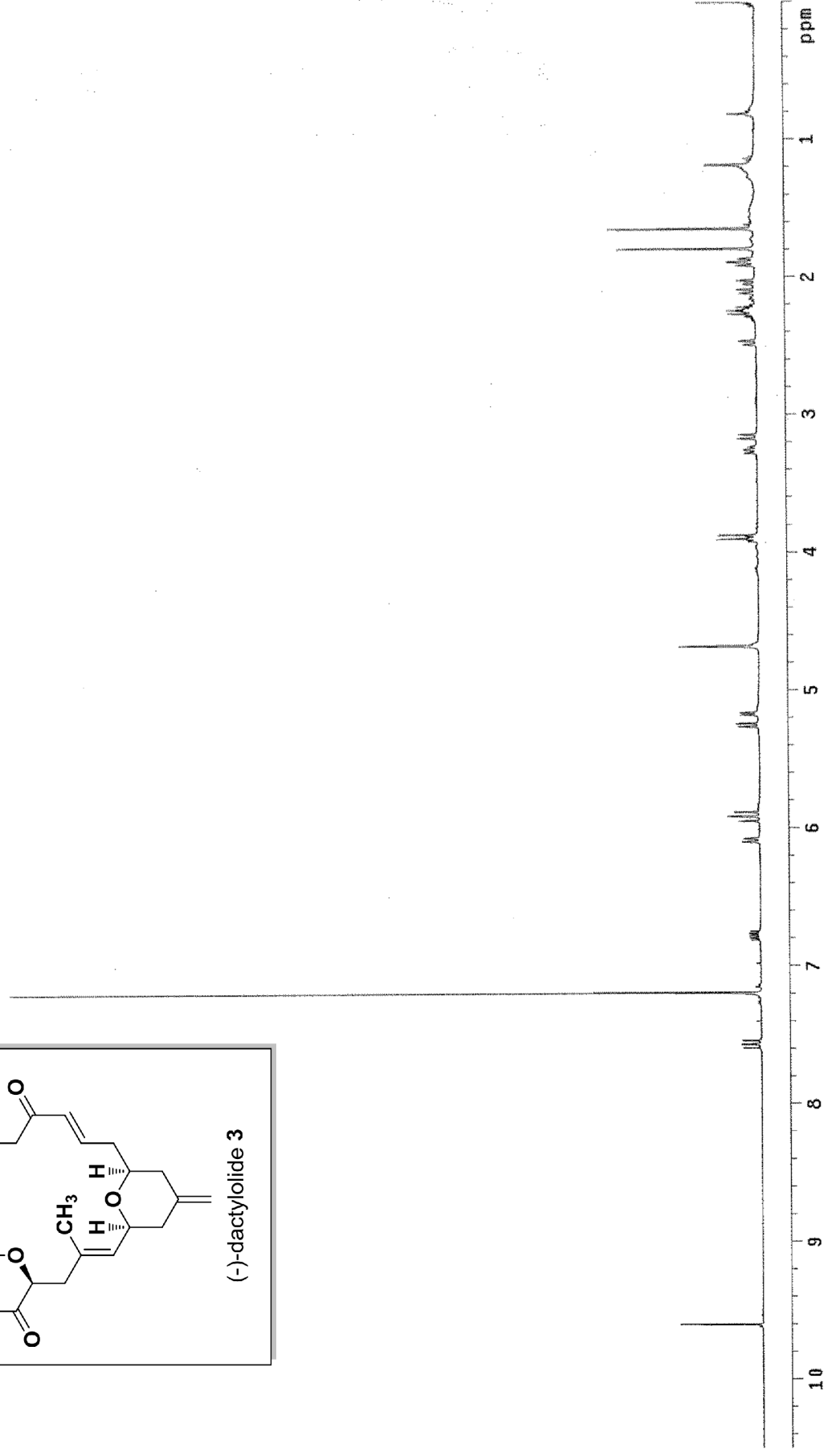
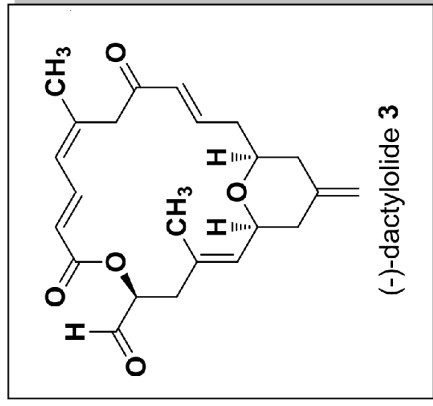
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 30 31 2 0 0 0
 30 32 1 0 0 0
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 40 41 1 0 0 0
 40 42 1 0 0 0
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Conformer C

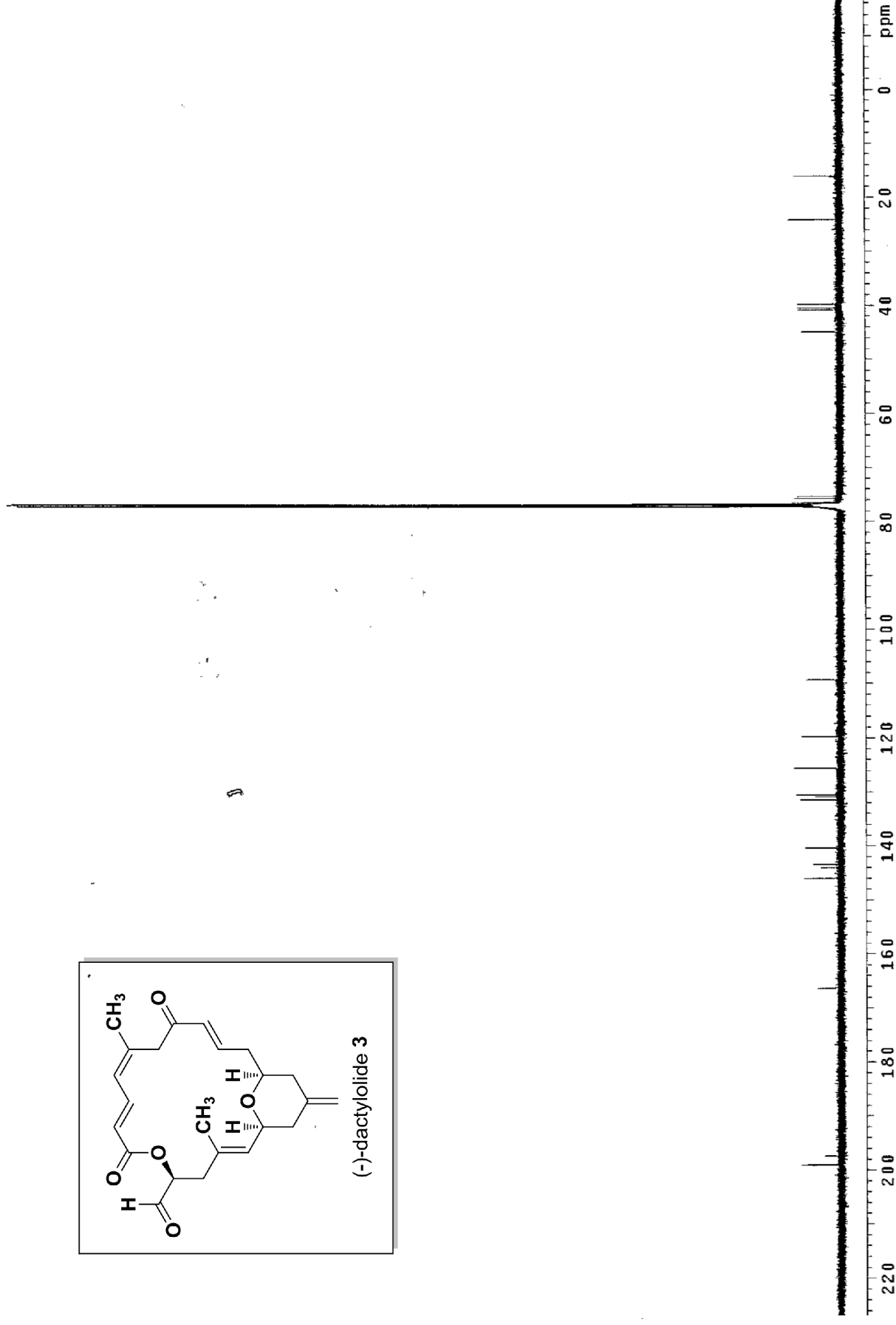
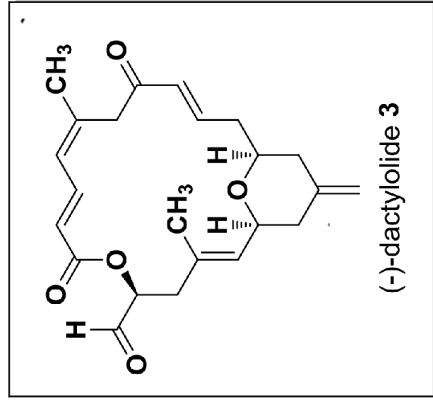
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 0.6632  8.7224 15.6727 O  0 0 0 0 0 0
 1.1287 10.0558 15.9087 C  0 0 2 0 0 0
 1.4716 10.2120 17.3960 C  0 0 0 0 0 0
 2.0605  7.7850 17.4117 C  0 0 0 0 0 0
 2.5457  7.9166 15.2887 H  0 0 0 0 0 0
 2.0390 10.2521 15.2961 H  0 0 0 0 0 0
 1.8489 11.2401 17.5955 H  0 0 0 0 0 0
 0.5633 10.0710 18.0240 H  0 0 0 0 0 0
 1.1965  7.5006 18.0552 H  0 0 0 0 0 0
 2.8691  7.0463 17.6124 H  0 0 0 0 0 0
 1.0073  6.4145 15.5904 C  0 0 0 0 0 0
 1.4371  5.4621 14.7433 C  0 0 0 0 0 0
 0.6250  4.1977 14.5323 C  0 0 0 0 0 0
 1.3177  3.3272 14.5902 H  0 0 0 0 0 0
-0.0936  4.0647 15.3735 H  0 0 0 0 0 0
-1.0990  5.2225 13.2277 O  0 0 0 0 0 0
-2.6335  6.7397 12.0362 C  0 0 0 0 0 0
-3.1548  7.2526 13.1579 C  0 0 0 0 0 0
-4.2033  8.2852 13.1248 C  0 0 0 0 0 0
-4.7440  8.8761 14.2049 C  0 0 0 0 0 0
-4.3780  8.5926 15.6463 C  0 0 0 0 0 0
-5.3158  8.4639 16.2330 H  0 0 0 0 0 0
-3.8395  7.6264 15.7471 H  0 0 0 0 0 0
-2.2330  9.9563 15.6153 C  0 0 0 0 0 0
-1.3141 10.7825 16.1291 C  0 0 0 0 0 0
 0.0239 11.0239 15.4646 C  0 0 0 0 0 0
 0.3416 12.0744 15.6546 H  0 0 0 0 0 0
-0.1010 10.9402 14.3599 H  0 0 0 0 0 0
 3.6878  9.4708 18.3285 C  0 0 0 0 0 0
 2.5014  9.1799 17.7820 C  0 0 0 0 0 0
 3.9735 10.5108 18.5579 H  0 0 0 0 0 0
 4.4172  8.6797 18.5696 H  0 0 0 0 0 0
 0.0577  6.2375 16.1275 H  0 0 0 0 0 0
-1.4965 11.2961 17.0888 H  0 0 0 0 0 0
-2.0288  9.4243 14.6721 H  0 0 0 0 0 0
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 2.6941  5.5534 13.9105 C  0 0 0 0 0 0
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 3.3560  6.3931 14.2061 H  0 0 0 0 0 0
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3.3005	4.6255	14.0024	H	0	0	0	0	0	0
-5.7937	9.9501	14.0436	C	0	0	0	0	0	0
-5.4506	10.9138	14.4803	H	0	0	0	0	0	0
-6.0450	10.1448	12.9780	H	0	0	0	0	0	0
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-1.5892	5.6949	12.0604	C	0	0	0	0	0	0
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-3.8875	10.3159	17.2517	O	0	0	0	0	0	0
-0.1485	4.1571	13.2073	C	0	0	2	0	0	0
0.5729	4.2887	12.3700	H	0	0	0	0	0	0
-1.8781	2.8494	12.5509	H	0	0	0	0	0	0
-0.8581	2.8207	13.0123	C	0	0	0	0	0	0
-0.3813	1.7432	13.2949	O	0	0	0	0	0	0
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14	16	1	0	0	0				
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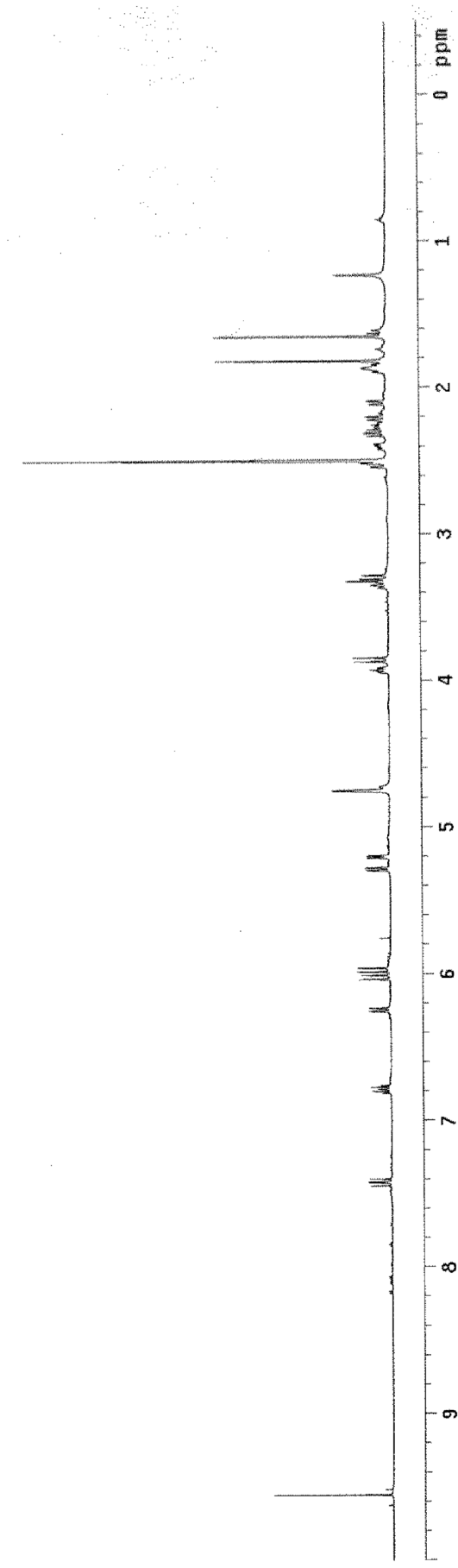
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¹H NMR spectrum of (-)-dactylolide in CDCl₃



^{13}C NMR spectrum of (-)-dactylolide in CDCl_3

¹H NMR spectrum of (-)-dactylolide in DMSO-d₆

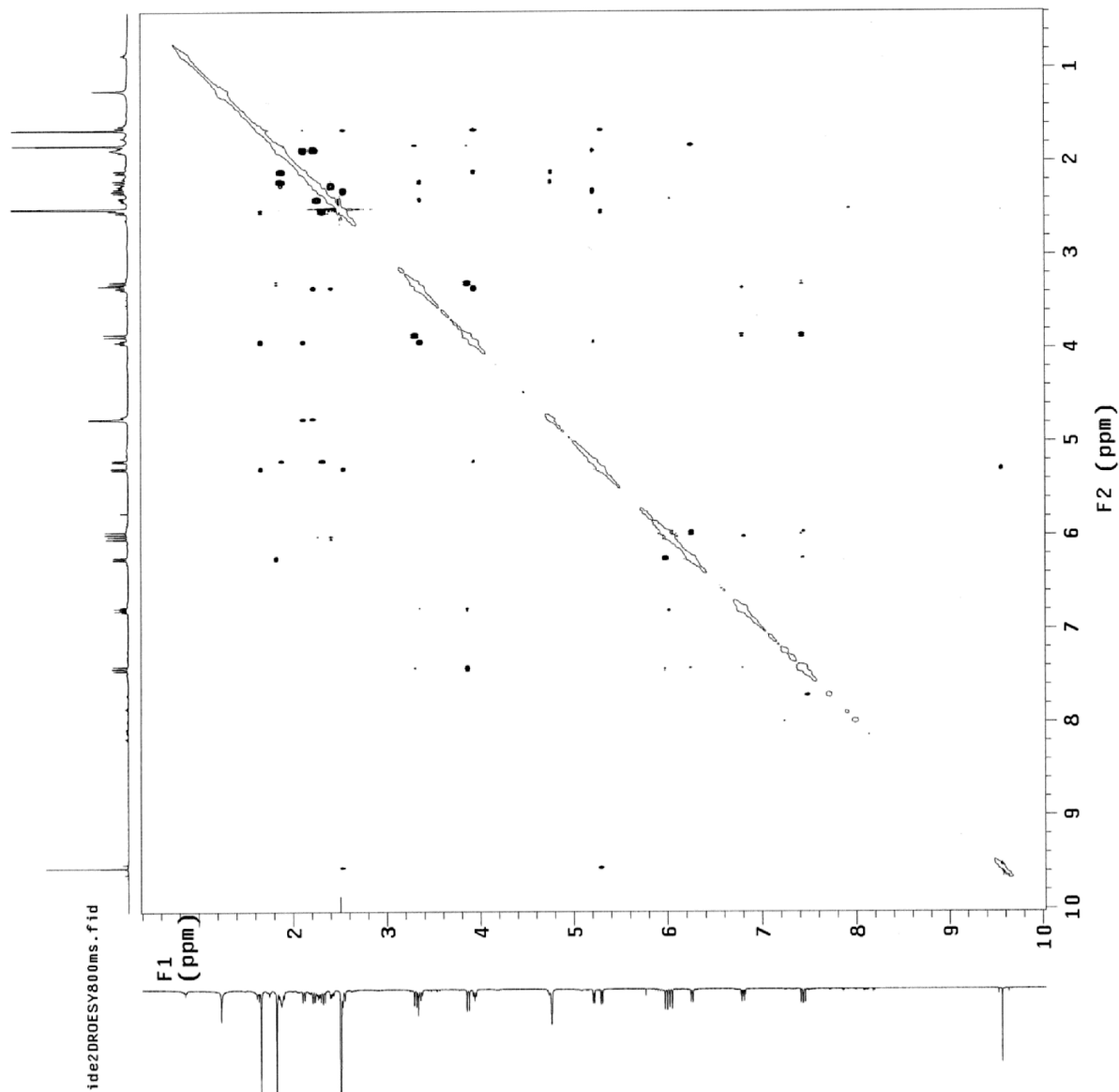
Std proton

File: afs/nd.edu/user23/mwilso16/Private/NMR/Dactylolide2DROESY800ms.fid

Pulse Sequence: ROESY

Solvent: dmsd
Temp. 22.0 C / 295.1 K
Operator: mwilso16
File: Dactylolide2DROESY800ms
VNMR-600 "nmr-600"

Relax. delay 4.000 sec
Mixing 0.800 sec
Acq. time 0.177 sec
Width 5787.0 Hz
2D Width 5787.0 Hz
32 repetitions
2 x 128 increments
OBSERVE H1, 599.8756950 MHz
DATA PROCESSING
Gauss apodization 0.082 sec
F1 DATA PROCESSING
Gauss apodization 0.041 sec
FT size 2048 x 2048
Total time 11 hr, 25 min, 53 sec



Std proton

File: afs/nd.edu/user23/mwilso16/Private/NMR/Dactylolide2DROESY800ms-B.fid

Pulse Sequence: ROESY

Solvent: dmsd

Temp. 22.0 C / 295.1 K

Operator: mwilso16

File: Dactylolide2DROESY800ms-B

VNMR5-600 "nmr600"

Relax. delay 4.000 sec

Mixing 0.800 sec

Acq. time 0.177 sec

Width 5787.0 Hz

2D Width 5787.0 Hz

32 repetitions

2 x 128 increments

OBSERVE H1 599.8757069 MHz

DATA PROCESSING

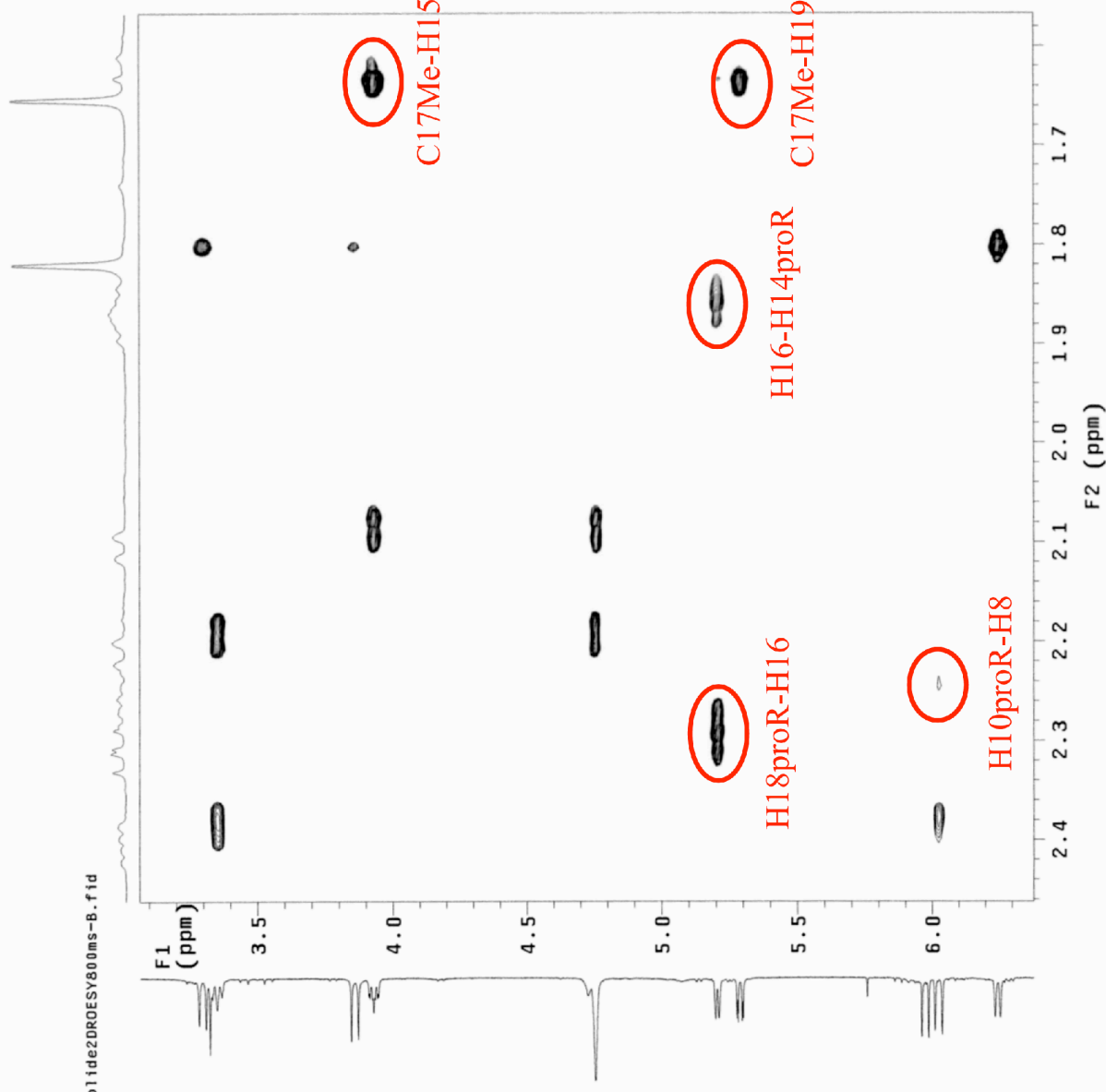
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F1 DATA PROCESSING

Gauss apodization 0.041 sec

FT size 2048 x 2048

Total time 11 hr, 25 min, 53 sec



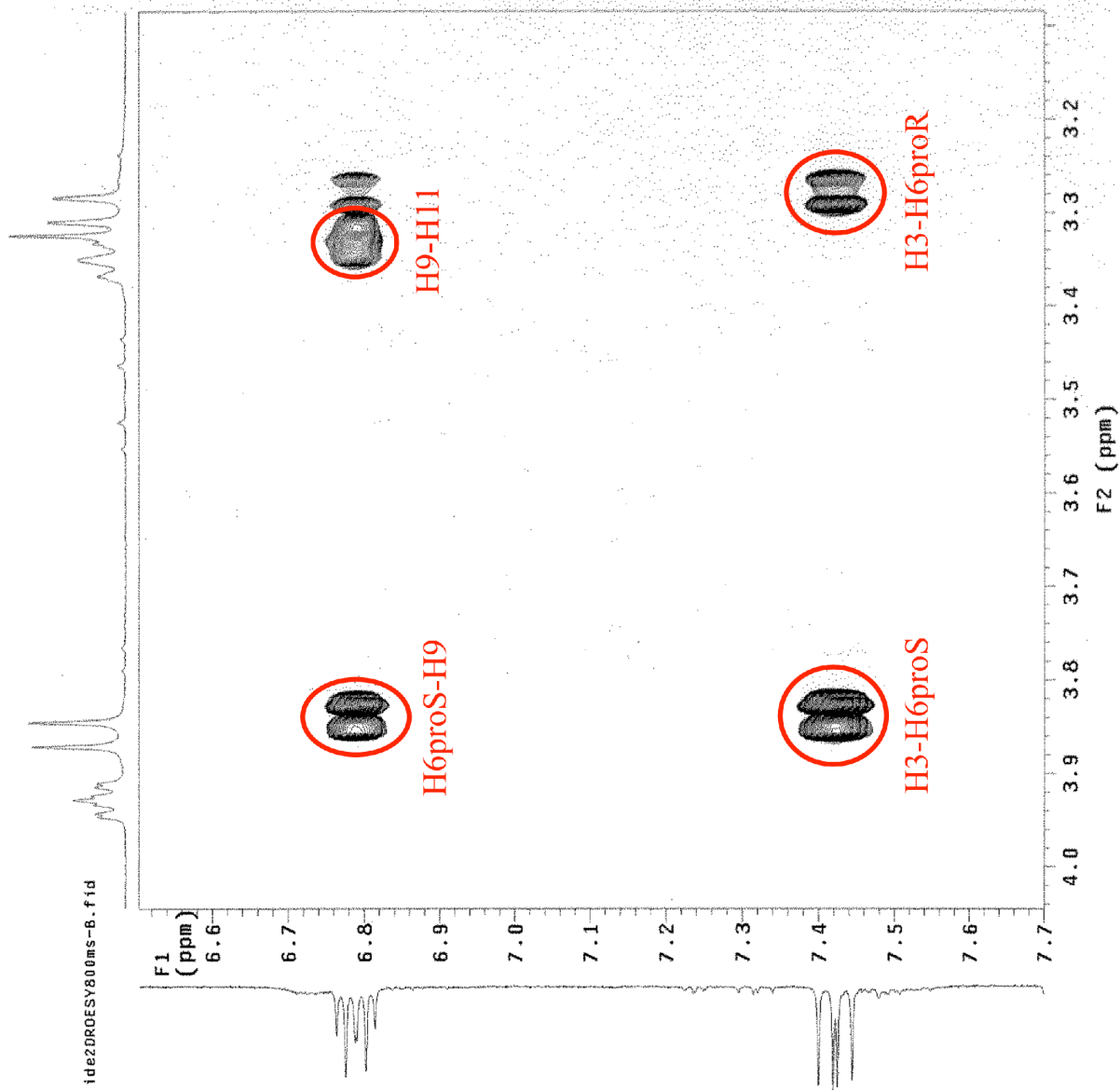
Std proton

File: afs/nd.edu/user23/mwilso16/Private/NMR/Dactylolide2DROESY800ms-B.fid

Pulse Sequence: ROESY

Solvent: dmsd
Temp. 22.0 C / 295.1 K
Operator: mwilso16
File: Dactylolide2DROESY800ms-B
VNMR5-600 "nmr600"

Relax. delay 4.000 sec
Mixing 0.800 sec
Acq. time 0.177 sec
Width 5787.0 Hz
2D Width 5787.0 Hz
32 repetitions
2 x 128 increments
OBSERVE H1, 599.8757069 MHz
DATA PROCESSING
Gauss apodization 0.082 sec
F1 DATA PROCESSING
Gauss apodization 0.041 sec
F1 size 2048 x 2048
Total time 11 hr, 25 min, 53 sec



Std proton

File: afs/nd.edu/user23/mwilso16/Private/NMR/Dactylolide2DROESY800ms-B.fid

Pulse Sequence: ROESY

Solvent: dmsd
Temp: 22.0 C / 295.1 K
Operator: mwilso16
File: Dactylolide2DROESY800ms-B
VNMR-600 "nmr600"

Relax. delay 4.000 sec
Mixing 0.800 sec
Acq. time 0.177 sec
Width 5787.0 Hz
2D Width 5787.0 Hz
32 repetitions
2 x 128 increments
OBSERVE H1, 599.8757069 MHz
DATA PROCESSING
Gauss apodization 0.082 sec
F1 DATA PROCESSING
Gauss apodization 0.041 sec
FT size 2048 x 2048
Total time 11 hr, 25 min, 53 sec

