Supplementary Material

Development of a Karplus equation for $^3J_{COCH}$ in ester-functionalized carbohydrates.

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Four parameter version of the general C(sp^2)OCH Karplus equation

The Karplus equation for $^3J_{C(sp2)OCH}$ presented in this research article can be written with an additional parameter to account for potential phase shift. However, the resulting equation is virtually identical to the three-parameter version presented here, because the phase shift is close to 0°:

$$^3J_{\mathrm{C-O-C-H}} = 5.81 \cdot \cos^2(\theta^* + 0.07°) - 1.42 \cdot \cos(\theta^* + 0.07°) + 1.05 \quad (1)$$

r^2= 0.997 rms = 0.11

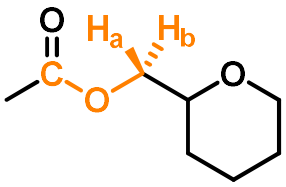
$$^3J_{\mathrm{C-O-C-H}} = 5.81 \cdot \cos^2\theta^* - 1.42 \cdot \cos\theta^* + 1.05 \quad (2)$$

r^2= 0.997 rms = 0.12

Preliminary data based on tetrahydropyran-2-methyl acetate

Note: The following data was first presented at the 251st ACS National Meeting in San Diego, CA, held March 13-17, 2016.[1]

A Karplus equation was generated using computational treatment of a model compound, tetrahydropyran-2-methyl acetate:



Computed Fermi contact values from 2 lowest energy conformers (obtained based on conformational search using Spartan14[2]) using Gaussian09[3] at the B3LYP/6-31G* level of theory and implicit PCM solvent model for chloroform for all rotamers ±10,20°.

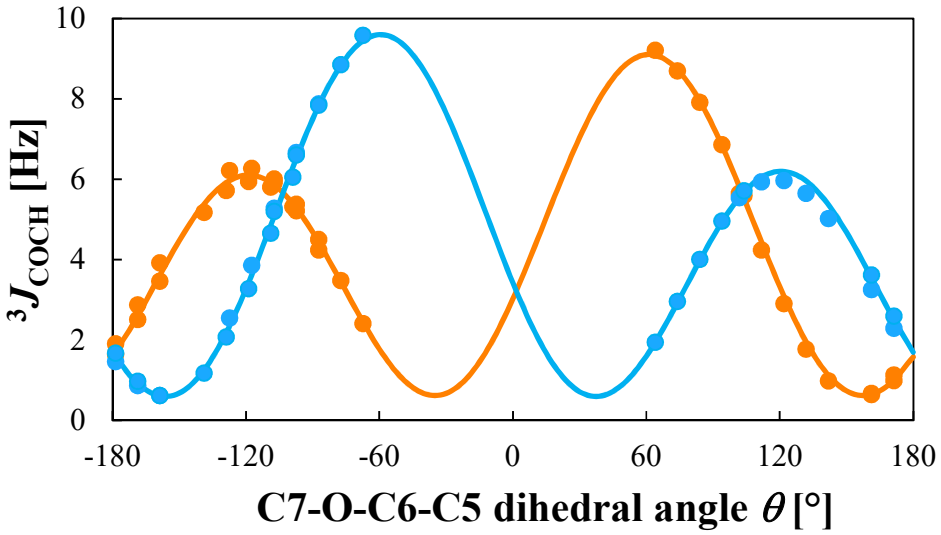


Figure S1 – Computationally determined Karplus relationship between C7-O-C6-C5 dihedral angle θ and $^3J_{COCH}$ for H6*proR* (blue) and H6*proS* (orange) based on tetrahydropyran-2-methyl acetate plotted along with Karplus equation for COCH coupling published by Tvaroška *et al.*.[4]

The Fermi contact values were plotted against the C7-O-C6-C5 dihedral angle θ and fitted using a four-parameter sinusoidal equation. The resulting Karplus equations for both $^3J_{C7\text{-}H6pro\text{-}R}$ and $^3J_{C7\text{-}H6pro\text{-}S}$, as shown in Figure S1, are given below:

$$^3J_{\mathrm{C}(sp2)\mathrm{OCH}proR} = 6.8 \cdot \cos^2(\theta + 118.7°) - 1.6 \cdot \cos(\theta + 118.7°) + 0.8$$

$$^3J_{\mathrm{C}(sp2)\mathrm{OCH}proS} = 7.1 \cdot \cos^2(\theta - 120.6°) - 1.7 \cdot \cos(\theta - 120.6°) + 0.8$$

Validation:	<u>*J*-HMBC experiment</u>	
	2.91 Hz	
	3.09 Hz	
Forcefield	<u>MD simulation</u>	
MM+ (500ps)	3.0 Hz	2.6 Hz

The following shows the Karplus equation for C(sp^3)OCH coupling published by Tvaroška *et al.*[4]. (in orange) for comparison of coefficients, which results in a different Karplus relationship around the maximum at 60° and -60° for the two equations, respectively, as depicted in Figure S2**Figure S1**:

$$^{3}J_{\mathrm{COCH}} = 5.7\ \cos^{2}(\theta^{*}) - 1.6 \cdot \cos(\theta^{*}) + 0.8$$

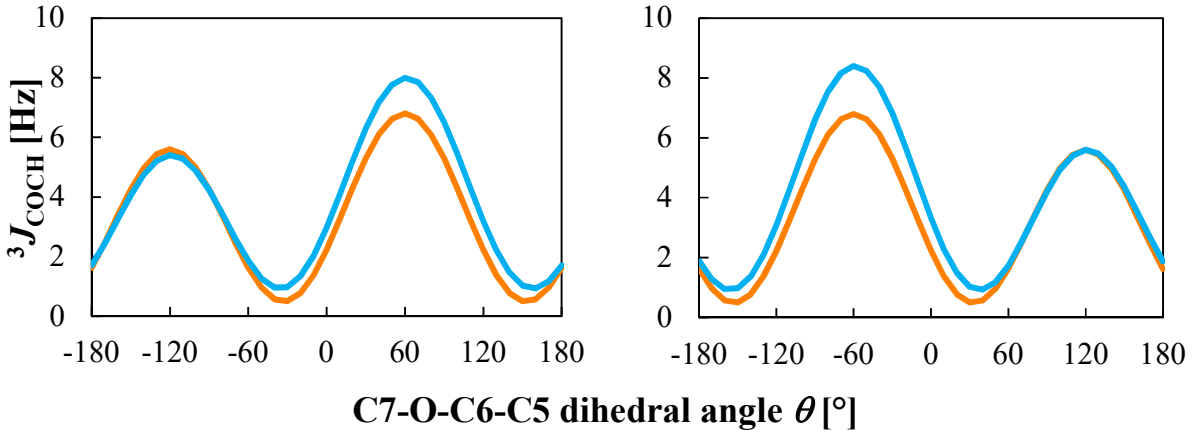
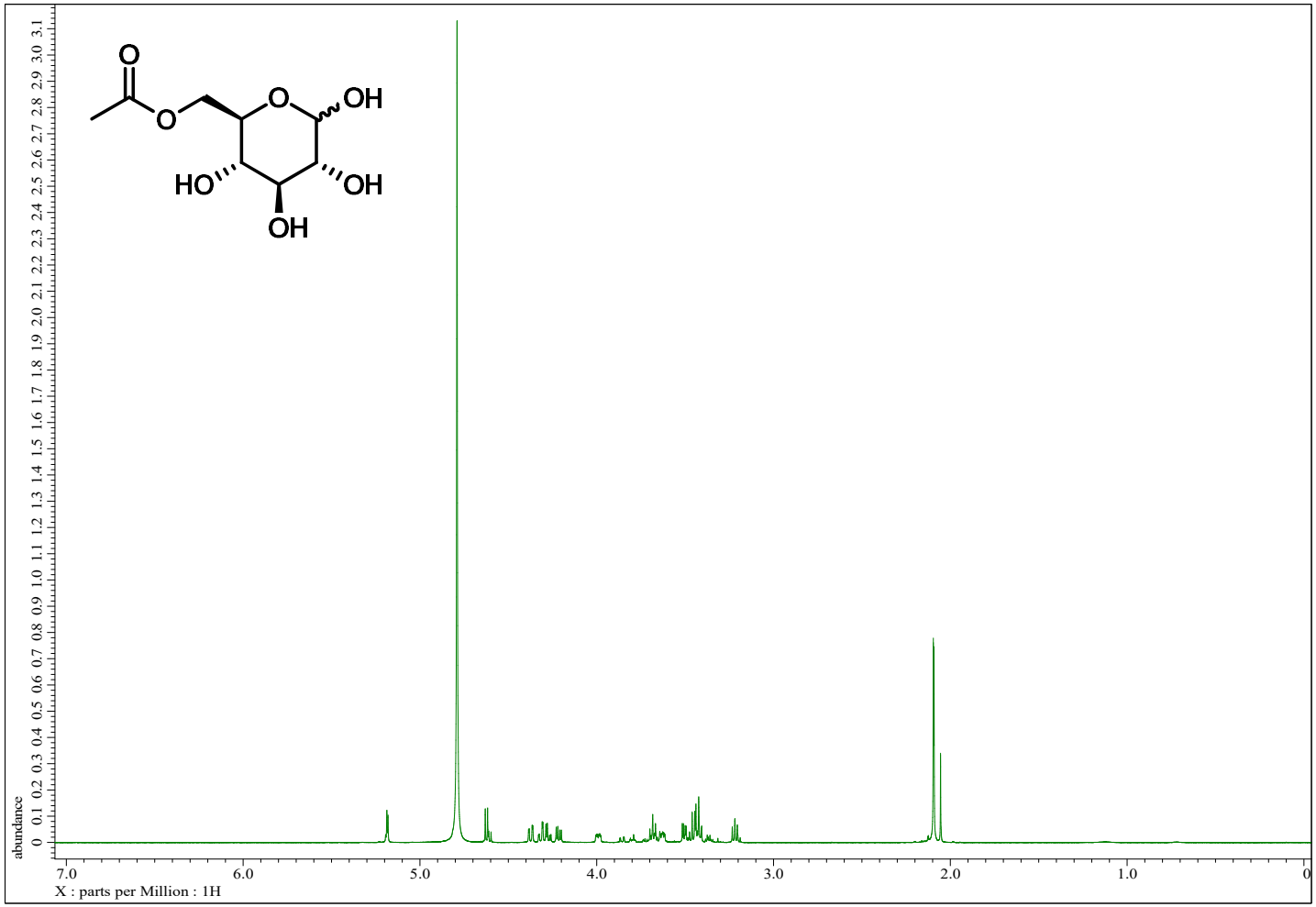


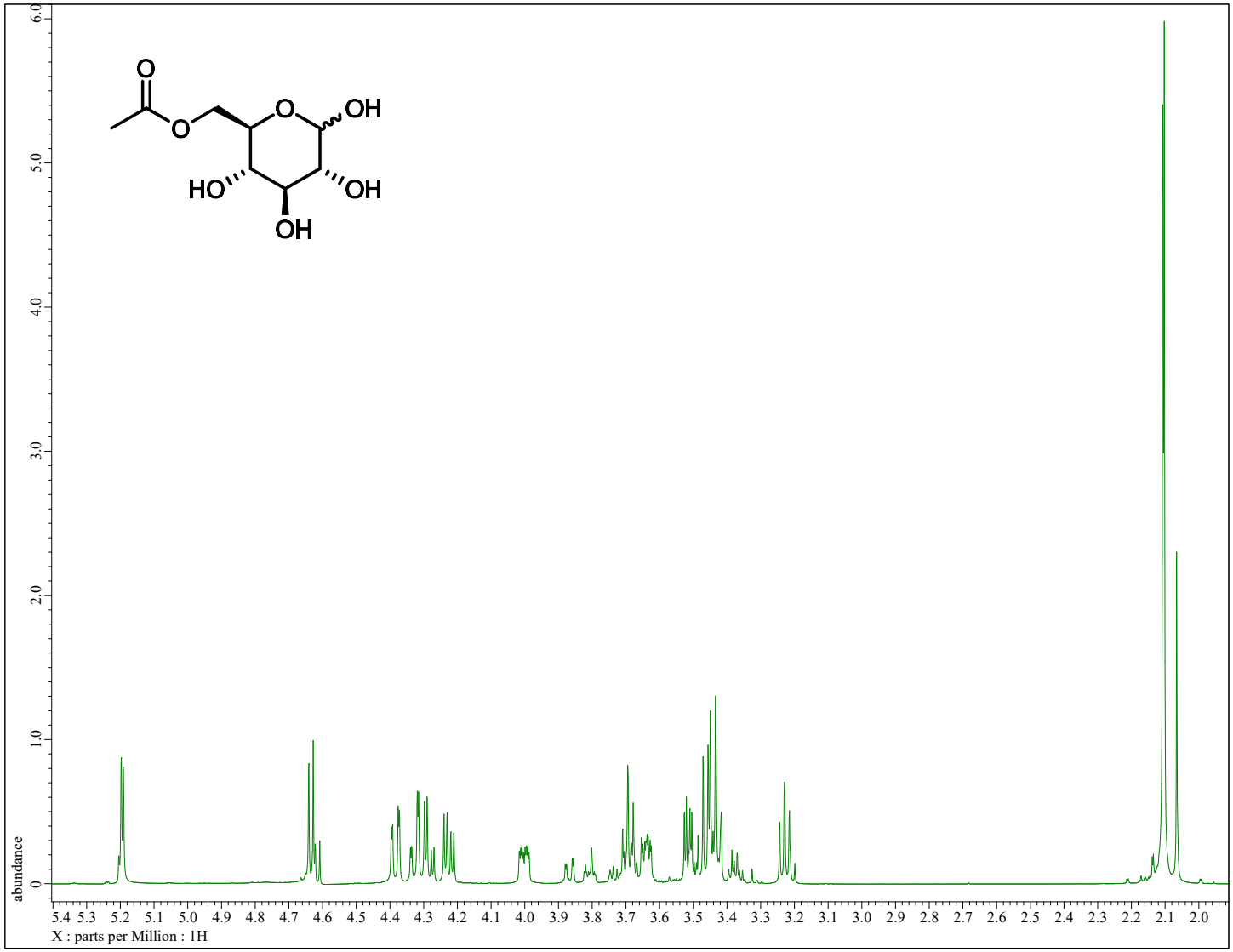
Figure S2 – Comparison of preliminary Karplus equations (blue) obtained based on tetrahydropyran-2-methyl acetate for C7-H6*proR* and C7-H6*proS* (left and right, respectively) and published equation based on Tvaroška *et al*. (orange).[4]

NMR spectral data

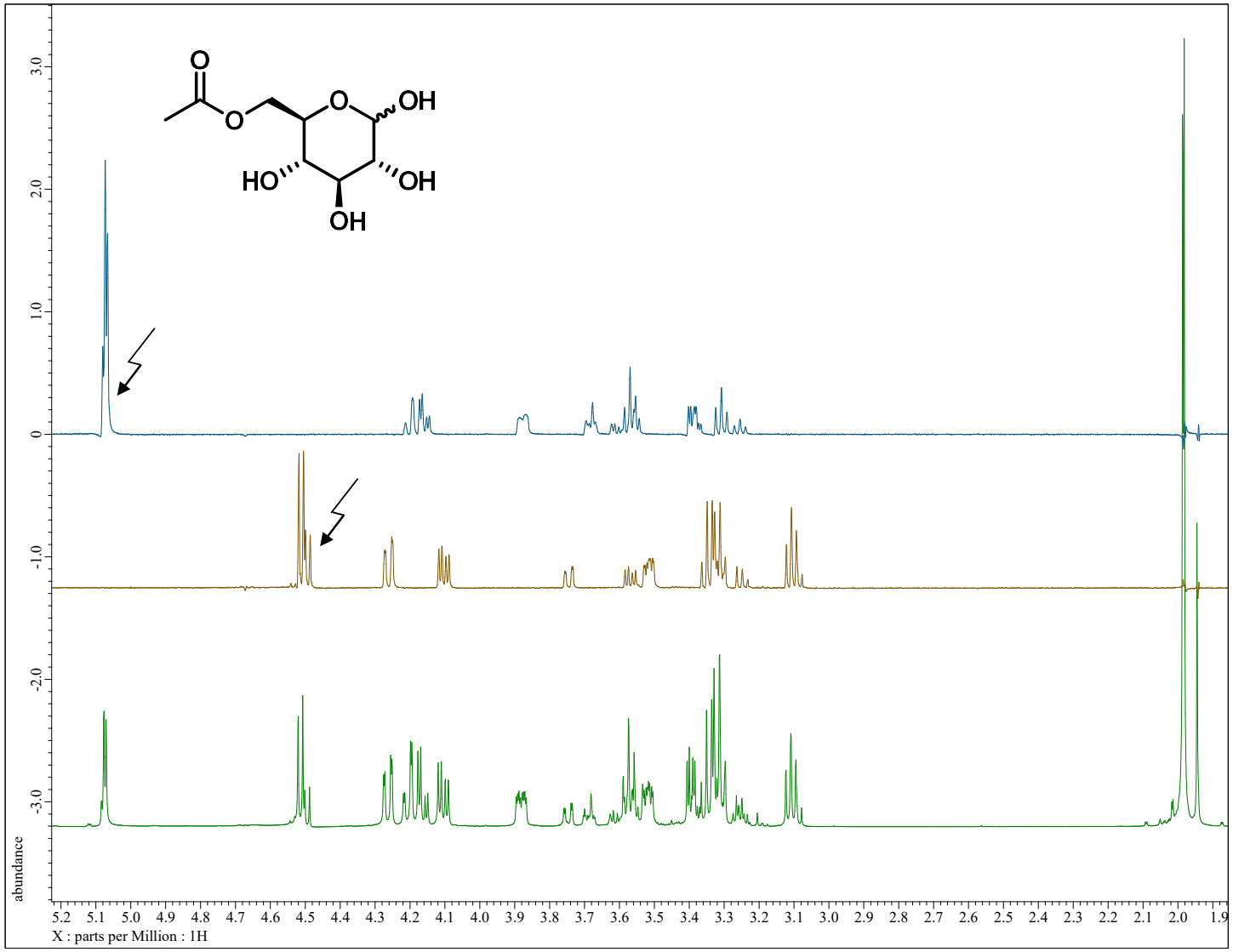
6-Acetyl-*α/β*-D-glucopyranose **Tõrge! Ei leia viiteallikat.**



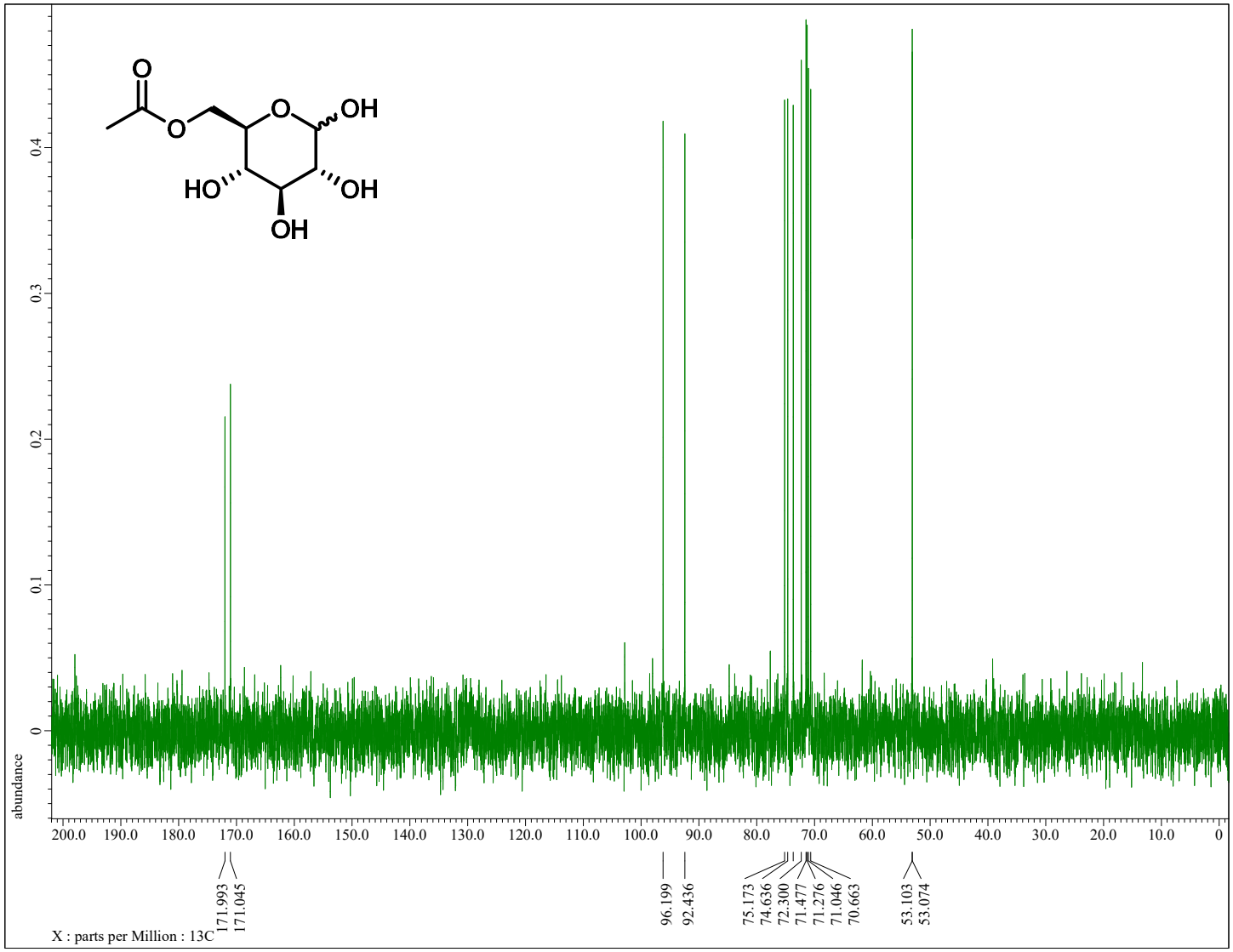
^{1}H NMR of Compound **1**



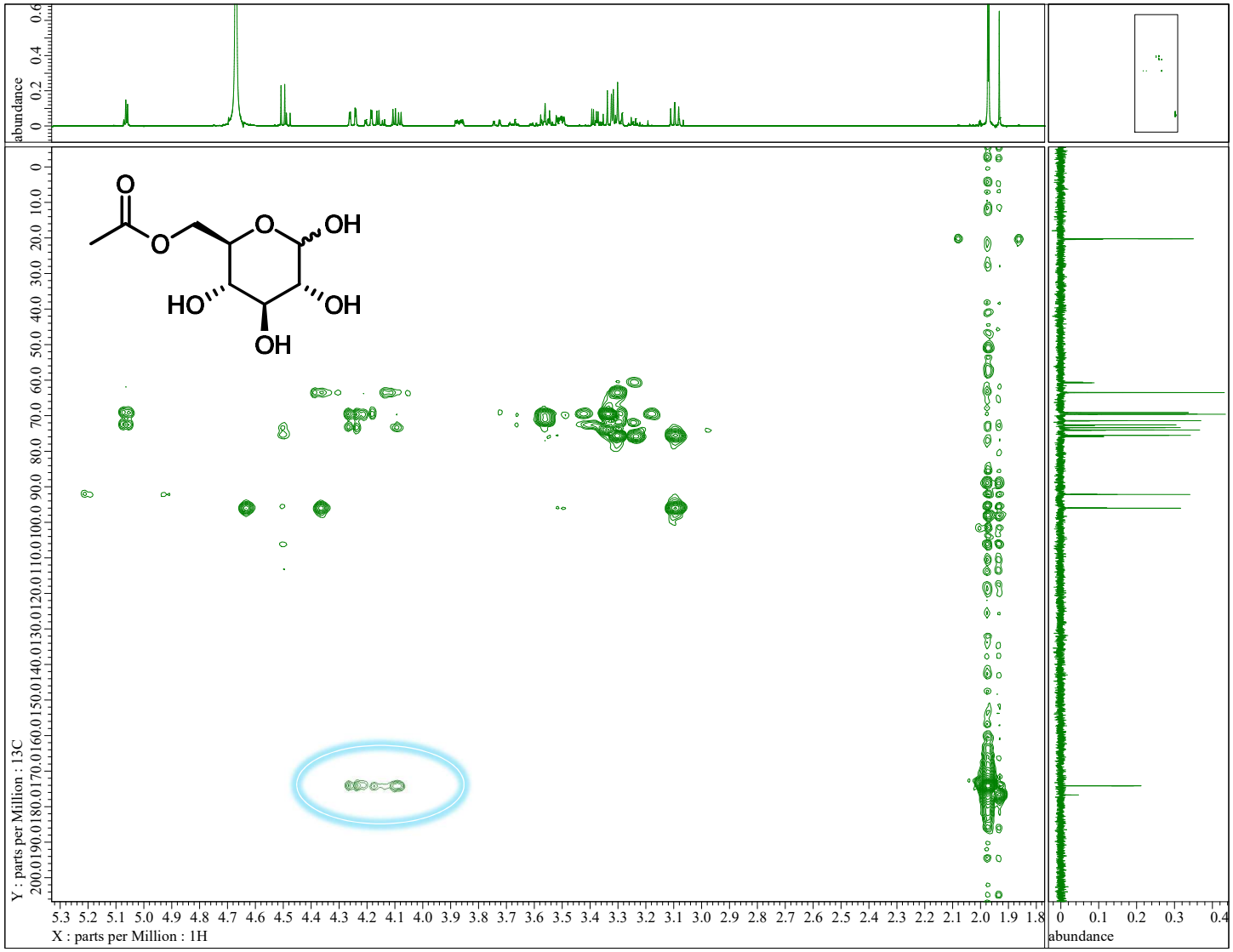
Presaturation ^{1}H NMR of Compound **1** expanded to show relevant range



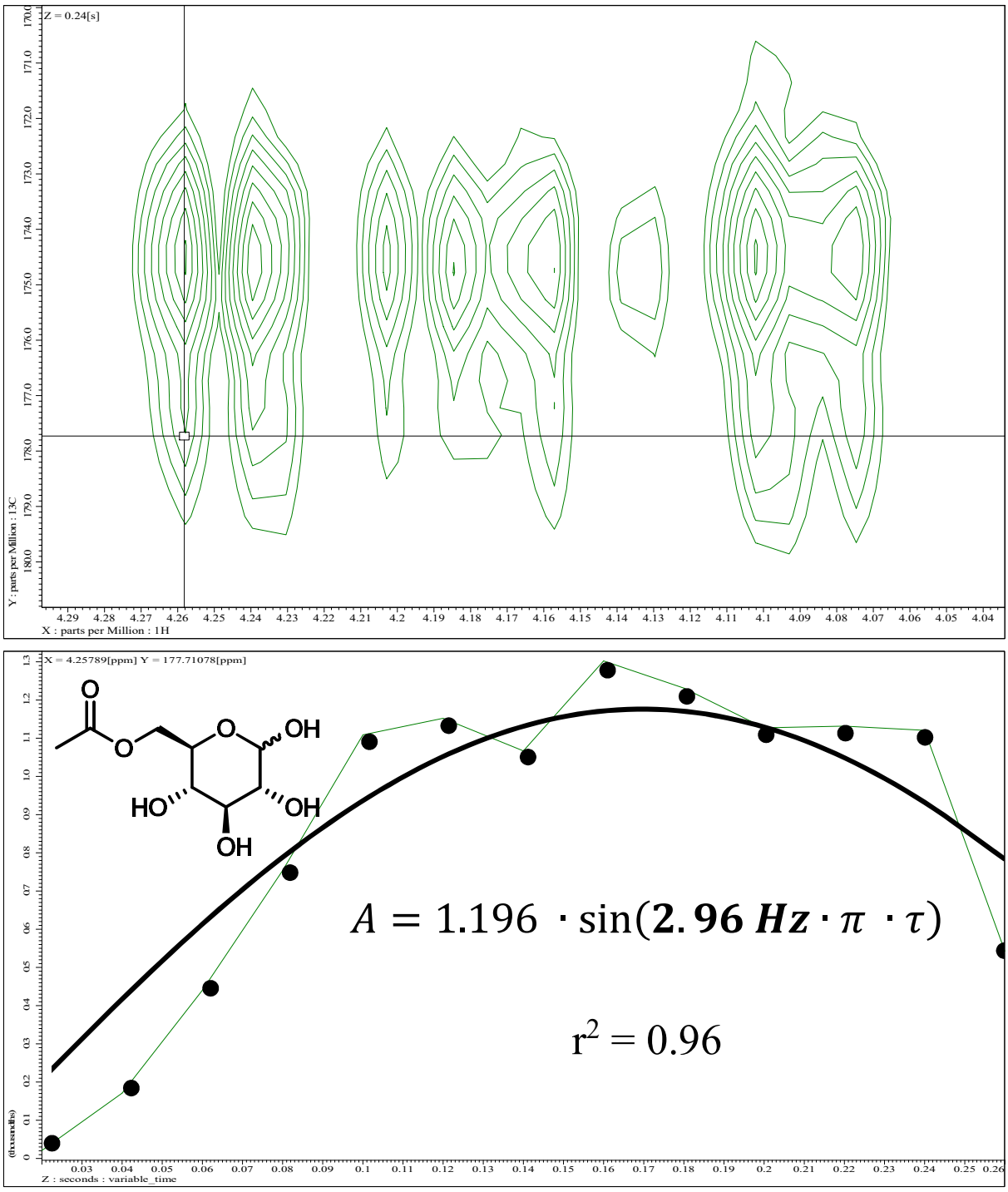
Presaturation ^{1}H NMR of Compound **1** overlayed with 1D TOCSY data for *α*-**1** (top) and *ß*-**1** (middle)



^{13}C NMR of Compound **1**

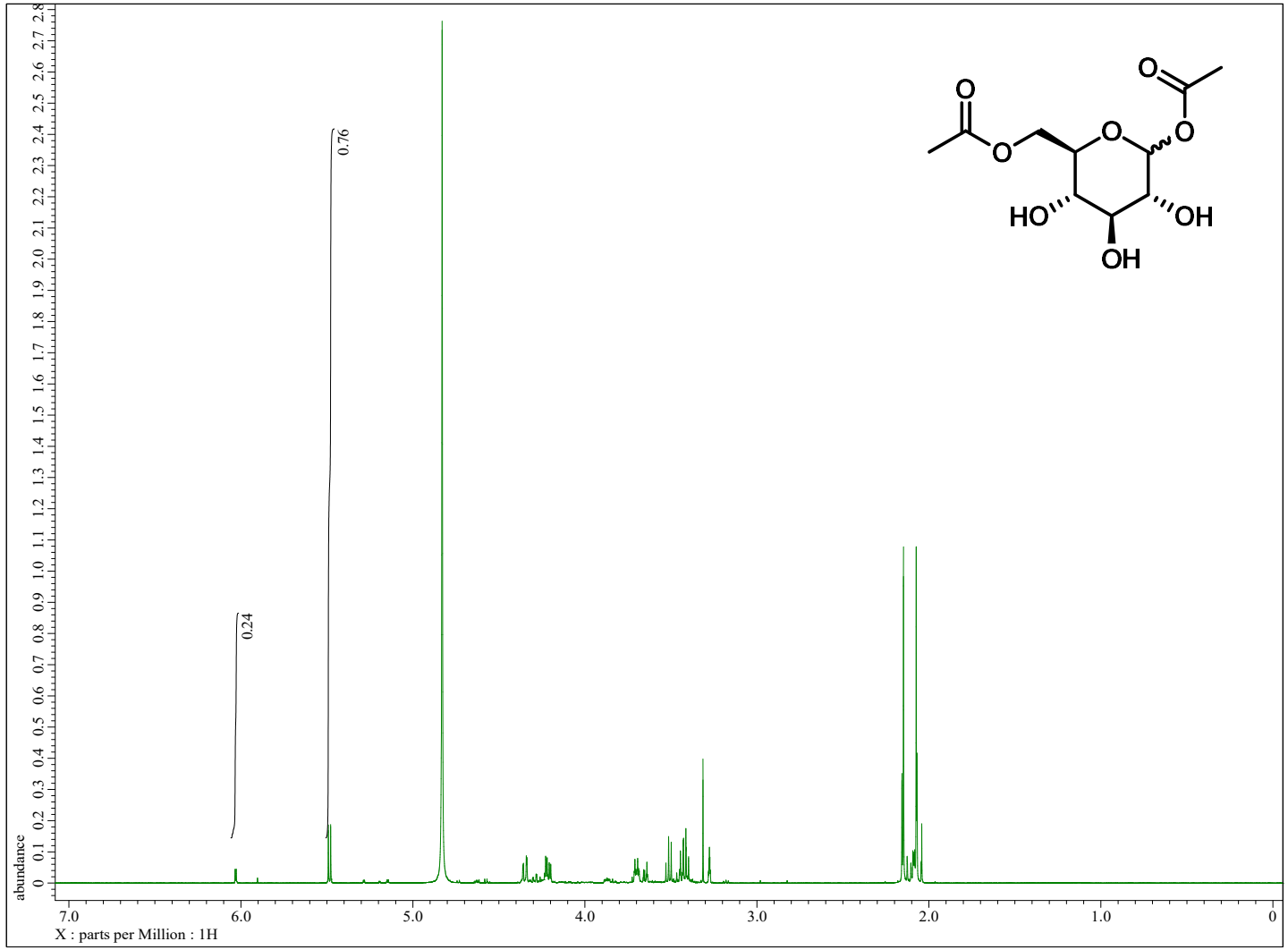


HMBC NMR of Compound **1** highlighting relevant cross-peaks used in determination of $^{3}J_{CH}$

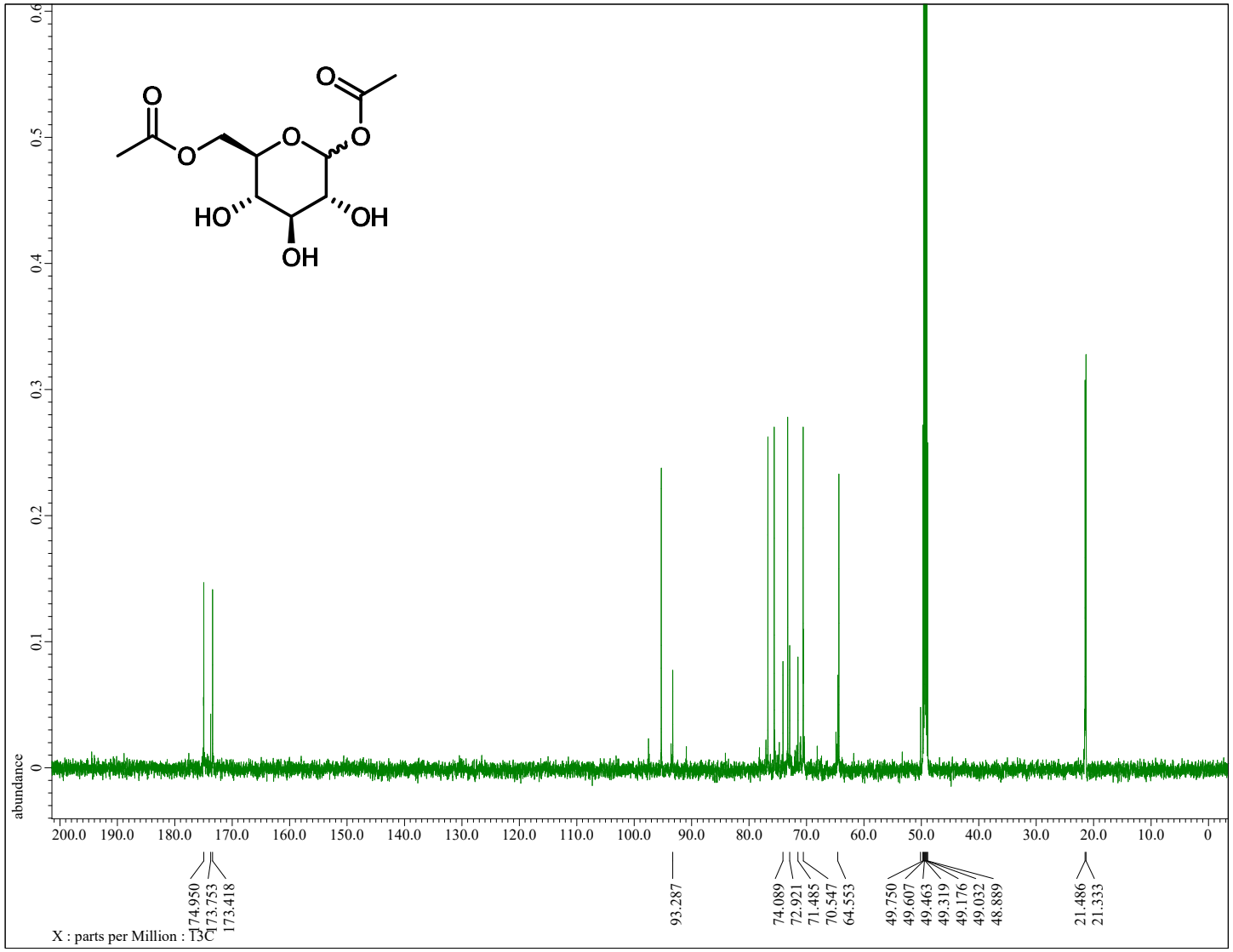


Expanded $^3J_{C5,H6a/b}$ cross-peak region of Compound **1** and example gradient enhanced *J*-HMBC data used in the determination of $^3J_{CH}$ (4.26 ppm – 168 ppm) overlaid with PSI-Plot fit.

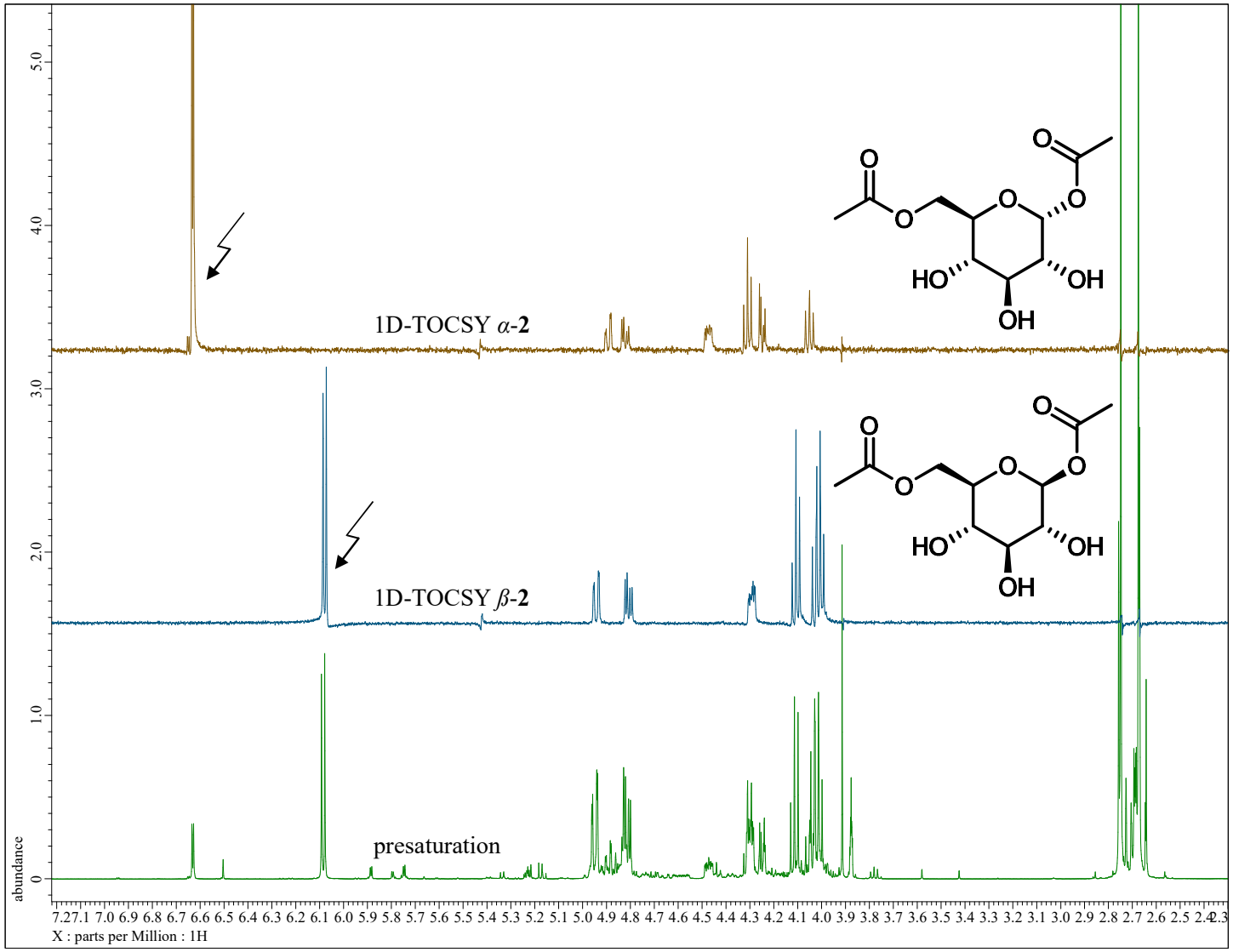
Acetyl 6-acetyl-α/ß-D-glucopyranose **2**



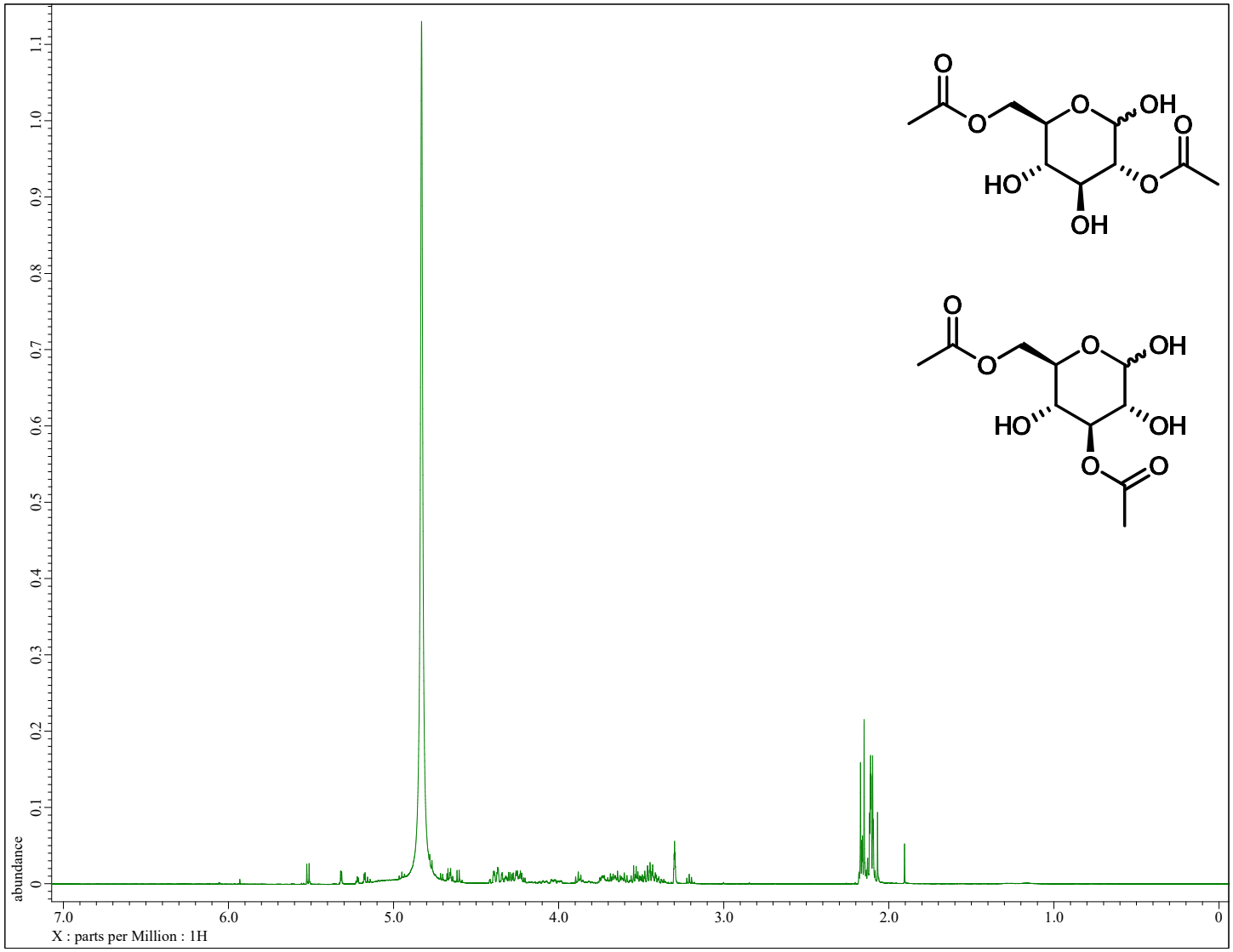
^{1}H NMR of Compound **2**



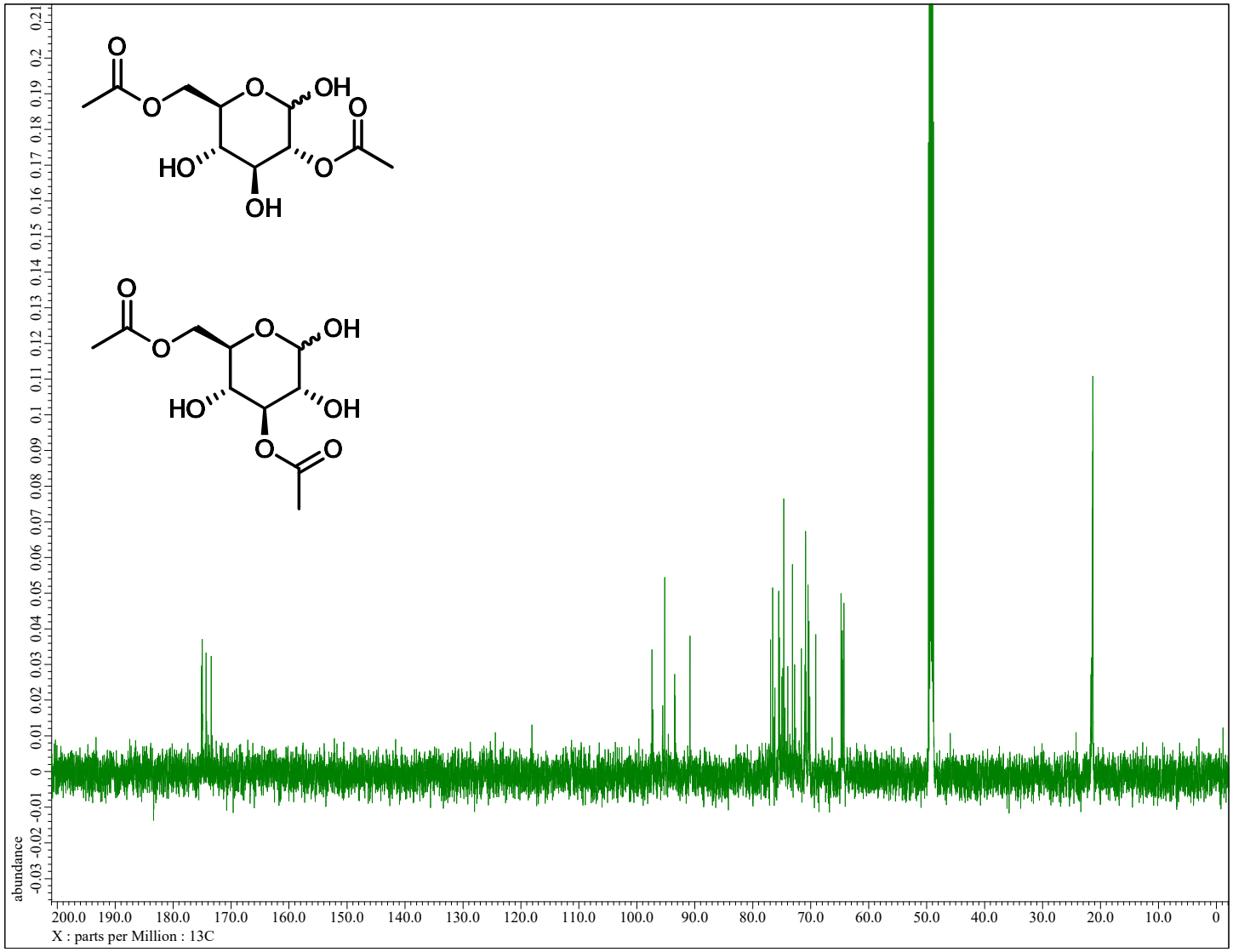
^{13}C NMR of Compound **2**



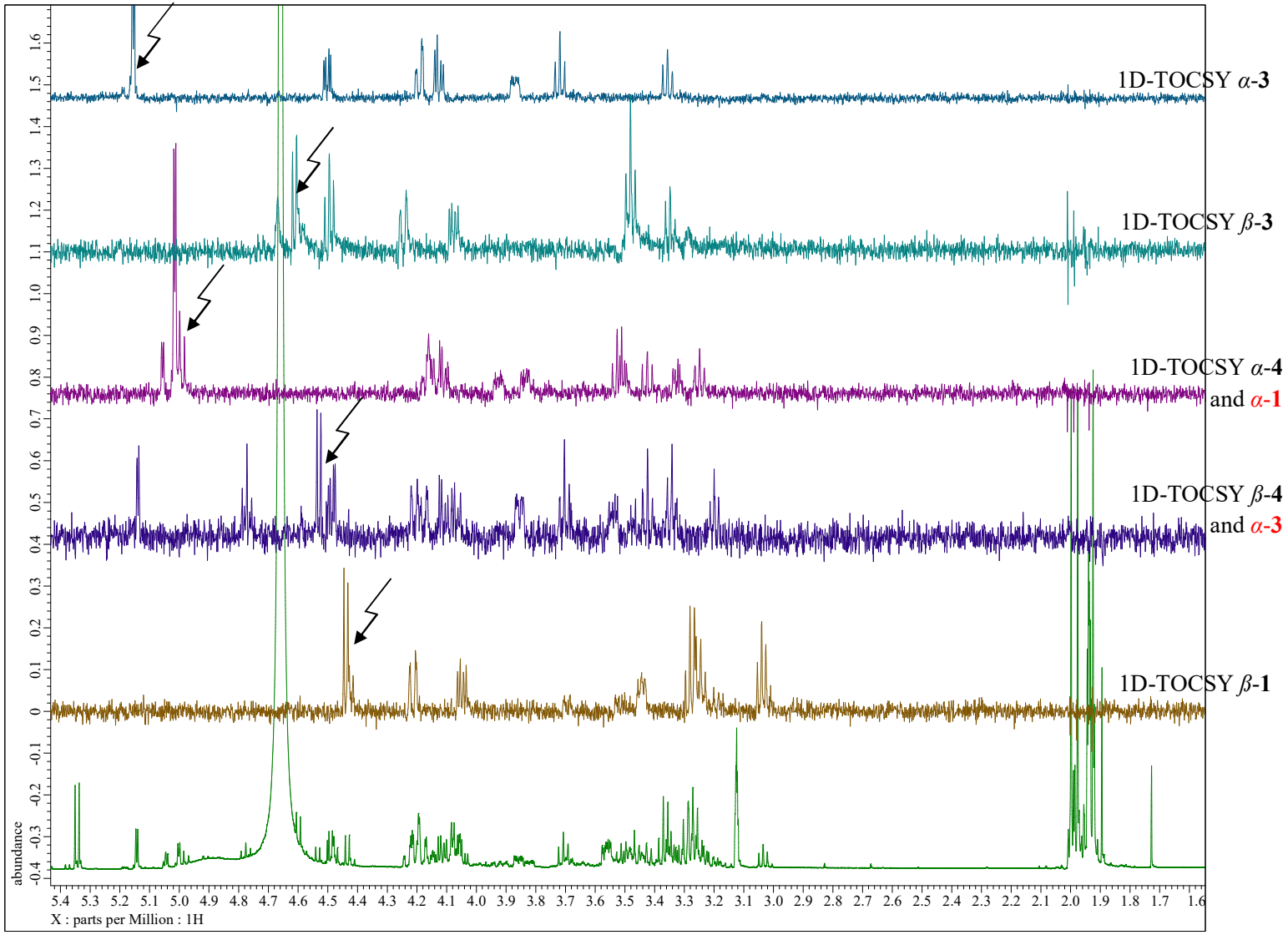
1D-TOCSY and presaturation experiments of Compound **2**



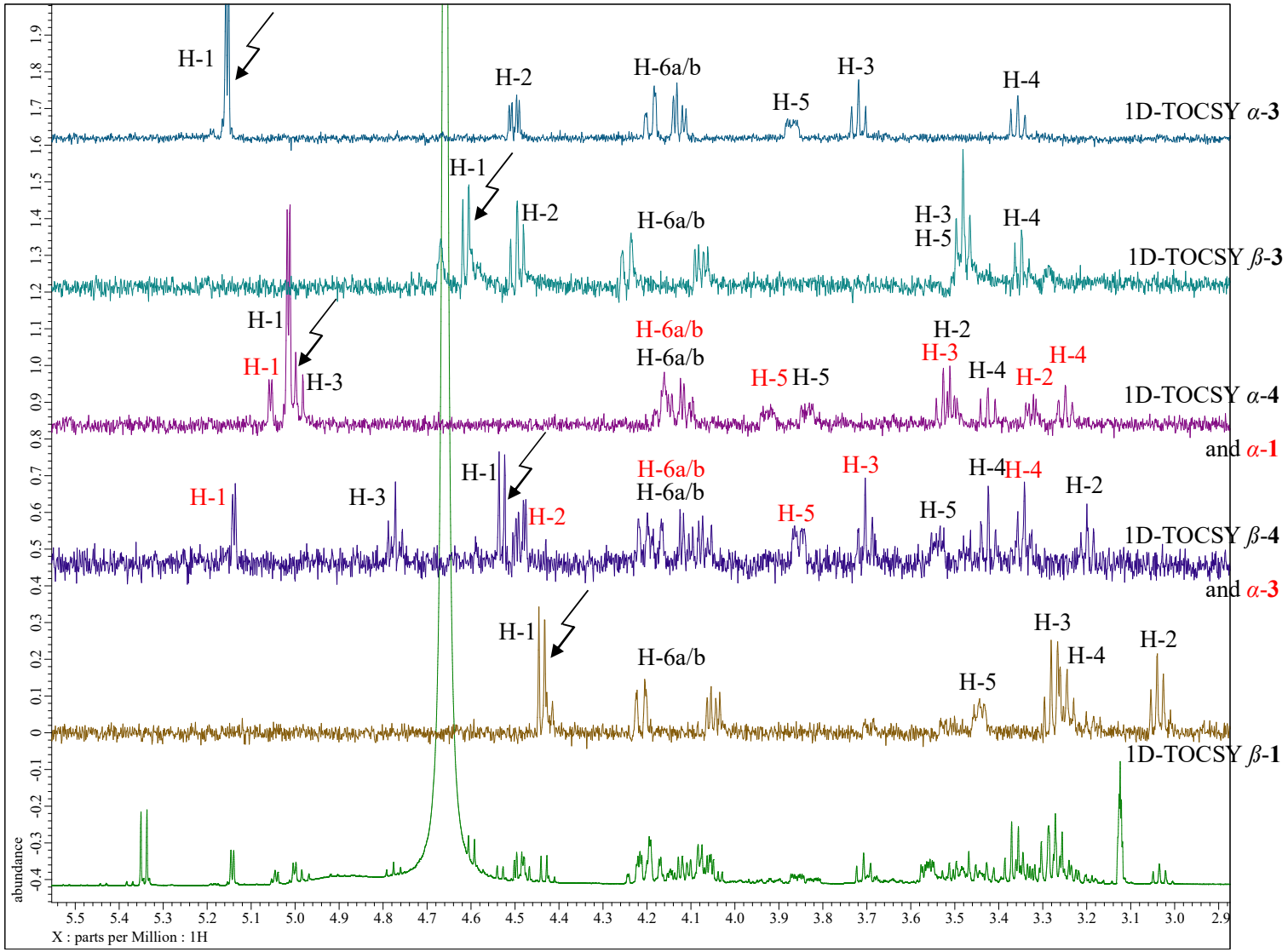
^{1}H NMR of the mixture containing *α/ß*-**3** and *α/ß*-**4**



^{13}C NMR of the mixture containing *α/ß*-**3** and *α/ß*-**4**



^{1}H NMR (bottom) and 1D TOCSY (500 ns mixing time) overlays for the mixture containing *α/ß*-**3** and *α/ß*-**4**

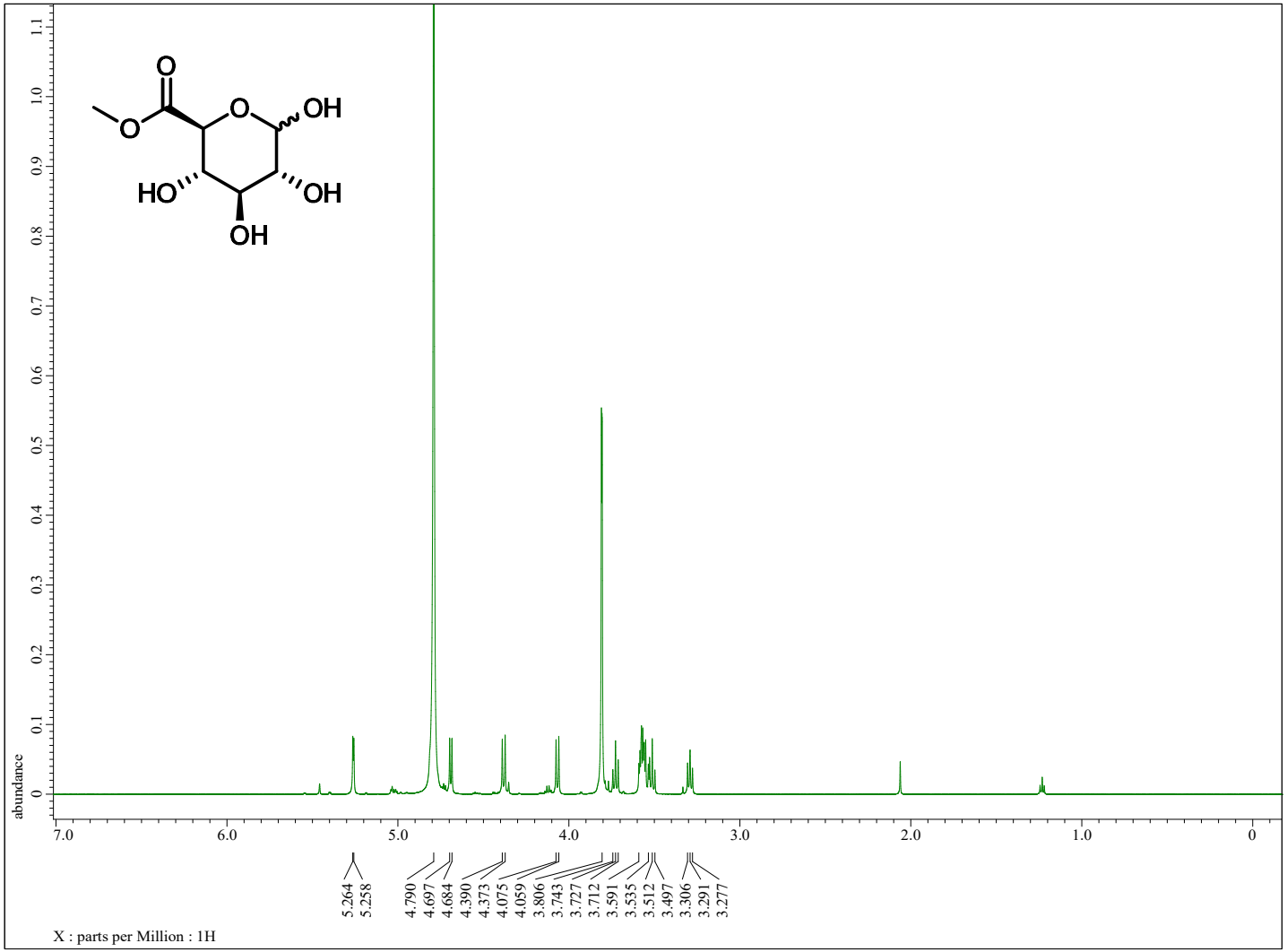


1D TOCSY overlays for the mixture containing *α*/*ß*-**3** and *α*/*ß*-**4** magnified to show assignment of hydrogens on pyranose ring

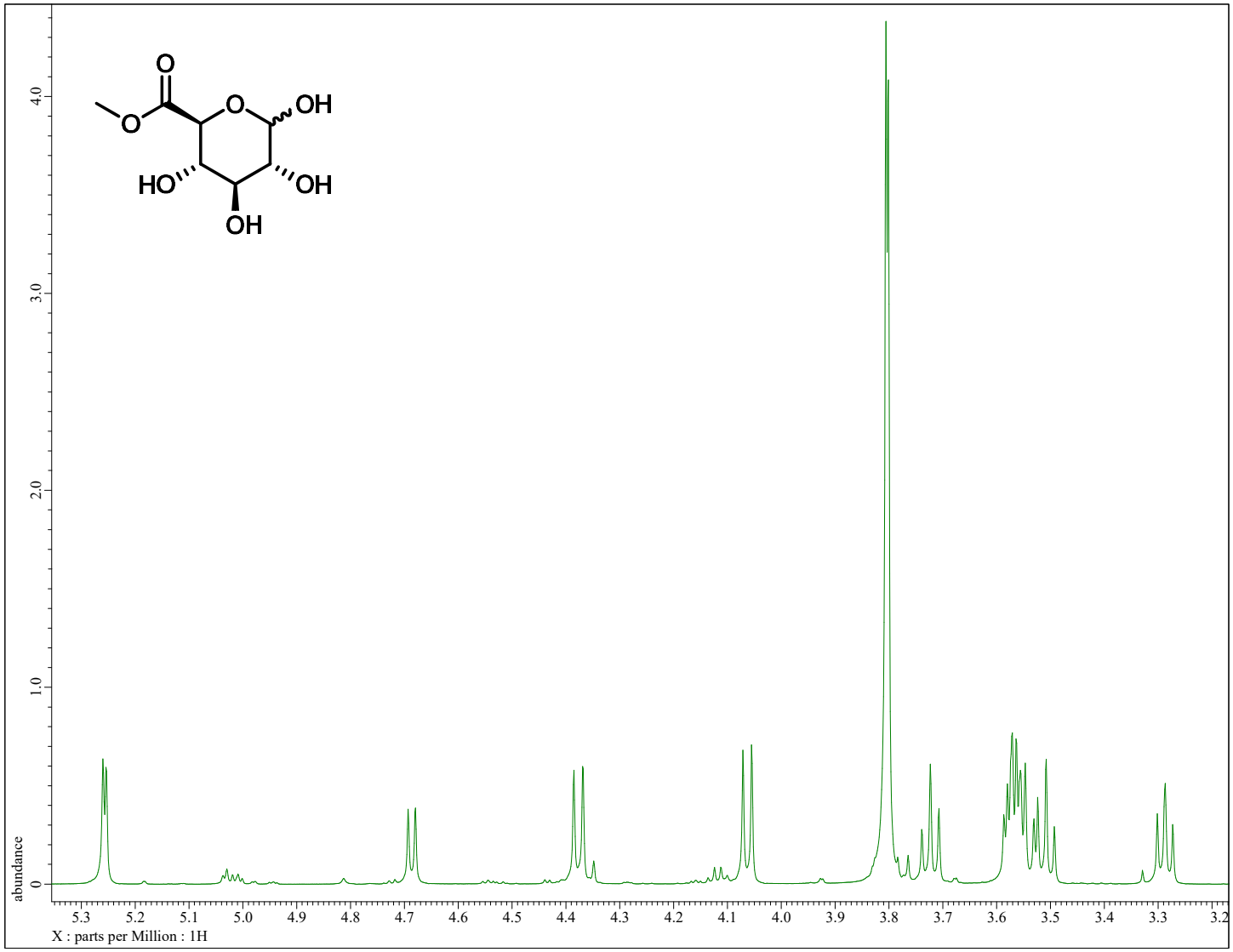
Tabular representation of ^{1}H chemical shifts for *α*/*ß*-**2**, *α*/*ß*-**3** and *α*/*ß*-**4**

^{1}H (δ / ppm)	H-1	H-2	H-3	H-4	H-5	H-6a	H-6b
α-**2**	6.03	3.65	3.71	3.45	3.87	4.29	4.22
ß-**2**	5.48	3.41	3.51	3.43	3.70	4.35	4.21
α-**3**	5.31	4.66	3.88	3.54	4.03	4.36	4.29
ß-**3**	4.77	4.65	3.66	3.54	3.67	4.40	4.24
α-**4**	5.18	3.69	5.16	3.61	3.99	4.32	4.29
ß-**4**	4.71	3.62	4.95	3.40	3.74	4.40	4.24

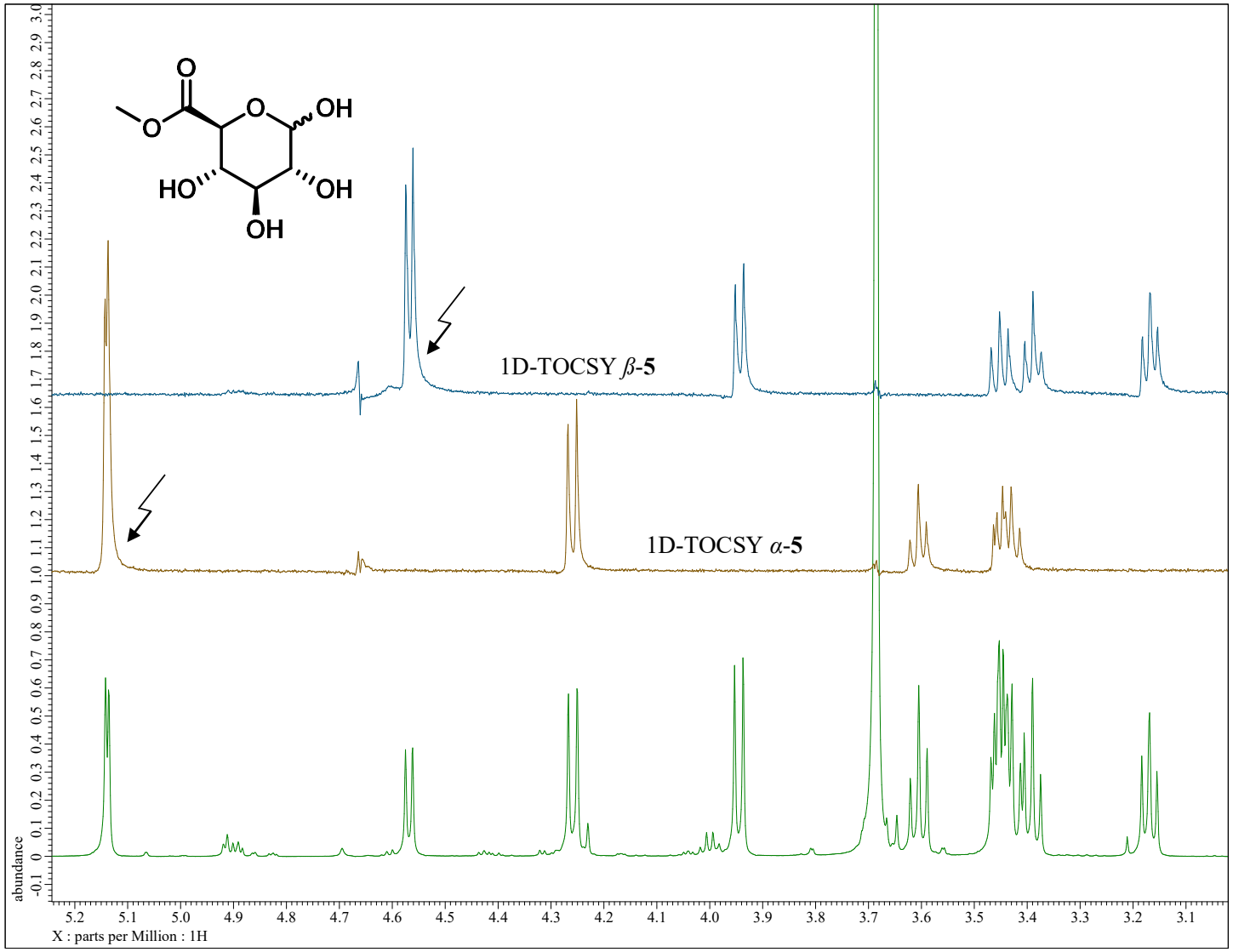
Methyl *α/β*-D-glucopyranuronate **5**



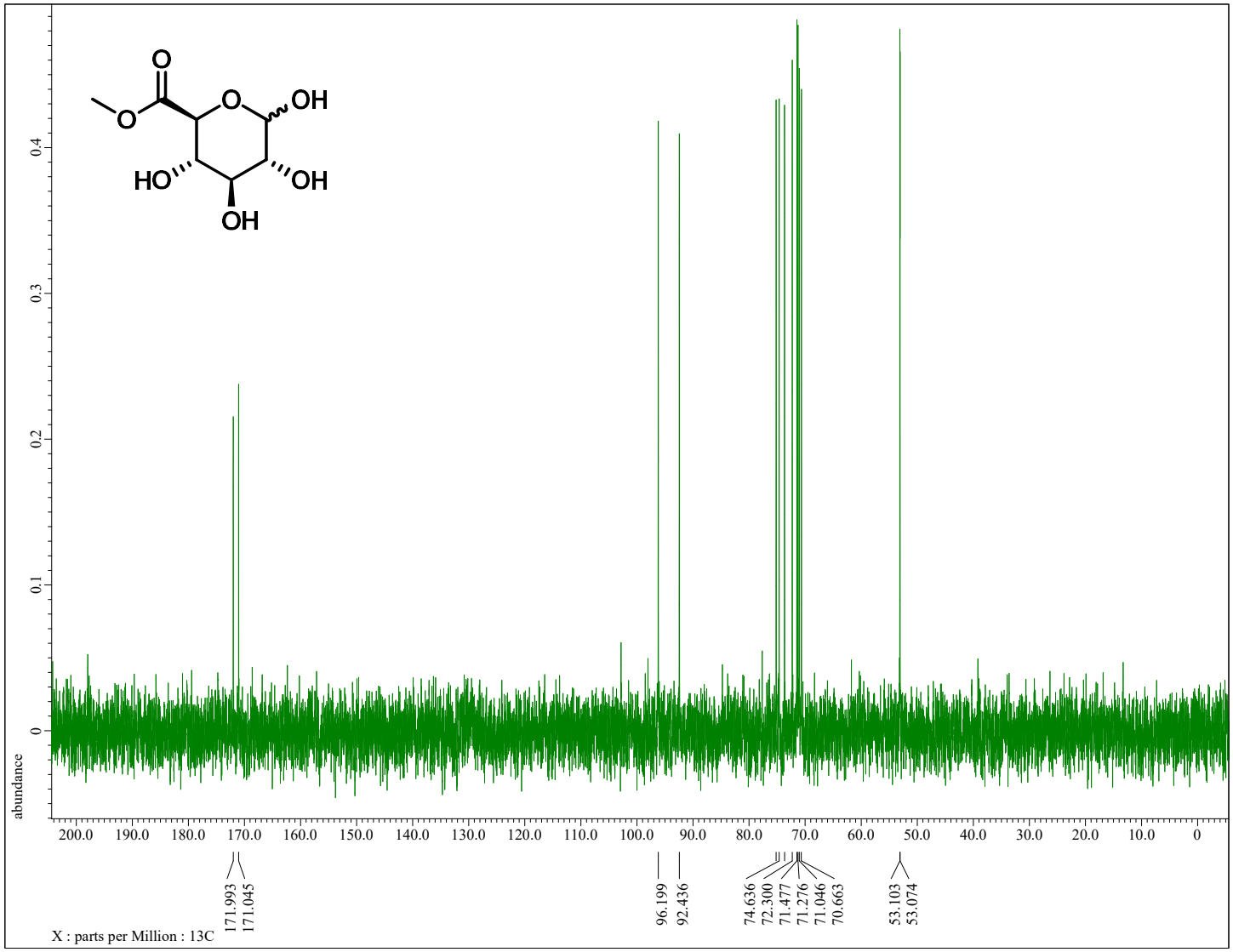
^{1}H NMR of Compound **5**



Presaturation ^{1}H NMR of Compound **5** expanded to show relevant range

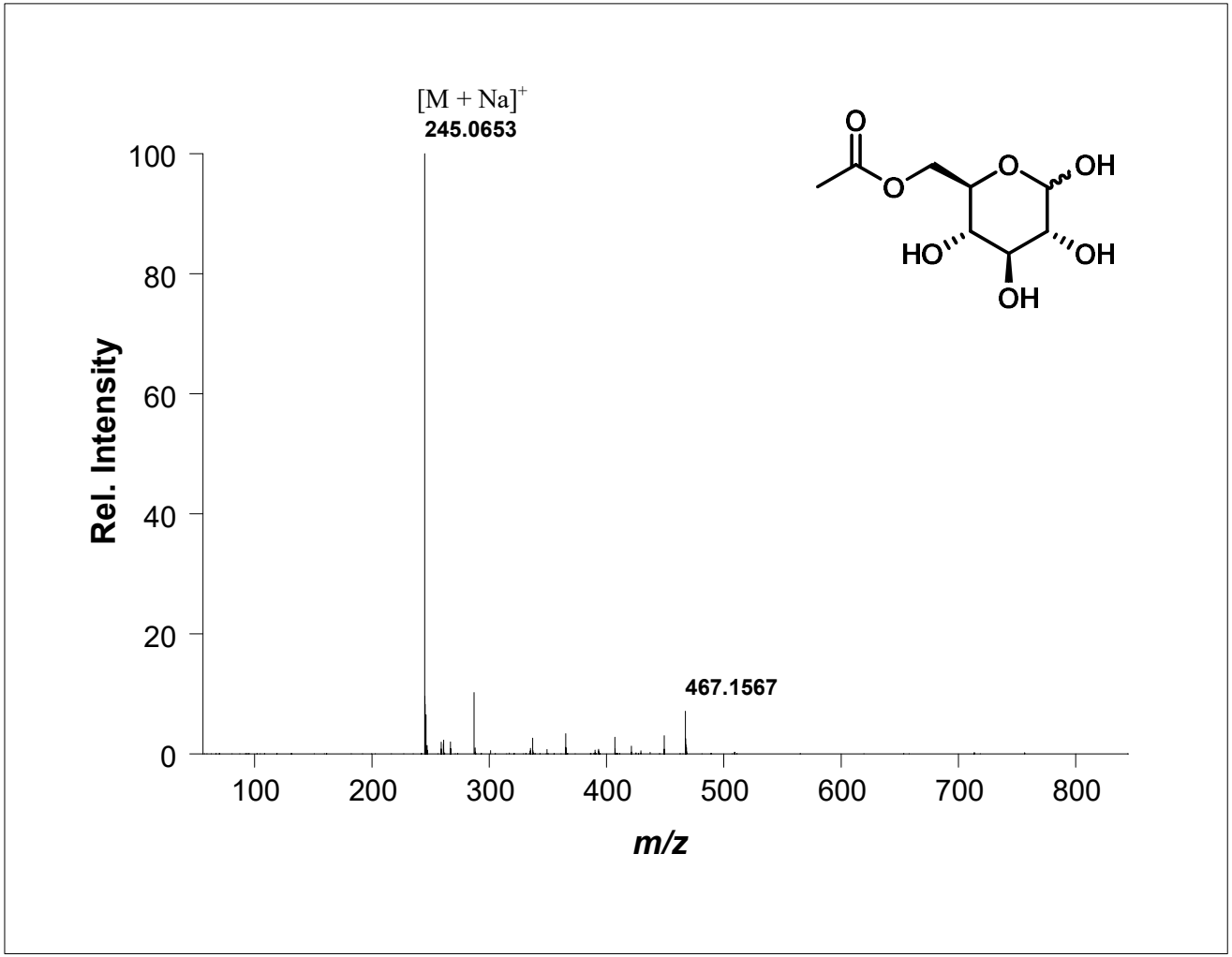


Presaturation ^{1}H NMR of Compound **5** overlayed with 1D TOCSY spectra

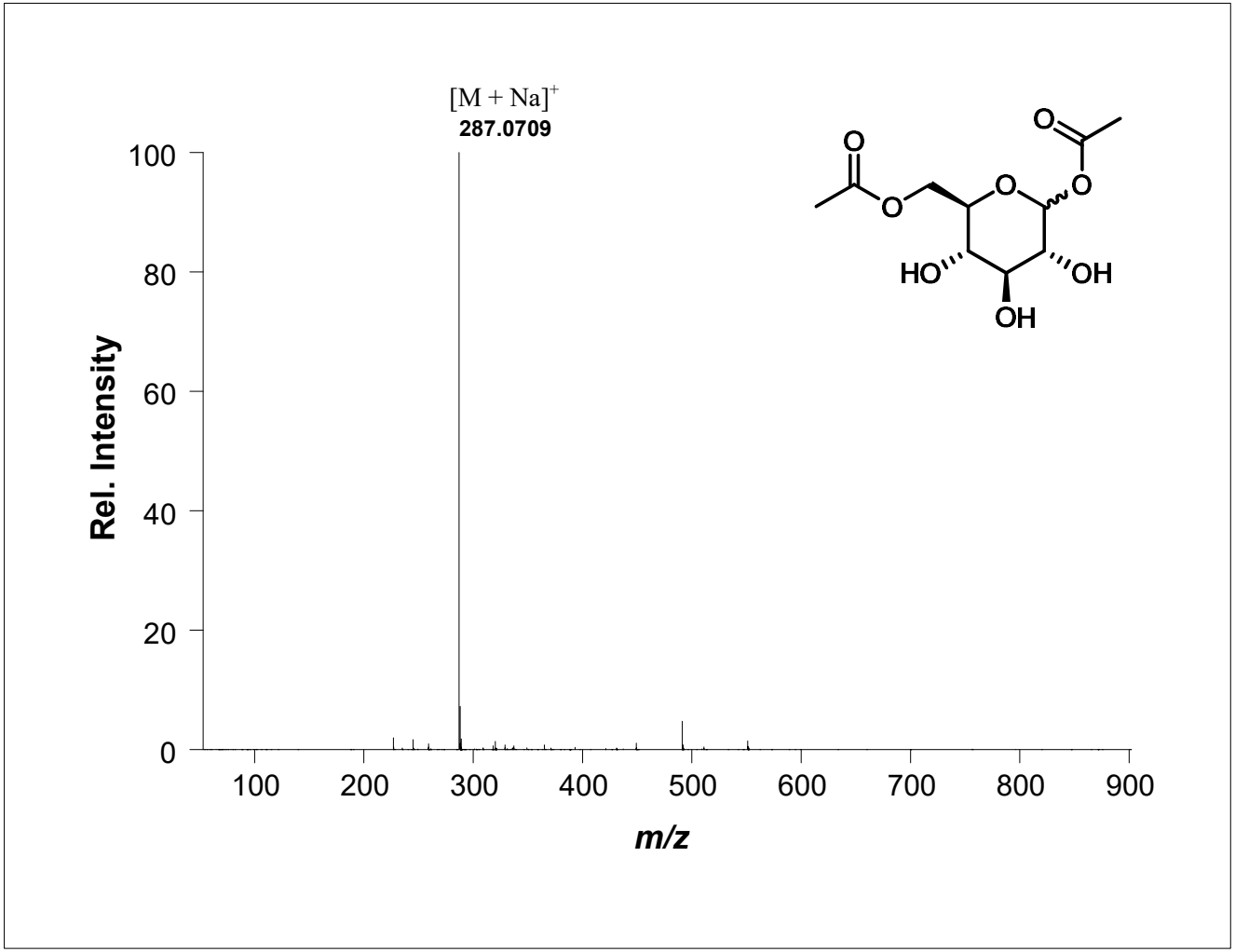


^{13}C NMR of Compound **5**

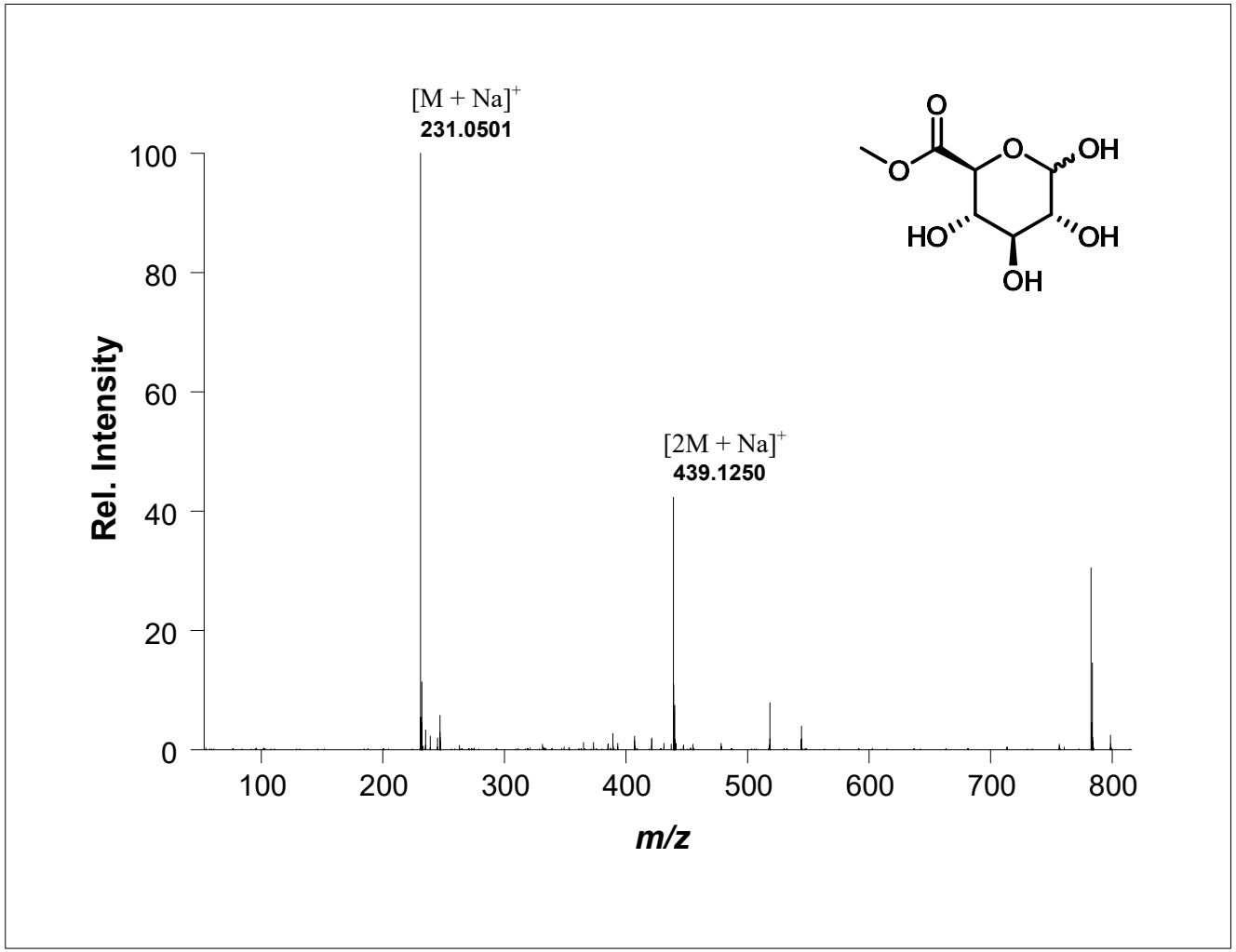
Mass spectral data.



ESI-HRMS of Compound **1**



ESI-HRMS of Compound **2**



ESI-HRMS of Compound **5**

Molecular Dynamics parameters.

Minimization Step 1

Minimize with solute held fixed
&cntrl
imin=1,
maxcyc=2000,
ncyc=1000,
ntpr=100,
ntb=1,
ntr=1,
cut=10.0,
/
Hold the sugar fixed
500.0
RES 1
END
END

Minimization Step 2

Minimize entire system
&cntrl
imin=1,
maxcyc=4500,
ncyc=1000,
ntb=1,
ntr=0,
cut=10.0,
/

Heating Step 1

Heat with weak constraints on solute for 20ps
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imin=0,
ntx=1,
irest=0,
ntb=1,
ntr=1,
nstlim=10000,
dt=0.002,
ntf=2,

ntc=2,
tempi=0.0,
temp0=300.0,
cut=8.0,
ntb=1,
ntt=3,
gamma_ln=1.0,
ig=-1,
ntpr=100, ntwx=100, ntwr=1000
/
Keep sugar fixed with weak restraints
10.0
RES 1
END
END

Heating Step 2

Heat for 100ps with full system without constraints
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ntb=2, pres0=1.0, ntp=1,
taup=2.0
ntr=0,
nstlim=50000,
dt=0.002,
ntf=2,
ntc=2,
tempi=300.0,
temp0=300.0,
cut=8.0,
ntt=3, gamma_ln=1.0,
ig=-1,
ntpr=100, ntwx=100, ntwr=1000
/

Production run

Production 500ns
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nstlim=500000000,
dt=0.001,

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ntc=2,
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ntt=3,
gamma_ln=1.0,
ig=-1,
/

Input geometries for Molecular Dynamics simulations

6-Acetyl-α-D-glucose *α*-**1**

HO1	6.065	8.253	-1.783
O1	6.341	8.899	-2.438
C1	5.585	8.705	-3.648
H1	5.816	7.715	-4.043
C2	5.936	9.770	-4.708
H2	5.484	9.457	-5.651
O2	7.363	9.804	-4.891
H2O	7.785	10.044	-4.062
C3	5.422	11.178	-4.354
H3	6.004	11.589	-3.526
O3	5.580	12.016	-5.513
H3O	6.505	12.034	-5.770
C4	3.924	11.147	-3.986
H4	3.325	10.952	-4.879
O4	3.569	12.435	-3.453
H4O	3.722	13.109	-4.120
C5	3.606	10.084	-2.916
H5	4.123	10.350	-1.993
O5	4.133	8.776	-3.382
C6	2.110	9.915	-2.609
H62	1.707	10.807	-2.128
H61	1.562	9.775	-3.542
O6	1.878	8.726	-1.757
C1A	2.141	8.551	-0.454
O1A	1.925	7.489	0.129
C2A	2.756	9.752	0.319
H1A	3.816	9.561	0.491
H2A	2.260	9.843	1.286
H3A	2.645	10.701	-0.199

6-Acetyl-β-D-glucose *β*-**1**

HO1	5.917	8.485	-1.724
O1	6.230	9.073	-2.414
C1	7.663	9.128	-2.382
H1	8.058	8.126	-2.556
O5	8.135	9.604	-1.067
C5	9.597	9.763	-0.917
H5	10.077	8.804	-1.123
C4	10.072	10.798	-1.954
H4	9.676	11.783	-1.698
O4	11.509	10.837	-1.915
H4O	11.829	11.478	-2.554
C3	9.646	10.408	-3.382
H3	10.222	9.538	-3.708
O3	9.931	11.517	-4.255
H3O	9.696	11.282	-5.156
C2	8.140	10.099	-3.480
H2	7.566	11.027	-3.424
O2	7.907	9.470	-4.753
H2O	6.974	9.260	-4.839
C6	9.872	10.153	0.539
H62	9.239	10.986	0.846
H61	10.913	10.457	0.639
O6	9.597	8.977	1.392
C1A	10.184	8.664	2.555
O1A	9.902	7.656	3.202
C2A	11.267	9.655	3.059
H1A	11.625	9.349	4.043
H2A	10.849	10.660	3.139
H3A	12.114	9.661	2.372

Acetyl 6-acetyl-α-D-glucopyranoside α-**2**

C5	-0.447	-0.098	0.659
C4	-0.478	1.422	0.548
C3	0.916	1.936	0.235
C2	1.466	1.252	-1.007
C1	1.369	-0.265	-0.881
O5	0.105	-0.662	-0.515
H1	1.595	-0.755	-1.810
H2	0.864	1.547	-1.857
H3	1.562	1.717	1.084
H4	-1.141	1.706	-0.263
H5	0.162	-0.368	1.517
C6	-1.807	-0.726	0.866
H61	-2.225	-0.397	1.805
H62	-1.714	-1.802	0.877
O6	-2.655	-0.335	-0.200
CA3	-3.886	-0.831	-0.209
CA4	-4.665	-0.343	-1.399
HA4	-5.661	-0.761	-1.375
HA5	-4.160	-0.637	-2.311
HA6	-4.716	0.739	-1.385
OA2	-4.300	-1.567	0.627
O4	-0.941	1.927	1.766
HO4	-0.902	2.875	1.732
O3	0.822	3.322	0.052
HO3	1.659	3.651	-0.251
O2	2.770	1.677	-1.285
HO2	3.361	1.277	-0.659
O1	2.332	-0.651	0.090
CA1	2.812	-1.907	0.054
CA2	3.732	-2.165	1.214
HA1	4.126	-3.167	1.145
HA2	3.189	-2.044	2.144
HA3	4.544	-1.446	1.211
OA1	2.540	-2.684	-0.794

Acetyl 6-acetyl-α-D-glucopyranoside β-**2**

C5	-0.710	0.293	1.231
C4	-0.952	1.253	0.066
C3	0.291	2.105	-0.119
C2	1.510	1.224	-0.344
C1	1.611	0.231	0.810
O5	0.431	-0.485	0.972
H1	1.844	0.779	1.715
H2	1.383	0.690	-1.276
H3	0.442	2.697	0.783
H4	-1.113	0.684	-0.844
H5	-0.557	0.889	2.132
C6	-1.852	-0.654	1.548
H61	-2.723	-0.096	1.856
H62	-1.543	-1.312	2.345
O6	-2.185	-1.515	0.468
CA3	-3.145	-1.176	-0.371
CA4	-3.406	-2.261	-1.377
HA4	-3.704	-3.167	-0.864
HA5	-2.493	-2.475	-1.920
HA6	-4.182	-1.946	-2.058
OA2	-3.727	-0.133	-0.331
O4	-2.023	2.116	0.313
HO4	-2.834	1.663	0.108
O3	0.182	2.951	-1.228
HO3	-0.612	3.464	-1.132
O2	2.686	1.978	-0.351
HO2	2.597	2.656	-1.010
O1	2.661	-0.682	0.700
CA1	2.761	-1.542	-0.319
CA2	3.965	-2.423	-0.135
HA1	4.857	-1.811	-0.068
HA2	4.043	-3.106	-0.968
HA3	3.874	-2.976	0.793
OA1	2.011	-1.598	-1.235

2,6-Diacetyl-α-D-glucose α-**3**

HO1	5.953	8.295	-1.837
O1	6.200	8.992	-2.448
C1	5.465	8.837	-3.678
H1	5.760	7.884	-4.118
C2	5.812	9.967	-4.684
H2	5.496	9.606	-5.665
C3	5.051	11.289	-4.400
H3	5.575	11.852	-3.628
C4	3.579	11.095	-3.977
H4	2.972	10.808	-4.839
C5	3.419	10.029	-2.886
H5	3.986	10.337	-2.007
C6	1.974	9.730	-2.459
H62	1.537	10.581	-1.934
H61	1.363	9.543	-3.343
O6	1.933	8.524	-1.603
O5	4.014	8.788	-3.421
O4	3.092	12.345	-3.458
H4O	3.146	13.016	-4.143
O3	4.994	12.041	-5.624
H3O	5.884	12.180	-5.957
O2	7.313	10.017	-4.691
C1A	2.279	8.383	-0.315
O1A	2.248	7.298	0.263
C2A	2.728	9.659	0.455
H1A	3.708	9.478	0.899
H2A	2.016	9.855	1.258
H3A	2.795	10.548	-0.164
C1A	8.290	10.931	-4.811
O1A	9.473	10.637	-4.649
C2A	7.905	12.376	-5.190
H1A	8.809	12.981	-5.276
H2A	7.287	12.830	-4.419
H3A	7.411	12.389	-6.160

2,6-Diacetyl-*β*-D-glucose *β*-**3**

HO1	6.119	8.482	-2.152
O1	6.462	9.174	-2.723
C1	7.880	9.282	-2.545
H1	8.349	8.355	-2.876
O5	8.215	9.522	-1.122
C5	9.644	9.741	-0.779
H5	10.188	8.813	-0.964
C6	9.720	10.094	0.711
H62	8.958	10.830	0.973
H61	10.694	10.533	0.922
O6	9.517	8.867	1.509
C4	10.232	10.861	-1.665
H4	9.864	11.831	-1.327
O4	11.664	10.819	-1.529
H4O	12.058	11.470	-2.115
C3	9.902	10.675	-3.152
H3	10.443	9.810	-3.541
O3	10.312	11.851	-3.871
H3O	10.133	11.725	-4.807
C2	8.389	10.485	-3.358
H2	7.885	11.375	-2.976
O2	8.059	10.399	-4.804
C1A	10.155	8.517	2.637
O1A	9.910	7.484	3.254
C2A	11.251	9.500	3.137
H1A	11.664	9.151	4.084
H2A	10.826	10.493	3.290
H3A	12.061	9.555	2.408
C1A	8.696	9.630	-5.689
O1A	9.306	8.585	-5.461
C2A	8.631	10.250	-7.100
H1A	9.514	9.960	-7.672
H2A	8.613	11.340	-7.035
H3A	7.736	9.906	-7.617

3,6-Diacetyl-α-D-glucose α-**4**

HO1	5.937	7.883	-1.936
O1	6.273	8.545	-2.541
C1	5.487	8.536	-3.749
H1	5.624	7.573	-4.241
C2	5.922	9.667	-4.704
H2	5.411	9.520	-5.657
O2	7.337	9.573	-4.947
H2O	7.810	9.681	-4.118
C3	5.568	11.064	-4.165
H3	6.134	11.255	-3.250
C4	4.064	11.133	-3.849
H4	3.488	11.056	-4.774
C5	3.635	10.018	-2.876
H5	4.160	10.162	-1.931
C6	2.126	9.958	-2.600
H62	1.778	10.877	-2.128
H61	1.588	9.854	-3.544
O6	1.798	8.792	-1.749
O5	4.050	8.710	-3.445
O4	3.795	12.406	-3.236
H4O	4.002	13.107	-3.857
O3	5.881	12.099	-5.176
C1A	2.015	8.618	-0.437
O1A	2.562	9.467	0.264
C2A	1.519	7.285	0.193
H1A	0.522	7.434	0.611
H2A	2.192	6.996	1.000
H3A	1.491	6.466	-0.524
C1A	7.004	12.821	-5.132
O1A	7.966	12.649	-4.383
C2A	6.967	13.976	-6.150
H1A	7.984	14.268	-6.419
H2A	6.461	14.831	-5.702
H3A	6.436	13.679	-7.056

3,6-Diacetyl-*β*-D-glucose *β*-**4**

HO1	5.922	8.530	-1.927
O1	6.297	9.155	-2.551
C1	7.723	9.184	-2.402
H1	8.119	8.189	-2.608
O5	8.092	9.568	-1.024
C5	9.535	9.713	-0.738
H5	10.028	8.754	-0.918
C6	9.681	10.092	0.740
H62	8.953	10.856	1.018
H61	10.676	10.498	0.908
O6	9.467	8.881	1.560
C4	10.116	10.768	-1.697
H4	9.727	11.754	-1.434
O4	11.546	10.768	-1.545
H4O	11.932	11.400	-2.157
C3	9.801	10.465	-3.171
H3	10.358	9.578	-3.485
C2	8.300	10.215	-3.393
H2	7.753	11.156	-3.307
O2	8.143	9.695	-4.724
H2O	7.216	9.510	-4.888
O3	10.209	11.642	-3.972
C1A	10.125	8.527	2.673
O1A	10.993	9.227	3.193
C2A	9.728	7.160	3.296
H1A	10.374	6.934	4.146
H2A	9.837	6.365	2.558
H3A	8.697	7.198	3.649
C1A	11.384	11.711	-4.599
O1A	12.211	10.806	-4.729
C2A	11.631	13.123	-5.159
H1A	12.678	13.235	-5.445
H2A	11.398	13.872	-4.399
H3A	11.002	13.288	-6.033

Methyl α-D-glucoronate α-**5**

C5	0.608	-0.041	-0.325
C4	-0.263	1.154	0.109
O5	0.246	-1.211	0.410
C1	-1.097	-1.614	0.231
C2	-2.092	-0.497	0.614
C3	-1.742	0.803	-0.126
C6	2.065	0.236	-0.035
H5	0.495	-0.232	-1.430
O62	2.847	-0.870	0.036
CM	4.240	-0.656	0.288
HM1	4.663	-1.690	0.298
HM2	4.374	-0.146	1.272
HM3	4.683	-0.038	-0.530
O61	2.581	1.352	0.096
O4	-0.005	2.296	-0.685
H4	-0.086	1.383	1.195
HO4	0.895	2.591	-0.479
O3	-2.595	1.807	0.392
H3	-1.929	0.678	-1.230
HO3	-2.308	2.643	0.000
O2	-3.371	-0.961	0.224
H2	-2.064	-0.325	1.724
HO2	-3.989	-0.233	0.379
O1	-1.169	-1.966	-1.129
H1	-1.213	-2.519	0.893
HO1	-2.104	-1.993	-1.373

Methyl *β*-D-glucoronate *β*-**5**

C5	0.652	-0.062	-0.363
C4	-0.122	1.162	0.162
O5	0.046	-1.280	0.065
C1	-1.307	-1.424	-0.353
C2	-2.179	-0.283	0.209
C3	-1.604	1.065	-0.241
C6	2.047	-0.084	0.233
H5	0.710	-0.037	-1.487
O62	3.003	-0.326	-0.709
CM	4.359	-0.340	-0.255
HM1	4.623	0.653	0.182
HM2	4.944	-0.549	-1.184
HM3	4.495	-1.144	0.507
O61	2.381	0.091	1.403
O4	0.465	2.301	-0.442
H4	-0.032	1.223	1.283
HO4	-0.030	3.065	-0.114
O3	-2.259	2.142	0.405
H3	-1.713	1.174	-1.356
HO3	-3.203	2.042	0.220
O2	-3.494	-0.360	-0.311
H2	-2.210	-0.339	1.333
HO2	-3.811	-1.256	-0.130
O1	-1.667	-2.663	0.189
H1	-1.398	-1.510	-1.470
HO1	-1.247	-2.751	1.058

GLYCAM Parameter fitting results for 1-acetyl linkage

1Ac.frcmod parameters:

Os-Cg-Os-C 1 -0.01 0.0 -3 SCEE=1.0 SCNB=1.0[1]

1 0.04 0.0 -2 SCEE=1.0 SCNB=1.0[1]

1 0.12 0.0 1 SCEE=1.0 SCNB=1.0[1]

H2-Cg-Os-C 1 0.00 0.0 1 SCEE=1.0 SCNB=1.0[1]

Acetyl 6-acetyl-α-D-glucopyranoside

Torsion angle (°)	ΔQM (kcal/mol)	ΔMM (kcal/mol)
82.42	0.38	1.59
112.42	1.03	1.91
142.42	0.00	0.00
172.42	3.14	1.75
202.42	3.56	5.00
232.42	4.84	6.18
262.42	6.29	6.11
292.42	7.84	6.06
322.42	8.46	8.72
352.42	8.90	9.71
22.42	7.10	6.37
52.42	2.92	3.18
	< Error >	0.85
	% of maximum barrier	8.8/9.6

[1] Based on suggestions from GLYCAM community (GLYCAM-L@LISTSERV.UGA.EDU)

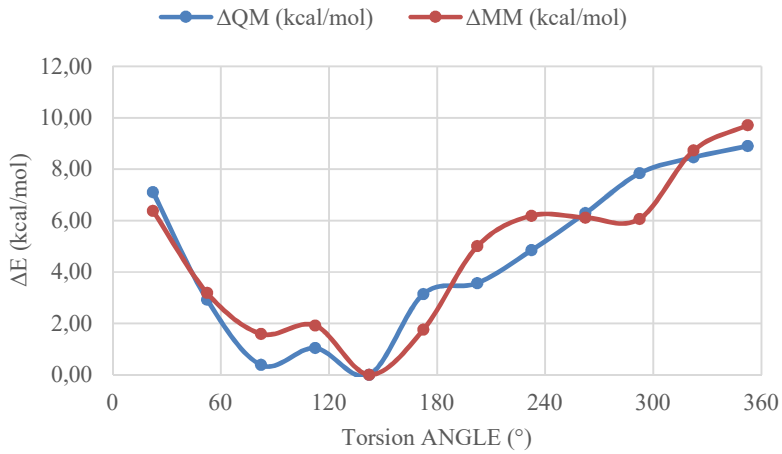
Acetyl 6-acetyl-*β*-D-glucopyranoside

Torsion angle (°)	ΔQM (kcal/mol)	ΔMM (kcal/mol)
64.46	3.88	1.04
94.46	5.41	4.04
124.46	8.90	7.70
154.46	6.56	7.26
184.46	5.20	5.17
214.46	4.36	5.47
244.46	0.63	0.43
274.46	0.00	0.00
304.46	2.59	1.57
334.46	8.31	5.78
4.46	10.99	7.48
34.46	7.07	3.21
	< Error >	1.53
	% of maximum barrier	19.9/13.9

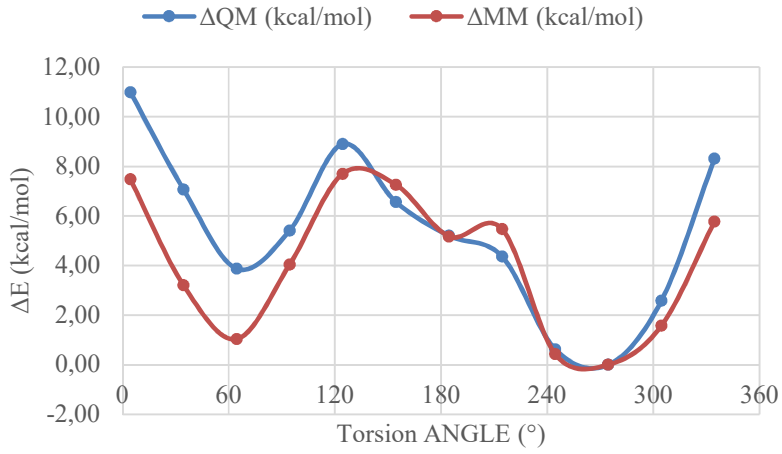
Tetrahydropyran-2-yl acetate

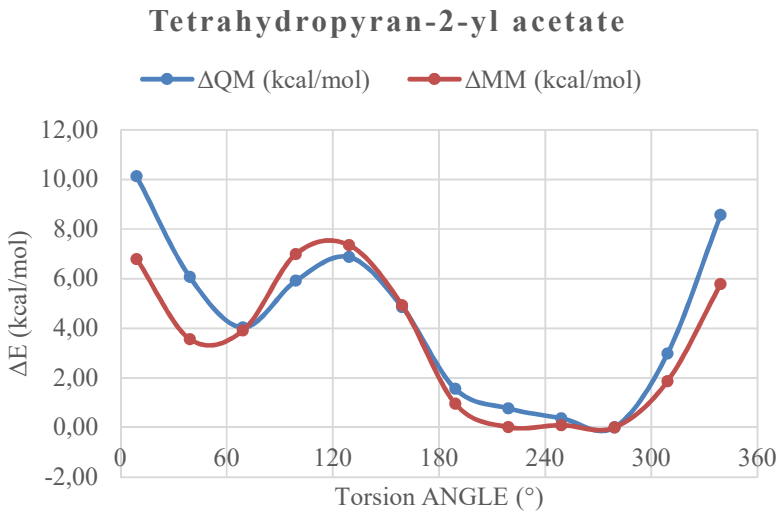
Torsion angle (°)	ΔQM (kcal/mol)	ΔMM (kcal/mol)
279.1	0.00	0.00
309.1	2.99	1.87
339.1	8.57	5.79
9.1	10.13	6.79
39.1	6.07	3.56
69.1	4.04	3.91
99.1	5.92	6.99
129.1	6.88	7.35
159.1	4.86	4.93
189.1	1.56	0.96
219.1	0.77	0.01
249.1	0.37	0.09
	< Error >	1.09
	% of maximum barrier	14.9/10.8

Acetyl 6-acetyl-*α*-D-glucopyranoside



Acetyl 6-acetyl-*β*-D-glucopyranoside





GLYCAM Parameter fitting results for 6-ester linkage

Minimization MM input

```
Minimize
&cntrl
imin=1,
maxcyc=6000, ncyc=2000,
ntb=0,
cut=10.0,
nmropt=1,
/
&wt type='END',
/
DISANG=methylmethoxyacetate_B3LYP_SPXX.RST
```

Example dihedral angle restraint input[2]

```
# 15 atoms read from pdb file methylmethoxyacetate_B3LYP_SP0.pdb.
# 1 mma OCCO:  (1 mma O1)-(1 mma C2)-(1 mma C3)-(1 mma O2) 180.0 180.0
 &rst    iat =    2,    6,    7,    8,
            r1 = 178.97, r2 = 179.97, r3 = 179.97, r4 = 180.97,
            rk2 =   5000.0, rk3 =   5000.0,                                    &end
```

Results:

MeDGlc.frcmod parameters:

```
Os-Cg-C -O    1    0.04   0.0     -3.     SCEE=1.0 SCNB=1.0
              1   -1.25   0.0     -2.     SCEE=1.0 SCNB=1.0
              1    0.01   0.0      1.     SCEE=1.0 SCNB=1.0
Os-C -Cg-Os   1    0.40   0.0      1.     SCEE=1.0 SCNB=1.0
Os-C -Cg-H1   1    0.00   0.0      1.     SCEE=1.0 SCNB=1.0
```

[2] See http://ambermd.org/tutorials/advanced/tutorial4/ for a helpful tutorial on torsional restraints in AMBER.

methyl THP-2-carboxylate

Torsion angle (°)	ΔQM (kcal/mol)	ΔMM (kcal/mol)
14.89	0.19	0.28
44.89	0.33	0.19
74.89	0.48	0.94
104.89	0.37	1.68
134.89	0.36	1.31
164.89	0.25	0.47
194.89	0.00	0.00
224.89	0.12	0.46
254.89	0.82	1.96
284.89	1.68	2.74
314.89	1.84	2.47
344.89	1.01	1.46
14.89	0.19	0.28
	< Error >	0.57
	% of maximum barrier	20.7 / 30.8

methyl methoxyacetate

Torsion angle (°)	ΔQM (kcal/mol)	ΔMM (kcal/mol)
180.00	0.00	0.00
210.00	0.51	0.38
240.00	1.31	1.02
270.00	1.31	1.19
300.00	0.82	0.84
330.00	0.30	0.57
0.00	0.12	0.53
30.00	0.30	0.57
60.00	0.82	0.84
90.00	1.31	1.19
120.00	1.31	1.03
150.00	0.51	0.38
180.00	0.00	0.00
	< Error >	0.17
	% of maximum barrier	14.5 / 13.1

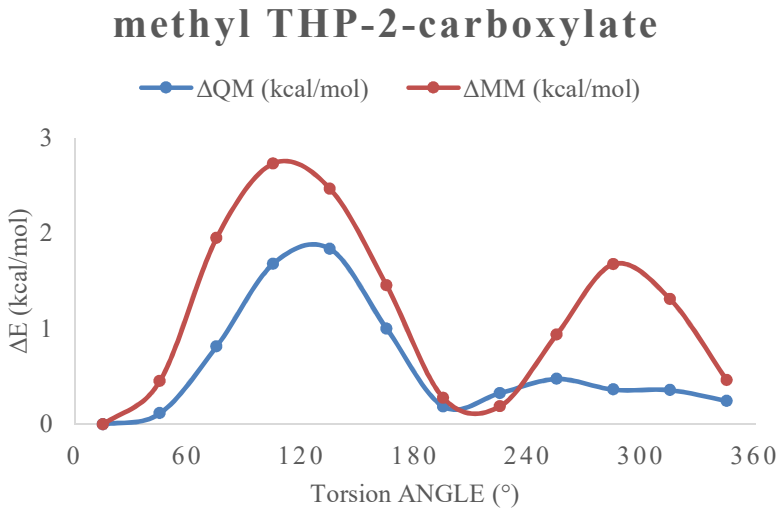
Average of both compounds

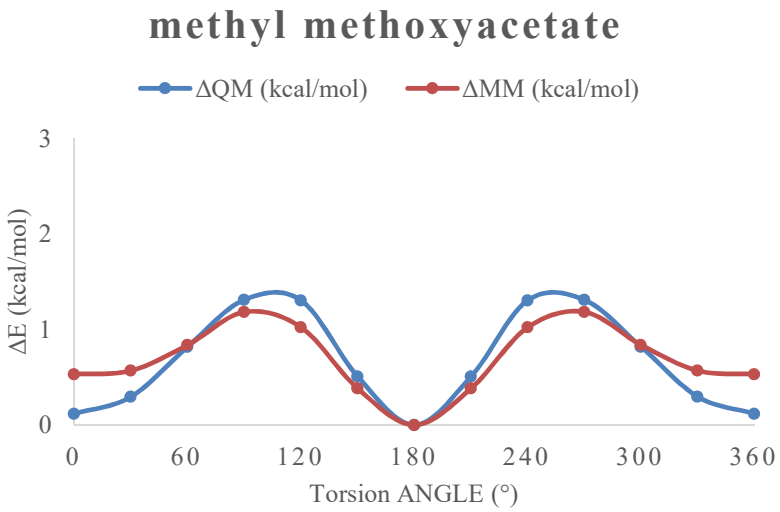
< Error >	0.37

% of maximum barrier 16.9 / 22.7

The above error and % of maximum barrier compare favorably to the results obtained for the carboxylate group (0.72 kcal/mol and 38.0%) in the original GLYCAM06 paper.[5]

Any correction to the torsion parameters to adjust the MM data to fit closer (lower) to the QM data in methyl THP-2-carboxylate would inevitably move it further away from the target QM values for methyl methoxyacetate (compare figures below). Thus, the established parameters above represent the best compromise on the basis of the mean <error> values for both compounds.





Atomic charges for *α*/*β*-**2** and *α*/*β*-**3** derived based on procedure by Cornell *et al*.[6]

Acetyl 6-acetyl-*α*-D-glucopyranoside *α*-**2**

C5	Cg	0.187680
C4	Cg	0.256063
C3	Cg	0.267703
C2	Cg	0.210290
C1	Cg	0.655238
O5	Os	-0.582957
H1	H2	0.000000
H2	H1	0.000000
H3	H1	0.000000
H4	H1	0.000000
H5	H1	0.000000
C6	Cg	0.398599
H61	H1	0.000000
H62	H1	0.000000
O6	Os	-0.508444
CA3	C	0.736774
CA4	Cg	0.044833
HA4	Hc	0.000000
HA5	Hc	0.000000
HA6	Hc	0.000000

OA2 O -0.600784
O4 Oh -0.695237
HO4 Ho 0.435529
O3 Oh -0.695870
HO3 Ho 0.446324
O2 Oh -0.703122
HO2 Ho 0.441322
O1 Os -0.465162
CA1 C 0.678461
CA2 Cg 0.056753
HA1 Hc 0.000000
HA2 Hc 0.000000
HA3 Hc 0.000000
OA1 O -0.563995

Acetyl 6-acetyl-α-D-glucopyranoside β-**2**

C5	Cg	0.157695
C4	Cg	0.256866
C3	Cg	0.282844
C2	Cg	0.252268
C1	Cg	0.595842
O5	Os	-0.508318
H1	H2	0.000000
H2	H1	0.000000
H3	H1	0.000000
H4	H1	0.000000
H5	H1	0.000000
C6	Cg	0.391920
H61	H1	0.000000
H62	H1	0.000000
O6	Os	-0.506155
CA3	C	0.739965
CA4	Cg	0.042963
HA4	Hc	0.000000
HA5	Hc	0.000000
HA6	Hc	0.000000
OA2	O	-0.600621
O4	Oh	-0.701072
HO4	Ho	0.439388
O3	Oh	-0.710394
HO3	Ho	0.448685
O2	Oh	-0.726056
HO2	Ho	0.450433
O1	Os	-0.514949
CA1	C	0.723895
CA2	Cg	0.057891
HA1	Hc	0.000000
HA2	Hc	0.000000
HA3	Hc	0.000000
OA1	O	-0.573091

Methyl α-D-glucoronate *α*-**5**

C5	Cg	0.203469
C4	Cg	0.240155
O5	Os	-0.625264
C1	Cg	0.598023
C2	Cg	0.205744
C3	Cg	0.411706
C6	C"	0.846180
H5	H1	0.000000
O62	Os	-0.483378
CM	Cg	0.306565
HM1	H1	0.000000
HM2	H1	0.000000
HM3	H1	0.000000
O61	O"	-0.604046
O4	Oh	-0.729197
H4	H1	0.000000
HO4	Ho	0.448741
O3	Oh	-0.747212
H3	H1	0.000000
HO3	Ho	0.446781
O2	Oh	-0.708367
H2	H1	0.000000
HO2	Ho	0.445286
O1	Oh	-0.712912
H1	H2	0.000000
HO1	Ho	0.457724

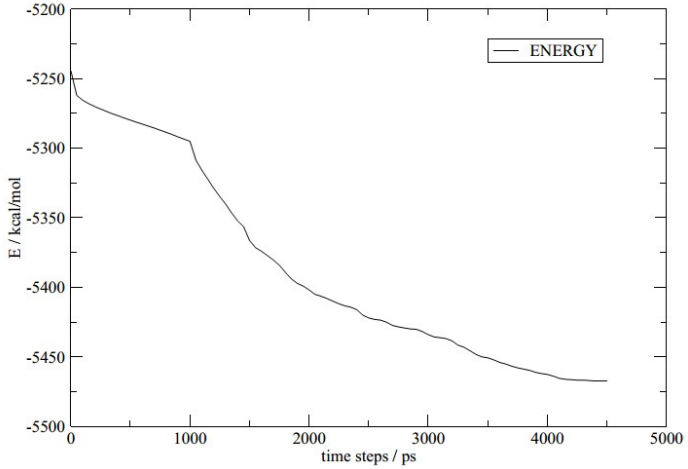
Methyl β-D-glucoronate *β*-**5**

C5	Cg	0.162756
C4	Cg	0.280145
O5	Os	-0.575959
C1	Cg	0.550484
C2	Cg	0.300668
C3	Cg	0.291477
C6	C	0.851559
H5	H1	0.000000
O62	Os	-0.482506
CM	Cg	0.309702
HM1	H1	0.000000
HM2	H1	0.000000
HM3	H1	0.000000
O61	O	-0.605135
O4	Oh	-0.733893
H4	H1	0.000000
HO4	Ho	0.459403
O3	Oh	-0.731423
H3	H1	0.000000
HO3	Ho	0.460004
O2	Oh	-0.745306
H2	H1	0.000000
HO2	Ho	0.456490
O1	Oh	-0.704345
H1	H2	0.000000
HO1	Ho	0.455875

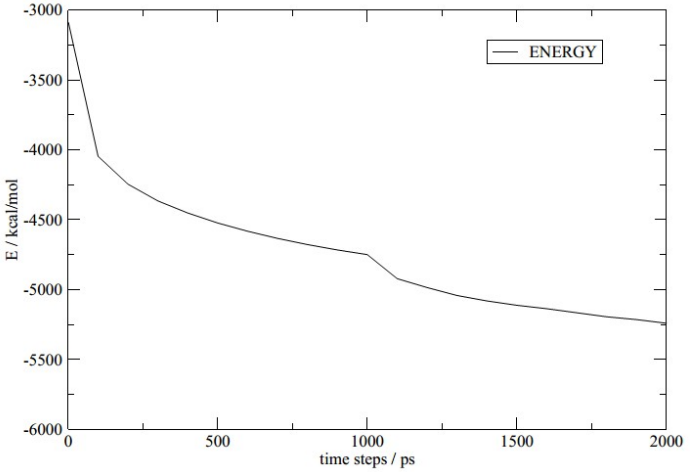
Summary of MD simulations

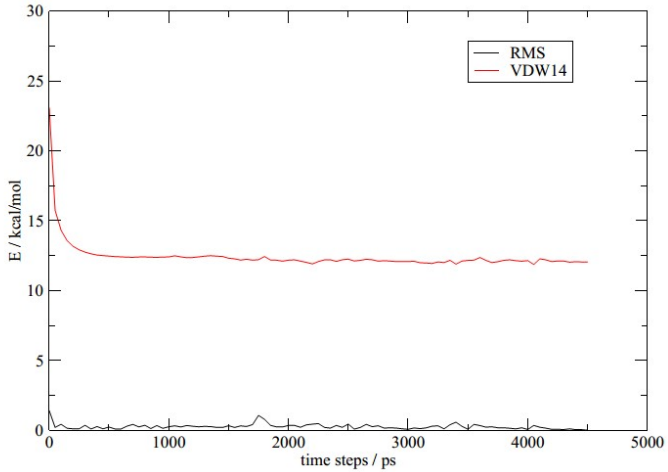
Representative example of Minimization and Heating convergence

Initial Restrained Minimization

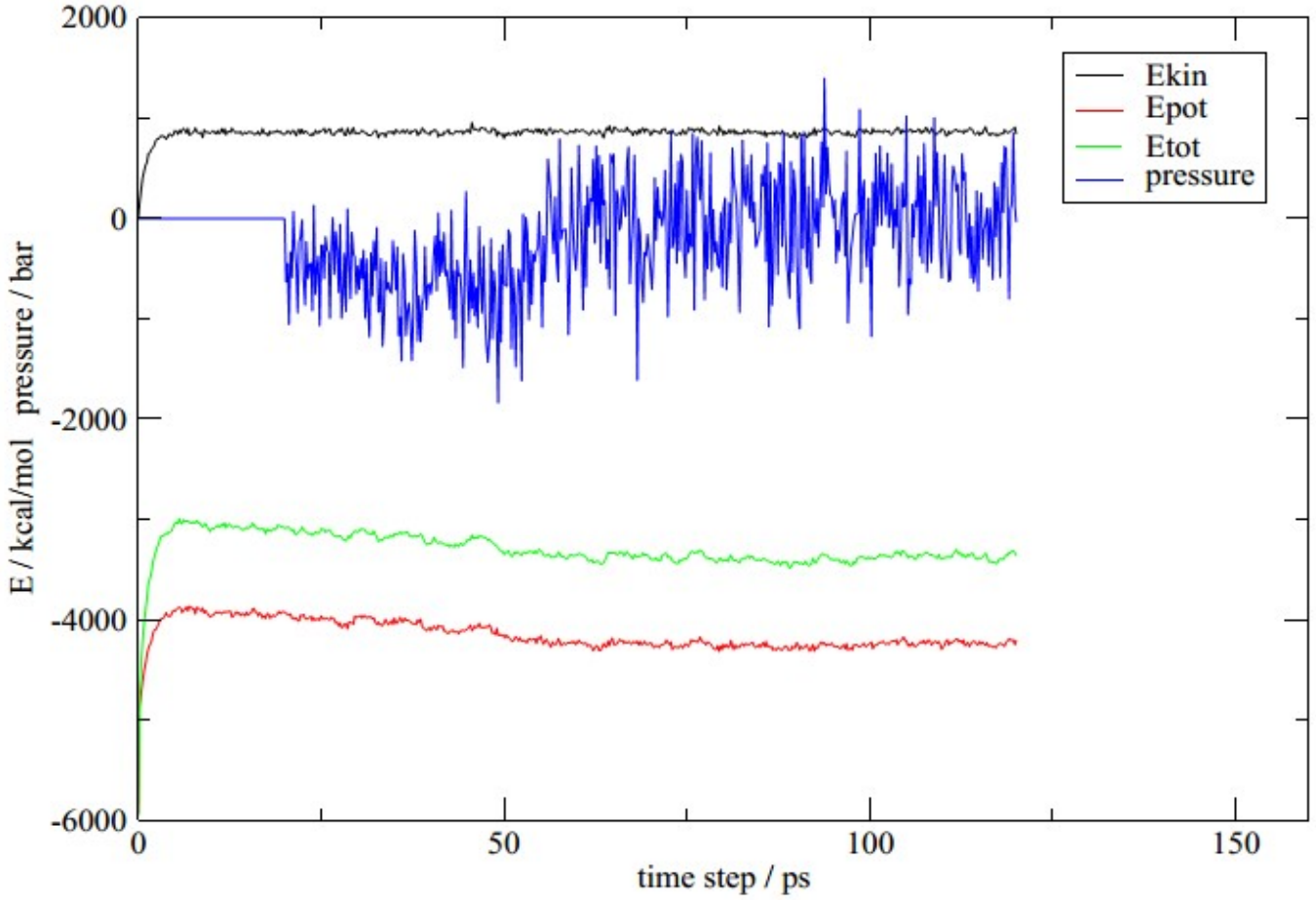


Full Minimization

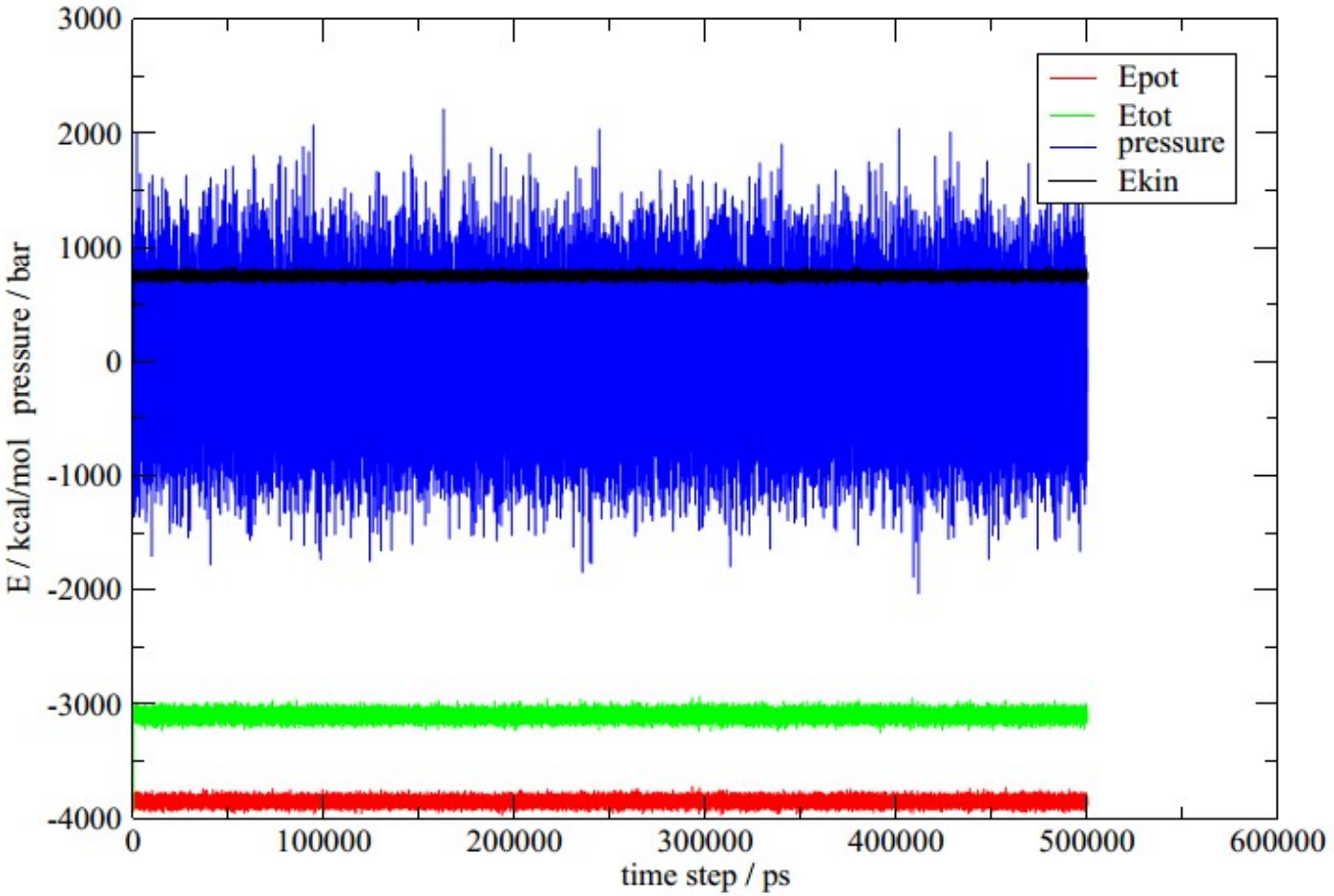




Heating



Production



Summaries of conformational analysis for compounds *α*/*ß*-**2**, *α*/*ß*-**3** and *α*/*ß*-**4** based on MD simulations

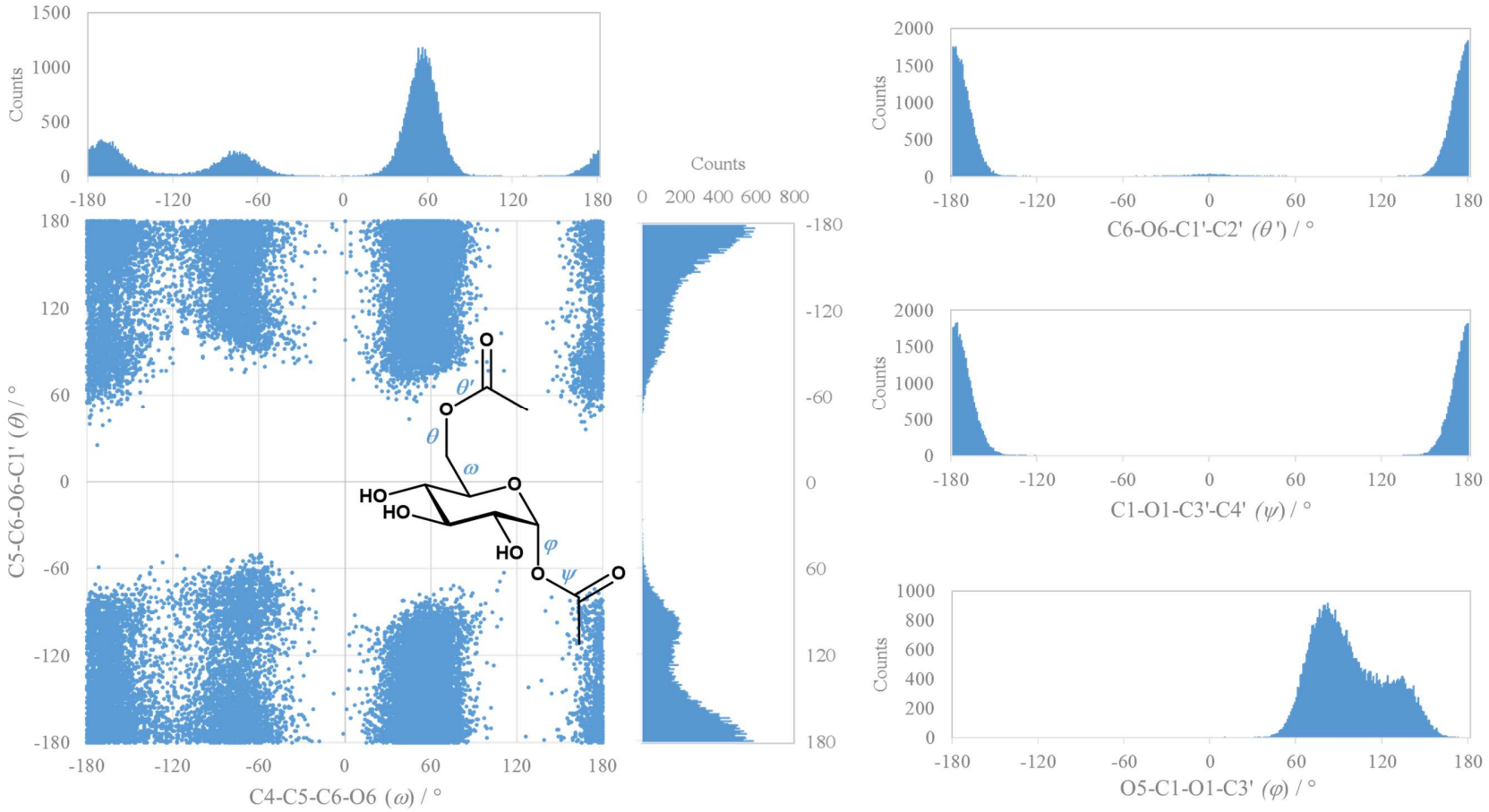


Figure S3 – Summary of the MD simulation for *α*-*Tõrge! Ei leia viiteallikat.* showing population histograms and Ramachandran plot data for the relevant dihedral angles θ(C5-C6-O6-C1'), ω(C4-C5-C6-O6) and θ' (C6-O6-C1'-C2') on the 6-acetyl and φ(O5-C1-O1-C3') and ψ(C1-O1-C3'-C4') on the 1-acetyl linkage.

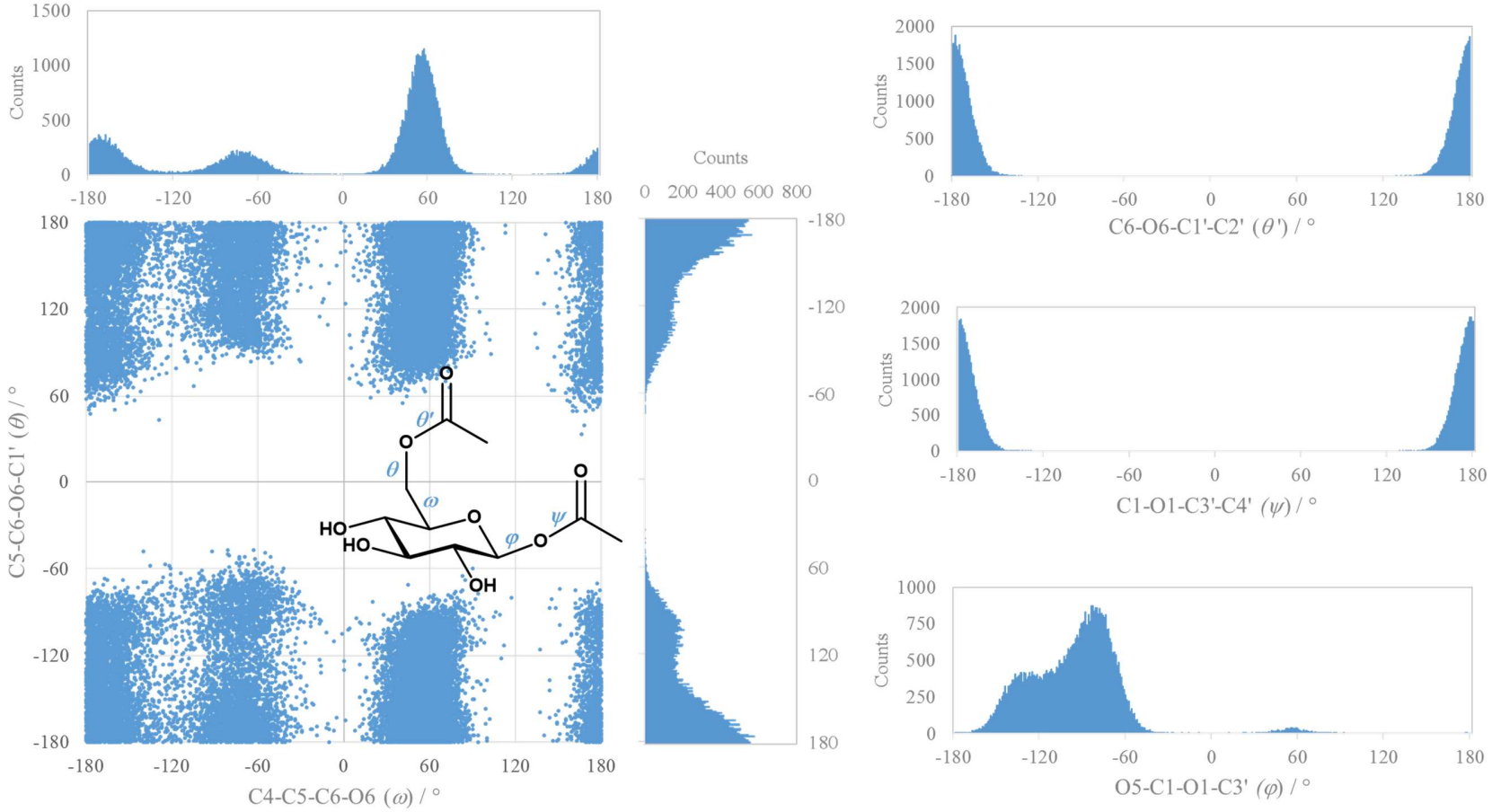


Figure S4 – Summary of the MD simulation for β-*Tõrge! Ei leia viiteallikat.* showing population histograms and Ramachandran plot data for the relevant dihedral angles θ(C5-C6-O6-C1'), ω(C4-C5-C6-O6) and θ' (C6-O6-C1'-C2') on the 6-acetyl and φ(O5-C1-O1-C3') and ψ(C1-O1-C3'-C4') on the 1-acetyl linkage.

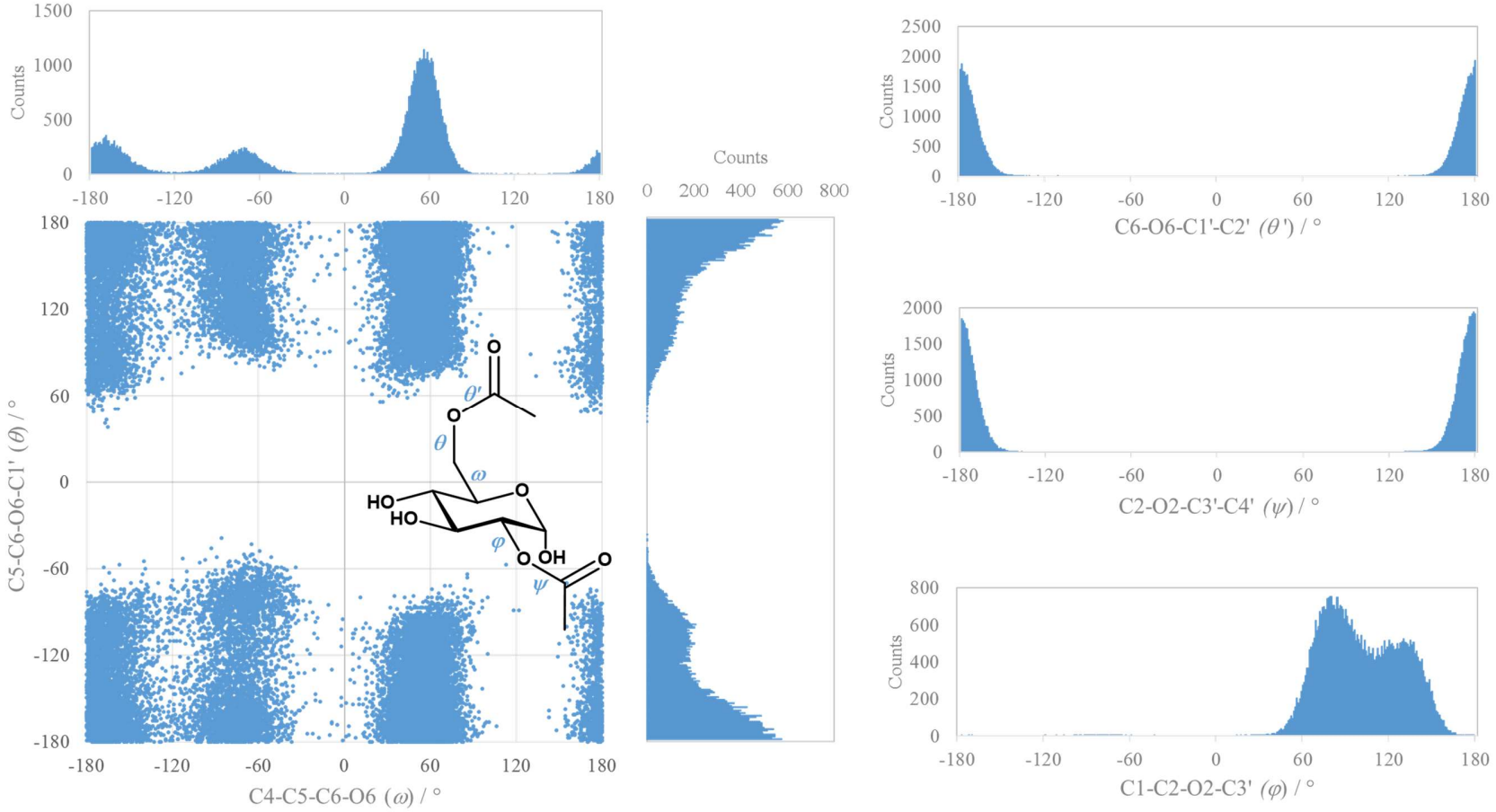


Figure S5 – Summary of the MD simulation for α-**3** showing population histograms and Ramachandran plot data for the relevant dihedral angles θ(C5-C6-O6-C1'), ω(C4-C5-C6-O6) and θ' (C6-O6-C1'-C2') on the 6-acetyl and φ(C1-C2-O2-C3') and ψ(C2-O2-C3'-C4') on the 2-acetyl linkage.

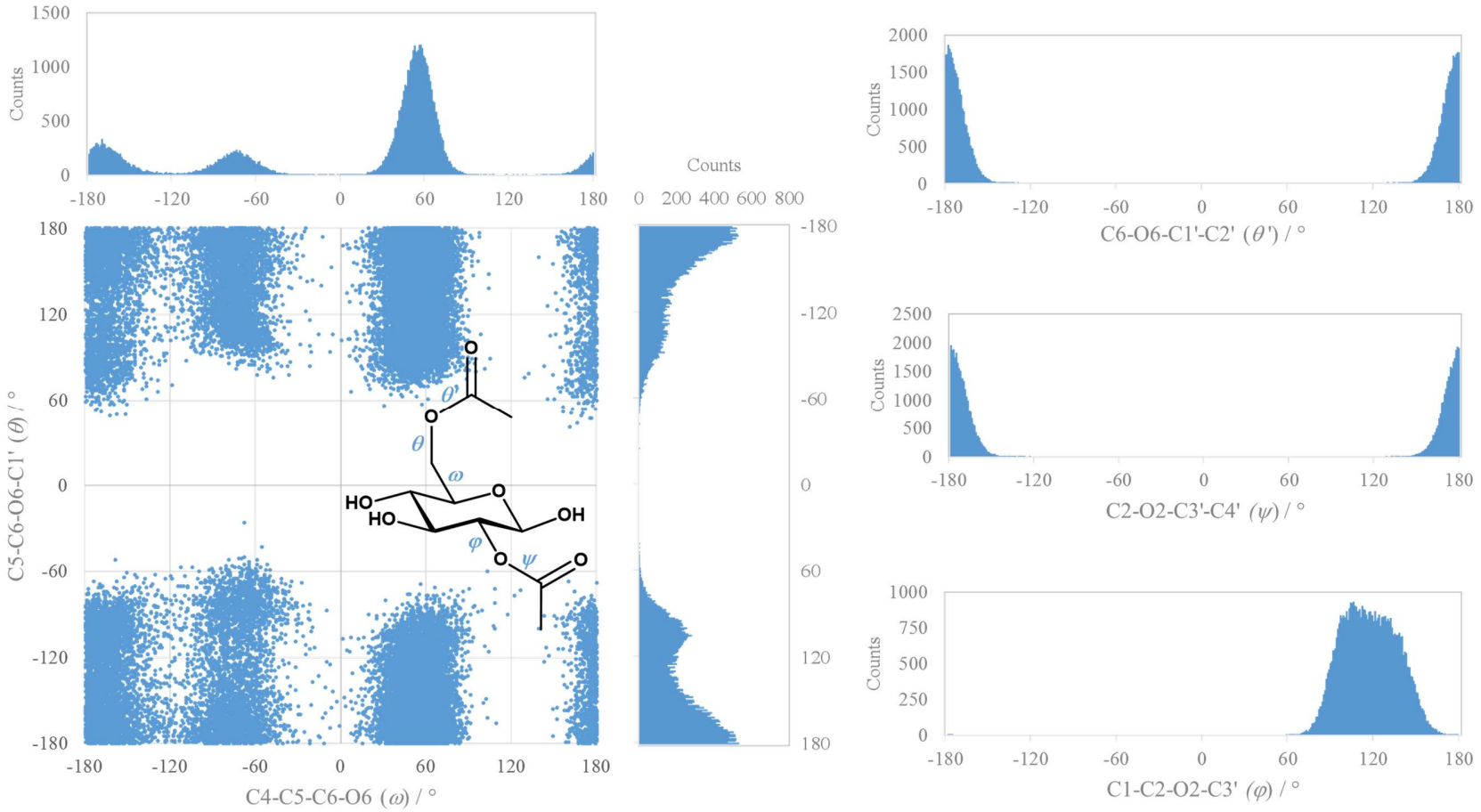


Figure S6 – Summary of the MD simulation for *β*-**3** showing population histograms and Ramachandran plot data for the relevant dihedral angles θ(C5-C6-O6-C1'), ω(C4-C5-C6-O6) and θ' (C6-O6-C1'-C2') on the 6-acetyl and φ(C1-C2-O2-C3') and ψ(C2-O2-C3'-C4') on the 2-acetyl linkage.

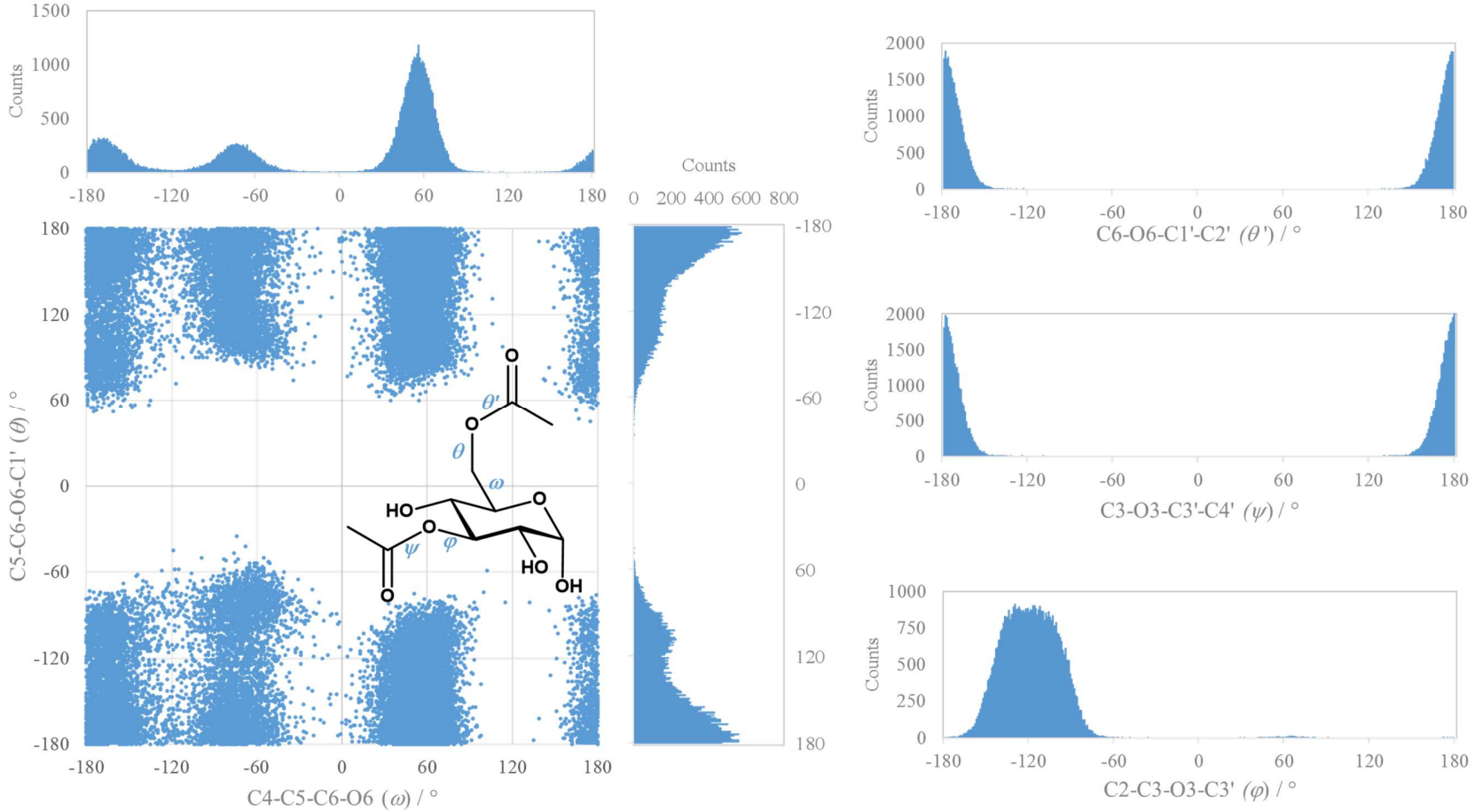


Figure S7 – Summary of the MD simulation for α-**4** showing population histograms and Ramachandran plot data for the relevant dihedral angles θ(C5-C6-O6-C1'), ω(C4-C5-C6-O6) and θ' (C6-O6-C1'-C2') on the 6-acetyl and φ(C2-C3-O3-C3') and ψ(C3-O3-C3'-C4') on the 2-acetyl linkage.

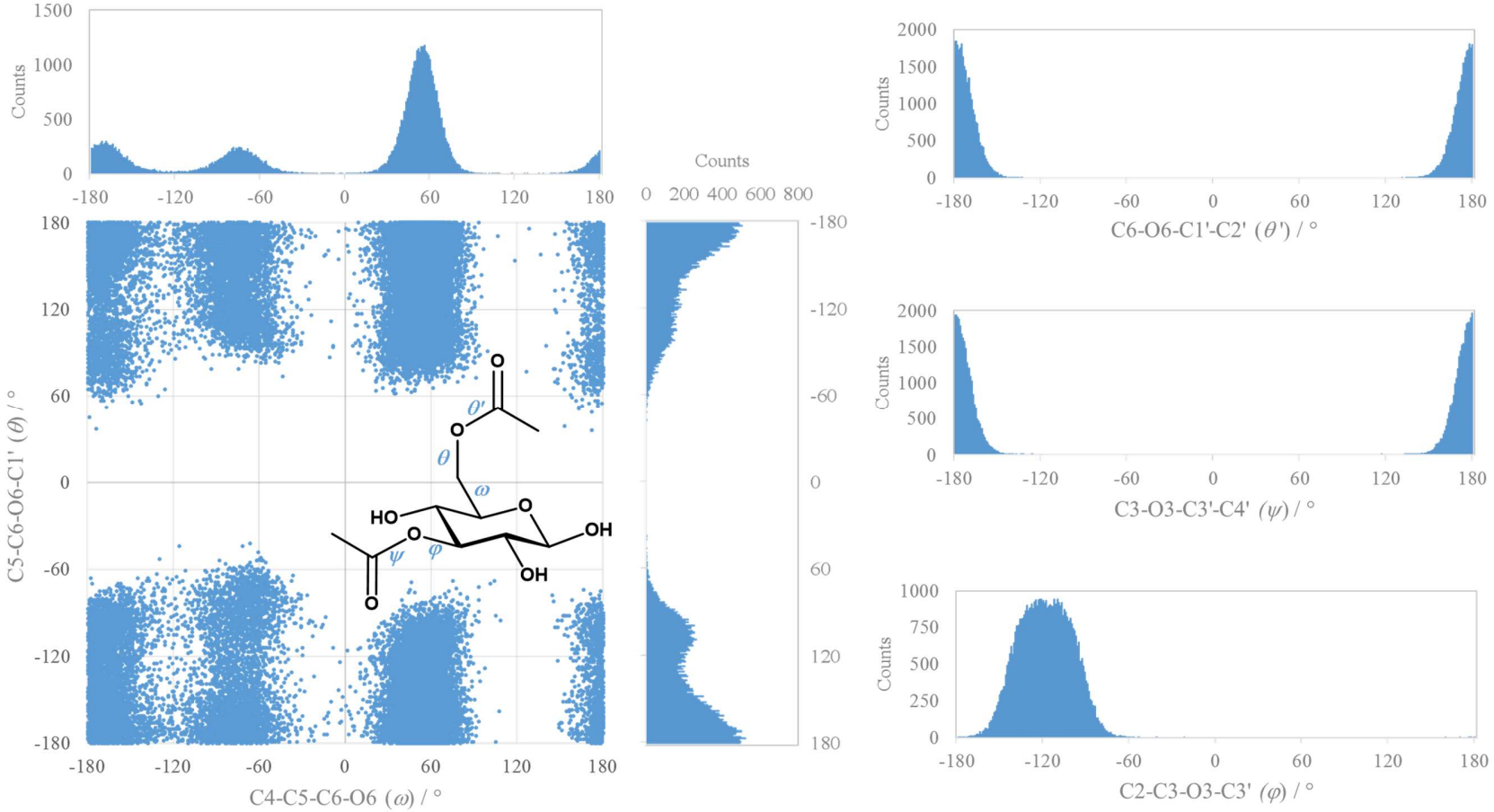


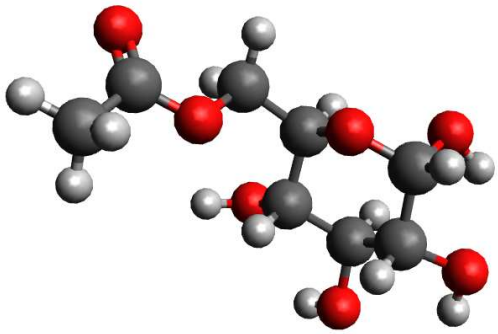
Figure S8 – Summary of the MD simulation for *β*-**4** showing population histograms and Ramachandran plot data for the relevant dihedral angles θ(C5-C6-O6-C1'), ω(C4-C5-C6-O6) and θ' (C6-O6-C1'-C2') on the 6-acetyl and φ(C2-C3-O3-C3') and ψ(C3-O3-C3'-C4') on the 2-acetyl linkage.

Geometries of QM optimized conformers for 6-Acetyl-α-D-glucose α-**1** (M05-2X/6-31G*)

Table S1: Summary of relevant dihedral angles

	ω / °		θ / °		θ' / °	
Conformer	C4-C5-C6-O6		C5-C6-O6-C1'		C6-O6-C1'-C2'	
#	QM	MD	QM	MD	QM	MD
1	**55**	58	**-178**	180	**180**	180
2	**58**	58	**103**	103	**-174**	180
3	**60**	58	**-96**	-106	**-175**	180
4	**-58**	-73	**-178**	180	**-179**	180
5	**-63**	-73	**96**	103	**-172**	180
6	**-46**	-73	**-70**	-106	**174**	180
7	**-173**	-168	**179**	180	**180**	180
8	**-177**	-168	**82**	103	**180**	180
9	**-175**	-168	**-105**	-106	**174**	180

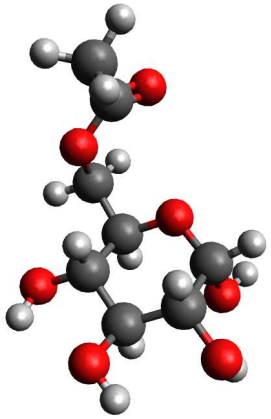
Conformer 1



H	-3.2296990000	-1.5874230000	-0.7737030000
O	-2.3136700000	-1.9050200000	-0.8348800000
C	-1.6886350000	-1.5115120000	0.3629990000
H	-1.8065650000	-2.2789860000	1.1301440000
C	-2.2800120000	-0.1852910000	0.8393890000
H	-1.8881450000	0.0440080000	1.8353590000
O	-3.6897500000	-0.3471860000	0.8677950000
H	-4.0707400000	0.5426280000	0.9114100000
C	-1.8931020000	0.9292110000	-0.1115290000
H	-2.3437050000	0.7320360000	-1.0919360000
O	-2.4021010000	2.1347720000	0.4310410000
H	-2.1116670000	2.8434050000	-0.1615460000
C	-0.3885530000	0.9718600000	-0.2778200000
H	0.0766000000	1.1830030000	0.6879470000
O	-0.1061560000	1.9980400000	-1.2197930000
H	0.7457380000	2.3950070000	-0.9999790000
C	0.0759820000	-0.3947420000	-0.7818340000
H	-0.3940880000	-0.5934170000	-1.7491600000
O	-0.3045500000	-1.3986960000	0.1627630000
C	1.5698000000	-0.4871360000	-0.9669350000
H	1.8596850000	-1.5032230000	-1.2304180000
H	1.8951060000	0.1918610000	-1.7541450000
O	2.1929390000	-0.1186250000	0.2752720000
C	3.5365450000	-0.1059000000	0.2673990000
O	4.1888420000	-0.3874160000	-0.7118940000
C	4.0868270000	0.2928380000	1.6064550000
H	3.7542590000	-0.4187960000	2.3625070000
H	3.7040290000	1.2759150000	1.8809040000

H	5.1716550000	0.3110550000	1.5614430000

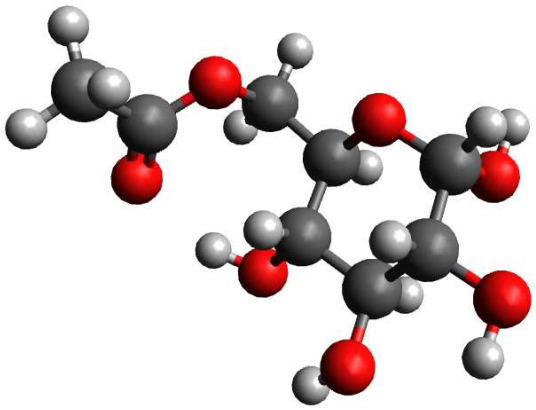
Conformer 2



H	-1.4826400000	-2.6203910000	-1.6097650000
O	-1.8462010000	-1.8465800000	-1.1581090000
C	-1.0864900000	-1.5938360000	-0.0016180000
H	-0.8986510000	-2.5128720000	0.5524980000
C	-1.9066270000	-0.6105670000	0.8271500000
H	-1.4301320000	-0.4828040000	1.7999840000
O	-3.2139050000	-1.1025480000	1.0623730000
H	-3.5244950000	-1.4409220000	0.2076620000
C	-1.9577280000	0.7364480000	0.1239540000
H	-2.4923570000	0.6279660000	-0.8277430000
O	-2.5899840000	1.7119930000	0.9367830000
H	-3.4620230000	1.3579440000	1.1641250000
C	-0.5537650000	1.2237400000	-0.1649890000
H	-0.0192150000	1.3498780000	0.7834160000
O	-0.5816580000	2.4347770000	-0.8990090000
H	-1.2082730000	3.0130860000	-0.4398850000
C	0.1680410000	0.1745770000	-1.0026680000
H	-0.3559740000	0.0605710000	-1.9564950000
O	0.1877210000	-1.0677230000	-0.2970830000
C	1.6062710000	0.5454540000	-1.2925220000
H	2.0940670000	-0.2354030000	-1.8691620000
H	1.6401540000	1.4932990000	-1.8235720000
O	2.3102170000	0.7398420000	-0.0556410000
C	3.1334990000	-0.2425020000	0.3594430000
O	3.3986320000	-1.2248000000	-0.2926100000
C	3.6714660000	0.0651830000	1.7279640000
H	2.8476080000	0.0647440000	2.4428990000

H	4.1193630000	1.0584920000	1.7346190000
H	4.4059840000	-0.6842440000	2.0075020000

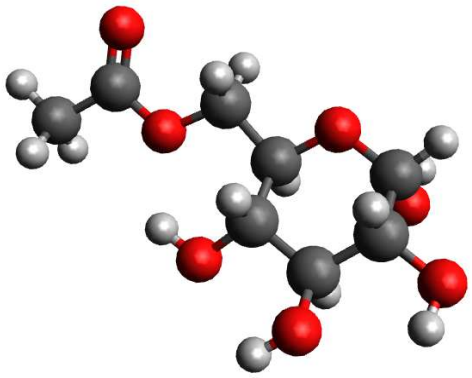
Conformer 3



H	-2.5657560000	-2.5178930000	-0.9286510000
O	-2.6338450000	-1.5741810000	-0.7270760000
C	-1.8978990000	-1.3325890000	0.4379890000
H	-2.1921400000	-2.0094890000	1.2404200000
C	-2.1145460000	0.1175600000	0.8511940000
H	-1.5663020000	0.2713270000	1.7884460000
O	-3.4943940000	0.3590340000	1.0308210000
H	-3.5806800000	1.3165800000	1.1467070000
C	-1.5263750000	1.0426510000	-0.1963500000
H	-2.0593250000	0.9022500000	-1.1432160000
O	-1.6965290000	2.3683890000	0.2786470000
H	-1.2398390000	2.9427600000	-0.3530700000
C	-0.0607940000	0.7158060000	-0.3995540000
H	0.4604300000	0.8943640000	0.5481430000
O	0.4266380000	1.5673360000	-1.4186920000
H	1.3951470000	1.5735810000	-1.3275990000
C	0.0661650000	-0.7589430000	-0.7783030000
H	-0.4584160000	-0.9202330000	-1.7253510000
O	-0.5127320000	-1.5676860000	0.2481000000
C	1.4924830000	-1.2234900000	-0.9735940000
H	1.5028790000	-2.2928170000	-1.1672880000
H	1.9552020000	-0.6894370000	-1.8002830000
O	2.2835740000	-1.0503680000	0.2197860000
C	3.0233460000	0.0584090000	0.3257770000

O	3.0031980000	0.9638570000	-0.4866200000
C	3.8716750000	0.0368770000	1.5617120000
H	3.2334750000	-0.0927120000	2.4359040000
H	4.4296840000	0.9651600000	1.6358150000
H	4.5540300000	-0.8121800000	1.5170800000

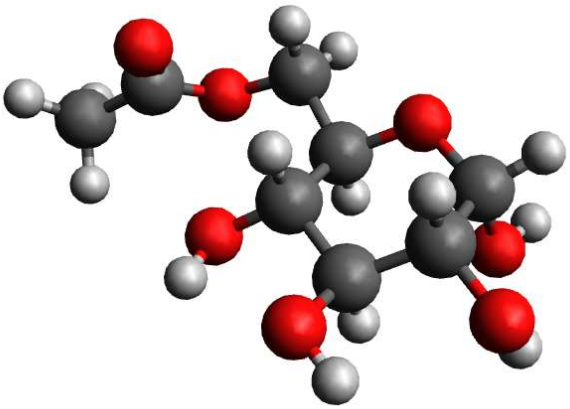
Conformer 4



H	2.1009030000	-2.4248640000	1.5914470000
O	2.3386060000	-1.5310490000	1.3079540000
C	2.1187310000	-1.4452760000	-0.0697380000
H	2.6039720000	-2.2634460000	-0.6023270000
C	2.6310560000	-0.0989630000	-0.5596610000
H	2.4622710000	-0.0622390000	-1.6424850000
O	4.0043720000	0.0296660000	-0.2582980000
H	4.2195760000	0.9612550000	-0.4135030000
C	1.8264690000	1.0057730000	0.0928260000
H	1.9787030000	0.9641980000	1.1761770000
O	2.3125170000	2.2327260000	-0.4305370000
H	1.8018580000	2.9374910000	-0.0076730000
C	0.3474250000	0.8313370000	-0.1940140000
H	0.1802230000	0.9622050000	-1.2710900000
O	-0.3089080000	1.8427040000	0.5526980000
H	-1.2607900000	1.7401730000	0.4112540000
C	-0.0944100000	-0.5779080000	0.2136930000
H	-0.0520550000	-0.6578280000	1.3029630000
O	0.7446820000	-1.5603380000	-0.3971580000
C	-1.4797160000	-0.9385810000	-0.2923220000
H	-1.4976170000	-0.9200570000	-1.3820800000
H	-1.7710820000	-1.9285530000	0.0532490000

O	-2.3996010000	0.0436410000	0.2177220000
C	-3.6969340000	-0.1515000000	-0.1058480000
O	-4.0626080000	-1.0945890000	-0.7645870000
C	-4.5674120000	0.9366240000	0.4497150000
H	-4.4122700000	1.0193680000	1.5251540000
H	-5.6076300000	0.7125990000	0.2333810000
H	-4.2897980000	1.8885620000	-0.0047230000

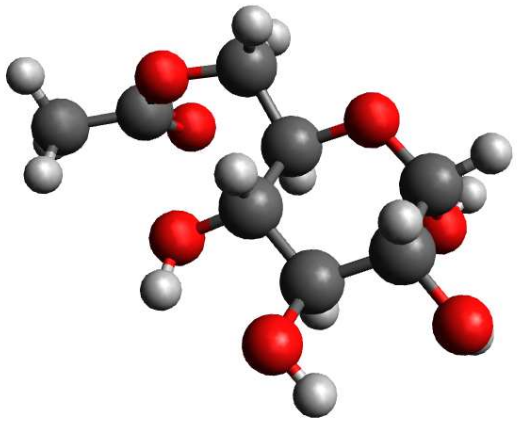
Conformer 5



H	2.6907400000	-2.3271940000	1.2634930000
O	2.5865230000	-1.3828700000	1.0840190000
C	2.2390340000	-1.2099590000	-0.2667280000
H	2.8606710000	-1.8272060000	-0.9144820000
C	2.4320840000	0.2718490000	-0.5632220000
H	2.2966780000	0.4415780000	-1.6319670000
O	3.7417910000	0.6987280000	-0.2326560000
H	3.9284140000	0.3223050000	0.6419420000
C	1.3985420000	1.0759350000	0.2058040000
H	1.5743290000	0.9475580000	1.2807810000
O	1.4561460000	2.4501830000	-0.1423700000
H	2.3668890000	2.7368330000	0.0181380000
C	-0.0062960000	0.5953370000	-0.1018360000
H	-0.2248860000	0.7684760000	-1.1624290000
O	-0.9301520000	1.2885530000	0.7234580000
H	-0.7099320000	2.2276640000	0.6320490000
C	-0.0986170000	-0.9008180000	0.1899150000
H	0.0269480000	-1.0581950000	1.2645460000
O	0.9129340000	-1.6009110000	-0.5410400000

C	-1.3893090000	-1.5523510000	-0.2865340000
H	-1.5012960000	-1.4202340000	-1.3600150000
H	-1.3668920000	-2.6118630000	-0.0429850000
O	-2.5167710000	-0.9993870000	0.3992580000
C	-3.1833870000	-0.0069520000	-0.2245390000
O	-2.9729870000	0.3294620000	-1.3669340000
C	-4.2024920000	0.6039120000	0.6901180000
H	-4.7585390000	-0.1719750000	1.2140420000
H	-4.8735330000	1.2394990000	0.1194420000
H	-3.6668110000	1.2009780000	1.4296890000

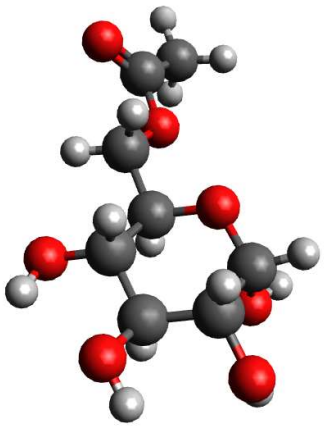
Conformer 6



H	-2.0575120000	-2.4876060000	-1.3819630000
O	-2.1217340000	-1.5386130000	-1.2091250000
C	-2.0952290000	-1.3241630000	0.1798370000
H	-2.7503740000	-2.0242790000	0.6973300000
C	-2.5463800000	0.1157220000	0.3898720000
H	-2.6681270000	0.2996240000	1.4578580000
O	-3.7988390000	0.3599120000	-0.2255150000
H	-3.7426710000	-0.0461380000	-1.1050880000
C	-1.4894420000	1.0538980000	-0.1648390000
H	-1.4115080000	0.8987850000	-1.2478180000
O	-1.8055500000	2.4085950000	0.1155230000
H	-2.6842250000	2.5695230000	-0.2578560000
C	-0.1263310000	0.7793070000	0.4421760000
H	-0.1642450000	0.9856990000	1.5197980000
O	0.8371590000	1.6002050000	-0.1998840000
H	0.4313130000	2.4778860000	-0.2653010000

C	0.2231600000	-0.6903120000	0.2180090000
H	0.3481100000	-0.8629810000	-0.8514070000
O	-0.8183480000	-1.5254770000	0.7392140000
C	1.4506180000	-1.1639860000	0.9905550000
H	1.2040110000	-1.1981860000	2.0491390000
H	1.7445050000	-2.1545510000	0.6473860000
O	2.5565170000	-0.2612720000	0.8946410000
C	3.1617740000	-0.1856370000	-0.3022070000
O	2.8771030000	-0.9036560000	-1.2342630000
C	4.1962180000	0.8997770000	-0.3149300000
H	3.6728100000	1.8567070000	-0.2857870000
H	4.7918470000	0.8293230000	-1.2204200000
H	4.8292770000	0.8309960000	0.5685670000

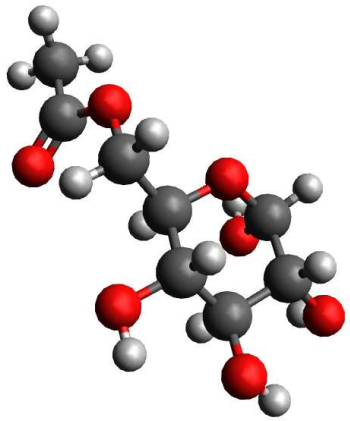
Conformer 7



H	0.9010000000	-2.7925580000	1.0614770000
O	1.4586680000	-2.0118000000	0.9425210000
C	1.3444610000	-1.5664870000	-0.3866460000
H	1.4078790000	-2.3995460000	-1.0858780000
C	2.4927700000	-0.5847170000	-0.5960820000
H	2.5380630000	-0.3111970000	-1.6509560000
O	3.7381860000	-1.1697000000	-0.2607170000
H	3.5947980000	-1.6258270000	0.5836480000
C	2.2517130000	0.6698160000	0.2284480000
H	2.2690310000	0.4100390000	1.2940080000
O	3.2244600000	1.6620570000	-0.0543580000
H	4.0883250000	1.2546710000	0.1048590000
C	0.8950760000	1.2602780000	-0.0952970000

H	0.8773790000	1.5446110000	-1.1556290000
O	0.6241460000	2.3757350000	0.7334500000
H	1.4192130000	2.9285060000	0.7080420000
C	-0.1709230000	0.1986050000	0.1539280000
H	-0.1668300000	-0.0727830000	1.2128490000
O	0.1034310000	-0.9515620000	-0.6490390000
C	-1.5381330000	0.6997820000	-0.2380980000
H	-1.7491690000	1.6471560000	0.2543160000
H	-1.6015680000	0.8308390000	-1.3184570000
O	-2.4921190000	-0.2897090000	0.1811440000
C	-3.7761850000	0.0023030000	-0.0781450000
O	-4.1195950000	1.0246760000	-0.6276360000
C	-4.6920540000	-1.0888200000	0.3980640000
H	-5.7202450000	-0.8245370000	0.1694750000
H	-4.5687850000	-1.2249120000	1.4726730000
H	-4.4268660000	-2.0266000000	-0.0903760000

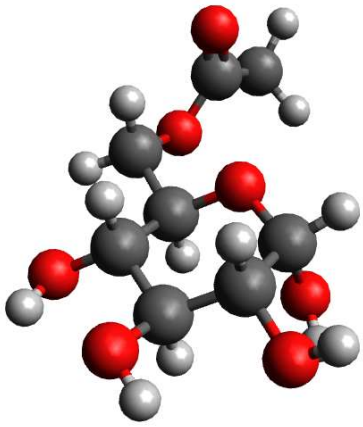
Conformer 8



H	-0.3555100000	-2.7051880000	-0.9800200000
O	-0.9820110000	-1.9694360000	-0.9494780000
C	-1.1806190000	-1.5942260000	0.3915960000
H	-1.3337310000	-2.4681400000	1.0239840000
C	-2.4109810000	-0.6930030000	0.3931850000
H	-2.6947690000	-0.4824600000	1.4250650000
O	-3.5160720000	-1.3282970000	-0.2243910000
H	-3.1684800000	-1.7269700000	-1.0378800000
C	-2.0882290000	0.6176930000	-0.3067160000
H	-1.8654070000	0.4177190000	-1.3619160000

O	-3.1633200000	1.5355610000	-0.1935050000
H	-3.9453980000	1.0895990000	-0.5498010000
C	-0.8714890000	1.2652590000	0.3212260000
H	-1.0957770000	1.4927610000	1.3719190000
O	-0.5075640000	2.4373380000	-0.3848280000
H	-1.3248840000	2.9429040000	-0.5058550000
C	0.2916530000	0.2811720000	0.2619720000
H	0.5298060000	0.0697180000	-0.7827300000
O	-0.0679230000	-0.9253100000	0.9399030000
C	1.5086980000	0.8391440000	0.9666550000
H	1.7661740000	1.8092130000	0.5494060000
H	1.3130170000	0.9221040000	2.0335730000
O	2.6274330000	-0.0564010000	0.8560910000
C	3.3324990000	0.0107990000	-0.2868140000
O	3.0638190000	0.7717090000	-1.1890670000
C	4.4706080000	-0.9688050000	-0.2784210000
H	5.1205220000	-0.7666600000	0.5730050000
H	5.0286660000	-0.8843680000	-1.2061260000
H	4.0780300000	-1.9797610000	-0.1665280000

Conformer 9



H	-1.7822420000	-2.1683500000	-1.3512630000
O	-0.8567140000	-1.9268920000	-1.1813740000
C	-0.7992770000	-1.5537250000	0.1739730000
H	-0.5968660000	-2.4218590000	0.8055440000
C	-2.1184880000	-0.8847650000	0.5766470000
H	-2.1418370000	-0.7382860000	1.6590110000
O	-3.2220040000	-1.6691480000	0.1340310000

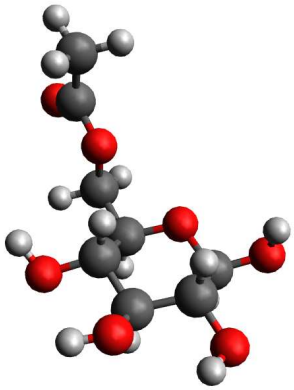
H	-3.3770890000	-2.3838880000	0.7661780000
C	-2.2544430000	0.4587310000	-0.1133700000
H	-2.3347950000	0.2936420000	-1.1940560000
O	-3.3796010000	1.1771650000	0.3627250000
H	-4.1596890000	0.6351390000	0.1781310000
C	-1.0321480000	1.3144190000	0.1463460000
H	-0.9536920000	1.5042990000	1.2247320000
O	-1.1141440000	2.5271570000	-0.5783410000
H	-2.0035930000	2.8761420000	-0.4179770000
C	0.2024960000	0.5522450000	-0.3173790000
H	0.1323540000	0.3684700000	-1.3922050000
O	0.2849440000	-0.6879140000	0.3858040000
C	1.4706070000	1.3173670000	-0.0129600000
H	1.4360640000	2.2934770000	-0.4897940000
H	1.6091400000	1.4211430000	1.0606000000
O	2.5867750000	0.6133230000	-0.5786590000
C	3.3838650000	-0.0761280000	0.2597580000
O	3.2791120000	-0.0575490000	1.4637820000
C	4.4120070000	-0.8543580000	-0.5113650000
H	3.9091640000	-1.6212600000	-1.1019300000
H	5.1107880000	-1.3172290000	0.1791410000
H	4.9376260000	-0.1932890000	-1.1997570000

Geometries of QM optimized conformers for 6-Acetyl-*β*-D-glucose *β*-**1** (M05-2X/6-31G*)

Table S2: Summary of relevant dihedral angles

	ω / °		θ / °		θ' / °	
Conformer	C4-C5-C6-O6		C5-C6-O6-C1'		C6-O6-C1'-C2'	
#	QM	MD	QM	MD	QM	MD
1	**55**	58	**-178**	180	**180**	180
2	**58**	58	**102**	103	**-174**	180
3	**60**	58	**-96**	-106	**-175**	180
4	**-58**	-73	**-177**	180	**-179**	180
5	**-63**	-73	**96**	103	**-172**	180
6	**-45**	-73	**-70**	-106	**174**	180
7	**-173**	-168	**179**	180	**180**	180
8	**-177**	-168	**82**	103	**180**	180
9	**-174**	-168	**-103**	-106	**175**	180

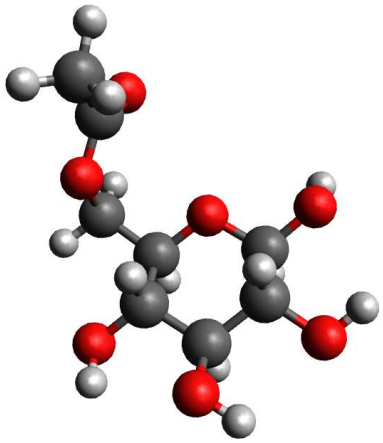
Conformer 1



C	-1.7761360000	-1.3944030000	-0.3892240000
H	-2.1665060000	-1.3136600000	-1.4083620000
O	-0.3584890000	-1.2786220000	-0.3999010000
C	0.0978830000	-0.0601180000	-0.9788220000
H	-0.3137420000	0.0549360000	-1.9905610000
C	-0.3803330000	1.1137140000	-0.1217090000
H	0.0335210000	1.0188490000	0.8847730000
O	-0.0375080000	2.3631660000	-0.7044560000
H	0.8101860000	2.6510340000	-0.3437300000
C	-1.8922640000	1.0616300000	-0.0470390000
H	-2.2949560000	1.1964930000	-1.0604430000
O	-2.4113710000	2.0519600000	0.8218680000
H	-2.0819010000	2.9019940000	0.4953890000
C	-2.3531110000	-0.2834310000	0.4796990000
H	-1.9639040000	-0.4132250000	1.4995280000
O	-3.7626380000	-0.3703910000	0.4553140000
H	-4.0870660000	0.4626540000	0.8285630000
C	1.5996880000	-0.1333260000	-1.1065680000
H	1.9774260000	0.7397800000	-1.6373290000
H	1.8931350000	-1.0329250000	-1.6453310000
O	2.1502070000	-0.1678060000	0.2204530000
O	-2.1102990000	-2.6600650000	0.0669160000
C	3.4922500000	-0.1966110000	0.2896400000
O	4.1986030000	-0.1933600000	-0.6923960000
C	3.9646980000	-0.2360970000	1.7142980000
H	-1.8764830000	-2.7114030000	1.0052660000
H	3.5729310000	0.6260350000	2.2541070000
H	5.0503660000	-0.2322310000	1.7361020000

H	3.5829210000	-1.1355530000	2.1979990000

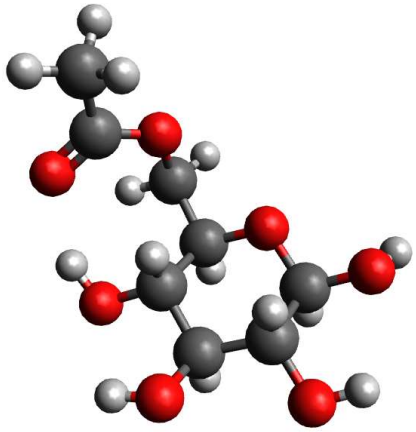
Conformer 2



C	-1.1533440000	-1.4340990000	-0.5669520000
H	-1.6075460000	-1.3494930000	-1.5629880000
O	0.1586590000	-0.8920600000	-0.6047800000
C	0.1711720000	0.4630140000	-1.0401760000
H	-0.3030590000	0.5544900000	-2.0266060000
C	-0.6047830000	1.3208710000	-0.0436050000
H	-0.1136210000	1.2541250000	0.9333070000
O	-0.6169610000	2.6536930000	-0.5196380000
H	-1.2586140000	3.1294320000	0.0281390000
C	-2.0187230000	0.7878340000	0.0823140000
H	-2.5207420000	0.8953460000	-0.8884210000
O	-2.6754650000	1.5700680000	1.0649730000
H	-3.5771930000	1.2282220000	1.1440770000
C	-1.9901480000	-0.6797110000	0.4525010000
H	-1.5148140000	-0.8020260000	1.4326930000
O	-3.3270610000	-1.1412690000	0.4623220000
H	-3.3006910000	-2.0814510000	0.6898040000
C	1.6171640000	0.8911000000	-1.1742190000
H	1.6643300000	1.9299670000	-1.4903920000
H	2.1409060000	0.2505620000	-1.8780640000
O	2.2569070000	0.8204340000	0.1092770000
O	-1.0874920000	-2.7564210000	-0.1469910000
C	3.0618870000	-0.2332710000	0.3505570000
O	3.3595820000	-1.0606440000	-0.4781460000
C	3.5331800000	-0.2200110000	1.7767500000
H	-0.7623510000	-3.3014980000	-0.8761180000

H	3.9802100000	0.7460110000	2.0097260000
H	4.2534770000	-1.0182980000	1.9291590000
H	2.6759370000	-0.3601620000	2.4365370000

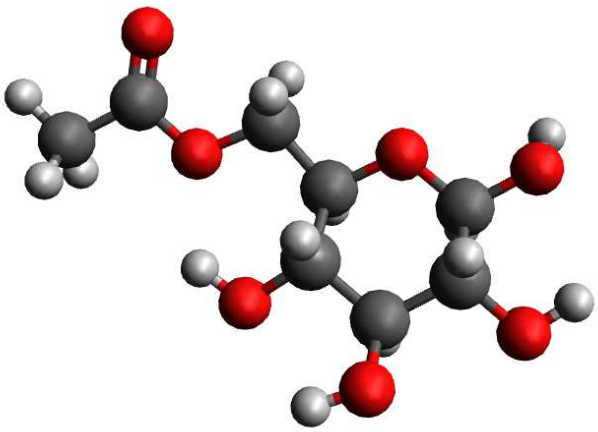
Conformer 3



C	-1.9683890000	-1.1675690000	-0.2425780000
H	-2.3914910000	-1.0524510000	-1.2494420000
O	-0.5832190000	-1.4515600000	-0.3500710000
C	0.1006420000	-0.4316380000	-1.0699220000
H	-0.3577970000	-0.2882590000	-2.0583630000
C	-0.0038130000	0.8784600000	-0.2907310000
H	0.4373790000	0.7381960000	0.7026820000
O	0.6070080000	1.9556470000	-0.9741910000
H	1.5630870000	1.8771800000	-0.8106970000
C	-1.4656680000	1.2533800000	-0.1019940000
H	-1.9092020000	1.4307170000	-1.0916240000
O	-1.5668750000	2.4119570000	0.7017520000
H	-0.9237020000	3.0343540000	0.3290010000
C	-2.2022000000	0.1077370000	0.5575770000
H	-1.7980090000	-0.0499140000	1.5649050000
O	-3.5842140000	0.4007180000	0.5930100000
H	-4.0194720000	-0.4013280000	0.9172580000
C	1.5217600000	-0.8967000000	-1.3056260000
H	2.0643080000	-0.1693220000	-1.9050400000
H	1.5093050000	-1.8603450000	-1.8076480000
O	2.2210830000	-1.1268060000	-0.0665770000
O	-2.5917160000	-2.1961350000	0.4551690000
C	2.9904380000	-0.1433880000	0.4129280000

O	3.0678500000	0.9602440000	-0.0930360000
C	3.7335750000	-0.5763900000	1.6405250000
H	-2.6928130000	-2.9582870000	-0.1306320000
H	4.3354930000	0.2477760000	2.0106030000
H	4.3664550000	-1.4303650000	1.3991870000
H	3.0190470000	-0.8938240000	2.4002910000

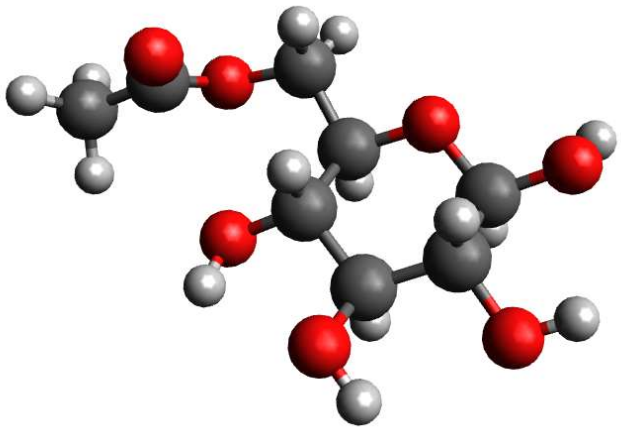
Conformer 4



C	2.1281400000	-1.2023240000	0.3513260000
H	2.1475730000	-1.1093650000	1.4449820000
O	0.8004130000	-1.4647040000	-0.0714000000
C	-0.1153890000	-0.4704670000	0.3747110000
H	-0.1117910000	-0.3992630000	1.4695100000
C	0.2800250000	0.8872930000	-0.2131100000
H	0.1755250000	0.8412520000	-1.3046000000
O	-0.4709110000	1.9612030000	0.3287580000
H	-1.4053890000	1.7933340000	0.1417130000
C	1.7287200000	1.2174210000	0.1199240000
H	1.8037580000	1.3469270000	1.2082840000
O	2.1186270000	2.4019850000	-0.5474700000
H	1.4198830000	3.0466040000	-0.3601440000
C	2.6399130000	0.0811720000	-0.2856960000
H	2.6075450000	-0.0475720000	-1.3742810000
O	3.9498300000	0.3538370000	0.1680970000
H	4.4645670000	-0.4485280000	-0.0024560000
C	-1.4627130000	-0.9699130000	-0.1161190000
H	-1.7150240000	-1.9175880000	0.3552370000
H	-1.4390060000	-1.1027370000	-1.1978360000

O	-2.4485050000	0.0204620000	0.2244350000
O	2.9545770000	-2.2295170000	-0.0873800000
C	-3.7249800000	-0.3012090000	-0.0832390000
O	-4.0182630000	-1.3524090000	-0.5986630000
C	-4.6710600000	0.7998530000	0.2941560000
H	2.8273760000	-3.0012770000	0.4805220000
H	-4.5484580000	1.0446010000	1.3489740000
H	-5.6904720000	0.4833040000	0.0951410000
H	-4.4381650000	1.6925050000	-0.2877900000

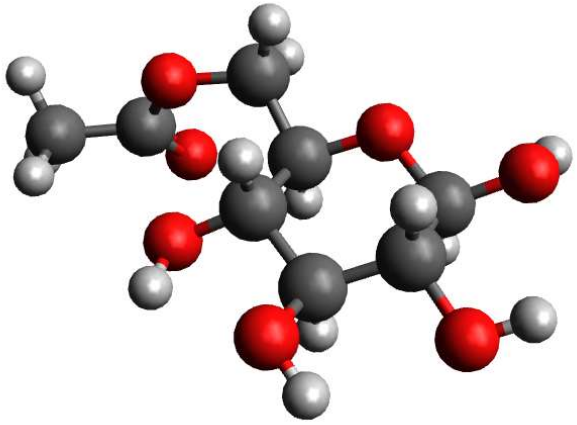
Conformer 5



C	-2.2385510000	-1.0326710000	-0.2769400000
H	-2.3001810000	-1.0059360000	-1.3725980000
O	-0.9736270000	-1.5487110000	0.1091090000
C	0.1202340000	-0.8182220000	-0.4395090000
H	0.0675350000	-0.8065790000	-1.5354470000
C	0.0771140000	0.6253240000	0.0653820000
H	0.2347470000	0.6268260000	1.1500510000
O	1.0810850000	1.3803560000	-0.5934270000
H	0.9085640000	2.3054000000	-0.3619540000
C	-1.2810420000	1.2322440000	-0.2421830000
H	-1.3868710000	1.2979940000	-1.3332050000
O	-1.2908130000	2.5287030000	0.3308720000
H	-2.1469270000	2.9266530000	0.1189650000
C	-2.3990890000	0.3651910000	0.2919940000
H	-2.3284830000	0.2948630000	1.3835170000
O	-3.6199220000	0.9521250000	-0.1145720000
H	-4.3308410000	0.3819140000	0.2108190000

C	1.3458820000	-1.6008680000	0.0108460000
H	1.2942710000	-2.6092030000	-0.3925870000
H	1.3859910000	-1.6360610000	1.0969800000
O	2.5414160000	-1.0131020000	-0.5098500000
O	-3.2385310000	-1.8236390000	0.2728810000
C	3.2030230000	-0.1583660000	0.2968900000
O	2.9236370000	0.0197390000	1.4598410000
C	4.3111100000	0.5234650000	-0.4483110000
H	-3.3077870000	-2.6420730000	-0.2367750000
H	4.8666890000	-0.1958090000	-1.0479480000
H	4.9686330000	1.0290500000	0.2530940000
H	3.8566170000	1.2526080000	-1.1207640000

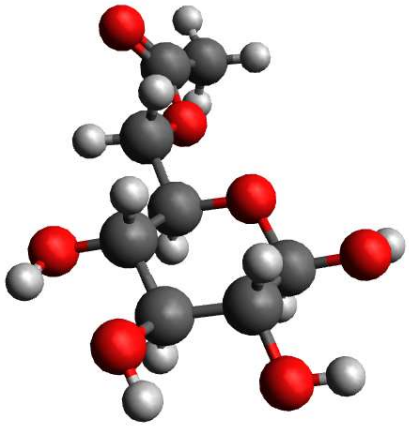
Conformer 6



C	-2.0782020000	-1.1162250000	-0.3179050000
H	-1.9130810000	-1.1179050000	-1.4031390000
O	-0.8820620000	-1.5000220000	0.3414620000
C	0.2369270000	-0.6836570000	-0.0033550000
H	0.4079450000	-0.7035950000	-1.0839990000
C	-0.0297730000	0.7618200000	0.4208840000
H	-0.0982970000	0.8106220000	1.5149690000
O	1.0074340000	1.5981990000	-0.0645270000
H	0.6736720000	2.5046970000	0.0151460000
C	-1.3476760000	1.2246710000	-0.1784430000
H	-1.2298580000	1.2508870000	-1.2700350000
O	-1.5881850000	2.5304000000	0.3185270000
H	-2.4084710000	2.8424380000	-0.0888740000
C	-2.4739030000	0.2715590000	0.1516790000

H	-2.6253350000	0.2300950000	1.2363690000
O	-3.6288720000	0.7374680000	-0.5186560000
H	-4.3412700000	0.1120820000	-0.3244620000
C	1.3944710000	-1.3463780000	0.7381240000
H	1.6580800000	-2.2833530000	0.2507580000
H	1.0819040000	-1.5369570000	1.7620540000
O	2.5478590000	-0.5078770000	0.8502680000
O	-3.0972370000	-1.9866890000	0.0460980000
C	3.2283330000	-0.2786550000	-0.2855020000
O	2.9595350000	-0.8154770000	-1.3365180000
C	4.3224100000	0.7228530000	-0.0664610000
H	-2.9855990000	-2.8191130000	-0.4325680000
H	4.9740220000	0.7507670000	-0.9349940000
H	4.8877460000	0.4774680000	0.8313630000
H	3.8552350000	1.6979130000	0.0800450000

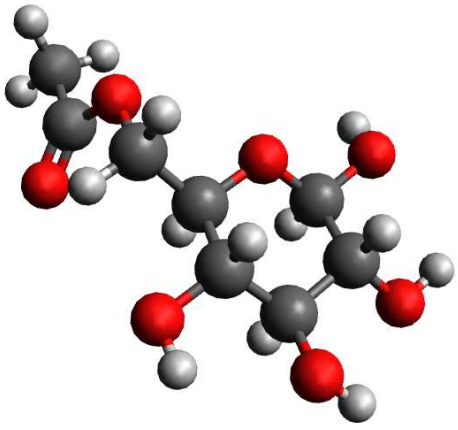
Conformer 7



C	-1.3665130000	1.4839330000	0.1731170000
H	-1.3183910000	1.5384230000	1.2686240000
O	-0.1364030000	0.9804040000	-0.3257580000
C	0.1923660000	-0.2861330000	0.2345720000
H	0.2195820000	-0.2223990000	1.3297700000
C	-0.8633870000	-1.3108050000	-0.1766950000
H	-0.8659160000	-1.3977370000	-1.2706160000
O	-0.5520810000	-2.5495230000	0.4316200000
H	-1.3290950000	-3.1143180000	0.3060760000
C	-2.2292740000	-0.8279600000	0.2740370000
H	-2.2384460000	-0.7935090000	1.3714580000

O	-3.1787890000	-1.7680790000	-0.1971960000
H	-4.0496820000	-1.4626430000	0.0935620000
C	-2.4986170000	0.5651370000	-0.2541790000
H	-2.5194050000	0.5463110000	-1.3499730000
O	-3.7373520000	0.9873630000	0.2817770000
H	-3.9004230000	1.8814580000	-0.0505690000
C	1.5550890000	-0.6776500000	-0.2794370000
H	1.5845070000	-0.6090780000	-1.3670710000
H	1.7974200000	-1.6937480000	0.0257990000
O	2.5034100000	0.2415450000	0.2852100000
O	-1.6107860000	2.7297980000	-0.3898940000
C	3.7845550000	0.0278750000	-0.0544780000
O	4.1287010000	-0.8742720000	-0.7841740000
C	4.6945090000	1.0405790000	0.5796840000
H	-1.0446750000	3.3846670000	0.0403770000
H	4.5748230000	1.0129340000	1.6627030000
H	4.4202650000	2.0390290000	0.2381340000
H	5.7234660000	0.8228700000	0.3093260000

Conformer 8



C	1.1861810000	1.4847510000	-0.1569410000
H	0.9004450000	1.4896070000	-1.2170670000
O	0.0986060000	1.0071450000	0.6197980000
C	-0.3322530000	-0.2847890000	0.2034000000
H	-0.5950850000	-0.2757480000	-0.8610380000
C	0.7966530000	-1.2892850000	0.4260620000
H	1.0371930000	-1.3205900000	1.4965360000
O	0.3731340000	-2.5569660000	-0.0377250000

H	1.1647150000	-3.1151750000	-0.0562980000
C	2.0275250000	-0.8317640000	-0.3338710000
H	1.7968710000	-0.8517420000	-1.4071250000
O	3.0658610000	-1.7489510000	-0.0362820000
H	3.8477760000	-1.4623870000	-0.5289760000
C	2.3925200000	0.5853740000	0.0545210000
H	2.6534040000	0.6201270000	1.1186330000
O	3.4796530000	0.9795680000	-0.7598140000
H	3.7016030000	1.8892320000	-0.5155420000
C	-1.5490800000	-0.6482330000	1.0263150000
H	-1.3247650000	-0.5317040000	2.0843800000
H	-1.8517890000	-1.6695450000	0.8106880000
O	-2.6371990000	0.2536590000	0.7679980000
O	1.5371180000	2.7549680000	0.2827360000
C	-3.3776800000	-0.0054090000	-0.3244700000
O	-3.1597920000	-0.9350040000	-1.0683730000
C	-4.4829680000	0.9991130000	-0.4792310000
H	0.8852400000	3.3902390000	-0.0426840000
H	-4.0559280000	1.9985820000	-0.5644490000
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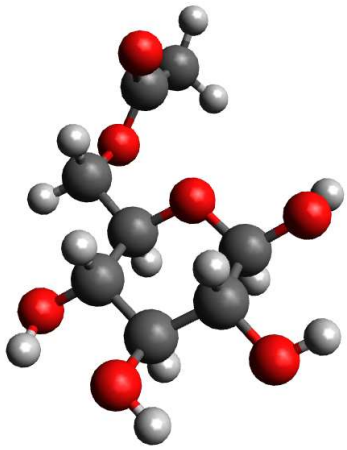
H	-5.0656200000	0.7634580000	-1.3647580000

Conformer 9



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O	-0.2552830000	0.6568060000	0.1446950000
C	-0.1891870000	-0.6819040000	-0.3329080000
H	-0.1460780000	-0.6893610000	-1.4296950000

C	1.0653060000	-1.3549220000	0.2181510000
H	1.0097440000	-1.3664260000	1.3140410000
O	1.1379330000	-2.6686080000	-0.3019900000
H	2.0258250000	-2.9936190000	-0.0911010000
C	2.2826590000	-0.5504030000	-0.1975640000
H	2.3621370000	-0.5849110000	-1.2921220000
O	3.4119010000	-1.1649680000	0.3979120000
H	4.1887230000	-0.6559950000	0.1263500000
C	2.1313930000	0.8944920000	0.2299170000
H	2.0797380000	0.9508940000	1.3234010000
O	3.2468330000	1.6027350000	-0.2745150000
H	3.1422180000	2.5261160000	-0.0046780000
C	-1.4439760000	-1.3931150000	0.1218570000
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H	-1.4129400000	-2.4336070000	-0.1902310000
O	-2.5790790000	-0.7964070000	-0.5221150000
O	0.6910230000	2.7413400000	0.1545270000
C	-3.3375830000	0.0480590000	0.2038770000
O	-3.1765470000	0.2595030000	1.3826980000
C	-4.4029690000	0.6690490000	-0.6541480000
H	0.0033620000	3.1925780000	-0.3534110000
H	-3.9314930000	1.2845700000	-1.4211380000
H	-5.0561360000	1.2792440000	-0.0374230000
H	-4.9739690000	-0.1115580000	-1.1562500000

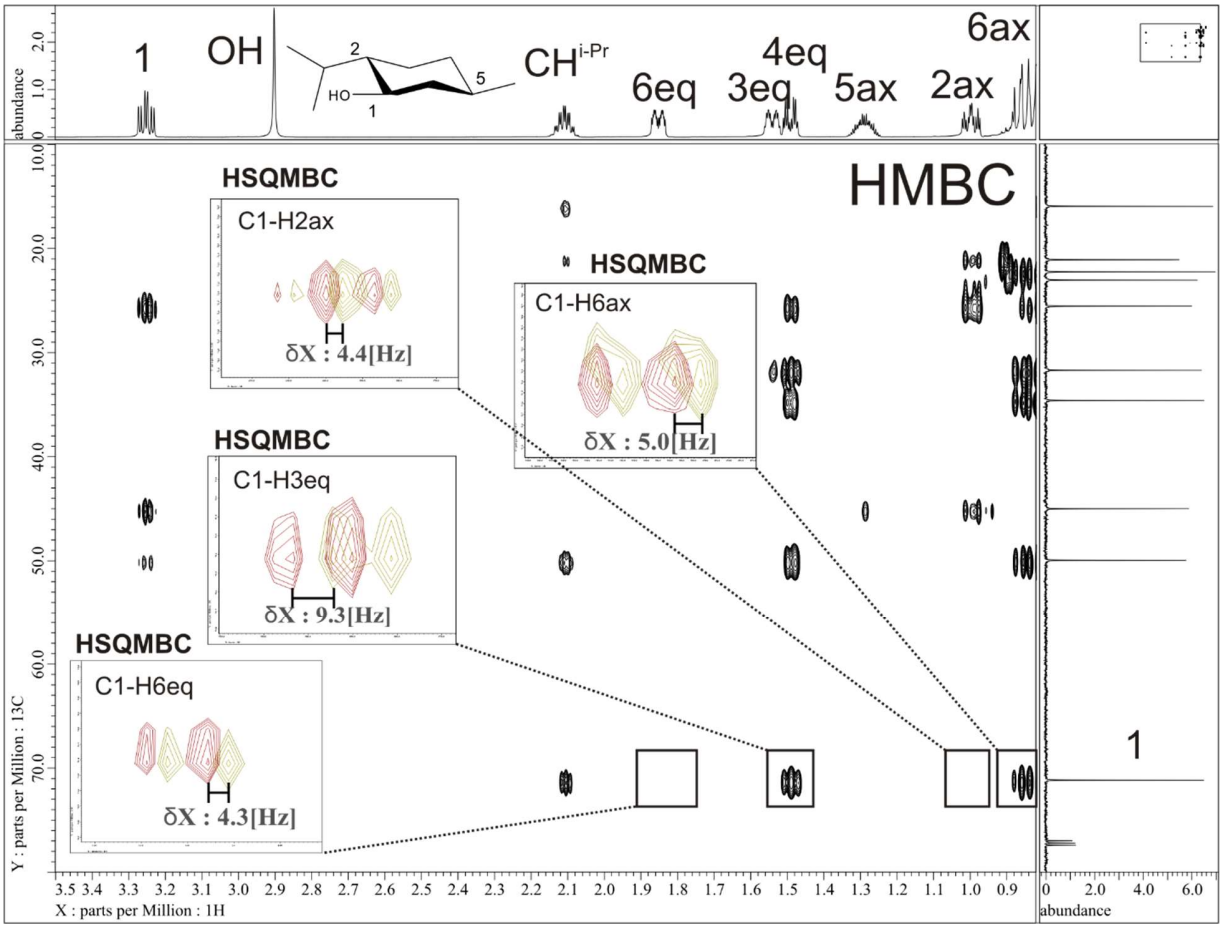

Figure S9. Menthol standard in $CDCl_3$. HMBC spectrum with HSQMBC ^{1}H-^{13}C-couplings (insets). The couplings of C1-H6eq and C1-H3eq matched the published values very well. [7] The value for C1-H2ax was reported by Vidal *et al.* with -6.3 Hz in the literature, but might be too high in magnitude (judged by the relative peak spacing; refer to Figure 4 of that publication). [7] The peak spacing shown in Vidal's paper actually corresponds much more to the magnitude determined by us here, namely 4.4 Hz.

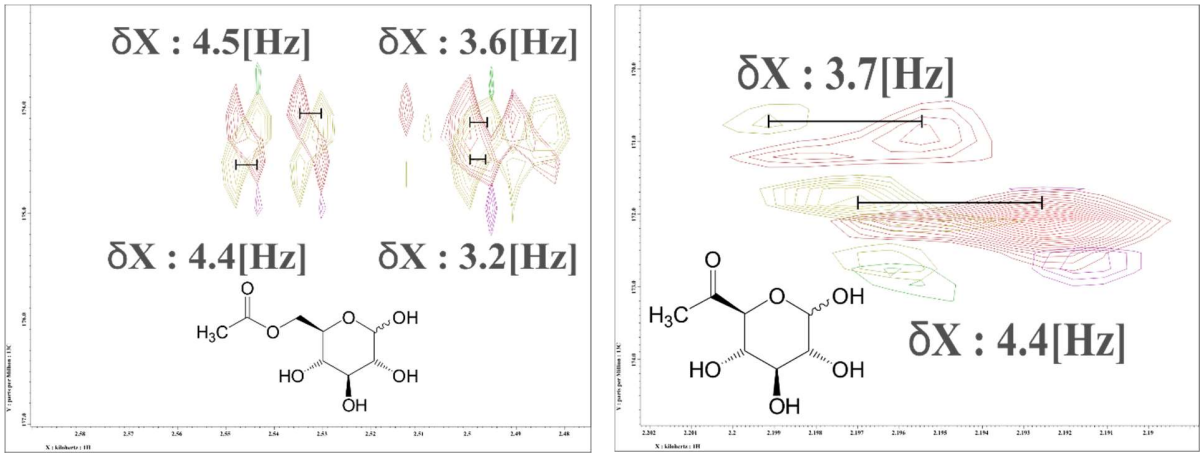

Figure S10. Experimental ipap-HSQMBC data of α/β-**1** (H6$_{R/S}$-C1') and α/β-**5** (H^{CH3}-C6').

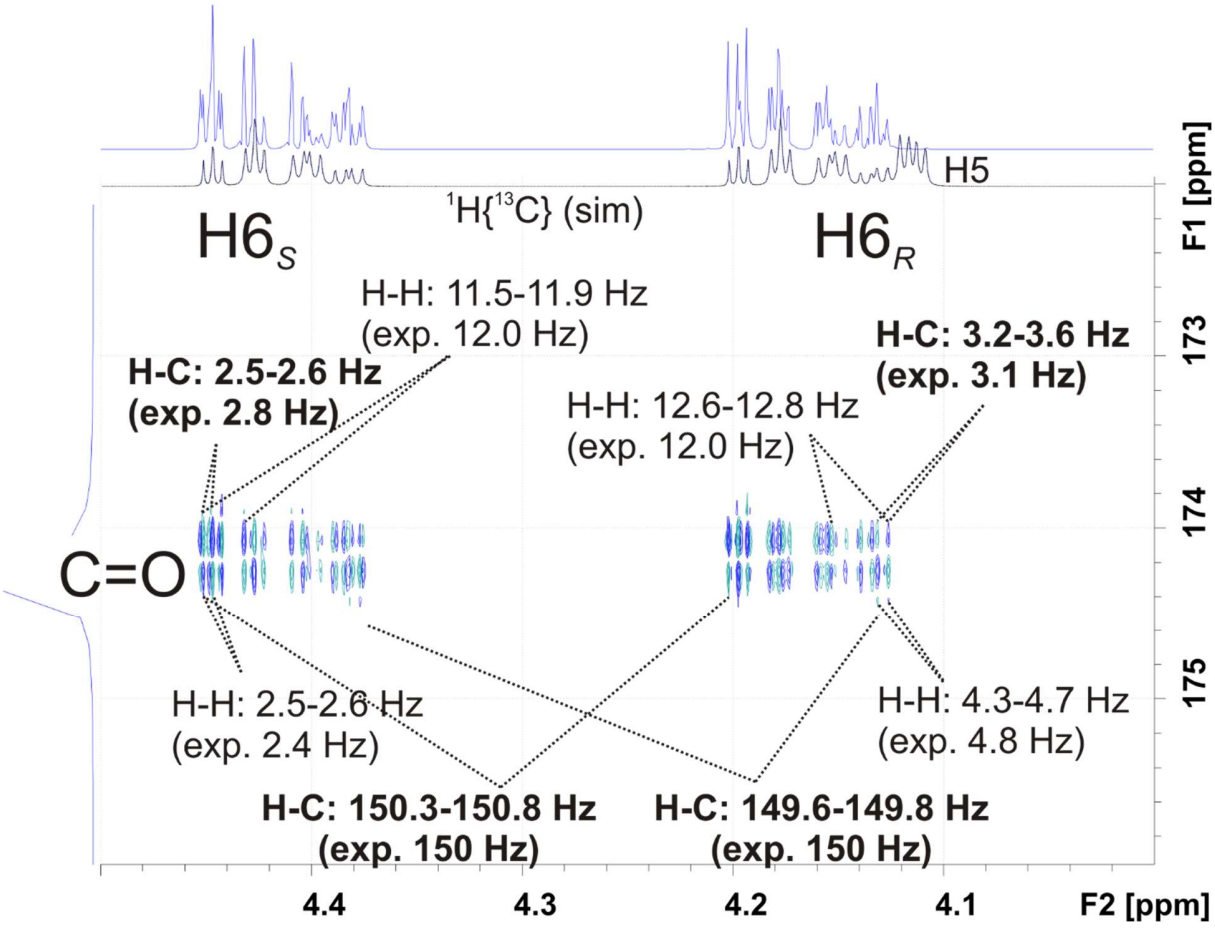

Figure S11. Simulated non-decoupled qf-HMBC spectrum (gradient-enhanced with low-pass filter; Bruker pulse sequence hmbcgplpndqf) of α-**1** and single-pulse coupled ^{1}H-spectrum of α-**1** (hairline inset; Bruker pulse sequence zg). Ranges of *J*-values are shown as a consequence of cumulative errors in the multi-pulse sequence. All compounds, α/β-**1**, α/β-**2**, α/β-**3**, and α/β-**4** were simulated in the same fashion (Figure S10). Errors for ^1J-values determined from the simulated spectral lines were found to be slightly larger (up to ~1.2 Hz) than for ^3J-values (up to ~0.5 Hz). The latter errors were of the same size as the experimental error associated with the determination of ^3J-values from *J*-HMBC experiments via cross-peak volume modulation and fitting to $y = \sin(\pi * J * x)$ model.

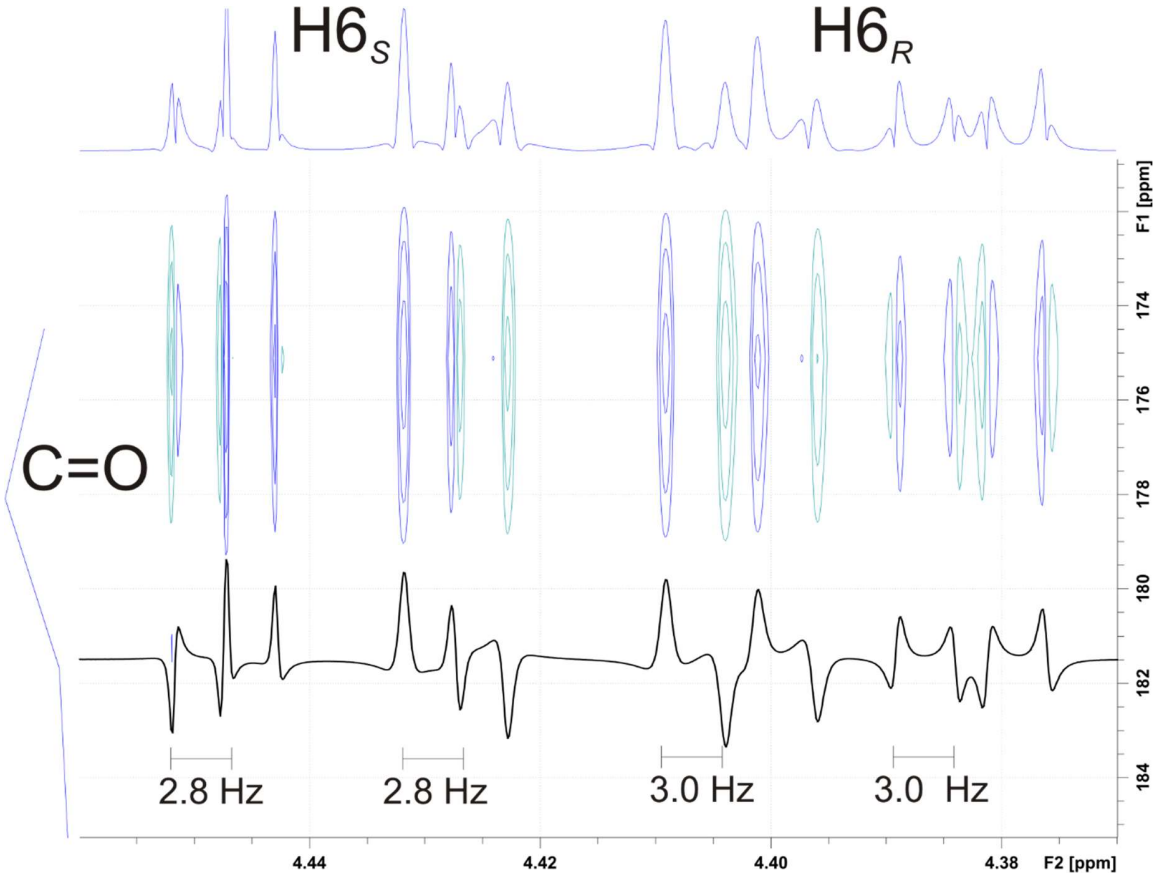

Figure S12. HSQMBC spectrum simulation of α-**1**.

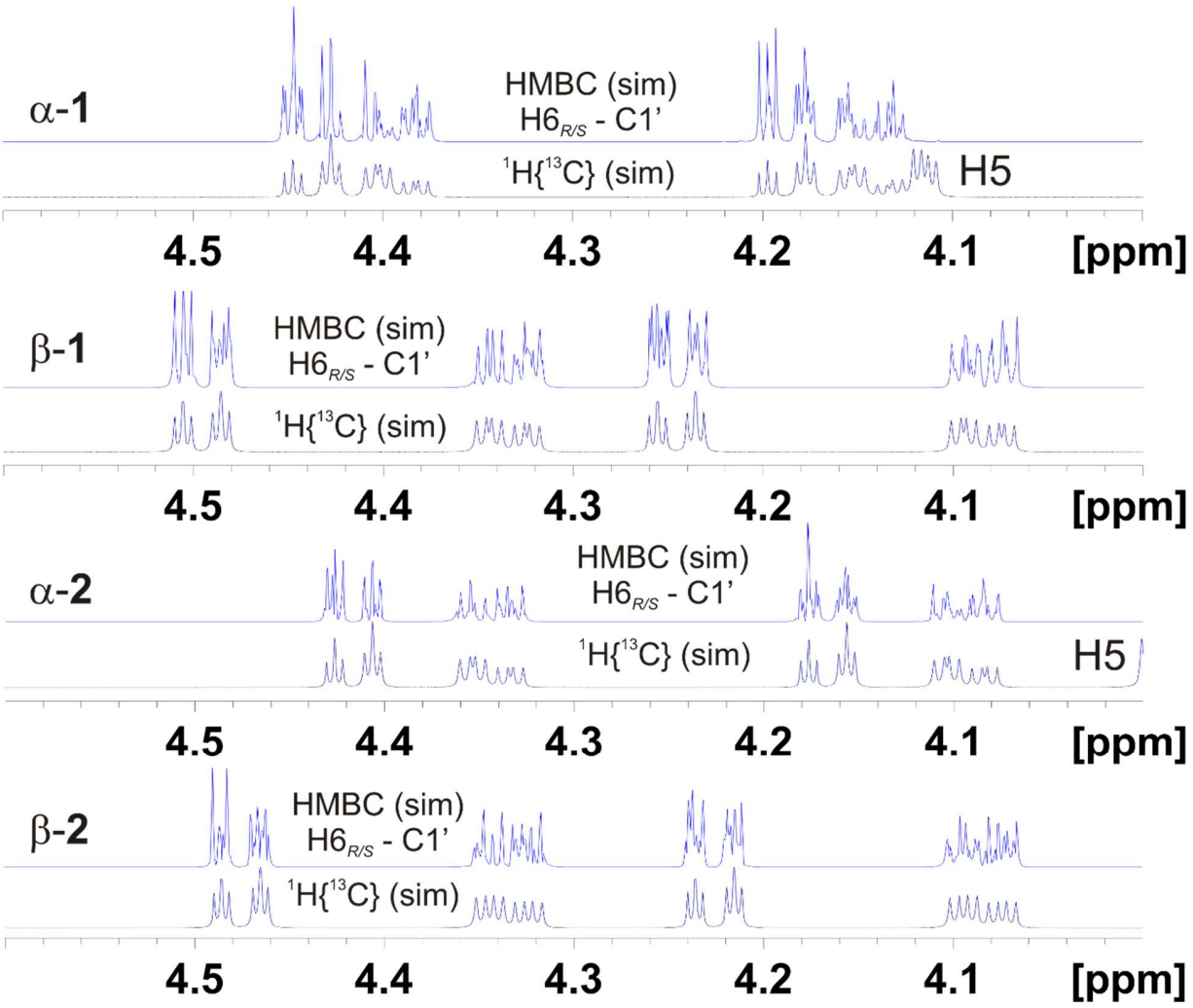

Figure S13. Simulated NMR spectra of the $CHCH_2OC(sp^2)$ spin system of α/β-**1** and α/β-**2**. The spectra were obtained by solving the Liouville equation that describes the time-evolution of the density matrix of a spin system during an NMR experiment. Calculations were carried out with the program NMRSim 6.0 as part of TopSpin 3.5 pl7 (Bruker, Germany). Proton-carbon *J*-values obtained from the HMBC pulse sequence as opposed to the fully coupled $^1H\{^{13}C\}$ spectrum had an error of 1-2 Hz for $^1J_{C,H}$ and 0.3-0.5 Hz for $^3J_{C,H}$. The error associated with $^1J_{C,H}$ values in the presence of strong ^1H-^1H-coupling was inline with the findings of Yu *et al.* in a recent paper. [8] For the three-bond *J*-values, the error from theoretical simulation of the spin system was of similar magnitude as the experimental error derived from multiple data sets describing the HMBC cross-peak volume evolution during the *J*-HMBC experiment.

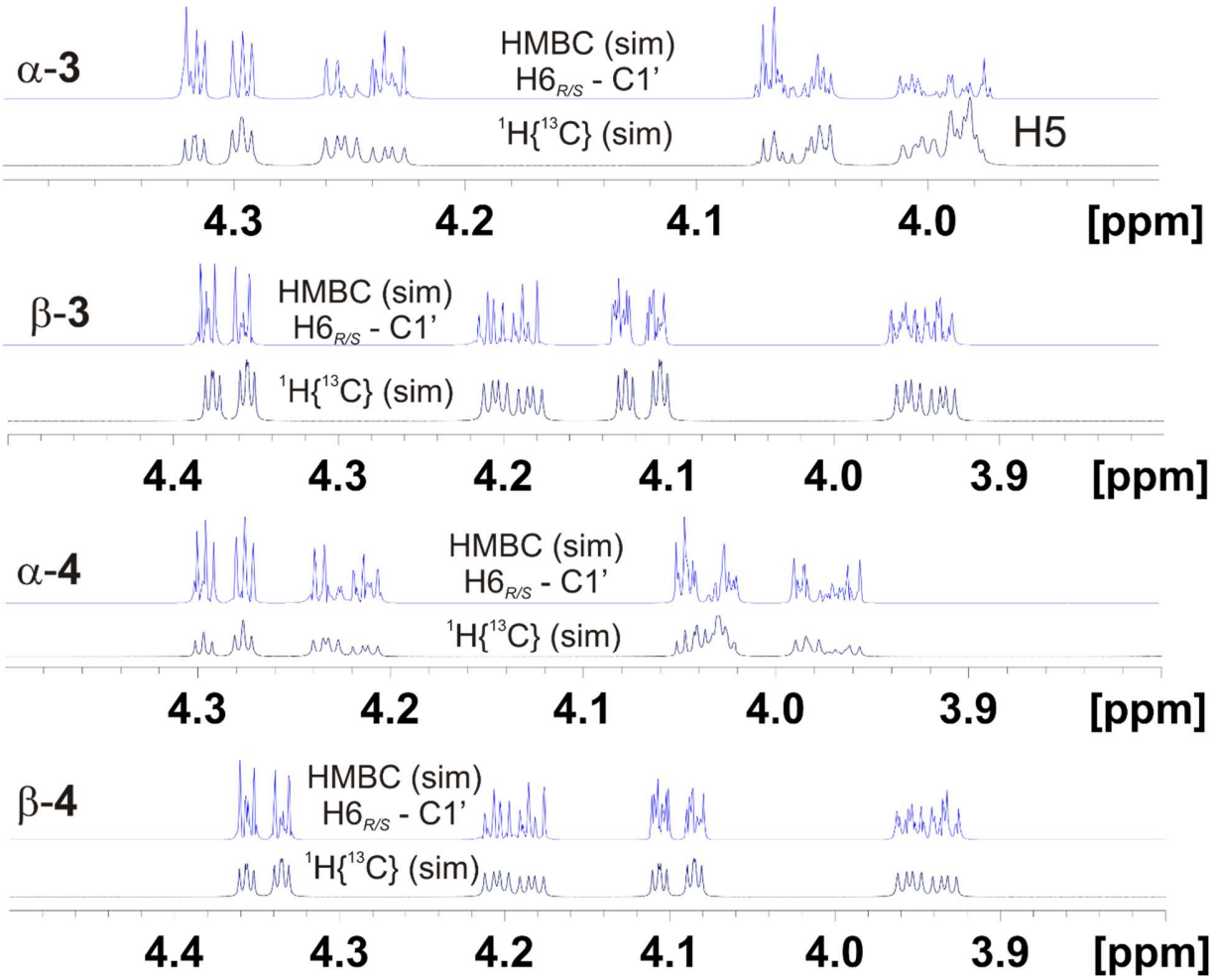

Figure S14. Simulated NMR spectra of the $CHCH_2OC(sp^2)$ spin system of α/β-**3** and α/β-**4**.

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