Selective Depletion and Enrichment of Constituents in "Curcumin" and Other *Curcuma longa* Preparations

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■ SUPPORTING INFORMATION

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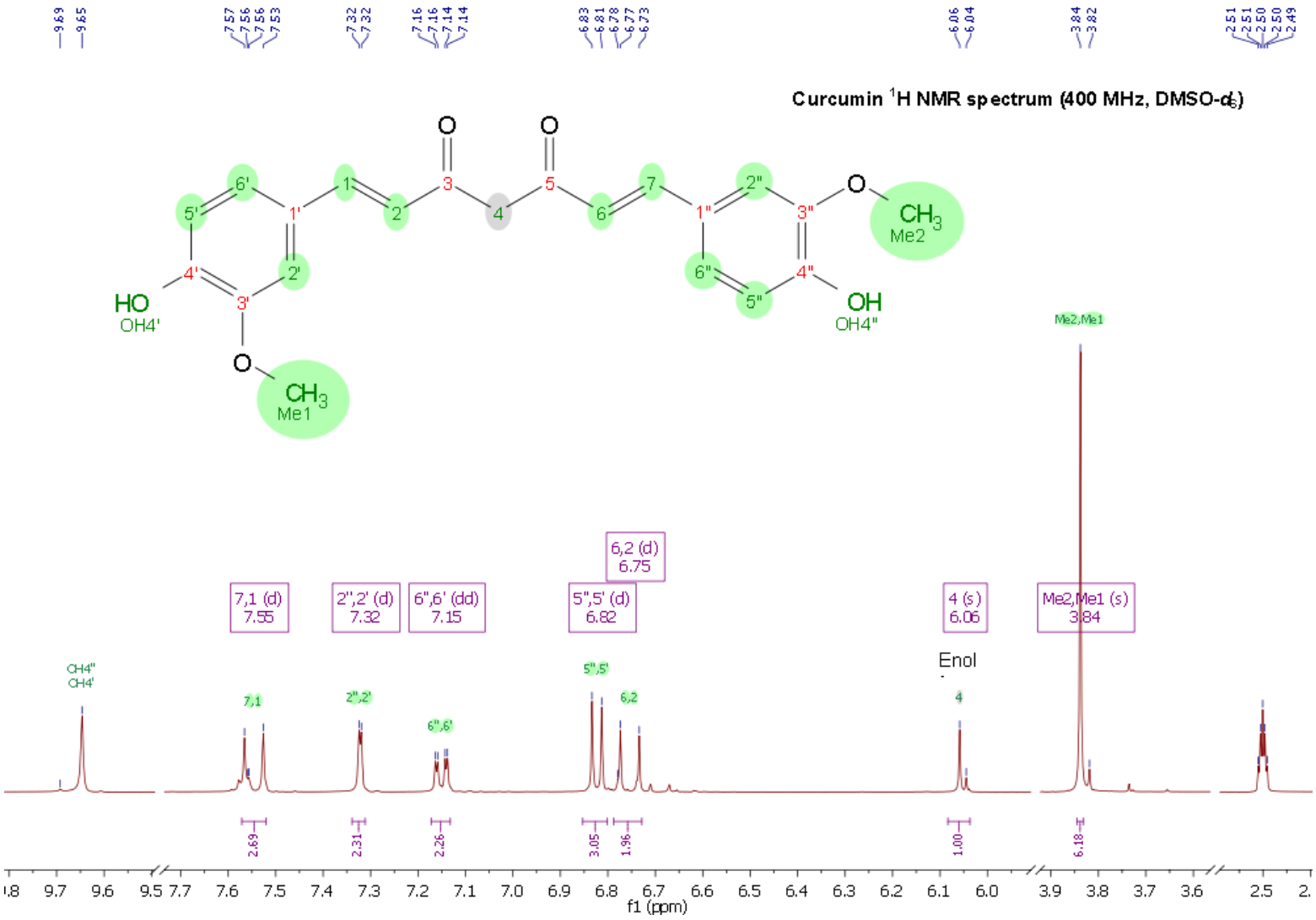
Figure S1. NMR Assignments of Curcumin (1) (400/100 MHz, DMSO-d_6)

1D ^{1}H NMR Spectrum (Curcuminoids_C1386_QHNMR_analysis)



1D ^{13}C NMR Spectrum

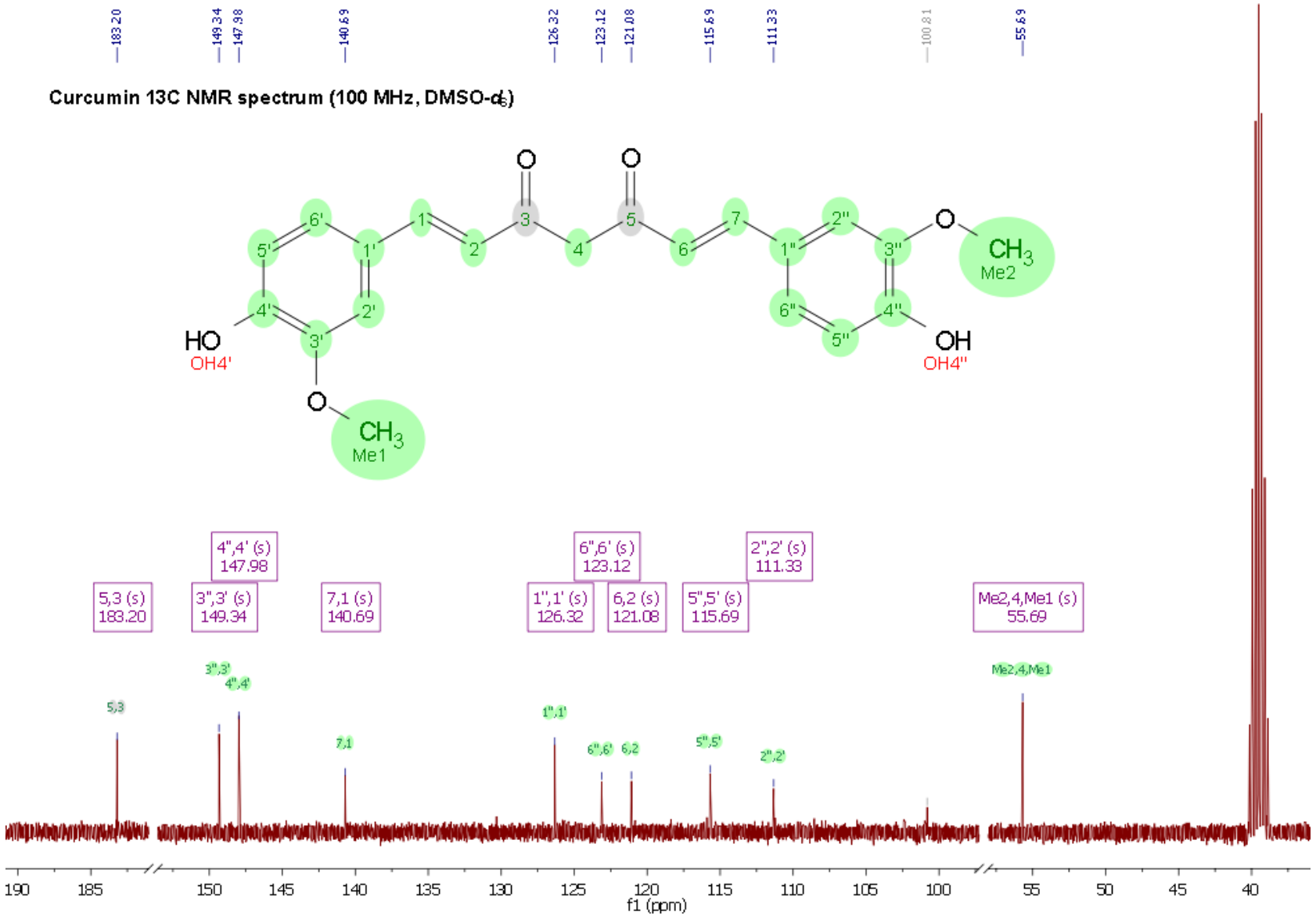


Figure S2. CPC separation of curcuminoid-enriched turmeric extract (CTE). Column volume 266 mL, flow rate 10 ml/min, rotation speed 3000 rpm, sample size 360 mg in 8 mL lower phase and 1 mL DMSO; Sf = 0.37.

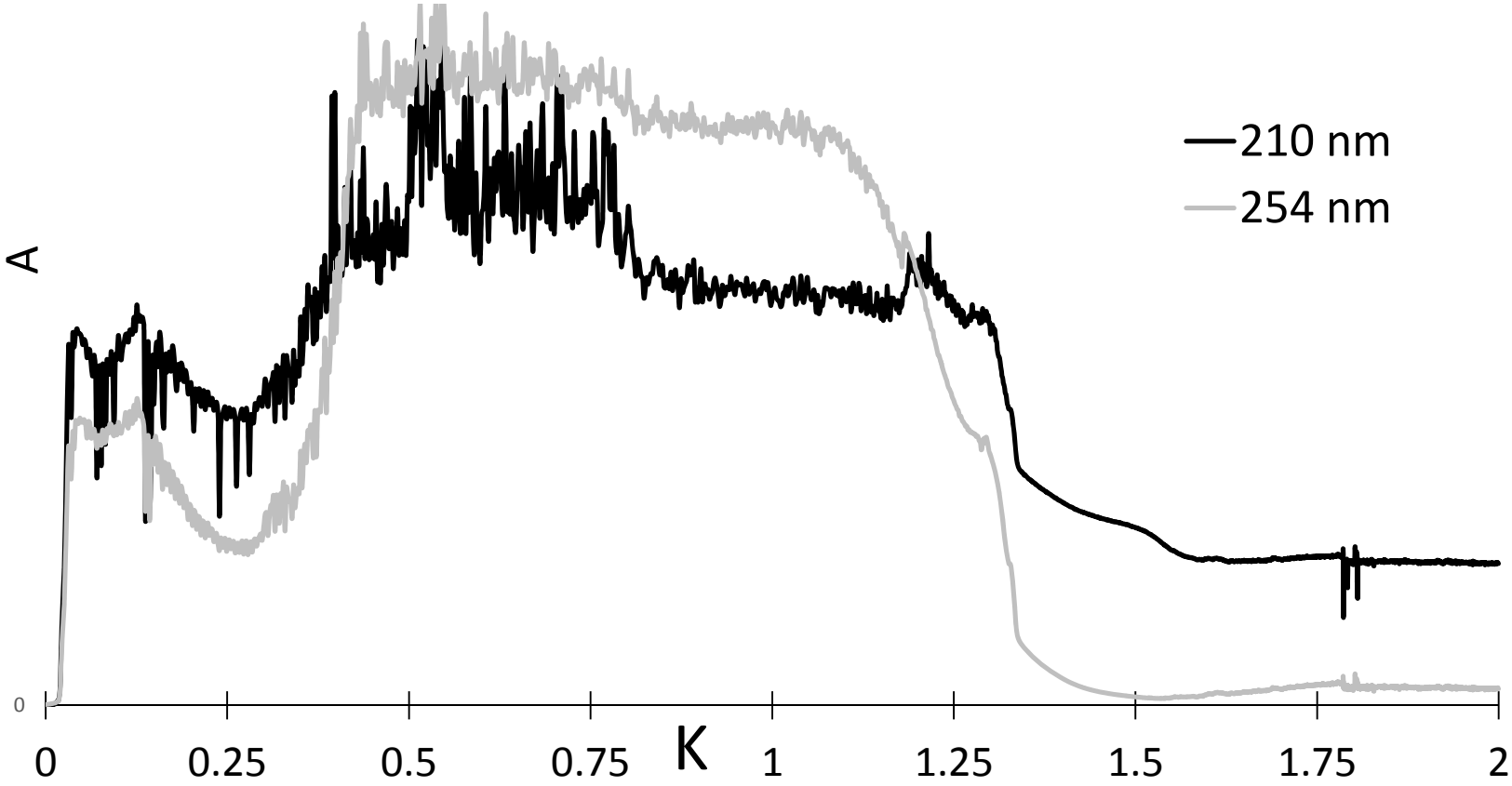


Figure S3 Volume percentages of individual solvents in the biphasic solvent systems *n*-hexane/dichloromethane/methanol/water.

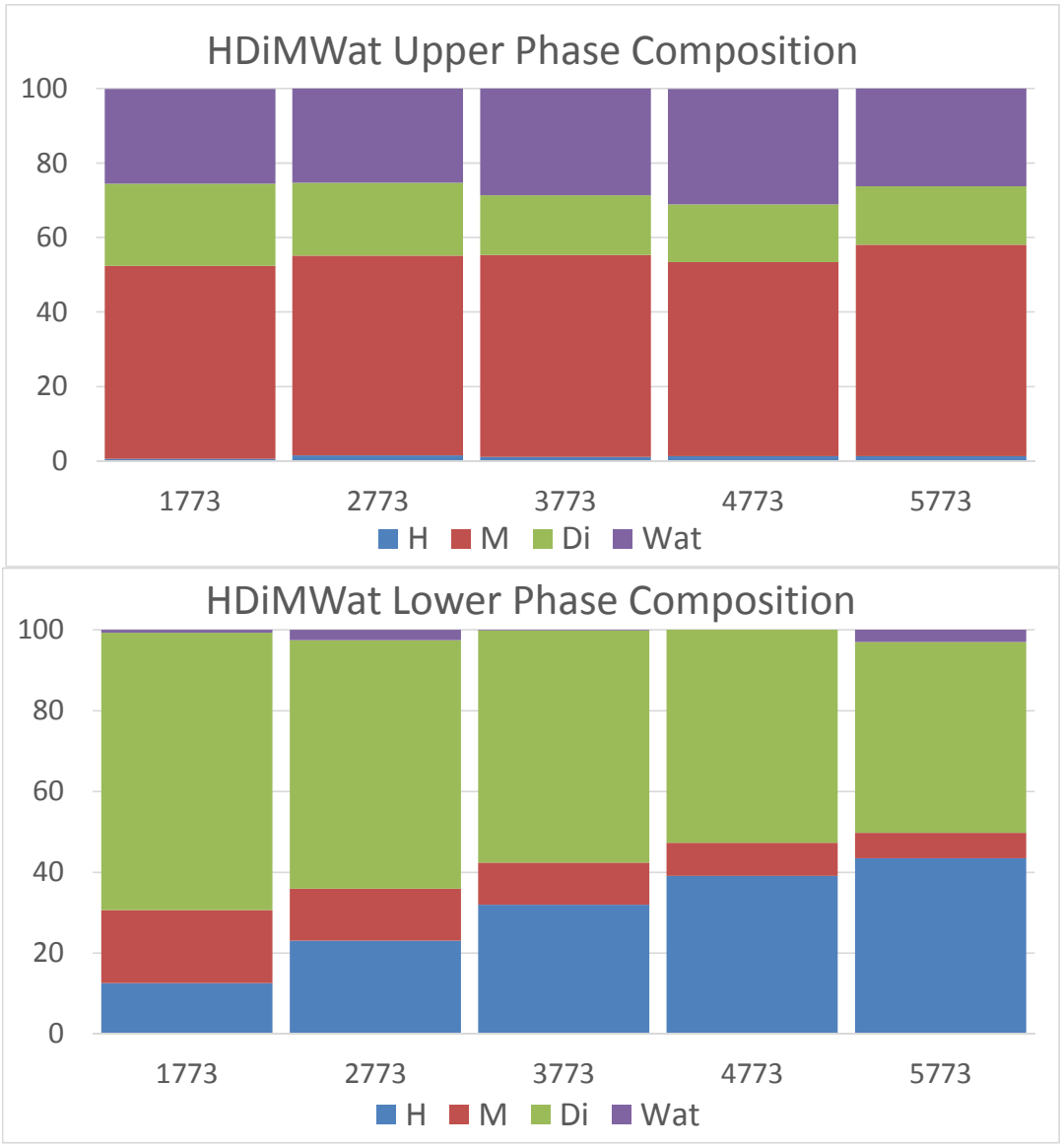


Table S4 The ^{1}H iterative full spin analysis (HiFSA) profiles of curcumin (**1**), demethoxycurcumin (**2**), and bisdemethoxycurcumin (**3**). These parameters (shown in perch.pms format) were subsequently for quantitation of the curcuminoid mixtures.

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ACTIVE SPECIES:1H
CHEMICAL SHIFTS(PPM):
1-CRCMN   2*SPIN= 1 SPECIES=1H    POPULATION(Y)=   0.44165
 1-H1   / 1    7.546789  1*2*1  STAT=Y  PRED= 7.222 RANGE= 0.503 WIDTH(Y)= 2.304 RESP(Y)= 1.0000 HSQC= C1
 1-H2   / 1    6.758370  1*2*1  STAT=Y  PRED= 6.648 RANGE= 0.818 WIDTH(Y)= 3.108 RESP(Y)= 1.0000 HSQC= C2
 1-H4   / 1    6.054990  1*1*1  STAT=Y  PRED= 8.037 RANGE= 0.148 WIDTH(Y)= 2.114 RESP(Y)= 1.0000 HSQC= C4
 1-H2'  / 1    7.320665  2*1*1  STAT=Y  PRED= 7.113 RANGE= 0.148 WIDTH(Y)= 1.740 RESP(Y)= 1.0000 HSQC= C2'
 1-H5'  / 1    6.821404  2*1*1  STAT=Y  PRED= 6.815 RANGE= 0.158 WIDTH(Y)= 1.972 RESP(Y)= 1.0000 HSQC= C5'
 1-H6'  / 1    7.148632  2*1*1  STAT=Y  PRED= 6.907 RANGE= 0.178 WIDTH(Y)= 1.444 RESP(Y)= 1.0000 HSQC= C6'
 1-H-Meth/ 1    3.836602  2*1*3  STAT=Y  PRED= 3.901 RANGE= 0.148 WIDTH(Y)= 0.934 RESP(Y)= 1.0000 HSQC= Methyl
2-DMCRCMN  2*SPIN= 1 SPECIES=1H    POPULATION(Y)=   0.45820
 2-H1A  / 2    7.539958  1*1*1  STAT=Y  PRED= 7.241 RANGE= 0.503 WIDTH(Y)= 1.465 RESP(Y)= 1.0000 HSQC= C1A
 2-H7A  / 2    7.545639  1*1*1  STAT=Y  PRED= 7.236 RANGE= 0.508 WIDTH(Y)= 1.449 RESP(Y)= 1.0000 HSQC= C7A
 2-H2A  / 2    6.753371  1*1*1  STAT=Y  PRED= 6.626 RANGE= 0.818 WIDTH(Y)= 1.419 RESP(Y)= 1.0000 HSQC= C2A
 2-H6A  / 2    6.689520  1*1*1  STAT=Y  PRED= 6.638 RANGE= 0.803 WIDTH(Y)= 1.704 RESP(Y)= 1.0000 HSQC= C6A
 2-H4A  / 2    6.040646  1*1*1  STAT=Y  PRED= 6.000 RANGE= 0.148 WIDTH(Y)= 1.763 RESP(Y)= 1.0000 HSQC= C4A
 2-H2'  / 2    7.321283  1*1*1  STAT=Y  PRED= 7.285 RANGE= 0.183 WIDTH(Y)= 1.390 RESP(Y)= 1.0000 HSQC= C2'
 2-H6'  / 2    7.141612  1*1*1  STAT=Y  PRED= 7.060 RANGE= 0.148 WIDTH(Y)= 3.585 RESP(Y)= 1.0000 HSQC= C6'
 2-H5'  / 2    6.818111  1*1*1  STAT=Y  PRED= 6.828 RANGE= 0.148 WIDTH(Y)= 3.107 RESP(Y)= 1.0000 HSQC= C5'
 2-H2"  / 2    7.564362  1*2*1  STAT=Y  PRED= 7.372 RANGE= 0.153 WIDTH(Y)= 1.762 RESP(Y)= 1.0000 HSQC= C2"
 2-H3"  / 2    6.821859  1*2*1  STAT=Y  PRED= 6.770 RANGE= 0.148 WIDTH(Y)= 1.054 RESP(Y)= 1.0000 HSQC= C3"
 2-methyl/ 2    3.835353  1*1*3  STAT=Y  PRED= 3.864 RANGE= 0.148 WIDTH(Y)= 0.839 RESP(Y)= 1.0000 HSQC= methyl
3-BDMCRCMN  2*SPIN= 1 SPECIES=1H    POPULATION(Y)=   0.10015
 3-H1   / 3    7.543196  1*2*1  STAT=Y  PRED= 7.519 RANGE= 0.513 WIDTH(Y)= 2.339 RESP(Y)= 1.0000 HSQC= C1
 3-H2   / 3    6.686903  1*2*1  STAT=Y  PRED= 6.631 RANGE= 0.798 WIDTH(Y)= 2.610 RESP(Y)= 1.0000 HSQC= C2
 3-H4   / 3    6.033727  1*1*1  STAT=Y  PRED= 6.009 RANGE= 0.148 WIDTH(Y)= 1.804 RESP(Y)= 1.0000 HSQC= C4
 3-H2'  / 3    7.560945  2*2*1  STAT=Y  PRED= 7.449 RANGE= 0.163 WIDTH(Y)= 3.084 RESP(Y)= 1.0000 HSQC= C2'
 3-H3'  / 3    6.823749  2*2*1  STAT=Y  PRED= 6.769 RANGE= 0.148 WIDTH(Y)= 2.532 RESP(Y)= 1.0000 HSQC= C3'

COUPLING CONSTANTS(HZ):
 J132_33   15.7886  J 1-H1    1-H2     STAT=Y  PRED= 15.690 RANGE= 1.000
 J115_31   -0.0037  J 1-H2'   1-H5'    STAT=Y  PRED= 0.477 RANGE= 1.000
 J114_31    2.0568  J 1-H2'   1-H6'    STAT=Y  PRED= 2.038 RANGE= 1.000
 J114_15    8.1027  J 1-H5'   1-H6'    STAT=Y  PRED= 8.224 RANGE= 1.000
 J231_32   15.7922  J 2-H1A   2-H2A     STAT=Y  PRED= 15.690 RANGE= 1.000
 J234_35   15.7996  J 2-H7A   2-H6A     STAT=Y  PRED= 15.565 RANGE= 1.000
 J214_30    2.0000  J 2-H2'   2-H6'    STAT=N  PRED= 2.000 RANGE= 1.000
 J215_30   -0.0966  J 2-H2'   2-H5'    STAT=Y  PRED= 0.477 RANGE= 1.000
 J214_15    7.6821  J 2-H6'   2-H5'    STAT=Y  PRED= 8.224 RANGE= 1.000
 J236_39    0.0033  J 2-H2"   2-H2"    STAT=Y  PRED= 0.409 RANGE= 1.000
 J237_36    8.3994  J 2-H3"   2-H2"    STAT=Y  PRED= 8.543 RANGE= 1.000
 J237_39    0.8884  J 2-H2"   2-H3"    STAT=Y  PRED= 0.456 RANGE= 1.000
 J237_29   -0.0062  J 2-H3"   2-H3"    STAT=Y  PRED= 0.526 RANGE= 1.000
 J328_29   15.1524  J 3-H1    3-H2     STAT=Y  PRED= 15.565 RANGE= 1.000
 J327_14   -0.0005  J 3-H2'   3-H2'    STAT=Y  PRED= 0.999 RANGE= 1.000
 J327_37    7.7306  J 3-H2'   3-H3'    STAT=Y  PRED= 8.543 RANGE= 1.000
 J327_15    0.0022  J 3-H3'   3-H2'    STAT=Y  PRED= 0.999 RANGE= 1.000
 J337_15   -0.0004  J 3-H3'   3-H3'    STAT=Y  PRED= 0.999 RANGE= 1.000
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Figure S5 ^{1}H NMR spectra of DESIGNER fractions with regions of interest (i – vii).