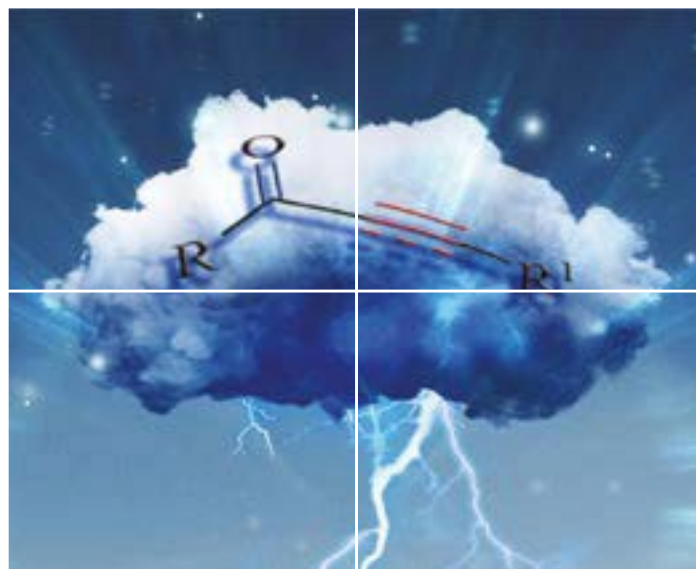


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## ARTICLE

# Synergistic Use of NMR Computation and Quantitative Interproton Distance Analysis in Structural Determination of Neokadcoccitane A, a Rearranged Triterpenoid Featuring an Aromatic Ring D from *Kadsura coccinea*

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Neokadcoccitane A (**1**), an unprecedented 14(13→12):28(14→8)-diabeo-3,4-secolanostane triterpenoid possessing an aromatic ring D and an unusual Me-21 orientation, along with two novel 14(13→12)-abeo-3,4-seco-norlanostane triterpenoids featuring three and one carbon degradation, respectively (**2** and **3**), were isolated from the roots of *Kadsura coccinea*. The absolute configuration of **1** was determined by synergistic use of NMR computation, quantitative interproton distance analysis, and TDDFT ECD calculation, while that of **2** was established by X-ray diffraction. **1** was found to exhibit moderate anti-platelet aggregation activity.

## Introduction

The Schisandraceae family, comprising only genera *Kadsura* and *Schisandra*, is an invaluable source of herbal medicines. Extensive research on species within this family has proven them to be versatile manufacturers of diverse and bioactive triterpenoids, which mainly falls into three classes: lanostanes, cycloartanes, as well as schinortriterpenoids (SNTs) exclusive to this family<sup>1</sup>. *K. coccinea*, or *hei lao hu* (meaning “black tiger”) in Chinese, is a traditional Chinese herbal medicine often used to treat rheumatic arthritis, postpartum abdominalgia with blood stasis, etc<sup>2</sup>. Previous investigations on the stems of this species by our lab have afforded six kinds of novel triterpene scaffolds<sup>3</sup> (Table S1), which were uniformly biosynthetically derived from lanostanes. In the present study, roots of this plant cultivated in Hunan Province, China, were fortunately obtained and brought into investigation to hunt for more structurally interesting and bioactive triterpenoids. Consequently, three novel lanostane-type triterpenoids, neokadcoccitane A–C (**1–3**) were obtained, and they were proposed to share the common biosynthetic precursor, seco-neokadsuranic acid A (sna A)<sup>4</sup> (Figure 1). Sna A possessed rare 14(13→12)-abeo-3,4-secolanostane scaffold<sup>3c</sup>, yet it was found to be a major constituent in the present

material. On the basis of sna A, **1** was proposed to form through 28(14→8)-migration and subsequent ring D aromatization, resulting in its unusual 14(13→12):28(14→8)-diabeo-3,4-secolanostane skeleton featuring a tetrasubstituted benzene ring D. To the best of our knowledge, only three lanostanes, daedaleic acid A, daedaleic acid A<sup>5</sup> and 19-nor-lanosta-5(10),6,8,24-tetraene-1 $\alpha$ ,3 $\beta$ ,12 $\beta$ ,22 $\delta$ -tetraol<sup>6</sup>, possess benzene rings within their intrinsic skeletons (all in ring B)<sup>7</sup> (Table S2). Besides, two SNTs with highly substituted aromatic ring D, rubrifloridilactones A and B, have also been reported by our group<sup>8</sup>, which aroused great interests in their synthetic study<sup>9</sup>. In addition, upon various degrees of carbon degradation occurring on sna A, **2** and **3** were generated and represented the first examples of 25,26,27-trinor-14(13→12)-abeo-3,4-secolanostane and 30-nor-14(13→12)-abeo-3,4-secolanostane triterpenoids, respectively. Notably, to address the challenges in stereochemical determination of **1**, quantum chemical calculation of NMR parameters (qccNMR)<sup>10</sup> and quantitative interproton distance analysis (QIDA)<sup>11</sup> were collaboratively

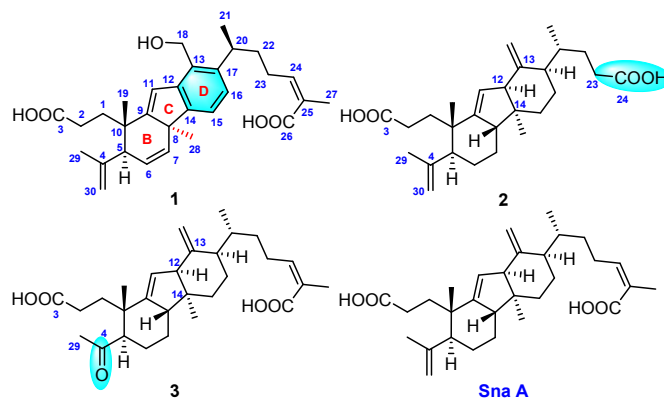


Figure 1. Chemical structures of compounds **1–3**, and sna A.

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<sup>†</sup> Electronic Supplementary Information (ESI) available: NMR data and 2D NMR correlations of **1–3**; General experimental procedures; Methods, relevant data and results for qccNMR and QIDA of **1**; The methods and results for bioactivity screening; NMR, MS, IR, ECD and UV spectra of **1–3**. See DOI: 10.1039/x0xx00000x

<sup>‡</sup> These authors contributed equally to the work.



Allowing for the imperfect results of the qccNMR method, as well as the unusual C-20 configuration in **1e**, the QIDA method was chosen to validate the proposed structure. To provide more accurate conformers for QIDA, all B3LYP-D3(BJ)/6-31G(d) geometries were reoptimized at M06-2X-D3/def2-SVP level, and energy of optimized conformers were evaluated at M06-2X-D3/def2-TZVP level. Solvation free energies were calculated at M05-2X/6-31G\* level with SMD solvation model<sup>19</sup>. To determine the feasibility of QIDA in current research, ensemble averaged interproton distances between 9 selected proton-pairs were calculated for **1a**, **1c**, and **1f**, respectively, and compared to those of **1e**, fortunately, the differences turned out to be distinguishable enough (Figure S21). Subsequently, NOE intensities between selected proton-pairs of **1** were extracted from 1D NOESY spectra (Figures S23–S25) and converted into interproton distances (Table S60) according to the peak amplitude normalization for improved cross-relaxation (PANIC) method<sup>11b, 20</sup>, which were taken into comparison with their theoretically predicted counterparts. As a result, the calculated interproton distances of **1e** were found to match the experimental ones best (Table 2 and Figure S22), which further proved its correctness. Noteworthy, the QIDA of H-20/H<sub>2</sub>-18, H-16/H<sub>3</sub>-21, H-5/H<sub>3</sub>-19, H-5/H-1b distances strongly supported the *S\** configurations of C-5 and C-20 (Figure 4), as well as clarified the confusing H-5/H<sub>3</sub>-19 NOESY correlation.

Table 2. The QIDA results of **1a**, **1c**, **1e**, and **1f**.

Proton-pairs	Exptl. distances (Å)	Calcd. distances (Å)			
		<b>1a</b>	<b>1c</b>	<b>1e</b>	<b>1f</b>
H-6/H-7	2.43	2.44	2.42	2.43	2.42
H-5/H-6	2.45	2.67	2.47	2.63	2.49
H-5/H <sub>3</sub> -19	3.39	3.57	2.47	3.48	2.49
H-5/H-1b	2.44	2.35	3.45	2.45	3.48
H-5/30b	2.50	2.78	2.42	2.63	2.53
H-7/H <sub>3</sub> -28	3.22	3.23	3.15	3.16	3.19
H-20/H <sub>2</sub> -18	2.32	3.59	4.21	2.34	2.34
H-16/H <sub>3</sub> -21	2.90	3.80	3.87	2.85	2.87
H-7/H-15	2.81	2.96	2.94	2.92	2.89
MAD		0.35	0.57	0.07	0.24

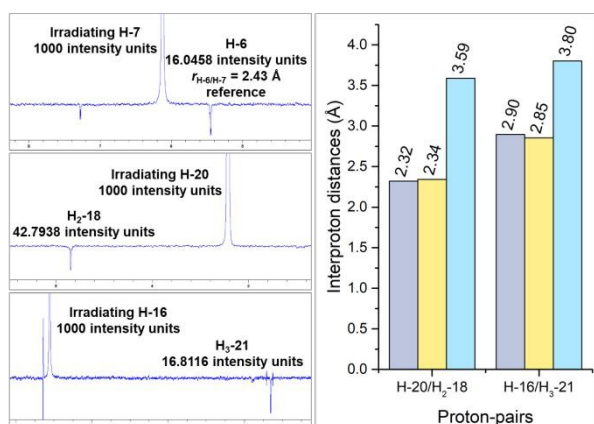


Figure 4. Left: 1D NOESY spectra of **1** when irradiating H-7, H-20, and H-16, respectively; Right: a comparison between the experimental H-20/H<sub>2</sub>-18, and H-16/H<sub>3</sub>-21 interproton distances (purple) and their calculated counterparts in **1e** (yellow) and **1a** (cyan).

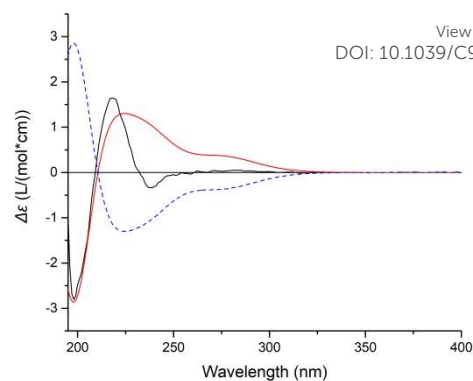


Figure 5. Experimental ECD spectrum of **1** (black); Calculated ECD spectra of (5S, 8S, 10S, 20S)-**1e** (shift = 8 nm, red) and (5R, 8R, 10R, 20R)-**1e** (shift = 8 nm, blue dash).

Finally, TDDFT ECD calculation<sup>21</sup> on one of the two possible enantiomers of **1e** at CAM-B3LYP/TZVP level in methanol with IEFPCM solvent model succeeded in establishing the absolute configuration of **1** as 5S, 8S, 10S, 20S, and 24Z (Figure 5). And this conclusion can be further reinforced by considering that C-5 and C-10 configurations are rather conserved in lanostane triterpenoids.

Neokadococitane B (**2**) was obtained as colorless acicular crystals with the molecular formula C<sub>27</sub>H<sub>40</sub>O<sub>4</sub> determined by HRESIMS ([M+Na]<sup>+</sup> *m/z* 451.2788, calcd 451.2819). Detailed analysis of the NMR data of **2** uncovered it to be closely analogous to sna A regarding their scaffolds. However, the H<sub>3</sub>-21/H-20/H-22/H-23 spin system observed in <sup>1</sup>H-<sup>1</sup>H COSY spectrum of **2**, together with the HMBC correlations from H<sub>2</sub>-22 and H-23 to C-24 (δ<sub>C</sub> 177.2) (Figure S2) indicated C-25–C-27 on the side chain were degraded. The excessively overlapped ROESY signals severely hampered the determination of the relative configuration of **2**. Fortunately, crystals of **2** were obtained and subjected to X-ray diffraction analysis through Cu Kα radiation (CCDC:1887346) (Flack parameter = 0.19(5)) (Figure 6), together with biosynthetic considerations, which verified the proposed planar structure of **2** and determined its absolute configuration to be 5S, 8S, 10S, 13R, 14S, 17R, and 20R.

Neokadococitane C (**3**) has the molecular formula of C<sub>29</sub>H<sub>42</sub>O<sub>5</sub> as supported by HRESIMS ([M-H]<sup>-</sup> *m/z* 469.2949, calcd 469.2959). Comprehensive analysis of the 1D and 2D NMR data revealed it to be also the derivative of sna A. As compared with **2**, **3** has an intact side chain but underwent C-30 degradation, which could be deduced from the HMBC correlations from H-5

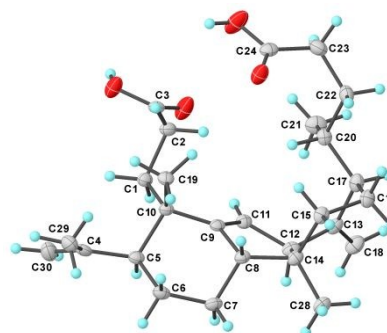


Figure 6. X-ray crystallographic structure of **2**.



**Table 3.** <sup>1</sup>H and <sup>13</sup>C NMR spectroscopic data for compounds **2** and **3** in pyridine-*d*<sub>5</sub> (δ in ppm, *J* in Hz)View Article Online  
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NO.	<b>2</b>		<b>3</b>		NO.	<b>2</b>		<b>3</b>	
	δ <sub>H</sub> <sup>a</sup>	δ <sub>C</sub> <sup>b</sup>	δ <sub>H</sub> <sup>a</sup>	δ <sub>C</sub> <sup>b</sup>		δ <sub>H</sub> <sup>a</sup>	δ <sub>C</sub> <sup>b</sup>	δ <sub>H</sub> <sup>a</sup>	δ <sub>C</sub> <sup>b</sup>
1a	2.25 (overlap)		2.32 (dd, 10.5, 3.9)		16a	1.89 (overlap)		1.79 (overlap)	
1b	2.11 (m)	34.6 t	2.19 (overlap)	34.8 t	16b	1.62 (overlap)	25.3 t	1.60 (overlap)	25.1 t
2a	2.79 (m)		2.81 (overlap)		17	1.96 (dd, 10.6, 4.3)	50.2 d	1.97 (m)	49.8 d
2b	2.66 (overlap)	30.7 t	2.72 (m)	30.5 t	18a	4.94 (d, 2.9)		4.92 (d, 2.9)	
3		177.6 s		176.9 s	18b	4.83 (d, 2.9)	112.9 t	4.81 (d, 2.8)	112.9 t
4		147.5 s		211.3 s	19	1.07 (3H, s)	18.0 q	1.32 (3H, s)	18.3 q
5	1.88 (overlap)	57.6 d	2.38 (dd, 12.7, 3.5)	60.9 d	20	2.21 (overlap)	32.0 d	2.02 (overlap)	32.6 d
6a	1.71 (overlap)		1.79 (overlap)		21	1.10 (3H, d, 6.6)	18.4 q	1.09 (3H, d, 6.5)	18.5 q
6b	1.50 (m)	29.1 t	1.68 (dd, 7.7, 3.1)	26.2 t	22a	2.32 (overlap)		1.81 (overlap)	
7a	1.61 (overlap)		1.58 (overlap)		22b	1.37 (br s)	30.2 t	1.19 (br s)	34.5 t
7b	1.03 (overlap)	29.3 t	1.03 (dd, 12.8, 3.8)	28.7 t	23a	2.67 (overlap)		2.87 (2H, m)	
8	2.02 (m)	54.9 d	2.03 (overlap)	54.3 d	23b	2.24 (overlap)	32.8 t		27.7 t
9		153.3 s		151.4 s	24		176.8 s	6.05 (t, 7.6)	142.4 d
10		42.0 s		41.3 s	25				129.6 s
11	5.30 (br s)	123.0 d	5.36 (s)	123.5 d	26				171.2 s
12	3.04 (s)	59.2 d	3.01 (s)	59.3 d	27			2.18 (3H, s)	22.1 q
13		150.9 s		150.7 s	28	1.01 (3H, s)	21.0 q	0.99 (3H, s)	21.2 q
14		44.4 s		44.2 s	29	1.73 (3H, s)	24.2 q	2.16 (3H, s)	32.6 q
15a	1.88 (overlap)		1.73 (overlap)		30a	4.92 (br s)			
15b	1.10 (overlap)	32.9 t	1.07 (overlap)	33.1 t	30b	4.78 (br s)	114.4 t		

<sup>a</sup>Recorded at 500 MHz, <sup>b</sup>Recorded at 125 MHz.

and H<sub>3</sub>-29 to C-4 (δ<sub>C</sub> 211.3) (Figure S3). Most of the stereochemistry of **3** can be resolved through ROESY spectrum analysis (Figure S3) and NMR data comparison with those of **2** and sna A, while that of C-5 can be determined according to the absence of both H-5/H<sub>3</sub>-19 and H-5/H-8 ROESY correlations, as well as through biosynthetic considerations.

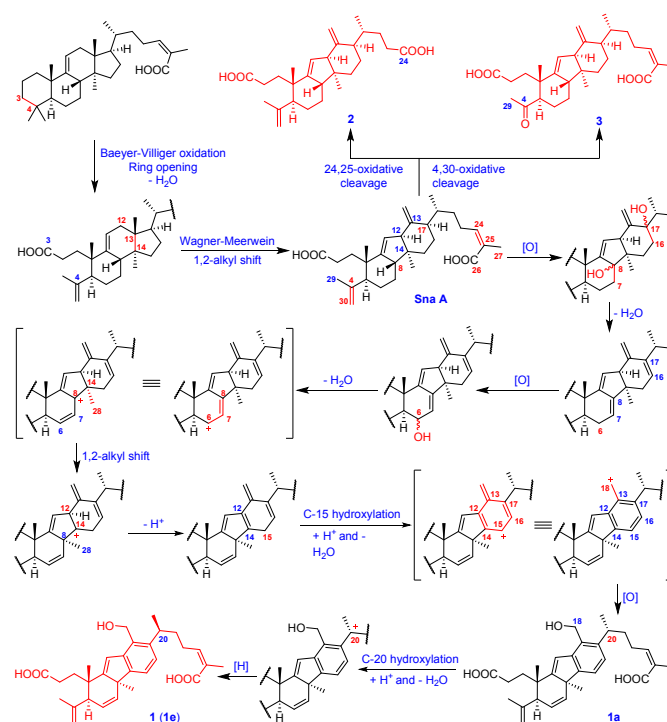
From the perspective of biosynthesis, **1–3** could be derived from a common precursor, sna A, which is proposed to generate mainly through Baeyer-Villiger oxidation, Wagner-Meerwein rearrangement, etc., starting from the intact lanostane. The oxidative cleavage of C-24/C-25 and C-4/C-30 double bonds upon sna A is the key process to yield **2** and **3**, respectively. As for **1**, multiple allylic oxidations and dehydrations lead to the transfer of Me-28 and aromatization of ring D (Scheme 1). Furthermore, the unusual configuration of C-20 in **1** may be explained by the tendency for benzylic oxidation (C-20), as well as that the fact that the lowest energy conformer of **1** (**1e-i**) has much lower energy (about 3 kcal/mol) than that of its C-20 epimer (**1a-i**) (Tables S15 and S38).

Compound **1–3** were screened for activities against platelet aggregation induced by colloid. The suppression ratio of **1** was 21.0 ± 9.4% (*p* < 0.001) under the concentration of 100 μM. The anticoagulant activity and cytotoxic activity of **1–3** were also evaluated but no remarkable activities were observed, and deficiency in sample quantity hampered further evaluations.

## Conclusions

In conclusion, three lanostane triterpenoids, neokadcocitanes A–C (**1–3**), were obtained from the roots of *K. coccinea*. The discovery of these novel compounds not only enriches the

skeletal diversity of the lanostane triterpenoids, but also manifested the strong ability of roots of *K. coccinea* in producing unique secondary metabolites. Moreover, together with our previous research<sup>12b</sup>, the QIDA method was further demonstrated to be a robust tool in structure elucidation of both rigid and flexible natural products, especially when it is used in combination with the qccNMR method.

**Scheme 1.** Plausible biogenetic pathways for **1–3**.

## Experimental Section

### Plant Materials

The roots of *K. coccinea* were collected from Jingzhou Miao and Dong Autonomous County in Hunan Province, People's Republic of China, in June 2016 and identified by Prof. Heng Li at Kunming Institute of Botany. A voucher specimen (KIB 2016062101) has been deposited in State Key Laboratory of Phytochemistry and Plant Resources in West China, Kunming Institute of Botany, Chinese Academy of Sciences.

### Physicochemical data of 1–3

Neokadococcitane A (**1**): Amorphous white powder;  $[\alpha]_D^{23}$   $-9.7$  (c 0.138, MeOH); UV (MeOH)  $\lambda_{\max}$  (log  $\epsilon$ ) 272 (3.42) nm, 223 (3.95) nm; IR (KBr)  $\nu_{\max}$  3437.93, 2927.84, 1701.80, 1637.10, 1383.62, 1262.36, 958.72, 582.62  $\text{cm}^{-1}$ ; CD (MeOH): 198 nm ( $\Delta\epsilon = -2.81$ ), 218 nm ( $\Delta\epsilon = +1.65$ ), 239 nm ( $\Delta\epsilon = -0.34$ );  $^1\text{H}$  and  $^{13}\text{C}$  NMR data, see Table 1 and Table S3; negative ESIMS  $m/z$  477  $[\text{M}-\text{H}]^-$ ; HRESIMS  $m/z$  477.2655  $[\text{M}-\text{H}]^-$  (calcd 477.2646).

Neokadococcitane B (**2**): Colorless acicular crystals; Melting point: 208 °C.  $[\alpha]_D^{26}$   $-139.0$  (c 0.118, MeOH); UV (MeOH)  $\lambda_{\max}$  (log  $\epsilon$ ) 205 (4.18) nm; IR (KBr)  $\nu_{\max}$  3432.55, 2927.40, 1701.93, 1637.13, 1413.86, 1260.53, 893.39, 590.39  $\text{cm}^{-1}$ ; CD (MeOH): 211 nm ( $\Delta\epsilon = -3.25$ );  $^1\text{H}$  and  $^{13}\text{C}$  NMR data, see Table 3; positive ESIMS  $m/z$  451  $[\text{M}+\text{Na}]^+$ ; HRESIMS  $m/z$  451.2788  $[\text{M}+\text{Na}]^+$  (calcd 451.2819).

Crystal data for neokadococcitane B (**2**):  $\text{C}_{27}\text{H}_{40}\text{O}_4$ ,  $M = 428.59$ ,  $a = 8.0610(2)$  Å,  $b = 10.8588(2)$  Å,  $c = 27.7356(6)$  Å,  $\alpha = 90^\circ$ ,  $\beta = 90^\circ$ ,  $\gamma = 90^\circ$ ,  $V = 2427.78(9)$  Å<sup>3</sup>,  $T = 100(2)$  K, space group  $P212121$ ,  $Z = 4$ ,  $\mu(\text{CuK}\alpha) = 0.605$   $\text{mm}^{-1}$ , 14256 reflections measured, 4413 independent reflections ( $R_{\text{int}} = 0.0418$ ). The final  $R_1$  values were 0.0358 ( $I > 2\sigma(I)$ ). The final  $wR(F^2)$  values were 0.0981 ( $I > 2\sigma(I)$ ). The final  $R_1$  values were 0.0360 (all data). The final  $wR(F^2)$  values were 0.0984 (all data). The goodness of fit on  $F^2$  was 1.085. Flack parameter = 0.19(5).

Neokadococcitane C (**3**): Amorphous white powder,  $[\alpha]_D^{26}$   $-71.4$  (c 0.154, MeOH), UV (MeOH)  $\lambda_{\max}$  (log  $\epsilon$ ) 209 (4.05) nm, 293 (2.91) nm. IR (KBr)  $\nu_{\max}$  3429.80, 2928.73, 1703.36, 1640.30, 1456.47, 1381.96, 1206.85, 1895.00, 575.12  $\text{cm}^{-1}$ .  $^1\text{H}$  and  $^{13}\text{C}$  NMR data, see Table 3; positive ESIMS  $m/z$  493  $[\text{M}+\text{Na}]^+$ ; HRESIMS  $m/z$  469.2949  $[\text{M}-\text{H}]^-$  (calcd 469.2959). CD (MeOH): 208 nm ( $\Delta\epsilon = -0.96$ ), 293 nm ( $\Delta\epsilon = -0.07$ )

### Computational method

Conformational analysis of **1a–1e** was initially performed in Spartan'16 (Wavenfunction, Irvine, CA, USA, 2016) using the Monte Carlo algorithm and Merck molecular force field (MMFF). To avoid losing relevant conformations during the conformational search stage, the "set torsions" function was used to give all rotatable bonds a 6-fold sampling. Maximum 20000 conformers were examined for each diastereoisomer, and those obtained conformers within 20 kcal/mol were kept (1000 ones for each diastereoisomer).

These conformers were subjected to semiempirical geometry optimization at PM6/DH+ level using MOPAC program (Stewart Computational Chemistry, Colorado Springs) in order to obtain conformers better correlating with DFT calculations. Subsequently, PM6 geometries were clustered according to a

criterion of 0.25 kcal (relative energy) and 0.25 (distance geometry). Then, clustered PM6 geometries were subjected to a DFT energy calculation at B3LYP/6-311G(d,p) level of theory, and those conformers within an energy window of 5 kcal/mol were kept. This step was completed with the aid of the Molclus program<sup>22</sup> (and its "isostat" module), which can call third-party programs (MOPAC, Gaussian, Openbabel, ORCA, XTb, etc) to run energy calculations or geometry optimizations on a large ensemble of conformers, as well as to undertake clustering analysis on them.

The above screened conformers were subjected to DFT geometry optimization at B3LYP/6-31G(d) level of theory with Grimme's DFT-D3 dispersion correction using Becke-Johnson damping function (EmpiricalDispersion=GD3BJ)<sup>23</sup> using Gaussian 09 program<sup>24</sup>. Frequency analysis of all optimized conformations were undertaken at the same level of theory to ensure they were true local minima on the potential energy surface. Then, energies of all optimized conformations were evaluated at B3LYP-D3(BJ)/6-311G(d,p) level of theory. Gibbs free energies of each conformers were calculated by adding "Thermal correction to Gibbs Free Energy" obtained by frequency analysis to electronic energies obtained at B3LYP-D3(BJ)/6-311G(d,p). Room-temperature (298.15 K) equilibrium populations were calculated according to Boltzmann distribution law:

$$p_i = \frac{n_i}{\sum_j n_j} = \frac{e^{-\Delta G_i/RT}}{\sum_j e^{-\Delta G_j/RT}} = \frac{Q_i(\text{Relative})}{Q(\text{Relative})}$$

Where  $P_i$  is the population of the  $i^{\text{th}}$  conformer;  $n_i$  the number of molecules in  $i^{\text{th}}$  conformer;  $\Delta G$  is the relative Gibbs free energy (kcal/mol);  $T$  is the temperature, usually the room temperature (298.15 K);  $R$  is the ideal gas constant (0.0019858995);  $Q$  is the partition function. Those conformers accounting for over 98% population were subjected to subsequent calculations.

NMR shielding constants were calculated with the GIAO method at mPW1PW91-SCRF/6-31+G(d,p) level with IEFPCM solvent model in chloroform solvent. The shielding constants obtained were converted into chemical shifts by referencing to TMS at 0 ppm ( $\delta_{\text{cal}} = \sigma_{\text{TMS}} - \sigma_{\text{cal}}$ ), where the  $\sigma_{\text{TMS}}$  was the shielding constant of TMS calculated at the same level. For each possible candidate, the parameters  $a$  and  $b$  of the linear regression  $\delta_{\text{cal}} = a\delta_{\text{exp}} + b$ ; the correlation coefficient,  $R^2$ ; the mean absolute error (MAE) defined as  $\sum_n |\delta_{\text{cal}} - \delta_{\text{exp}}|/n$ ; the corrected mean absolute error, CMAE, defined as  $\sum_n |\delta_{\text{corr}} - \delta_{\text{exp}}|/n$ , where  $\delta_{\text{corr}} = (\delta_{\text{cal}} - b)/a$ , were calculated<sup>10, 18</sup>. The DP4+ probabilities of each possible candidate were calculated with the EXCEL spreadsheet provided by Sarotti, *et al*<sup>17</sup>.

To provide more accurate geometries for the QIDA, all B3LYP-D3(BJ)/6-31G(d) optimized conformers were reoptimized at M06-2X-D3/def2-SVP level, and energy of optimized conformers were evaluated at M06-2X-D3/def2-TZVP level ( $E_{\text{def2TZVP}}$ ). Frequency analysis of all optimized conformations were undertaken at the same level of theory to ensure they were true local minima on the potential energy surface and to obtain the "Thermal correction to Gibbs Free Energy" ( $G_{\text{correction}}$ ). Solvation free energies of optimized conformers

were calculated by subtracting energy calculated at M05-2X/6-31G\* level in gas ( $E_{\text{gas}}$ ) from energy calculated at M05-2X/6-31G\* level with SMD solvation model ( $E_{\text{solvent}}$ ) (chloroform for QIDA, and methanol for TDDFT ECD calculation described below<sup>21</sup>). Gibbs free energies of each conformers were calculated according to the following equation:

$$G_{\text{solvent}} = E_{\text{def2TZVP}} + G_{\text{correction}} + (E_{\text{solvent}} - E_{\text{gas}}) + 1.89 \text{ kcal/mol}$$

Room-temperature (298.15 K) equilibrium populations were calculated according to Boltzmann distribution law. Those conformers accounting for over 98% population were subjected to QIDA and TDDFT ECD calculation described below.

TDDFT ECD calculations were run at CAM-B3LYP/TZVP level of theory in MeOH with IEFPCM solvent model. For each conformer, 30 excited states were calculated. The calculated ECD curves were generated using Multiwfn 3.6 software<sup>25</sup>.

### Quantitative interproton distance analysis<sup>11, 26</sup>

#### (1) The acquisition of calculated interproton distances

$r_{\text{cal}}$  was the calculated interproton distances (Å) extracted from DFT optimized conformers obtained with method as stated above; For molecules with multiple conformers,  $r_{\text{cal}}$  were obtained by weighting interproton distances from individual conformers according to their Boltzmann populations:

$$r_{H_a-H_b, \text{ calcd.}} = \left( \sum p_i \times r_{H_a-H_b, i}^{-6} \right)^{-1/6}$$

where  $r_{H_a-H_b, \text{ calcd}}$  is the interproton distance of interest (between  $H_a$  and  $H_b$ ) in conformer  $i$ , and  $p_i$  is the population of conformer  $i$ .

To obtain Boltzmann averaged distance between a single proton ( $H_x$ ) and three chemically equivalent methyl protons ( $H_{\text{abc}}$ ), the following equation is used:

$$r_{H_x-H_{\text{abc}}, \text{ calc}} = \left\{ \frac{\sum_i [(r_{H_x-H_{a,i}})^{-6} \times p_i + (r_{H_x-H_{b,i}})^{-6} \times p_i + (r_{H_x-H_{c,i}})^{-6} \times p_i]}{3} \right\}^{-1/6}$$

To obtain Boltzmann averaged distance between a single proton (H) and two overlapped methylene protons ( $H_{\text{ab}}$ ), the following equation is used:

$$r_{H_x-H_{\text{ab}}, \text{ calcd.}} = \left\{ \frac{\sum_i [(r_{H_x-H_{a,i}})^{-6} \times p_i + (r_{H_x-H_{b,i}})^{-6} \times p_i]}{2} \right\}^{-1/6}$$

#### (2) The acquisition of experimental interproton distances

The 1D selective NOESY spectra was collected using the "selnogpzs" pulse program; Before the measurement, the mixing time for the 1D experiments were optimized by selective irradiation of  $H_3$ -19 (Figure S23). During a gradient of mixing time (100–1000 ms, step = 100 ms), the  $H_3$ -19/ $H$ -11 intensities were recorded. Then the PANIC NOE build-up curve (Figure S24) was plotted. According to the curve, as well as in consideration of the signal/noise ratio under different mixing time, a mixing time of 700 ms was adopted.

$r_{\text{exptl.}}$  was experimental interproton distances (Å) determined by using equation below and the above obtained intensities from the 1D NOESY spectra:

$$r_{H_a-H_b, \text{ exp}} = r_{\text{ref}} \times \left( \frac{\eta_{H_a-H_b, \text{ exp}}}{\eta_{\text{ref}}} \right)^{-1/6}$$

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Where  $r$  is interproton distance, and  $\eta$  is NOESY signal intensity derived from the 1D NOESY spectra. Peak amplitude normalization for improved cross-relaxation (PANIC) method was employed by setting the irradiated peak in each 1D NOESY spectrum to 1000 intensity units as shown in Figure S25. The distances between methylene protons H-6 and H-7 (2.43 Å), which were insensitive to molecular conformation, was chosen to be the reference distance ( $r_{\text{ref}}$ ).

To obtain the averaged experimental distance between a single proton ( $H_x$ ) and three chemically equivalent methyl protons ( $H_{\text{abc}}$ ):

(a) When irradiating  $H_x$ , set the irradiated peak to 1000, and then average the observed  $H_x$ - $H_{\text{abc}}$  intensity  $[(\eta_{H_x-H_{\text{abc}}, \text{ exp}})/3]$ , and then use this intensity to calculate the averaged  $r_{H_x-H_{\text{abc}}, \text{ exp}}$ ;

(b) When irradiating  $H_{\text{abc}}$ , set the irradiated peak to 1000, and then use observed  $H_x$ - $H_{\text{abc}}$  intensity ( $\eta_{H_x-H_{\text{abc}}, \text{ exp}}$ ) directly to calculate the averaged  $r_{H_x-H_{\text{abc}}, \text{ exp}}$ .

To obtain the averaged experimental distance between a single proton ( $H_x$ ) and two overlapped methylene protons ( $H_{\text{ab}}$ ):

(a) When irradiating  $H_x$ , set the irradiated peak to 1000, and then average the observed  $H_x$ - $H_{\text{ab}}$  intensity  $[(\eta_{H_x-H_{\text{ab}}, \text{ exp}})/2]$ , and then use this intensity to calculate the averaged  $r_{H_x-H_{\text{ab}}, \text{ exp}}$ ;

(b) When irradiating  $H_{\text{ab}}$ , set the irradiated peak to 1000, and then use observed  $H_x$ - $H_{\text{ab}}$  intensity ( $\eta_{H_x-H_{\text{ab}}, \text{ exp}}$ ) directly to calculate the averaged  $r_{H_x-H_{\text{ab}}, \text{ exp}}$ .

#### (3) The evaluation of fitness between experimental and calculated interproton distances

The mean absolute deviation (MAD) was defined as:

$$MAD = \frac{\sum_n |r_{\text{cal}} - r_{\text{exp}}|}{n}$$

#### Conflicts of interest

There are no conflicts to declare.

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