Supporting Information

Novel Anthraquinone Derivatives as Inhibitors of Protein Tyrosine Phosphatases and Indoleamine 2,3-Dioxygenase 1 from the Deep-sea Derived Fungus *Alternaria tenuissima* DFFSCS013

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EXPERIMENTAL SECTION

Phosphatase Enzyme Inhibition Assays. Recombinant human phosphatase PTP1B, PTP1B, SHP1, SHP2, MEG2 and TCPTP were expressed in *Escherichia coli* and purified. The enzyme inhibition assays were measured using *p*-nitrophenyl phosphate (pNPP) as a substrate in a 96-well plate with a final volume of 100 μ L. Human recombinant PTP1B, SHP1, SHP2, MEG2 or TCPTP (0.05 μ g) in 50 μ L reaction buffer (pH 6.5) containing 50 mM HEPES, 100 mM NaCl, 1 mM EDTA, and 1 mM dithiothreitol (DTT) and test compounds were added to each well of a 96-well plate. Na₃VO₄ was used as the positive control and DMSO as the negative control to evaluate the high-throughput screening (HTS) system. After preincubation for 15 min at room temperature, 50 μ L of reaction buffer containing 50 mM pNPP was added and incubated at 37 °C for 60 min. The phosphatase activity was determined by measuring the absorbance at 405 nm for the amount of produced *p*-nitrophenol. IC₅₀ values were determined by analyzing the data using Gen5 software (Synergy2 Multi-Mode Microplate Reader, BioTek Instruments, Inc.). Each compound was assayed in triplicate.

IDO Enzyme Inhibition Assays. Recombinant human IDO was expressed in *E. coli* and purified. Briefly, the reaction mixture (200 μ L) contained potassium phosphate buffer (50 mM, pH 6.5), ascorbic acid (10 mM), methylene blue (5 μ M), purified recombinant IDO1 (43 μ M), L-Trp (100 μ M), and DMSO (10 μ L). The inhibitors were serially diluted 3-fold from 50 to 0.02 mM in pure DMSO. The reaction was conducted at 37 °C for 6 min and stopped by addition of 30% (w/v) trichloroacetic acid (40 μ L). To convert N-formylkynurenine to kynurenine, the tubes were incubated at 37 °C for 30 min, followed by centrifugation at 20,000 g for 20 min. Finally, 150 μ L of supernatant is added to 150 μ L of *p*-dimethylaminobenzaldehyde (pDMAB) (2%, v/v) in acetic acid to generate a Schiff base with kynurenine that was detected at a wavelength of 480 nm. We used NLG919 as the positive control and DMSO as the negative control to evaluate the high-throughput screening (HTS) system. IC₅₀ values were determined by analyzing the data using Gen5 software (Synergy2 Multi-Mode Microplate Reader, BioTek Instruments, Inc.). Each compound was assayed in triplicate.

Calcium imaging assay. The calcium imaging assay was performed by an automated, cell-based fluorescence-imaging system (Arrayscan) by a previously reported method with slight modification. The human embryonic kidney 293 (HEK293) cells were seeded in medium containing 10% FBS and incubated at 37 °C with 5% CO₂ to a suitable quantity, and then cells were plated in poly-D-lysine-coated 96-well plates at a density of approximately 20000 cells/well for 24 h. Later, the cells were stained with 5 μ M Fluo-4 AM for 60 min and subsequently washed three times with HBSS buffer. And then the cells were treated with up-to 10 μ M of the tested samples in a 96-well plate containing 50 μ l HBSS/well. For the bioactive compound **1**, its bioactivity was further tested at concentrations of 10, 5, 2.5, 1.25, and 0.625 μ M, respectively. The purities of the tested compounds were >95%. The experiment was repeated three times. The false positive activity caused by the color of the tested samples was excluded. Calcium images of cells in HBSS buffer were acquired and analyzed using an Array Scan VTI HCS Reader (Cellomics, Thermo Scientific, Pittsburgh, PA, USA).

Figure S1. ¹H NMR spectrum of compound 1





Figure S2. ¹³C NMR spectrum of compound 1



Figure S3. DEPT NMR spectrum of compound 1



Figure S4. HSQC spectrum of compound 1







Figure S6. ¹H-¹H COSY spectrum of compound 1



Figure S7. NOESY spectrum of compound 1



Figure S8. HRESIMS spectrum of compound 1

		Mass	Spectrum	n SmartFor	mula Re	eport		
Analysis Info Analysis Name	D:\Data\MS\data	a\201709\nandongvan	PDY-DP-25 pos	23 01 3564 d	Ad	equisition Date	9/14/2017 4	:02:13 PM
Method Sample Name Comment	LC_Direct Infusion_pos_70-500mz.m pandongyan_PDY-DP-25_pos					perator S strument m	CSIO naXis	255552.00029
Acquisition Parame Source Type Focus Scan Begin Scan End	ter ESI Active 70 m/z 1500 m/z	lon P Set C Set E Set C Set C	olarity apillary nd Plate Offset harging Voltage orona	Positive 4500 ∨ -500 ∨ 0 ∨ 0 nA	2	Set No Set Di Set Di Set Di Set Af	ebulizer ry Heater ry Gas vert Valve PCI Heater	0.4 Bar 180 °C 4.0 l/min Waste 0 °C
Intens.								+MS, 0.3min #18
5000								
4000							1+	
3000							511.1575	
2000 1000 481.2611	484.4717	489.1754	496.5059	500.0755 ⁵	505.332	23 507.1332509.1416	512.5035	517.1661 519.3156
480	485	490	495	500	505	51	D	515 m/z
Meas. m/z 489.175356 511.157498 999.324805	# Ion Formula 1 C25H29O10 1 C25H28NaO10 1 C50H56NaO20	Score m/z 100.00 489.175524 100.00 511.157468 100.00 999.325715	err [ppm] err [-0.3 -0.1 -0.9	[mDa] mSigma -0.2 83.0 -0.0 17.5 -0.9 32.9	rdb e Conf 11.5 even 11.5 even 22.5 even	f N-Rule ok ok ok		

pandongyan_PDY-DP-25_pos_23_01_3564.d					
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Figure S11. Crystal data and structure refinement for compound 1

Datablock: pdy-dp-25_collect

Bond precision:	C-C = 0.0034 A	L	Wavelength	n=1.54184
Cell:	a=11.9189(4)	b=6.5987(2	2)	c=26.7335(10)
Temperature:	alpha=90 100 K	beta=100.1	124 (4)	gamma=90
	Calculated		Reported	
Volume	2069.83(12)		2069.83(1	12)
Space group	I 2		I 1 2 1	
Hall group	I 2y		I 2y	
Moiety formula	C25 H28 O10		C25 H28 (010
Sum formula	C25 H28 O10		C25 H28 C	010
Mr	488.47		488.47	
Dx,g cm-3	1.567		1.568	
Z	4		4	
Mu (mm-1)	1.025		1.025	
F000	1032.0		1032.0	
F000'	1035.67			
h,k,lmax	14,8,33		14,8,32	
Nref	4189[2285]		4013	
Tmin,Tmax	0.929,0.980		0.911,1.0	000
Tmin'	0.857			
Correction metho AbsCorr = MULTI	od= # Reported T -SCAN	Limits: T	min=0.911	Tmax=1.000
Data completene	ss= 1.76/0.96	Theta(m	nax)= 73.80	57
R(reflections) =	0.0330(3819)	wR2(ref	lections):	= 0.0915(4013)
S = 1.095	Npar	= 326		

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_cell_length_b	6. 59866 (19)
_cell_length_c	26.7335(10)
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_cell_angle_beta	100. 124 (3)
_cell_angle_gamma	90. 0
_cell_volume	2069.83(12)
_cell_measurement_temperature	100.00(10)
_cell_measurement_reflns_used	7548
_cell_measurement_theta_min	3. 8600
_cell_measurement_theta_max	73. 4340
_cell_oxdiff_length_a	11.9174(3)
_cell_oxdiff_length_b	6. 5979(2)
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_cell_oxdiff_angle_beta	100. 1294 (19)
_cell_oxdiff_angle_gamma	89.994(2)
_cell_oxdiff_volume	2069. 83 (9)
_cell_oxdiff_measurement_refln	s_used 7656
_exptl_absorpt_correction_T_mix	n 0. 91061
_exptl_absorpt_correction_T_max	x 1.00000
_exptl_absorpt_correction_type	multi-scan
_exptl_absorpt_process_details	

CrysAlisPro 1. 171. 39. 33c (Rigaku Oxford Diffraction, 2017) Empirical absorption correction using spherical harmonics, implemented in SCALE3 ABSPACK scaling algorithm.; oxdiff exptl absorpt empirical full min 0.532 oxdiff exptl absorpt empirical full max 1.454 oxdiff exptl absorpt empirical details; Empirical correction (ABSPACK) includes: - Absorption correction using spherical harmonics - Frame scaling: diffrn ambient temperature 100.00(10)diffrn ambient environment $N^{\sim}2^{\sim}$ diffrn source 'Rotating-anode X-ray tube' diffrn source type 'Rigaku (Cu) X-ray Source' diffrn radiation probe x-ray diffrn radiation type 'Cu K\a' diffrn radiation wavelength 1.54184 diffrn radiation monochromator mirror diffrn measurement device 'four-circle diffractometer' diffrn measurement device type 'XtaLAB AFC12 (RINC): Kappa single' diffrn detector 'CCD plate' diffrn reflns number 9974 diffrn reflns av R equivalents 0.0267 diffrn reflns av sigmaI/netI 0.0287 diffrn reflns limit h min -14 diffrn reflns limit h max 9 diffrn reflns limit k min -8 diffrn reflns limit k max 8 diffrn reflns limit 1 min -32 diffrn reflns limit 1 max 31

diffrn reflns theta min 3.8457 diffrn reflns theta max 73.8670 diffrn measured_fraction_theta_max 0.9816 diffrn reflns theta full 66.9682 diffrn measured fraction theta full 0.9970 diffrn orient matrix type 'CrysAlisPro convention (1999, Acta A55, 543-557)' diffrn orient matrix UB 11 0.0112845000 _diffrn_orient_matrix_UB_12 0.2312972000 diffrn orient matrix UB 13 0.0070148000 diffrn orient matrix UB 21 0.0070015000 diffrn orient matrix UB 22 0.0238222000 _diffrn_orient_matrix_UB_23 -0.0566787000diffrn orient matrix UB 31 -0.1306357000_diffrn_orient_matrix_UB_32 0.0212824000 diffrn orient matrix UB 33 -0.0127748000diffrn measurement details;

List of Runs (angles in degrees, time in seconds):

#	Туре	Start	End	Width	t~exp~	$\setminus w$	/d	∖k	\f	Frames
	 ,									
1	\w	-17.00	22.00	0.50	2.80		0.00	-57.00	-30.00	78
2	$\setminus w$	-58.00	-31.00	0.50	2.80		0.00	-19.00	30.00	54
3	$\setminus w$	-23.00	2.00	0.50	2.80		0.00	-19.00	30.00	50
4	$\setminus w$	-89.00	-24.00	0.50	2.80		0.00	-57.00	-30.00	130
5	$\setminus w$	-30.00	31.00	0.50	2.80		0.00	-82.00	30.00	122
6	$\setminus w$	-25.00	5.00	0.50	2.80		0.00	-82.00-	-150.00	60
7	$\setminus w$	6.00	31.00	0.50	25.36		94.60	-82.00	-30.00	50
8	$\setminus w$	136.00	183.00	0.50	25.36		94.60	0.00	-60.00	94
9	$\setminus w$	6.00	115.00	0.50	25.36		94.60	-61.00	90.00	218

10	$\setminus w$	5.00	100.00	0.50	25.36	 94.60	-30.00-150.00	190
11	$\setminus w$	9.00	106.00	0.50	25.36	 94.60	-30.00 120.00	194
12	$\setminus w$	64.00	123.00	0.50	25.36	 94.60	-82.00-180.00	118
13	$\setminus w$	8.00	116.00	0.50	25.36	 94.60	-61.00 -30.00	216
14	$\setminus w$	96.00	123.00	0.50	25.36	 94.60	30.00 -30.00	54
15	$\setminus w$	141.00	183.00	0.50	25.36	 94.60	30.00 -30.00	84
16	$\setminus w$	53.00	121.00	0.50	25.36	 94.60	-82.00 -30.00	136
17	$\setminus w$	7.00	125.00	0.50	25.36	 94.60	-82.00 90.00	236
18	$\setminus w$	5.00	108.00	0.50	25.36	 94.60	0.00 -60.00	206
19	$\setminus w$	39.00	64.00	0.50	25.36	 94.60	-61.00-180.00	50
20	$\setminus w$	67.00	118.00	0.50	25.36	 94.60	-61.00-180.00	102
21	$\setminus w$	91.00	118.00	0.50	25.36	 94.60	-82.00 -60.00	54
22	$\setminus w$	87.00	114.00	0.50	25.36	 94.60	-82.00 60.00	54
23	$\setminus w$	89.00	116.00	0.50	25.36	 94.60	-82.00-124.97	54;

_diffrn_measurement_method '\w scans' _diffrn_oxdiff_ac3_digest_frames; 01b2acda7ae51b05d43ce613c0d38c5c4f000266271; _diffrn_oxdiff_ac3_digest_hkl; 016084d2f544d8d9ee8649c850f30d2c7d04b9; _space_group_IT_number 12 _space_group_crystal_system monoclinic _space_group_name_H-M_alt 'I 1 2/m 1' _reflns_odcompleteness_completeness 99.70 _reflns_odcompleteness_theta 66.97 _reflns_odcompleteness_iscentric 1 _chemical_oxdiff_formula 'C H 0'

Figure S12. ¹H NMR spectrum of compound 2





Figure S13. ¹³C NMR spectrum of compound 2



2







Figure S15. HSQC spectrum of compound 2











fl (ppm)







fl (ppm)

Figure S19. HRESIMS spectrum of compound 2

				Mass S	Spectru	ım Sma	artFori	mula	a Report			
Analysis	Info	D:\Data\MS	\data\201700\pa	ndonavan PE	V.D.9.31	DOE 24 01	2562 d		Acquisitio	n Date	9/14/2017 3:58:44 PN	1
Method Sample N Commen	vame t	LC_Direct Infusion_pos_70-500mz.m ame pandongyan_PDY-DP-31_pos					Operator Instrumer	SCSIC nt maXis	25555	2.00029		
Acquisiti Source Ty Focus Scan Begi Scan End	ion Parameter ^{pe} n	ESI Active 70 m/z 1500 m/s	z	lon Pola Set Cap Set End Set Cha Set Core	rity illary Plate Offset rging Voltage ona	e	Positive 4500 V -500 V 0 V 0 nA			Set Nebuliz Set Dry Hea Set Dry Ga Set Divert \ Set APCI H	ter 0.4 ater 180 s 4.0 /alve Wa leater 0 °C	Bar °C I/min ste
Intens. x10 ⁵⁻												+MS, 0.3min #18
0.8-												
0.6-							1+ 492.1270)				
0.4-												
0.2-							4	1+ 193.129	5 1+			
0.0 480	.0	482.5	485.0	487.5	488.8718	490.0	492.	5	494.1328 495.0	497	500.0916 .5 500.0	m/z
	Meas. m/z 492.126975 961.263376	 # Ion Formu 1 C24H23NN 1 C48H46N2 	ila Score IaO9 100.00 NaO18 100.00	m/z 492.126502 961.263783	err [ppm] -1.0 0.4	err [mDa] -0.5 0.4	mSigma 12.5 13.8	rdb 13.5 26.5	e [—] Conf N- even even	-Rule ok ok		

pandongyan_PDY-DP-31_pos_24_01_3563.d					
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1	Ð	383.60	0. 195	
2	Ŧ	312.80	0.357	
3	Ŧ	285.60	1.121	
4	Ŧ	203.00	1.085	

Figure S22. ¹H NMR spectrum of compound 3











Figure S24. HMBC spectrum of compound 3



Figure S25. ¹H-¹H COSY spectrum of compound 3



Figure S26. NOESY spectrum of compound 3



(ung) 13

Figure S27. HRESIMS spectrum of compound 3

Mass Spectrum SmartFormula Report

Analysis Info							Acqu	uisition D	ate 1	/23/2018 2:48:39 PM	
Analysis Name Method Sample Name Comment	LC_Direct Infusion_pos_70-500mz.m pandongyan_PDY-DP-33-1_pos						Ope Instr	rator ument	SCSIO maXis	255552.0	00029
Acquisition Parameter Source Type Focus Scan Begin Scan End	r ESI Active 70 m/z 1500 m/z	lon Set Set Set	Polarity Capillary End Plate Offs Charging Volta Corona	et age	Positive 4500 ∨ -500 ∨ 0 ∨ 0 nA	5			Set Nebulizer Set Dry Heater Set Dry Gas Set Divert Valv Set APCI Heat	0.4 Ba 180 °C 4.0 l/m ve Waste er 0 °C	ur C hin
Intens. x104 5 4 3 2 1	434.47	52 487.3	037	400.0	492.127	493.12	294 494,1336		407.6	* •	MS, 0.3min #18
480.0 Meas. m/z 492.1270 961.2650	482.5 4 # Ion Formula 1 C24H23NNaO9 1 C48H46N2NaO18	85.0 48 Score m/2 100.00 492.1263 100.00 961.263	7.5 err [ppm] 5 -1.1 -1.3	490.0 err [mDa] -0.5 -1.3	492 mSigma 13.8 69.6	2.5 rdb 13.5 26.5	e Conf even even	95.0 N-Rule ok ok	497.5	500.0	m/z

pandongyan_PDY-DP-33-1_pos_43_01_4190.d					
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Figure S29. UV spectrum of compound 3







Table S1. Stable conformers of compounds 2 and 3 used for ECD calculation



Conformer	Conformation	Energy (Kcal/mol)	Percent (%)
(13 <i>R</i> ,18 <i>S</i>)- 2 -1		-1041599.686146	6.20
(13 <i>R</i> ,18 <i>S</i>)- 2 -2		-1041599.444617	4.12
(13 <i>R</i> ,18 <i>S</i>)- 2 -3		-1041599.444554	4.12
(13 <i>R</i> ,18 <i>S</i>)- 2 -4		-1041600.177862	14.22

(13 <i>R</i> ,18 <i>S</i>)- 2 -5		-1041599.151884	2.51
(13 <i>R</i> ,18 <i>S</i>)- 2 -6		-1041599.535230	4.80
(13 <i>R</i> ,18 <i>S</i>)- 2 -7		-1041599.621387	5.56
(13 <i>R</i> ,18 <i>S</i>)- 2 -8		-1041600.425101	21.60
(13R,18S)- 2 -9		-1041600.002034	10.57
(13 <i>R</i> ,18 <i>S</i>)- 2 -10	9.40x	-1041599.777009	7.23

(13 <i>R</i> ,18 <i>S</i>)- 2 -11		-1041600.178552	14.24
(13 <i>R</i> ,18 <i>S</i>)- 2 -12		-1041599.535355	4.80
Conformer	Conformation	Energy (Kcal/mol)	Percent (%)
(13 <i>S</i> ,18 <i>S</i>)- 3 -1		-1041600.026507	44.67
(13 <i>S</i> ,18 <i>S</i>)- 3 -2		-1041598.761071	5.27

(13 <i>S</i> ,18 <i>S</i>)- 3 -4	-1041598.363795	2.69
(13 <i>S</i> ,18 <i>S</i>)- 3 -5	-1041598.761699	5.27
(13 <i>S</i> ,18 <i>S</i>)- 3 -6	-1041598.583737	3.91
(13 <i>S</i> ,18 <i>S</i>)- 3 -7	-1041598.952211	7.28
(13 <i>S</i> ,18 <i>S</i>)- 3 -8	-1041599.403578	15.60

Table S2. Stable conformers of $(13R^*, 18S^*)$ -2 and their calculated ¹³C NMR data used for the ¹³C NMR calculation of $(13R^*, 18S^*)$ -2



conformer		E(au)		ф Е(au)	k	cal/mol		$\Delta G(\text{kcal/mol})$		Pi		bolzt	
q4 9	-166	0.27893	92	-1660.2	78939	-1041	840.640	970	-0.79091	3	3.80	2980	0.22728	34
q4_12	-166	0.27853	33	-1660.2	78533	-1041	840.386	264	-0.53620	7	2.47	3435	0.14782	4
q4 13	-166	0.27853	32	-1660.278533		-1041	840.386	201	-0.53614	4	2.47	3173	0.14780	9
a4 18	-166	0.27768	38	-1660.2	77684	-1041	839.853	195	-0.00313	8	1.00	5313	0.06008	32
a4 21	-166	0 27883	18	-1660 2	78832	-1041	840 573	576	-0 72351	8	3 39	3838	0 20283	2
q1_21 q4_22	-166	0.27654	57	-1660.2	76546	-10/1	830 130	026	0.71103	1	0.30	0032	0.01708	5
q4_22	-100	0.27034	60	1660.2	70540	-1041	039.139	020	0.71103	1 7	0.30	0701	0.01/90	20
q4_25	-100	0.27660	60	-1660.2	/6606	-1041	839.176	865	0.6/319	2	0.32	0/91	0.01917	2
q4_28	-166	0.27767	88	-1660.2	.77679	-1041	839.850	057	0.00000	0	1.00	0000	0.05976	5
q4_30	-166	0.27669	56	-1660.2	76696	-1041	839.233	090	0.61696	7	0.35	2747	0.02108	32
q4_37	-166	0.27655	10	-1660.2	76551	-1041	839.142	352	0.70770	5	0.30	2627	0.01808	6
q4 40	-166	0.27768	39	-1660.2	77684	-1041	839.853	257	-0.00320	0	1.00	5420	0.06008	9
a4 47	-166	0.27654	59	-1660.2	76546	-1041	839.139	152	0.71090	5	0.30	0996	0.01798	9
1.7											16 73	2251		
											10.75	2231		
conformer	a4 9	o4 12	a4_13	o4 18	a4 21	o4 22	o4 25	o4 2	8 a4 30		14 37	a4 40	o4 47	bolzt
no	δC	δC	δC	δC	δC	δC	δC	- <u>-</u> 2	δC	-	δC	δC	δC	
1	168.4	169.25	169.25	167.58	169.3	167.65	167.56	169.9	7 169.91	1	170.03	167.58	167.65	168.85
2	127.64	126.63	126.63	128.53	126.66	128.59	128.45	127.3	7 127.46		127.73	128.53	128.58	127.30
3	171.26	168.59	168.59	171.57	168.59	171.54	171.53	168.7	3 168.74		168.7	171.57	171.54	169.73
4	107.59	107.57	107.57	107.55	107.6	107.48	107.5	107.3	3 107.27	1	107.23	107.55	107.48	107.54
4a	138.3	138.84	138.84	138.88	138.83	138.89	138.93	138.7	5 138.8	1	138.77	138.88	138.89	138.72
5	137.11	137.22	137.22	137.05	137.2	137.32	137.06	137.1	5 137.16	1	137.43	137.05	137.32	137.17
6	139.36	139.57	139.57	139.17	139.56	135.35	139.19	139.3	7 139.41	1	135.59	139.17	135.35	139.23
7	167.33	167.32	167.32	167.26	167.31	167.72	167.28	167.3	2 167.32	1	167.76	167.26	167.72	167.33
8	115.94	115.91	115.91	115.85	115.92	117.53	115.86	115.8	6 115.87	1	117.59	115.85	117.53	116.00
8a	138.55	138.35	138.35	138.58	138.36	139.28	138.56	138.4	9 138.47		139.2	138.58	139.28	138.49
9	192.86	193.19	193.19	192.7	193.25	192.79	192.68	192.9	7 193.02	1	193.07	192.7	192.79	193.03
9a	114.14	114.01	114.01	113.76	114.02	113.92	113.79	114.1	6 114.17	1	114.31	113.76	113.92	114.02
10	186.53	186.51	186.51	186.67	186.5	186.57	186.66	186.6	2 186.61	1	186.53	186.67	186.57	186.55
10a	130.25	130.2	130.2	130.23	130.27	129.89	130.21	130.2	3 130.24	1	129.88	130.23	129.89	130.21
11	20.08	20.11	20.11	20.05	20.12	17.12	20.05	20.09	20.09		17.12	20.05	17.12	19.93
12	57.56	57.74	57.74	56.99	57.76	56.98	56.99	57.63	3 57.68		57.61	56.99	56.98	57.56
13	76.62	72.83	72.83	68.95	72.29	68.95	69.05	68.83	68.7		68.77	68.95	68.95	72.50
14	50.29	50.47	50.47	47.37	49.46	47.36	47.55	47.2	47.35		47.18	47.37	47.36	49.36
15	180.16	181.14	181.14	184.49	180.73	184.44	184.63	182.0	6 182.02	1	181.96	184.48	184.44	181.51
16	32.33	33.6	33.6	33.17	33.05	33.18	33.4	33.19	33.39		33.2	33.17	33.18	33.09
17	28.76	29.53	29.53	29.32	29.72	29.31	30.09	28.91	28.87		28.89	29.32	29.31	29.31
18	65.12	67.76	67.76	63.13	65.34	63.1	64.53	61.59	63.24		61.52	63.13	63.1	65.31
19	183.29	181.84	181.84	182.98	184.03	182.98	182.79	182.9	7 182.91	1	182.97	182.98	182.98	182.92
20	55.27	54.57	54.57	55.34	54.72	55.34	55.4	55.23	3 55.28		55.22	55.34	55.34	54.96

Table S3. Stable conformers of $(13S^*, 18S^*)$ -**3** and their calculated ¹³C NMR data used for the ¹³C NMR calculation of $(13S^*, 18S^*)$ -**3**

0 ŅН OH (S) .OH 0 (13S*,18S*)-**3**

A		В			С		D		E		F	
Conformer		E(au)		k	cal/mol		∆G(kcal/mol)		Pi		bolzt	
q3_4	-16	60.2793	176	-1041	840.8784	20	0.000000		00	1.000000		0.324209
q3 5	-16	60.2760	190	-1041838.808517				2.0699	03	0.030	322	0.009831
a3 10	-16	60.2779	329	-1041	-1041840 009507			0.8689	12	0.230	497	0.074729
a3 14	-16	60 2781	742	-1041	840 1609	25		0 7174	94	0 297	665	0.096506
a3 17	-16	60 2778	349	-1041	839 9480	11		0.9304	08	0.207	758	0.067357
q5_17	16	60.27760	100	1041	020 0005	17		2.0600	02	0.207	222	0.000931
q5_20	-10	60.2700	190	-1041	020.0002	05		2.0099	25	0.030	522	0.009831
q5_25	-10	00.2767	4/4	-1041	839.2033	95		1.0128	25	0.005	017	0.0212/4
q3_24	-16	60.2768	145	-1041	839.3077	01		1.5707	19	0.070	453	0.022841
q3_28	-16	60.2765	164	-1041	839.1206	40		1.7577	79	0.051	368	0.016654
q3_33	-16	60.2788	216	-1041	840.5671	75		0.3112	45	0.591	162	0.191660
q3_49	-16	60.2786	809	-1041	840.4788	84		0.3995	35	0.509	268	0.165109
										3.084	430	
Á	B	C	П	म	म	G		Н	Т	Т	K	T
Conformer	a3 4	a3 10	a3 14	a3 17	a3 20	a3 2	3	a3 24	a3 28	a3 33	a3 49	bolzt
no.	δC	δC	δC	δC	δC	δC		δC	δC	δC	δC	
1	170.66	167.03	170.72	168.28	169.35	168.3	37	167.1	169.22	168.32	170.71	167.95
2	127.68	130.45	127.76	129.09	126.49	129.1	19	130.53	126.5	129.21	129.41	127.38
3	169.64	172.19	169.62	174.59	168.57	174.	6	172.17	168.47	174.69	168.83	169.46
4	106.98	107.83	106.92	110.42	107.63	110.3	39	107.77	107.58	110.52	107.47	107.08
4a	138.58	138.29	138.59	138.7	138.85	138.7	72	138.31	138.8	138.63	138.83	137.26
5	137.16	137.01	137.44	137.13	137.19	137.	4	137.27	137.2	137.13	137.05	135.81
6	139.38	139.1	135.59	139.49	139.57	135.6	53	135.34	139.58	139.5	139.32	137.48
7	167.3	167.23	167.76	167.23	167.3	167.	7	167.67	167.3	167.24	167.31	165.70
8	115.86	115.83	117.58	115.89	115.92	117.6	55	117.51	115.94	115.91	115.92	114.98
8a	138.46	138.62	139.15	138.43	138.34	139.1	13	139.32	138.45	138.4	138.67	137.23
9	193.11	192.7	193.21	193.63	193.26	193.7	13	192.8	193.19	193.65	193.75	191.44
9a	114.07	113.82	114.22	113.46	114.04	113.6	51	113.98	114.04	113.4	114.7	112.87
10	186.66	186.67	186.56	186.5	186.5	186.	4	186.58	186.52	186.5	186.58	184.75
10a	130.26	130.31	129.92	130.39	130.24	130.0)3	129.97	130.27	130.38	130.23	128.97
11	20.1	20.05	17.14	20.11	20.11	17.1	7	17.12	20.07	20.11	20.09	19.48
12	57.64	57.33	57.62	59.59	57.8	59.5	9	57.32	57.75	59.66	57.61	57.60
13	69.23	72.37	69.23	69.1	75.47	69.1	3	72.35	74.12	69.1	75.38	69.98
14	4/.68	53.83	47.72	47.75	47.37	47.7	/	53.85	46.26	47.53	52.54	48.57
15	180.14	182.21	180.11	180.65	180.44	180.6	o/	182.22	1/9.08	180.47	187.4	1/9.86
16	32.62	34.66	32.63	32.71	32.8	32.7	2	34.68	34.63	32.5	33.28	32.63
17	29.28	28.5	29.26	29.69	28.25	29.6	2	28.52	29.26	28.76	29.81	28.93
18	64.24	68.55	64.24	64.51	64.17	64.5	6	68.58	64.19	63.2	65.57	64.07
19	182.95	185.95	182.97	182.92	183.55	182.	9	185.96	183.56	182.9	182.43	181.36
20	22.5	oo.25	33.5	22.55	22.17	35.3	2	<u>33.25</u>	54.88	55.21	55.14	54.70

Table S4. DP4⁺ analysis result table for compound **2** (experimental for **2**, isomer 1 for $(13S^*, 18S^*)$ -**3**, isomer 2 for $(13R^*, 18S^*)$ -**2**)





(13R*,18S*)-2 isomer 2

(13S*,18S*)-**3** isomer 1

Funct	ional	Solv	ent?	Basis	Basis Set		f Data
nPV1	P¥91	PC		6-3110	;(d,p)	Unscale	l Shifts
		DP4+	H dl 0.00% dl 00.00% – – – –		-		
Nuclei	sp2?	xperimenta	Isomer 1	Isomer 2	Isomer 3	Isomer 4	Isomer 5
С	x	162.4	168.0	168.8			
С	x	122.1	127.4	127.3			
С	x	164.3	169.5	169.7			
С	x	103.1	17.1	107.5			
С	x	134.7	137.3	138.7			
С	x	130.5	135.8	137.2			
С	x	132.7	137.5	139.2			
С	x	162.1	165.7	167.3			
С	х	111.8	115.0	116.0			
С	x	125	137.2	138.5			
С	x	187.8	191.4	193.0			
С	х	111.1	112.87	114.02			
С	x	180.9	184.75	186.55			
С	х	133.4	128.97	130.21			
С		16.6	19.48	19.93			
С		56.9	57.60	57.56			
С		62.3	69.98	72.50			
С		45.6	48.57	49.36			
С	x	175.2	179.86	181.50			
С		29.3	32.63	33.09			
С		23.2	28.93	29.31			
С		59.7	64.07	65.31			
С	x	172.9	181.36	182.92			
С		52.6	54.70	54.96			

Functional	Solv Solv	rent?	Basis	s Set	Type of Data	
mPW1PW91	P		6-311G(d, p)		Unscaled Shifts	
	Isomer 1	Isomer 2	Isomer 3	Isomer 4	Isomer 5	Isomer 6
sDP4+ (H data)	_	-	_	_	_	_
sDP4+ (C data)	oll 0. 00%	📲 00. 00%	—	-	-	-
sDP4+ (all data)	all 0. 00%	📲 00. 00%	-	-	-	—
uDP4+ (H data)	-	-	_	_	_	_
uDP4+ (C data)	oll 0. 00%	📲 00. 00%	-	-	-	_
uDP4+ (all data)	all 0. 00%	📲 00. 00%	-	-	-	_
DP4+ (H data)	-	-	-	-	-	_
DP4+ (C data)	all 0. 00%	📲 00. 00%	_	-	_	_
DP4+ (all data)	nl 0. 00%	all 00. 00%	_	_	_	_

Table S5. DP4+ analysis result table for compound 3 (experimental for 3, isomer 1 for(13S*,18S*)-3, isomer 2 for (13R*,18S*)-2)

Funct:	ional P¥91 —	Solv _P(ent?	Basis 6-3110	Set (d.n)	Type o Unscale	f Data 1 Shifts
		DP4+	세 87. 50%	ⅆ 12. 50%	_	_	_
Nuclei	sp2?	xperimenta	Isomer 1	Isomer 2	Isomer 3	Isomer 4	Isomer 5
С	х	161	168.0	168.8			
С	х	121	127.4	127.3			
С	х	163.2	169.5	169.7			
С	х	102.1	107.1	107.5			
С	х	133.5	137.3	138.7			
С	х	129.5	135.8	137.2			
С	х	131.6	137.5	139.2			
С	х	161	165.7	167.3			
С	х	110.6	115.0	116.0			
С	х	124.1	137.2	138.5			
С	х	186.6	191.4	193.0			
С	х	109.9	112.87	114.02			
С	х	179.8	184.75	186.55			
С	х	132.3	128.97	130.21			
С		15.5	19.48	19.93			
С		55.9	57.60	57.56			
С		62.7	69.98	72.50			
С		44.5	48.57	49.36			
С	х	173.6	179.86	181.50			
С		28.1	32.63	33.09			
С		21.9	28.93	29.31			
С		59.2	64.07	65.31			
С	х	172.1	181.36	182.92			
С		51.6	54.70	55.22			

Functional	Solv	ent?	Basis	s Set	Type of Data	
mPW1PW91	P(6-311G(d, p)		Unscaled Shifts	
	Isomer 1	Isomer 2	Isomer 3	Isomer 4	Isomer 5	Isomer 6
sDP4+ (H data)	_	-	-	-	-	-
sDP4+ (C data)	🔊 83. 25%	16.75%	-		-	—
sDP4+ (all data)	al 83. 25%	16.75%		1		—
uDP4+ (H data)	-	-	-	-	_	-
uDP4+ (C data)	11 58. 47%	41.53%	-	1	1	—
uDP4+ (all data)	11 58. 47%	41.53%				—
DP4+ (H data)	-	_	-	_	_	-
DP4+ (C data)	11 87.50%	12. 50%	_	-	-	_
DP4+ (all data)	1187. 50%	12. 50%	_	-	-	_