Supporting information for:

Strecker-derived methodology for library synthesis of N-acylated *a*-aminonitriles

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Examples of unstable 4-tolylsulfonyl adducts

The compounds were prepared using the same protocol as described in *general method (A) for synthesis of phenyl-N-(3-phenyl-1-tosylpropyl)acetamide*. But we were unable to purify them and could only confirm the presence of the compound with UPLC-MS for **(S1)** or NMR for **(S2)**. In these two cases, change of color was associated with degradation.

Compound (S1)



Sample 1 Vial 2:65 ID GQ-2018-001-1-FR018 File GQ-2018-001-1-FR018 Date 07-Mar-2018 Time 11:28:49 Description

Figure S.1 – Chromatogram of compound (S1) after flash chromatography

Compound (S2)



Figure S.2 – NMR spectra of compound (S2) after flash chromatography

Supercritical chiral chromatography



Scheme S.1 – Synthetic scheme for the synthesis of chiral standard



Figure S.3 – SFC chromatograms: chiral standard (left) and compound (11) (right)

Chiral HPLC chromatograms

Despite the peak having different shapes the area under the curve is the same.



Compound (9)

Figure S.4 – Chromatogram from chiral HPLC for compound (9)

Compound (11)



Figure S.5 – Chromatogram from chiral HPLC for compound (11). Normal reaction conditions.



Figure S.6 – Chromatogram from chiral HPLC for compound **(11).** Attempt to induce enantioselectivity by adding quinine with KCN and maintaining reaction at -10°C.



Figure S.7 – Chromatogram from chiral HPLC for compound **(11).** Attempt to induce enantioselectivity by adding quinine at beginning and maintaining reaction at room temperature. This reaction did not produce any product when performed at -10°C from beginning until the end.







Compound (13)

Figure S.9 – Chromatogram from chiral HPLC for compound (13).

Compound (21)



Figure S.10 – Chromatogram from chiral HPLC for compound (21).

LC-MS screening

In order to screen a considerable number of conditions, the initial target-molecule was compound **(11)** which allows following the product formation with UPLC-MS. A calibration curve was performed for each method, the longer method was only used when there was peak overlap.

Calibration curve:

Generic method, 13 concentrations in triplicate, R² = 0,9933, measured in a random order. Method: 0-0.15 minutes: 95% H2O+FA 0.1% 5% ACN+FA 0.1%; (gradient); 2-2.25 minutes: 100% H2O+FA 0.1%; 0.7 mL/min



Figure S.11 – Calibration curve for generic method on the UPLC-MS system. Prepared samples ran during working hours (blue), night (orange), and reaction mixture with known concentration (gray)

 Purity method, 13 concentrations in duplicate, R² = 0,9948, measured in a random order. Method: 0-0.15 minutes: 95% H2O+FA 0.1% 5% ACN+FA 0.1%; (gradient); 5-5.25 minutes: 100% H2O+FA 0.1%



Figure S.12 – Calibration curve for purity method on the UPLC-MS system. Prepared samples ran during working hours.

NMR spectra

Compound (9)



Figure S.13 – HNMR compound (9) in CDCl₃.



Figure S.14 – COSY compound (9) in CDCl₃.



Figure S.16 – HMQC compound (9) in CDCl₃.

Compound (11)



Figure S.18 – COSY compound (11) in CDCl₃.







Figure S.21 – HNMR compound (11) in DMSO-d6.



Figure S.22 – APT compound (11) in DMSO-d6.



Figure S.23 – HMQC compound (11) in DMSO-d6.



Figure S.24 – HMBC compound (11) in DMSO-d6.

Compound (12)



Figure S.26 – COSY compound (12) in DMSO-d6.





Figure S.29 – HMBC compound (12) in DMSO-d6.

Compound (13)



Figure S.30 – HNMR compound (13) in Acetone-d6.



Figure S.31 – COSY compound (13) in Acetone-d6.







Figure S.33 – HMQC compound (13) in Acetone-d6.



Figure S.34 – HMBC compound (13) in Acetone-d6.

Compound (14)



Figure S.36 – COSY compound (14) in CDCl₃.



Figure S.38 – HMQC compound (14) in CDCl₃.



Figure S.39 – HMBC compound (14) in CDCl₃.





Figure S.40 – HNMR compound (15) in CDCl₃.



Figure S.41 – COSY compound (15) in CDCl₃.



Figure S.42 – APT compound (15) in CDCl₃.



Figure S.43 – HMQC compound (15) in CDCl₃.



Figure S.44 – HMBC compound (15) in CDCl₃.

Compound (16)



Figure S.46 – COSY compound (16) in Acetone-d6.



Figure S.48 – HMQC compound (16) in Acetone-d6.



Figure S.49 – HMBC compound (16) in Acetone-d6.







Figure S.51 – COSY compound (17) in CDCl₃.





Figure S.54 – HMBC compound (17) in CDCl₃.

Compound (18)



Figure S.56 – COSY compound (18) in CDCl₃.



Figure S.58 – HMQC compound (18) in CDCl₃.



Figure S.59 – HMBC compound (18) in CDCl₃.







Figure S.61 – COSY compound (19) in CDCl₃.



Figure S.62 – APT compound (19) in CDCl₃.



Figure S.63 – HMQC compound (19) in CDCl₃.



Figure S.64 – HNMR compound (19) in CDCl₃.

Compound (20)



Figure S.66 – COSY compound (20) in CDCl₃.



Figure S.68 – HMQC compound (20) in CDCl₃.



Figure S.69 – HMBC compound (20) in CDCl₃.





Figure S.70 – HNMR compound (21) in CDCl₃.



Figure S.71 – COSY compound (21) in CDCl₃.



Figure S.72 – APT compound (21) in CDCl₃.



Figure S.73 – HMQC compound (21) in CDCl₃.



Figure S.74 – HMBC compound (21) in CDCl₃.

Compound (22)



Figure S.76 – COSY compound (22) in MeOD-d4.





Figure S.78 – HMQC compound (22) in MeOD-d4.



Figure S.79 – HMBC compound (22) in MeOD-d4.







Figure S.81 – COSY compound (23) in CDCl₃.



Figure S.82 – APT compound (23) in CDCl₃.



Figure S.83 – HMQC compound (23) in $CDCI_3$.



Figure S.84 – HMBC compound (23) in CDCl₃.

Compound (24)



Figure S.86 – COSY compound (24) in CDCl₃.



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Figure S.89 – HMBC compound (24) in CDCl₃.

HRMS

The samples were used as delivered. 10μ I of each sample was injected using the CapLC system (Waters, Manchester, UK) and electrosprayed using a standard electrospray source. Samples were injected with an interval of 3 minutes. Positive ion mode accurate mass spectra were acquired using a Q-TOF II instrument (Waters, Manchester, UK). The MS was calibrated prior to use with a 0.1% H3PO4 solution.

The spectra were lock mass corrected using the know mass of the nearest H3PO4 cluster or a known background ion.

Analytes were detected as protonated molecule unless stated otherwise. The measured masses, best fitting elemental composition and corresponding calculated monoisotopic masses are given in the attached spectra. All measured masses are within a difference of 5ppm compared to the calculated mass unless specified otherwise. The presented MS data does allow to calculate the elemental composition of the analytes, but does not decide on structure or purity of the samples.

Accurate ma	ss	sar	nple	e su	ıbn	nis	sior	n li	st						
Name:	Pe	dro	San	tos	Go	nç	alve	s	_	_					
Data file(s):	GV	H_2	2019	012	22_	06	.rav	v							
							-	-	-						
						_		_	_					(M+H)+	
sample Code	С	н	Ν	0	F	CI	Br	1	s	Ρ	Mol weight	(M+H)+	Structure (Chemdraw)	measured	error (ppm)
PSG2018-051	18	18	2	1							278,141913	279,1492		279,1499	2,55
PSG2018-031-1	28	33	3	5							491,242021	492,2493		492,2503	2,04
PSG2018-044-1	12	14	2	1							202,110613	203,1179		203,1187	4,00
PSG2018-045	15	12	2	1							236,094963	237,1022		237,1022	-0,16
PSG2018-046-1	13	23	3	3							269,173941	270,1812		270,1812	-0,06
PSG2018-035-2	13	14	2	1							214,110613	215,1179		215,1181	0,99
PSG2018-056-2	13	16	2	1					1		248,098334	249,1056		249,1049	-2,85
PSG2018-049-1	11	13	3	1							203,105862	204,1131		204,1124	-3,61
PSG2018-053-2	10	11	3	1							189,090212	190,0975		190,0970	-2,56

Table S.1 – Results from HRMS analysis (1 of 3)

Accurate r	nas	s s	am	ple	submission	list						
Name:	Pe	dro H 2	Sar	itos 1060	Gonçalves							
ata me(o).	0.		.010		0_10.10W				(M+H)+		(M+Na)+	
ample Code	С	Н	N	0	Mol weight	(M+H)+	(M+Na)+	Structure	measured	error (ppm)	measured	error (ppm)
PSG2018-059	14	16	2	3	260,116092	261,1234	283,105312	HN OH		-1000000,00		-1000000,00
	15	20	2	4	292,142307	293,1496	315,131527	+ Methanol	293,1502	2,11	315,1330	4,67
PSG2018-058-1	11	19	3	3	241,142641	242,1499	264,131861		242,1505	2,41	264,1328	3,55
PSG2018-061	15	18	2	1	242,141913	243,1492	265,131133		243,1502	4,16	265,1335	8,93
PSG2018-050-1	17	23	3	4	333,168856	334,1761	356,158076		334,1774	3,80	356,1597	4,56
PSG2018-055-1iso	14	16	2	3	260,116092	261,1234	283,105312		261,1236	0,89	283,1066	4,55

Table S.2 – Results from HRMS analysis (2 of 3)

Accurate	mas	s s	am	ple	sul	bmi	ssi	on	list	:						
Name:	Pe	dro	Gor	nçal	ves	5										
)ata file(s):	G٧	′H_2	2019	9111	15_	03.	raw									
	G٧	Ή2	2019	9112	29	05.	raw									
															(M+H)+	
ample Cod	l C	Н	Ν	0	F	CI	Br	I	S	Ρ	Mol weight	(M+H)+	(M+Na)+	Structure	measured	error (ppm)
PSG2018-059-3fcprep	14	16	2	3							260,116092	261,1234	283,105312		261,1241	2,81

Table S.3 – Results from HRMS analysis (3 of 3)

LC-MS Chromatograms



Sample 1 Vial 2:13 ID PSG2016-009-fc-w File PSG2016-009-fc-w Date 06-Jan-2017 Time 16:09:53 Description

Figure S.90 – Details of UPLC-MS report of compound (9) using generic method.



Sample 1 Vial 1:8 ID PSG2018-051-2fc File PSG2018-051-2fc Date 05-Nov-2018 Time 10:33:41 Description

Figure S.91 – Details of UPLC-MS report of compound (11) using generic method.





Figure S.92 – Details of UPLC-MS report of compound (12) using generic method.



Figure S.93 – Details of UPLC-MS report of compound (13) using generic method.



Sample 1 Vial 1:30 ID PSG2018-056-1nmr File PSG2018-056-1nmr Date 09-Nov-2018 Time 14:26:29 Description

Figure S.94 – Details of UPLC-MS report of compound (14) using generic method.







Sample 1 Vial 2:75 ID PSG2018-055-1iso-pTLC2 File PSG2018-055-1iso-pTLC2 Date 16-Apr-2019 Time 15:41:31 Description

Figure S.96 – Details of UPLC-MS report of compound **(15)** using generic method; peaks number 9 and 10 are present in every run when the sample is diluted or does not produce strong MS signals.



Figure S.97 – Details of UPLC-MS report of compound (15) using generic method (continued).

Sample 1 Vial 2:36 ID PSG-brnmr1 File PSG-brnmr1 Date 21-Nov-2018 Time 10:38:27 Description



Figure S.98 – Details of UPLC-MS report of compound **(16)** using generic method; peak 10 is present in every run when the sample is diluted or does not produce strong MS signals.





Figure S.99 – Details of UPLC-MS report of compound (18) using generic method.





Figure S.100 – Details of UPLC-MS report of compound **(19)** using generic method; peak 7 and 8 is present in every run when the sample is diluted or does not produce strong MS signals.



Sample 1 Vial 2:96 ID PSG2018-050-3prepTLC3 File PSG2018-050-3prepTLC3 Date 06-Feb-2019 Time 14:22:35 Description

Figure S.101 – Details of UPLC-MS report of compound **(20)** using generic method; peak 7 and 8 are present in every run when the sample is diluted or does not produce strong MS signals.



Sample 1 Vial 2:28 ID PSG2018-031-1pTLCfr40-45 File PSG2018-031-1pTLCfr40-45 Date 07-Jun-2018 Time 16:31:44 Description

Figure S.102 – Details of UPLC-MS report of compound (21) using generic method.





Figure S.103 – Details of UPLC-MS report of compound (22) using generic method.

Sample 1 Vial 1:64 ID PSG2018-049-2fr12 File PSG2018-049-2fr12 Date 11-Dec-2018 Time 10:18:05 Description



Figure S.104 – Details of UPLC-MS report of compound **(23)** using generic method; peak 9 and 11 is present in every run when the sample is diluted or does not produce strong MS signals.





Figure S.105 – Details of UPLC-MS report of compound (23) using purity method.

FT-IR Chromatograms for Selected Compounds

Note: the nitrile band is apparently missing (low signal-to-noise ratio) for some compounds; this phenomenon is common with ATR FT-IR (these spectra acquired with a Bruker Alpha Platinum ATR apparatus), due to the high absorbance of diamond in that region (see for example: Larkin, P. J. Instrumentation and Sampling Methods. In Infrared and Raman Spectroscopy; Second Edition, Elsevier: Amsterdam, **2018**; pp 29–61).



Figure S.106 – FT-IR spectra of compound (11)



Figure S.107 – FT-IR spectra of compound (12)



Figure S.108 – FT-IR spectra of compound (14)



Figure S.109 – FT-IR spectra of compound (15)



Figure S.110 – FT-IR spectra of compound (16)



Figure S.111 – FT-IR spectra of compound (17)



Figure S.112 – FT-IR spectra of compound (18)



Figure S.113 – FT-IR spectra of compound (20)



Figure S.114 – FT-IR spectra of compound (21)



Figure S.115 – FT-IR spectra of compound (22)