Supporting Information

Structure-based design of selective salt-inducible kinase (SIK) inhibitors

Roberta Tesch[a,bŦ], Marcel Rak[a,bŦ], Monika Raab[c], Lena M. Berger[a,b], Thales Kronenberger[d,e] Andreas C. Joerger[a,b], Benedict-Tilman Berger[a,b], Ismahan Abdi[a,b], Thomas Hanke[a,b], Antti Poso[d,e], Klaus Strebhardt[c], Mourad Sanhaji[c], Stefan Knapp[a,b]*

[Ŧ]These authors contributed equally to the work.

[a]Institute of Pharmaceutical Chemistry, Johann Wolfgang Goethe University, Max-von-Laue-Str. 9, 60438, Frankfurt am Main, Germany.

[b]Structural Genomics Consortium (SGC), Buchmann Institute for Life Sciences, Johann Wolfgang Goethe University, Max-von-Laue-Str. 15, 60438, Frankfurt am Main, Germany.

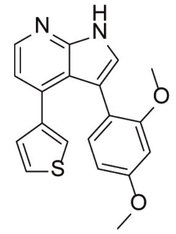
[c]Department of Obstetrics and Gynaecology, School of Medicine, Johann Wolfgang Goethe-University, Theodor-Stern-Kai 7, 60590, Frankfurt am Main, Germany.

[d]University Hospital Tübingen, Dept. of Internal Medicine VIII, Otfried-Müller-Strasse 14, 72076 Tübingen, Germany

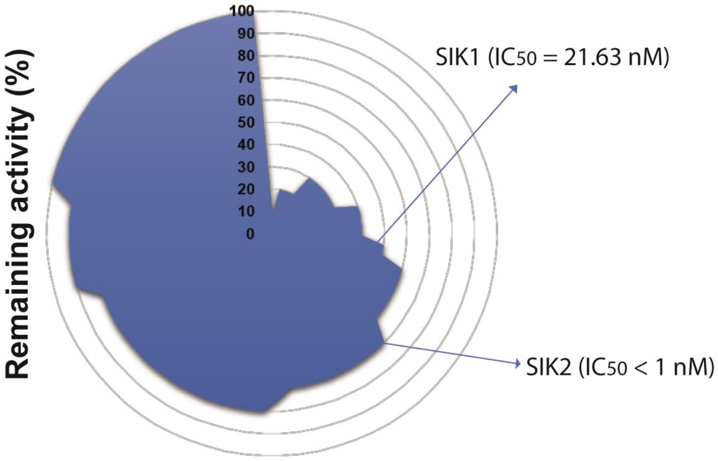
[e]School of Pharmacy, University of Eastern Finland, Yliopistonranta 1, 70210 Kuopio, Finland.

[f]German translational cancer network (DKTK) and Frankfurt Cancer Institute (FCI). 60438 Frankfurt am Main, Germany

Table of Content

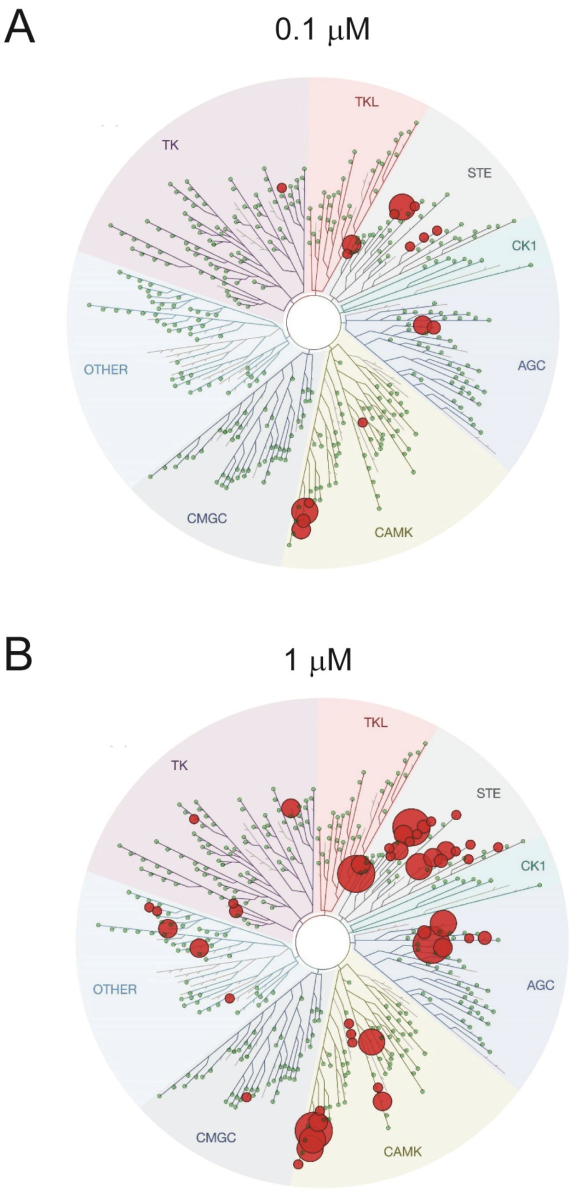


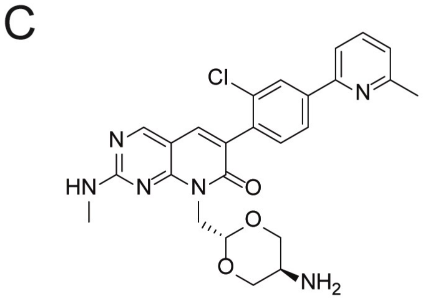
ARN-3236
(**5**)



ARN-3236 screening on 74 kinases

Figure S1. Selectivity profile of SIK2 inhibitor ARN-3236 (5) at a concentration of 500 nM against a panel of 74 kinases. Data report as percent of activity remaining in presence of inhibitor relative to activity measured in absence of inhibitor (100%). Graph created from the information on the supplementary material from Lombardi, M. S.; Gilliéron, C.; Dietrich, D.; Gabay, C. SIK inhibition in human myeloid cells modulates TLR and IL-1R signaling and induces an anti-inflammatory phenotype. *Journal of leukocyte biology* **2016**, *99* (5), 711–721.





	remaining activity (%)	
Targets	0.1 µM	1 µM
KIAA0999 (SIK3)	0.2	0
MST4	0.5	0
SIK1	1.4	0.6
STK32B	3.5	3.7
PAK1	4.4	4.5
STK32A	5.3	3.7
SIK2	6.5	0.8
CDPK1	9.1	0.4
MAP2K5	13	0
PAK2	13	0
STK24	15	1.7
MAP4K5	18	5.3
NUAK2	19	2
MAP2K1	24	1
LTK	28	4.1
DCLK3	29	0.5
MAP2K2	33	1.4
STK36	36	2.9
AURKC	37	20
STK10	37	2.1
STK25	40	36
CAMK1D	43	2.5
MARK3	45	18
MAST1	47	0.4
MYO3B	48	57
PIP5K1A	48	67
MAP2K4	49	9.6

Figure S2. Selectivity profile of G-5555. (A) Kinome tree of G-5555 screened at a concentration of 0.1 µM using scanMAX^{SM} kinase assay panel of 468 kinases (*Eurofins Scientific*). (B) Kinome tree of G-5555 screened at a concentration of 1 µM using scanMAX^{SM} kinase assay panel of 468 kinases (*Eurofins Scientific*). (C) Top off-targets at 0.1 µM and 1 µM.

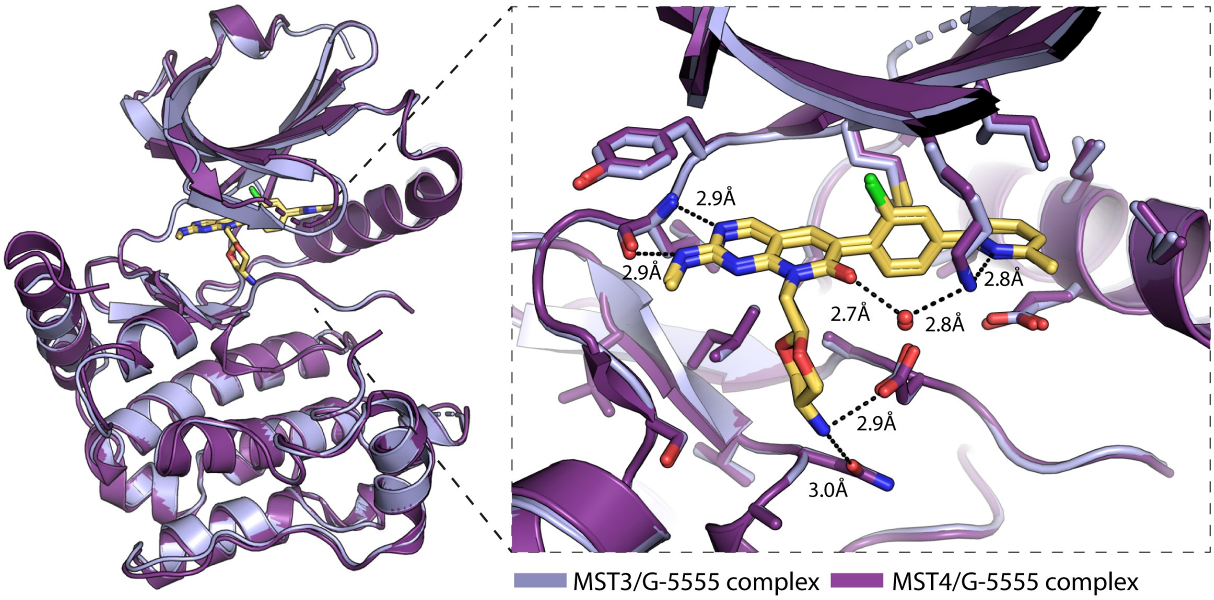
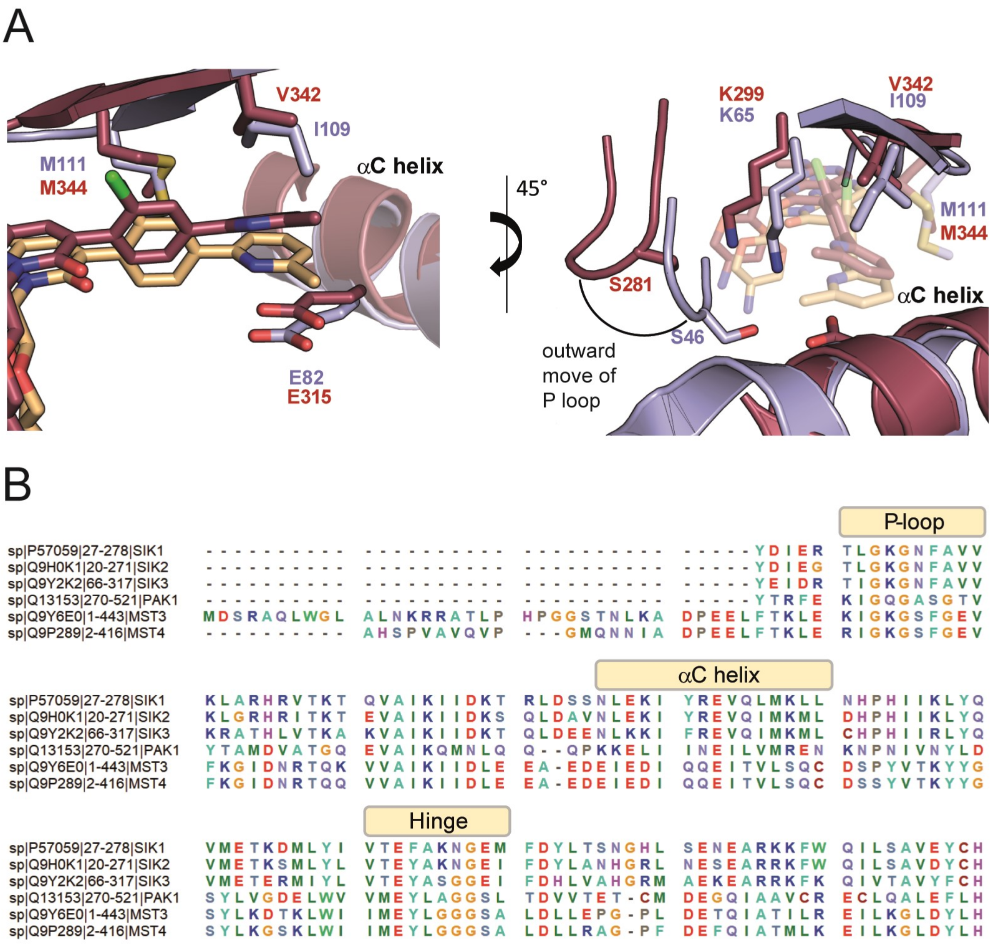


Figure S3. Comparison of the crystal structures of MST3 (light purple) and MST4 (violet) highlighting the conservation of amino acids in the binding site, interactions with G-5555 and conservation of a water molecule in the binding site.



```
sp|P57059|27-278|SIK1     ----------  ----------  ----------  -----YDIER  TLGKGNFAVV
sp|Q9H0K1|20-271|SIK2     ----------  ----------  ----------  -----YDIEG  TLGKGNFAVV
sp|Q9Y2K2|66-317|SIK3     ----------  ----------  ----------  -----YEIDR  TIGKGNFAVV
sp|Q13153|270-521|PAK1    ----------  ----------  ----------  -----YTRFE  KIGQGASGTV
sp|Q9Y6E0|1-443|MST3      MDSRAQLWGL  ALNKRRATLP  HPGGSTNLKA  DPEELFTKLE  KIGKGSFGEV
sp|Q9P289|2-416|MST4      ----------  AHSPVAVQVP  ---GMQNNIA  DPEELFTKLE  RIGKGSFGEV

sp|P57059|27-278|SIK1     KLARHRVTKT  QVAIKIIDKT  RLDSSNLEKI  YREVQLMKLL  NHPHIIKLYQ
sp|Q9H0K1|20-271|SIK2     KLGRHRITKT  EVAIKIIDKS  QLDAVNLEKI  YREVQIMKML  DHPHIIKLYQ
sp|Q9Y2K2|66-317|SIK3     KRATHLVTKA  KVAIKIIDKT  QLDEENLKKI  FREVQIMKML  CHPHIIRLYQ
sp|Q13153|270-521|PAK1    YTAMDVATGQ  EVAIKQMNLQ  Q--QPKKELI  INEILVMREN  KNPNIVNYLD
sp|Q9Y6E0|1-443|MST3      FKGIDNRTQK  VVAIKIIDLE  EA-EDEIEDI  QQEITVLSQC  DSPYVTKYYG
sp|Q9P289|2-416|MST4      FKGIDNRTQQ  VVAIKIIDLE  EA-EDEIEDI  QQEITVLSQC  DSSYVTKYYG

sp|P57059|27-278|SIK1     VMETKDMLYI  VTEFAKNGEM  FDYLTSNGHL  SENEARKKFW  QILSAVEYCH
sp|Q9H0K1|20-271|SIK2     VMETKSMLYL  VTEYAKNGEI  FDYLANHGRL  NESEARRKFW  QILSAVDYCH
sp|Q9Y2K2|66-317|SIK3     VMETERMIYL  VTEYASGGEI  FDHLVAHGRM  AEKEARRKFK  QIVTAVYFCH
sp|Q13153|270-521|PAK1    SYLVGDELWV  VMEYLAGGSL  TDVVTET-CM  DEGQIAAVCR  ECLQALEFLH
sp|Q9Y6E0|1-443|MST3      SYLKDTKLWI  IMEYLGGGSA  LDLLEPG-PL  DETQIATILR  EILKGLDYLH
sp|Q9P289|2-416|MST4      SYLKGSKLWI  IMEYLGGGSA  LDLLRAG-PF  DEFQIATMLK  EILKGLDYLH
```

Figure S4. (A) Comparison of the crystal structures of MST3 (purple) and PAK1 (dark red) highlighting the main differences between the binding mode of G-5555 in the back-pocket region. (B) Sequence alignment of SIKs and main off-targets of G-5555, MSTs and PAK1 (BioEdit 7.2).

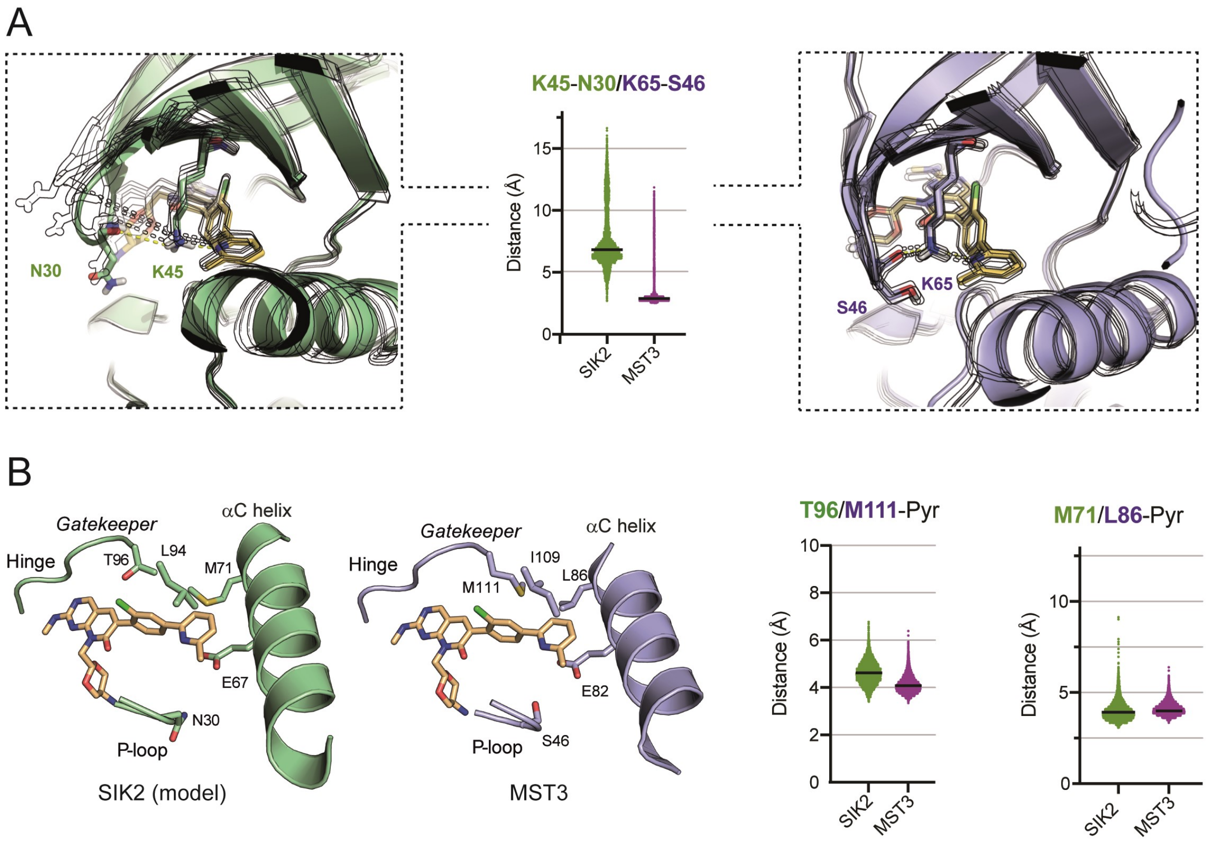


Figure S5. Binding pocket fluctuation in MD simulations. (A) Comparison of the movement of the P-loop region relative to the catalytic lysine in SIK2 and MST3. The distance from Ser46 in MST3 and Asn30 in SIK2 to the catalytic lysine was calculated for snapshots of the MD trajectory to assess the flexibility of this region. The oxygen from the carbonyl group of the main chain of Ser36 and Asn30 and the nitrogen from the catalytic lysine were chosen for the distance calculation. (B) Distribution of the distance between back-pocket residues of SIK2 and MST3 and the pyridine moiety of G-5555 along the MD trajectory. The first atom of the side chain of the back pockets was chosen for distance calculation with the center of mass of the pyridine ring.

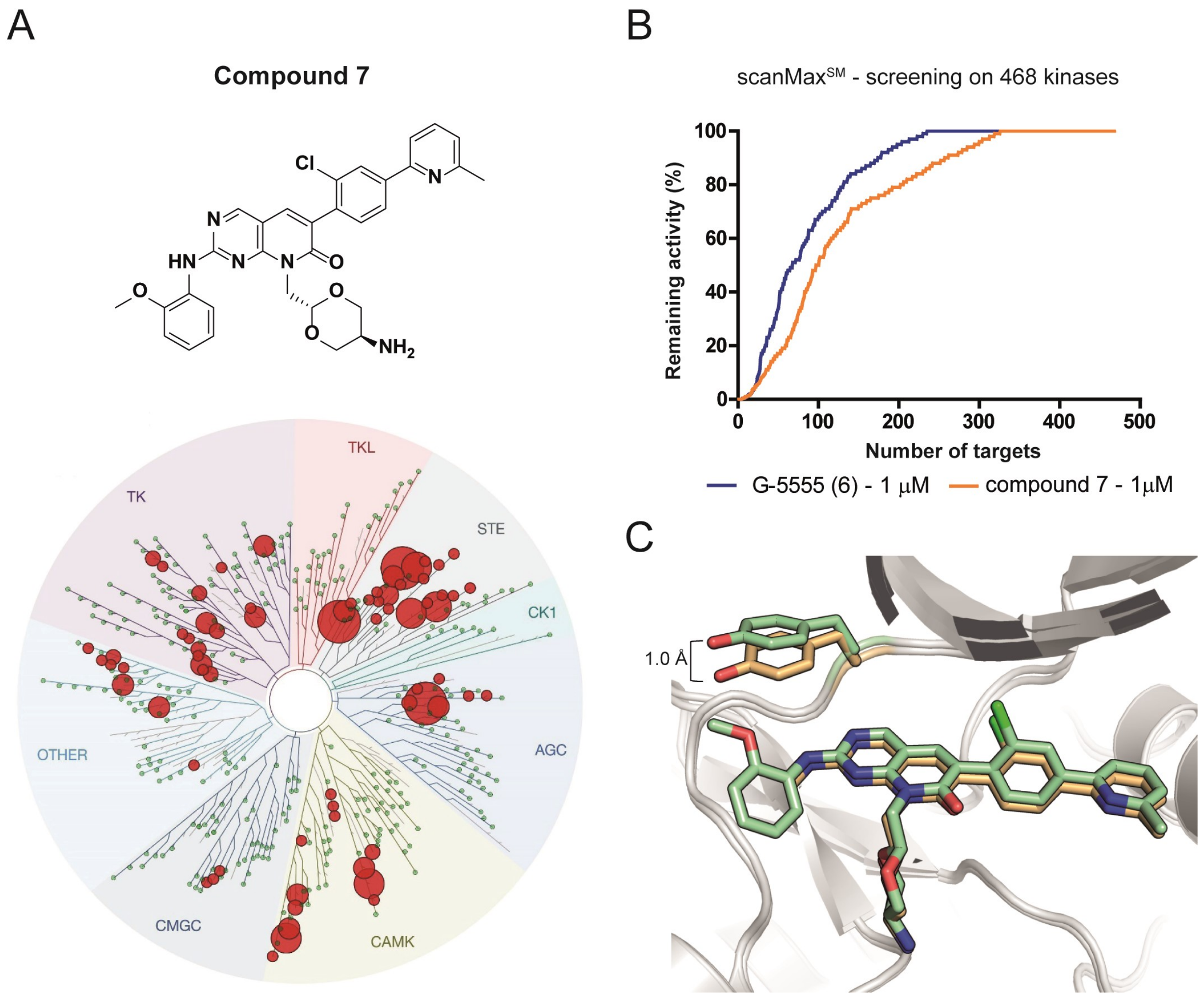


Figure S6. Comparison of the selectivity profile of G-5555 and compound **7**. (A) Kinome tree of compound **7** screened at 1 µM using scanMAX^{SM} kinase assay panel of 468 kinases (*Eurofins Scientific*). (B) Comparison of selectivity profile of G-5555 and compound **7**. (C) Comparison of the binding mode of G-5555 in yellow (PDB code 7B30) and compound **7** in green (PDB code 7B32).

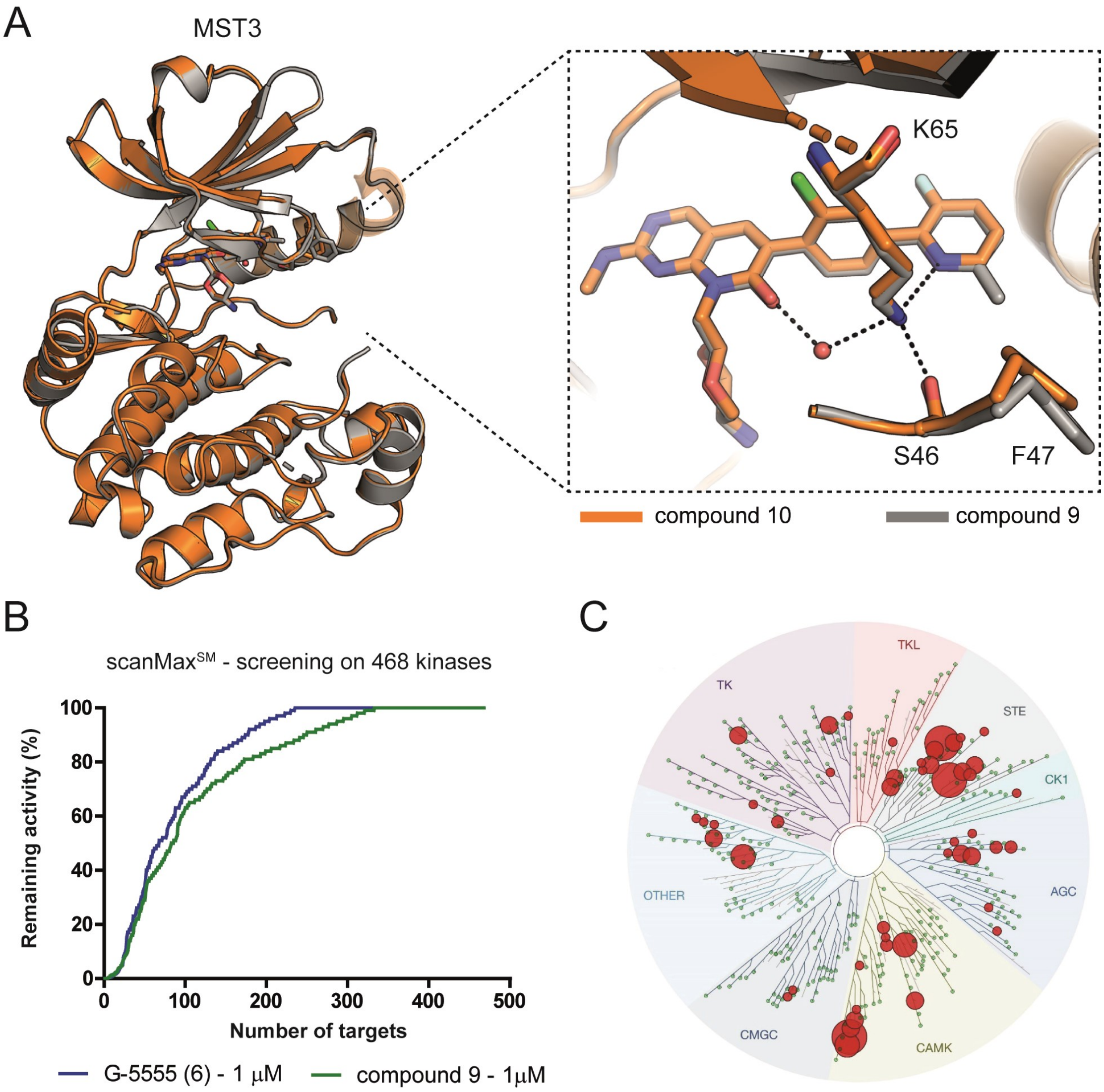


Figure S7. Binding mode of compounds **9** and **10** (MRIA9) in MST3. (A) Comparison of the binding mode of compound **9** (gray, PDB code 7B34) and compound **10** (MRIA9) (orange, PDB code 7B31). (B) Selectivity profile of G-5555 and compound **9** using scanMAX^{SM} kinase assay panel of 468 kinases (*Eurofins Scientific*). (C) Kinome tree of compound **9** screened at 1 µM in scanMAX^{SM} kinase assay (*Eurofins Scientific*).

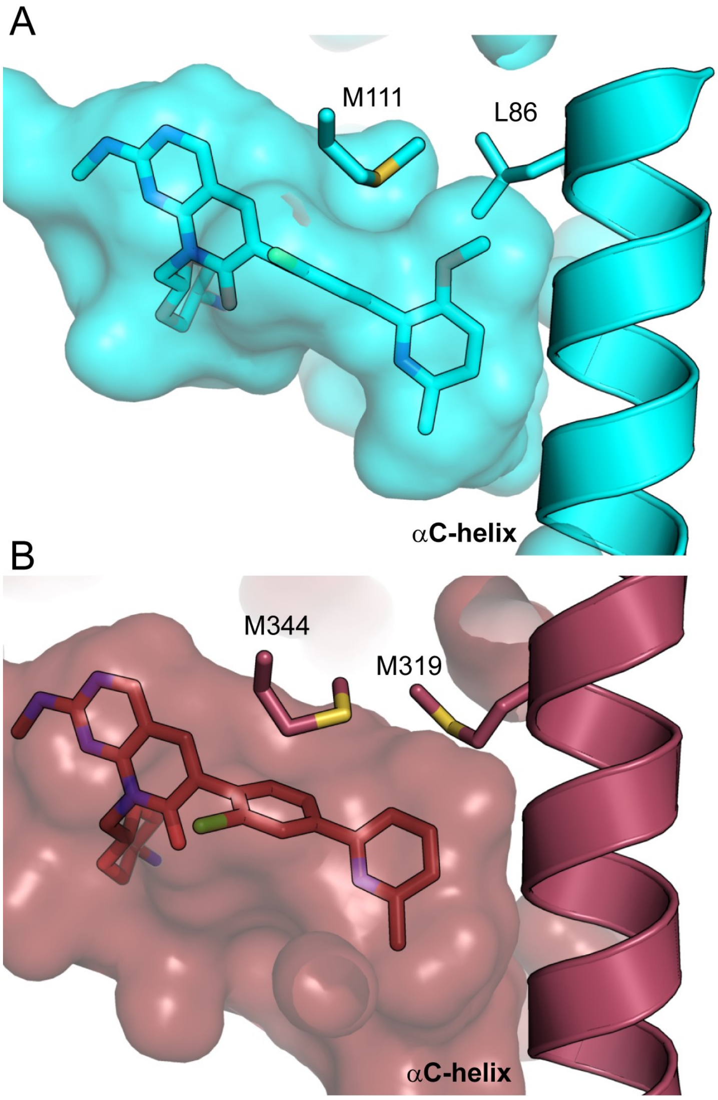


Figure S8. Comparison of the MST3 and PAK1 back pocket. (A) Binding mode of compound **14** in MST3 (cyan) and accommodation of the methoxy group in the back pocket (PDB code 7B35). (B) Binding mode of compound G-5555 in PAK1 (dark red), highlighting the back-pocket region (PDB code 5DEY).

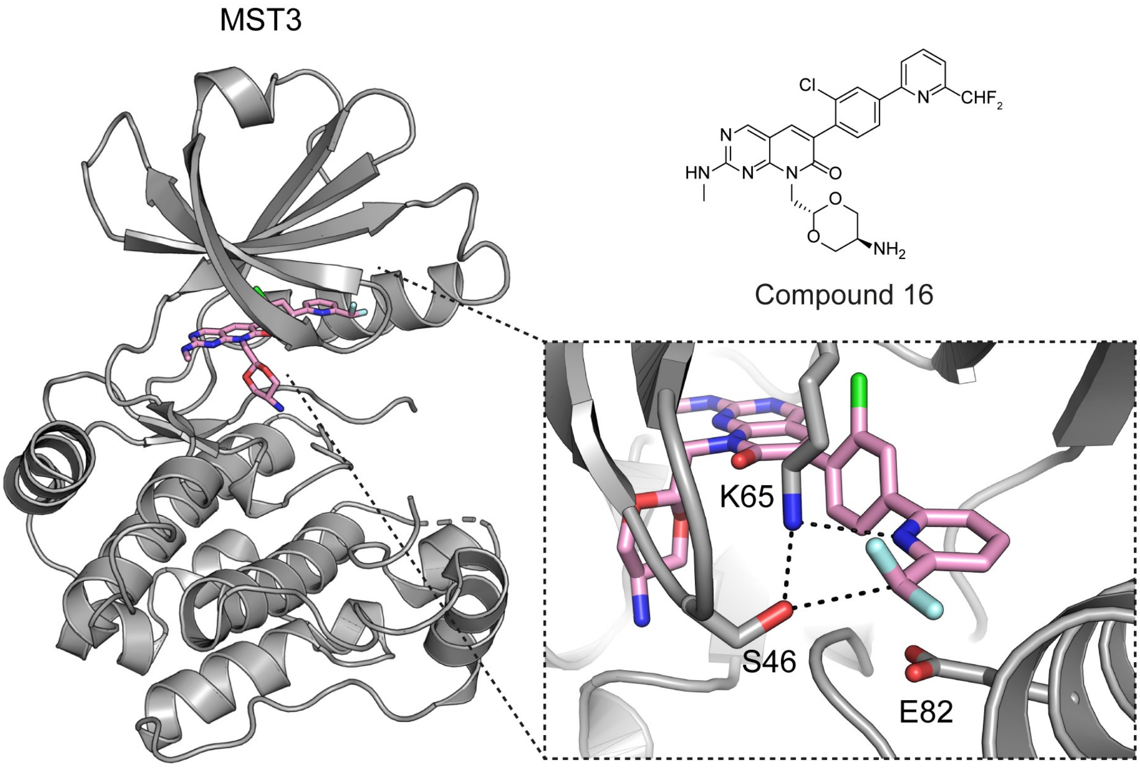


Figure S9. Binding mode of compound **16** with MST3 (PDB 7B33) and main interactions in the back pocket. The CHF_2 moiety contributes to binding to MST3 through direct interaction with Ser46.

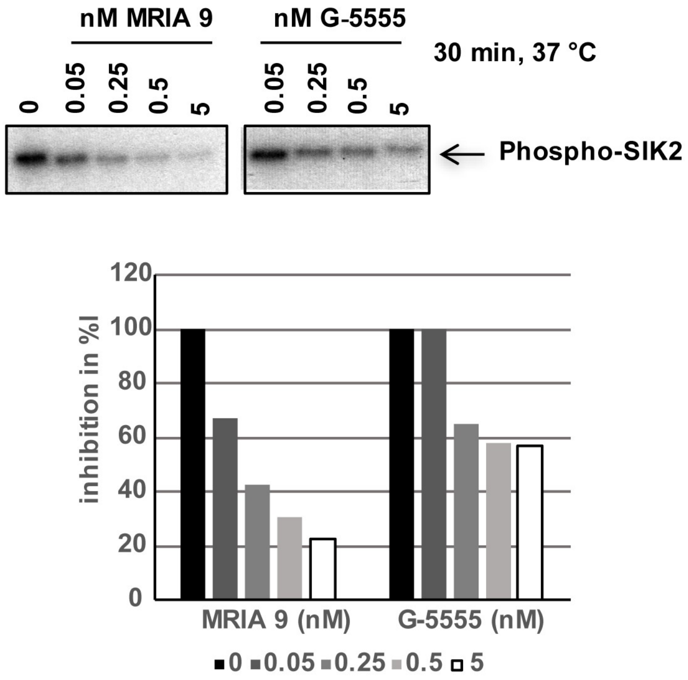
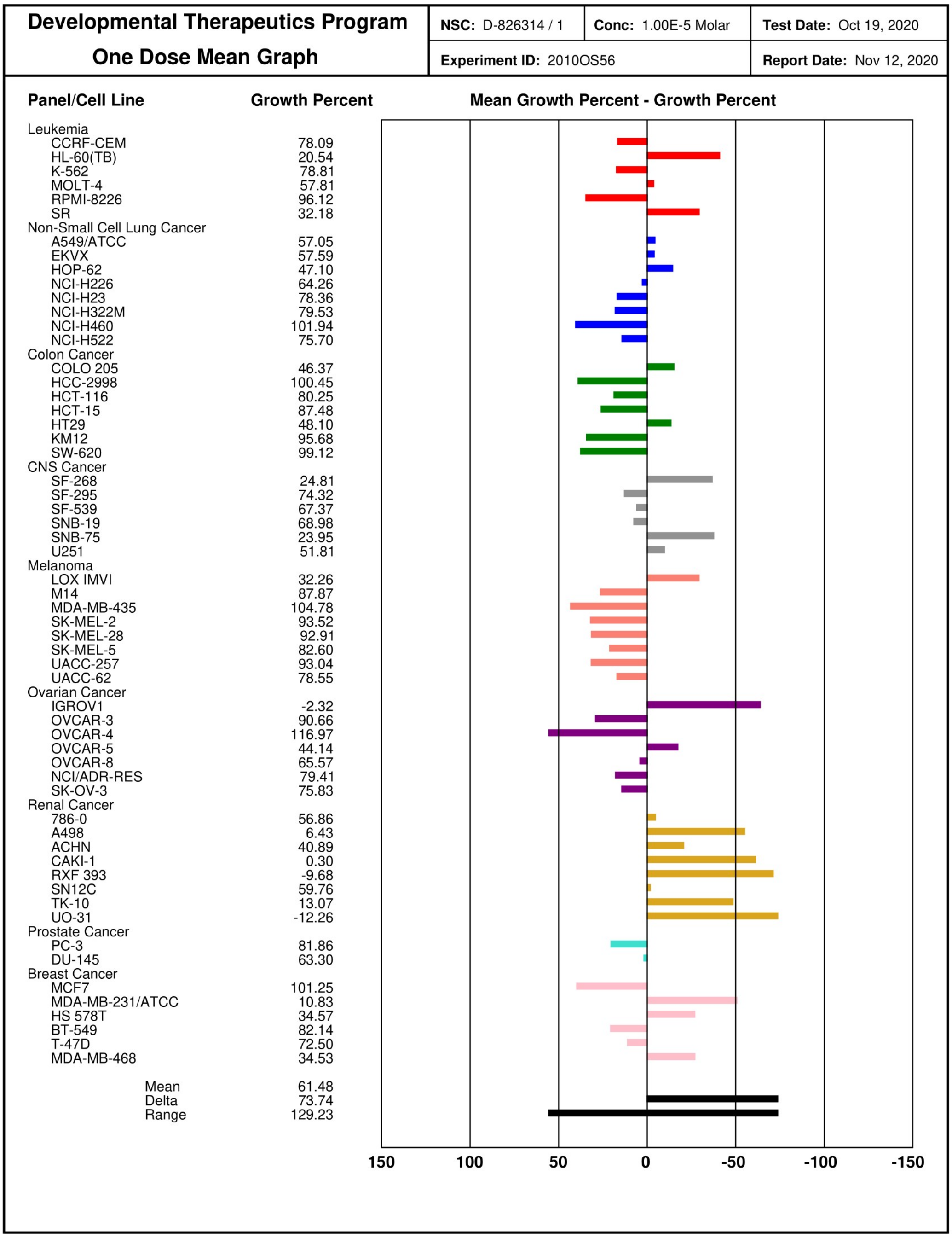


Figure S10. MRIA9 potently inhibits SIK2 *in vitro*. Representative *in vitro* kinase assay in which the autophosphorylation of SIK2 has been assessed for increasing concentrations of MRIA9 and G-5555. Band intensities were quantified and are represented as a bar graph.



Developmental Therapeutics Program

One Dose Mean Graph

NSC: D-826314 / 1

Conc: 1.00E-5 Molar

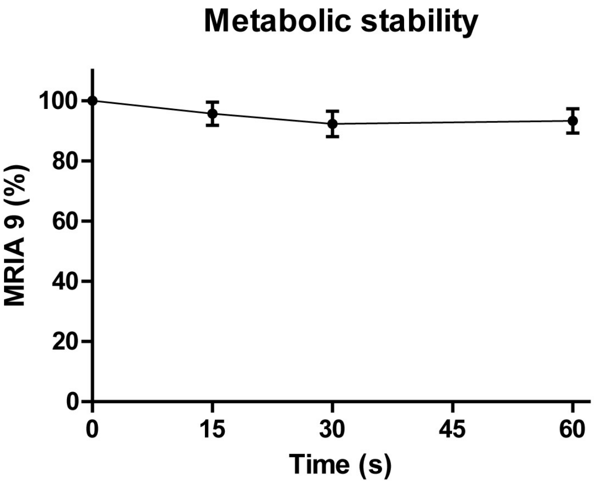
Test Date: Oct 19, 2020

Experiment ID: 2010OS56

Report Date: Nov 12, 2020

Panel/Cell Line	Growth Percent
Leukemia	
CCRF-CEM	78.09
HL-60(TB)	20.54
K-562	78.81
MOLT-4	57.81
RPMI-8226	96.12
SR	32.18
Non-Small Cell Lung Cancer	
A549/ATCC	57.05
EKVX	57.59
HOP-62	47.10
NCI-H226	64.26
NCI-H23	78.36
NCI-H322M	79.53
NCI-H460	101.94
NCI-H522	75.70
Colon Cancer	
COLO 205	46.37
HCC-2998	100.45
HCT-116	80.25
HCT-15	87.48
HT29	48.10
KM12	95.68
SW-620	99.12
CNS Cancer	
SF-268	24.81
SF-295	74.32
SF-539	67.37
SNB-19	68.98
SNB-75	23.95
U251	51.81
Melanoma	
LOX IMVI	32.26
M14	87.87
MDA-MB-435	104.78
SK-MEL-2	93.52
SK-MEL-28	92.91
SK-MEL-5	82.60
UACC-257	93.04
UACC-62	78.55
Ovarian Cancer	
IGROV1	-2.32
OVCAR-3	90.66
OVCAR-4	116.97
OVCAR-5	44.14
OVCAR-8	65.57
NCI/ADR-RES	79.41
SK-OV-3	75.83
Renal Cancer	
786-0	56.86
A498	6.43
ACHN	40.89
CAKI-1	0.30
RXF 393	-9.68
SN12C	59.76
TK-10	13.07
UO-31	-12.26
Prostate Cancer	
PC-3	81.86
DU-145	63.30
Breast Cancer	
MCF7	101.25
MDA-MB-231/ATCC	10.83
HS 578T	34.57
BT-549	82.14
T-47D	72.50
MDA-MB-468	34.53
Mean	61.48
Delta	73.74
Range	129.23

Figure S11. Results of compound **10** (MRIA9) tested against 60 cancer cell lines in the NCI-60 Human Tumor Cell Lines Screen at a single-dose concentration of 1 µM. Growth inhibition (values between 0 and 100) and lethality (values between 0 and -100) are shown as a bar chart.



Descriptor	Interpretation	Limit Values	G-5555^{+}	G-5555	MRIA9^{+}	MRIA9
PCaco	Predicted apparent Caco-2 cell permeability in nm/sec[a]. Caco-2 cells are a model for the gut-blood barrier	<25 poor, >500 great	110	140.1	93.9	92.2
logBB	Predicted brain/blood partition coefficient[b]	-3.0 – 1.2	-0.8	-0.8	-0.8	-0.8
PPMDCK	Predicted apparent MDCK cell permeability in nm/sec[a]. MDCK cells are considered to be a good mimic for the blood-brain barrier	<25 poor, >500 great	95.2	125.4	123.2	121.6
logKp	Predicted skin permeability	-8.0 – -1.0	-4.5	-4.4	-4.6	-4.7
logK'hsa	Prediction of binding to human serum albumin	-1.5 – 1.5	0.1	0.1	0.0	0.0
Oral Abs	Predicted human oral absorption on 0 to 100% scale. The prediction is based on a quantitative multiple linear regression model	>80% is high <25% is poor	80	81	77	76

Figure S12. Metabolism of MRIA9. The compound was treated with activated microsomes and measured at 0, 15, 30 and 60 minutes via HPLC. Data are given as mean ± S.E.M. obtained in 3 independent experiments. Predicted ADME properties for the selected compounds. Predictions were generated using QikProp (Schrödinger, 2020) and compared with literature values. [a]Predictions are for non-active transport. [b]Predictions are for orally delivered drugs so, for example, dopamine and serotonin are CNS negative because they are too polar to cross the blood-brain barrier.

Table S1. Selectivity screening results of G-5555 (**6**) at 100 nM.

DiscoveRx Gene Symbol	Entrez Gene Symbol	Percent Control	Compound Concentration (nM)
QSK	KIAA0999	0.2	100
MST4	MST4	0.5	100
SIK	SIK1	1.4	100
YANK2	STK32B	3.5	100
PAK1	PAK1	4,4	100
YANK1	STK32A	5.3	100
SIK2	SIK2	6.5	100
PFCDPK1 (*P. falciparum*)	CDPK1	9.1	100
MEK5	MAP2K5	13	100
PAK2	PAK2	13	100
MST3	STK24	15	100
MAP4K5	MAP4K5	18	100
SNARK	NUAK2	19	100
MEK1	MAP2K1	24	100
LTK	LTK	28	100
DCAMKL3	DCLK3	29	100
MEK2	MAP2K2	33	100
STK36	STK36	36	100
AURKC	AURKC	37	100
LOK	STK10	37	100
YSK1	STK25	40	100
CAMK1D	CAMK1D	43	100
MARK3	MARK3	45	100
MAST1	MAST1	47	100

MYO3B	MYO3B	48	100
PIP5K1A	PIP5K1A	48	100
MEK4	MAP2K4	49	100
GAK	GAK	51	100
MELK	MELK	51	100
PIK3CD	PIK3CD	53	100
FLT3(ITD,F691L)	FLT3	56	100
SgK110	SgK110	56	100
LATS1	LATS1	57	100
LATS2	LATS2	58	100
LCK	LCK	58	100
DYRK1B	DYRK1B	61	100
EPHB6	EPHB6	61	100
MAP4K2	MAP4K2	63	100
EPHA1	EPHA1	64	100
MST2	STK3	64	100
DRAK2	STK17B	66	100
PIP5K2B	PIP4K2B	68	100
PRKD1	PRKD1	68	100
YSK4	MAP3K19	70	100
AURKB	AURKB	72	100
MAP3K15	MAP3K15	72	100
MRCKB	CDC42BPB	73	100
MST1R	MST1R	73	100
NLK	NLK	73	100
PIK3CA(H1047Y)	PIK3CA	73	100
MLCK	MYLK3	74	100

MEK3	MAP2K3	75	100
MYLK	MYLK	75	100
PLK2	PLK2	75	100
GCN2(Kin.Dom.2,S808G)	EIF2AK4	76	100
MET(M1250T)	MET	76	100
PIK3CA(M1043I)	PIK3CA	76	100
ERBB3	ERBB3	77	100
KIT(V559D,V654A)	KIT	77	100
MINK	MINK1	77	100
TRKA	NTRK1	77	100
HPK1	MAP4K1	78	100
ABL1(H396P)-nonphosphorylated	ABL1	79	100
CAMK2A	CAMK2A	79	100
CDC2L5	CDK13	79	100
DRAK1	STK17A	79	100
PIP5K2C	PIP4K2C	79	100
RSK1(Kin.Dom.1-N-terminal)	RPS6KA1	79	100
DCAMKL1	DCLK1	80	100
JNK1	MAPK8	80	100
MEK6	MAP2K6	80	100
PIK3CA(C420R)	PIK3CA	80	100
KIT(A829P)	KIT	81	100
MAP3K1	MAP3K1	81	100
PRKCQ	PRKCQ	81	100
CDKL5	CDKL5	82	100
KIT-autoinhibited	KIT	82	100

PLK1	PLK1	82	100
PRKCH	PRKCH	82	100
GRK3	ADRBK2	83	100
LRRK2	LRRK2	83	100
MTOR	MTOR	83	100
ROCK1	ROCK1	83	100
RSK2(Kin.Dom.2-C-terminal)	RPS6KA3	83	100
TESK1	TESK1	83	100
MAP3K4	MAP3K4	84	100
PLK4	PLK4	84	100
SNRK	SNRK	84	100
TRKC	NTRK3	84	100
TYK2(JH2domain-pseudokinase)	TYK2	84	100
FLT3(D835V)	FLT3	85	100
MAP4K3	MAP4K3	85	100
PIK3CA(E545K)	PIK3CA	85	100
PIK3CA(Q546K)	PIK3CA	85	100
RIOK3	RIOK3	85	100
ABL1(Q252H)-nonphosphorylated	ABL1	86	100
HIPK3	HIPK3	86	100
MAP3K3	MAP3K3	86	100
MKK7	MAP2K7	86	100
p38-delta	MAPK13	86	100
PLK3	PLK3	86	100
PRKG2	PRKG2	86	100
RET(V804M)	RET	86	100

VPS34	PIK3C3	86	100
ABL1(F317I)-phosphorylated	ABL1	87	100
ARK5	NUAK1	87	100
BTK	BTK	87	100
CDK11	CDK19	87	100
HASPIN	GSG2	87	100
PIK3CA(I800L)	PIK3CA	87	100
PIK3CG	PIK3CG	87	100
TIE2	TEK	87	100
CSNK2A1	CSNK2A1	88	100
DDR2	DDR2	88	100
FLT3(ITD,D835V)	FLT3	88	100
PIK3C2B	PIK3C2B	88	100
PIK3CA(E545A)	PIK3CA	88	100
ALK	ALK	89	100
CDKL3	CDKL3	89	100
CSF1R	CSF1R	89	100
DMPK2	CDC42BPG	89	100
EGFR(E746-A750del)	EGFR	89	100
FLT3(D835H)	FLT3	89	100
GRK7	GRK7	89	100
MET	MET	89	100
NIM1	MGC42105	89	100
PIK3CA(E542K)	PIK3CA	89	100
SLK	SLK	89	100
ABL1(T315I)-nonphosphorylated	ABL1	90	100

BMPR1A	BMPR1A	90	100
CSNK1D	CSNK1D	90	100
MAK	MAK	90	100
MST1	STK4	90	100
PFPK5 (*P. falciparum*)	MAL13P1.279	90	100
RIPK5	DSTYK	90	100
ULK3	ULK3	90	100
ANKK1	ANKK1	91	100
NEK10	NEK10	91	100
ERN1	ERN1	92	100
IKK-alpha	CHUK	92	100
JAK1(JH2domain-pseudokinase)	JAK1	92	100
JNK3	MAPK10	92	100
PAK6	PAK6	92	100
PRKD2	PRKD2	92	100
S6K1	RPS6KB1	92	100
TNK2	TNK2	92	100
AMPK-alpha2	PRKAA2	93	100
IKK-beta	IKBKB	93	100
LIMK1	LIMK1	93	100
MYLK2	MYLK2	93	100
NEK3	NEK3	93	100
PRP4	PRPF4B	93	100
SGK3	SGK3	93	100
ABL1-nonphosphorylated	ABL1	94	100
FLT1	FLT1	94	100
FLT3(D835Y)	FLT3	94	100

FLT3-autoinhibited	FLT3	94	100
PIK3CA	PIK3CA	94	100
RET(V804L)	RET	94	100
ROCK2	ROCK2	94	100
RSK2(Kin.Dom.1-N-terminal)	RPS6KA3	94	100
SRPK1	SRPK1	94	100
TYK2(JH1domain-catalytic)	TYK2	94	100
VRK2	VRK2	94	100
ABL1(F317L)-phosphorylated	ABL1	95	100
ABL1-phosphorylated	ABL1	95	100
AKT3	AKT3	95	100
AMPK-alpha1	PRKAA1	95	100
BMPR1B	BMPR1B	95	100
HIPK4	HIPK4	95	100
INSR	INSR	95	100
IRAK3	IRAK3	95	100
IRAK4	IRAK4	95	100
MERTK	MERTK	95	100
PIK3C2G	PIK3C2G	95	100
PRKCE	PRKCE	95	100
PRKD3	PRKD3	95	100
CASK	CASK	96	100
CDK2	CDK2	96	100
CSNK2A2	CSNK2A2	96	100
FLT3(R834Q)	FLT3	96	100
RET	RET	96	100

TYRO3	TYRO3	96	100
WNK4	WNK4	96	100
ABL1(H396P)-phosphorylated	ABL1	97	100
ABL1(Q252H)-phosphorylated	ABL1	97	100
ABL1(Y253F)-phosphorylated	ABL1	97	100
ACVR1	ACVR1	97	100
CAMK1B	PNCK	97	100
CLK4	CLK4	97	100
CSF1R-autoinhibited	CSF1R	97	100
EIF2AK1	EIF2AK1	97	100
GRK2	ADRBK1	97	100
GSK3B	GSK3B	97	100
IRAK1	IRAK1	97	100
MAP3K2	MAP3K2	97	100
NDR1	STK38	97	100
p38-beta	MAPK11	97	100
PDGFRB	PDGFRB	97	100
PIK4CB	PI4KB	97	100
PRKCI	PRKCI	97	100
RIPK4	RIPK4	97	100
RSK4(Kin.Dom.1-N-terminal)	RPS6KA6	97	100
ZAK	ZAK	97	100
AURKA	AURKA	98	100
ERK5	MAPK7	98	100
FAK	PTK2	98	100

KIT(V559D,T670I)	KIT	98	100
SBK1	SBK1	98	100
SRPK2	SRPK2	98	100
TSSK1B	TSSK1B	98	100
VEGFR2	KDR	98	100
WEE1	WEE1	98	100
ADCK4	ADCK4	99	100
ASK1	MAP3K5	99	100
EPHA3	EPHA3	99	100
FGFR3(G697C)	FGFR3	99	100
JAK2(JH1domain-catalytic)	JAK2	99	100
KIT(V559D)	KIT	99	100
OSR1	OXSR1	99	100
PDPK1	PDPK1	99	100
SGK	SGK1	99	100
SRMS	SRMS	99	100
TAOK2	TAOK2	99	100
TGFBR1	TGFBR1	99	100
YANK3	STK32C	99	100
AAK1	AAK1	100	100
ABL1(E255K)-phosphorylated	ABL1	100	100
ABL1(F317I)-nonphosphorylated	ABL1	100	100
ABL1(F317L)-nonphosphorylated	ABL1	100	100
ABL1(M351T)-phosphorylated	ABL1	100	100
ABL1(T315I)-	ABL1	100	100

phosphorylated			
ABL2	ABL2	100	100
ACVR1B	ACVR1B	100	100
ACVR2A	ACVR2A	100	100
ACVR2B	ACVR2B	100	100
ACVRL1	ACVRL1	100	100
ADCK3	CABC1	100	100
AKT1	AKT1	100	100
AKT2	AKT2	100	100
ALK(C1156Y)	ALK	100	100
ALK(L1196M)	ALK	100	100
ASK2	MAP3K6	100	100
AXL	AXL	100	100
BIKE	BMP2K	100	100
BLK	BLK	100	100
BMPR2	BMPR2	100	100
BMX	BMX	100	100
BRAF	BRAF	100	100
BRAF(V600E)	BRAF	100	100
BRK	PTK6	100	100
BRSK1	BRSK1	100	100
BRSK2	BRSK2	100	100
BUB1	BUB1	100	100
CAMK1	CAMK1	100	100
CAMK1G	CAMK1G	100	100
CAMK2B	CAMK2B	100	100
CAMK2D	CAMK2D	100	100

CAMK2G	CAMK2G	100	100
CAMK4	CAMK4	100	100
CAMKK1	CAMKK1	100	100
CAMKK2	CAMKK2	100	100
CDC2L1	CDK11B	100	100
CDC2L2	CDC2L2	100	100
CDK3	CDK3	100	100
CDK4	CDK4	100	100
CDK4-cyclinD1	CDK4	100	100
CDK4-cyclinD3	CDK4	100	100
CDK5	CDK5	100	100
CDK7	CDK7	100	100
CDK8	CDK8	100	100
CDK9	CDK9	100	100
CDKL1	CDKL1	100	100
CDKL2	CDKL2	100	100
CHEK1	CHEK1	100	100
CHEK2	CHEK2	100	100
CIT	CIT	100	100
CLK1	CLK1	100	100
CLK2	CLK2	100	100
CLK3	CLK3	100	100
CSK	CSK	100	100
CSNK1A1	CSNK1A1	100	100
CSNK1A1L	CSNK1A1L	100	100
CSNK1E	CSNK1E	100	100
CSNK1G1	CSNK1G1	100	100

CSNK1G2	CSNK1G2	100	100
CSNK1G3	CSNK1G3	100	100
CTK	MATK	100	100
DAPK1	DAPK1	100	100
DAPK2	DAPK2	100	100
DAPK3	DAPK3	100	100
DCAMKL2	DCLK2	100	100
DDR1	DDR1	100	100
DLK	MAP3K12	100	100
DMPK	DMPK	100	100
DYRK1A	DYRK1A	100	100
DYRK2	DYRK2	100	100
EGFR	EGFR	100	100
EGFR(G719C)	EGFR	100	100
EGFR(G719S)	EGFR	100	100
EGFR(L747-E749del, A750P)	EGFR	100	100
EGFR(L747-S752del, P753S)	EGFR	100	100
EGFR(L747-T751del,Sins)	EGFR	100	100
EGFR(L858R)	EGFR	100	100
EGFR(L858R,T790M)	EGFR	100	100
EGFR(L861Q)	EGFR	100	100
EGFR(S752-I759del)	EGFR	100	100
EGFR(T790M)	EGFR	100	100
EPHA2	EPHA2	100	100
EPHA4	EPHA4	100	100
EPHA5	EPHA5	100	100

EPHA6	EPHA6	100	100
EPHA7	EPHA7	100	100
EPHA8	EPHA8	100	100
EPHB1	EPHB1	100	100
EPHB2	EPHB2	100	100
EPHB3	EPHB3	100	100
EPHB4	EPHB4	100	100
ERBB2	ERBB2	100	100
ERBB4	ERBB4	100	100
ERK1	MAPK3	100	100
ERK2	MAPK1	100	100
ERK3	MAPK6	100	100
ERK4	MAPK4	100	100
ERK8	MAPK15	100	100
FER	FER	100	100
FES	FES	100	100
FGFR1	FGFR1	100	100
FGFR2	FGFR2	100	100
FGFR3	FGFR3	100	100
FGFR4	FGFR4	100	100
FGR	FGR	100	100
FLT3	FLT3	100	100
FLT3(ITD)	FLT3	100	100
FLT3(K663Q)	FLT3	100	100
FLT3(N841I)	FLT3	100	100
FLT4	FLT4	100	100
FRK	FRK	100	100

FYN	FYN	100	100
GRK1	GRK1	100	100
GRK4	GRK4	100	100
GSK3A	GSK3A	100	100
HCK	HCK	100	100
HIPK1	HIPK1	100	100
HIPK2	HIPK2	100	100
HUNK	HUNK	100	100
ICK	ICK	100	100
IGF1R	IGF1R	100	100
IKK-epsilon	IKBKE	100	100
INSRR	INSRR	100	100
ITK	ITK	100	100
JAK1(JH1domain-catalytic)	JAK1	100	100
JAK3(JH1domain-catalytic)	JAK3	100	100
JNK2	MAPK9	100	100
KIT	KIT	100	100
KIT(D816H)	KIT	100	100
KIT(D816V)	KIT	100	100
KIT(L576P)	KIT	100	100
LIMK2	LIMK2	100	100
LKB1	STK11	100	100
LRRK2(G2019S)	LRRK2	100	100
LYN	LYN	100	100
LZK	MAP3K13	100	100
MAP4K4	MAP4K4	100	100

MAPKAPK2	MAPKAPK2	100	100
MAPKAPK5	MAPKAPK5	100	100
MARK1	MARK1	100	100
MARK2	MARK2	100	100
MARK4	MARK4	100	100
MET(Y1235D)	MET	100	100
MKNK1	MKNK1	100	100
MKNK2	MKNK2	100	100
MLK1	MAP3K9	100	100
MLK2	MAP3K10	100	100
MLK3	MAP3K11	100	100
MRCKA	CDC42BPA	100	100
MUSK	MUSK	100	100
MYLK4	MYLK4	100	100
MYO3A	MYO3A	100	100
NDR2	STK38L	100	100
NEK1	NEK1	100	100
NEK11	NEK11	100	100
NEK2	NEK2	100	100
NEK4	NEK4	100	100
NEK5	NEK5	100	100
NEK6	NEK6	100	100
NEK7	NEK7	100	100
NEK9	NEK9	100	100
NIK	MAP3K14	100	100
p38-alpha	MAPK14	100	100
p38-gamma	MAPK12	100	100

PAK3	PAK3	100	100
PAK4	PAK4	100	100
PAK7	PAK7	100	100
PCTK1	CDK16	100	100
PCTK2	CDK17	100	100
PCTK3	CDK18	100	100
PDGFRA	PDGFRA	100	100
PFTAIRE2	CDK15	100	100
PFTK1	CDK14	100	100
PHKG1	PHKG1	100	100
PHKG2	PHKG2	100	100
PIK3CA(H1047L)	PIK3CA	100	100
PIK3CB	PIK3CB	100	100
PIKFYVE	PIKFYVE	100	100
PIM1	PIM1	100	100
PIM2	PIM2	100	100
PIM3	PIM3	100	100
PIP5K1C	PIP5K1C	100	100
PKAC-alpha	PRKACA	100	100
PKAC-beta	PRKACB	100	100
PKMYT1	PKMYT1	100	100
PKN1	PKN1	100	100
PKN2	PKN2	100	100
PKNB (*M. tuberculosis*)	pknB	100	100
PRKCD	PRKCD	100	100
PRKG1	PRKG1	100	100
PRKR	EIF2AK2	100	100

PRKX	PRKX	100	100
PYK2	PTK2B	100	100
RAF1	RAF1	100	100
RET(M918T)	RET	100	100
RIOK1	RIOK1	100	100
RIOK2	RIOK2	100	100
RIPK1	RIPK1	100	100
RIPK2	RIPK2	100	100
ROS1	ROS1	100	100
RPS6KA4(Kin.Dom.1-N-terminal)	RPS6KA4	100	100
RPS6KA4(Kin.Dom.2-C-terminal)	RPS6KA4	100	100
RPS6KA5(Kin.Dom.1-N-terminal)	RPS6KA5	100	100
RPS6KA5(Kin.Dom.2-C-terminal)	RPS6KA5	100	100
RSK1(Kin.Dom.2-C-terminal)	RPS6KA1	100	100
RSK3(Kin.Dom.1-N-terminal)	RPS6KA2	100	100
RSK3(Kin.Dom.2-C-terminal)	RPS6KA2	100	100
RSK4(Kin.Dom.2-C-terminal)	RPS6KA6	100	100
SGK2	SGK2	100	100
SRC	SRC	100	100
SRPK3	SRPK3	100	100
STK16	STK16	100	100
STK33	STK33	100	100
STK35	STK35	100	100

STK39	STK39	100	100
SYK	SYK	100	100
TAK1	MAP3K7	100	100
TAOK1	TAOK1	100	100
TAOK3	TAOK3	100	100
TBK1	TBK1	100	100
TEC	TEC	100	100
TGFBR2	TGFBR2	100	100
TIE1	TIE1	100	100
TLK1	TLK1	100	100
TLK2	TLK2	100	100
TNIK	TNIK	100	100
TNK1	TNK1	100	100
TNNI3K	TNNI3K	100	100
TRKB	NTRK2	100	100
TRPM6	TRPM6	100	100
TSSK3	TSSK3	100	100
TTK	TTK	100	100
TXK	TXK	100	100
ULK1	ULK1	100	100
ULK2	ULK2	100	100
WEE2	WEE2	100	100
WNK1	WNK1	100	100
WNK2	WNK2	100	100
WNK3	WNK3	100	100
YES	YES1	100	100
ZAP70	ZAP70	100	100

Table S2. Selectivity screening results of G-5555 (**6**) at 1 μM.

DiscoveRx Gene Symbol	Entrez Gene Symbol	Percent Control	Compound Concentration (nM)
QSK	KIAA0999	0	1000
MST4	MST4	0	1000
YANK2	STK32B	0	1000
PAK2	PAK2	0	1000
MEK5	MAP2K5	0.2	1000
PFCDPK1 (*P. falciparum*)	CDPK1	0.4	1000
MAST1	MAST1	0.4	1000
DCAMKL3	DCLK3	0.5	1000
SIK	SIK1	0.6	1000
SIK2	SIK2	0.8	1000
MEK1	MAP2K1	1	1000
MEK2	MAP2K2	1.4	1000
MST3	STK24	1.7	1000
GAK	GAK	1.7	1000
SNARK	NUAK2	2	1000
LOK	STK10	2.1	1000
CAMK1D	CAMK1D	2.5	1000
STK36	STK36	2.9	1000
YANK1	STK32A	3.7	1000
LTK	LTK	4.1	1000
PAK1	PAK1	4.5	1000
MAP4K5	MAP4K5	5.3	1000
MRCKB	CDC42BPB	5.3	1000
LATS2	LATS2	8	1000

EPHB6	EPHB6	9	1000
MEK4	MAP2K4	9.6	1000
LCK	LCK	11	1000
DMPK2	CDC42BPG	15	1000
PRKD1	PRKD1	17	1000
NLK	NLK	17	1000
MARK3	MARK3	18	1000
WNK4	WNK4	18	1000
YSK4	MAP3K19	19	1000
AURKC	AURKC	20	1000
PRKD3	PRKD3	20	1000
AURKB	AURKB	23	1000
MAP4K3	MAP4K3	23	1000
MAP3K3	MAP3K3	23	1000
ARK5	NUAK1	24	1000
MINK	MINK1	26	1000
HPK1	MAP4K1	26	1000
PIP5K2C	PIP4K2C	26	1000
MST2	STK3	27	1000
PRKD2	PRKD2	27	1000
MEK3	MAP2K3	29	1000
MEK6	MAP2K6	30	1000
CAMK1B	PNCK	30	1000
MAP4K2	MAP4K2	32	1000
SLK	SLK	33	1000
EPHA1	EPHA1	34	1000
YSK1	STK25	36	1000

MET	MET	40	1000
AMPK-alpha1	PRKAA1	40	1000
LATS1	LATS1	41	1000
JNK1	MAPK8	41	1000
FLT3(ITD,F691L)	FLT3	43	1000
AURKA	AURKA	43	1000
MET(M1250T)	MET	45	1000
PAK6	PAK6	45	1000
MELK	MELK	47	1000
AMPK-alpha2	PRKAA2	47	1000
MAP3K15	MAP3K15	48	1000
MST1R	MST1R	48	1000
AKT3	AKT3	48	1000
DYRK1B	DYRK1B	49	1000
IRAK1	IRAK1	49	1000
MARK2	MARK2	49	1000
MST1	STK4	51	1000
DCAMKL2	DCLK2	51	1000
PKNB (*M. tuberculosis*)	pknB	51	1000
TNIK	TNIK	51	1000
MAP3K4	MAP3K4	52	1000
TIE2	TEK	52	1000
ULK3	ULK3	52	1000
ERK5	MAPK7	52	1000
CSNK1E	CSNK1E	52	1000
DDR1	DDR1	53	1000
PRKCQ	PRKCQ	55	1000

ABL1(H396P)-nonphosphorylated	ABL1	56	1000
MYO3B	MYO3B	57	1000
RSK3(Kin.Dom.1-N-terminal)	RPS6KA2	57	1000
S6K1	RPS6KB1	58	1000
CDKL2	CDKL2	58	1000
LIMK1	LIMK1	59	1000
CAMK1	CAMK1	59	1000
SGK3	SGK3	60	1000
NEK2	NEK2	60	1000
GCN2(Kin.Dom.2,S808G)	EIF2AK4	63	1000
KIT(A829P)	KIT	63	1000
RSK2(Kin.Dom.2-C-terminal)	RPS6KA3	63	1000
BTK	BTK	63	1000
PRKCI	PRKCI	63	1000
TRKA	NTRK1	64	1000
RSK2(Kin.Dom.1-N-terminal)	RPS6KA3	65	1000
RIPK2	RIPK2	65	1000
PIP5K1A	PIP5K1A	67	1000
PLK4	PLK4	67	1000
FLT3(D835V)	FLT3	67	1000
MAP3K2	MAP3K2	67	1000
MARK1	MARK1	68	1000
TBK1	TBK1	68	1000
RSK1(Kin.Dom.1-N-terminal)	RPS6KA1	69	1000
STK16	STK16	69	1000

WNK1	WNK1	69	1000
NDR1	STK38	70	1000
SRPK2	SRPK2	70	1000
ASK2	MAP3K6	70	1000
MRCKA	CDC42BPA	70	1000
SgK110	SgK110	71	1000
PRKCE	PRKCE	71	1000
ASK1	MAP3K5	71	1000
PDPK1	PDPK1	71	1000
FRK	FRK	71	1000
GRK3	ADRBK2	72	1000
NEK3	NEK3	72	1000
EPHA8	EPHA8	72	1000
FLT3(ITD,D835V)	FLT3	74	1000
TYK2(JH1domain-catalytic)	TYK2	74	1000
ERK1	MAPK3	74	1000
LYN	LYN	74	1000
ABL1(Q252H)-nonphosphorylated	ABL1	75	1000
JNK2	MAPK9	75	1000
STK33	STK33	75	1000
MKK7	MAP2K7	77	1000
PAK4	PAK4	77	1000
PRKCH	PRKCH	78	1000
IKK-epsilon	IKBKE	78	1000
DCAMKL1	DCLK1	79	1000
YANK3	STK32C	79	1000

EPHB2	EPHB2	79	1000
IKK-beta	IKBKB	80	1000
KIT-autoinhibited	KIT	81	1000
MYLK2	MYLK2	81	1000
FLT3(D835Y)	FLT3	81	1000
RSK1(Kin.Dom.2-C-terminal)	RPS6KA1	81	1000
PAK7	PAK7	82	1000
MTOR	MTOR	83	1000
JAK2(JH1domain-catalytic)	JAK2	83	1000
CSNK1G2	CSNK1G2	83	1000
PLK2	PLK2	84	1000
ALK	ALK	84	1000
CSF1R-autoinhibited	CSF1R	84	1000
PDGFRB	PDGFRB	84	1000
EGFR(L747-E749del, A750P)	EGFR	84	1000
FES	FES	84	1000
TSSK3	TSSK3	84	1000
MYLK	MYLK	85	1000
BMPR1A	BMPR1A	85	1000
ABL1-nonphosphorylated	ABL1	85	1000
CSK	CSK	85	1000
EGFR(L858R)	EGFR	85	1000
EGFR(T790M)	EGFR	85	1000
ULK1	ULK1	85	1000
PIK3CA(H1047Y)	PIK3CA	86	1000
ERBB3	ERBB3	86	1000

TNK2	TNK2	86	1000
CDK7	CDK7	86	1000
ERK2	MAPK1	86	1000
PIP5K2B	PIP4K2B	87	1000
ANKK1	ANKK1	87	1000
JNK3	MAPK10	87	1000
ABL1(F317L)-nonphosphorylated	ABL1	87	1000
FYN	FYN	87	1000
TAOK1	TAOK1	87	1000
CAMK2A	CAMK2A	88	1000
EPHA3	EPHA3	88	1000
EGFR	EGFR	88	1000
MLK2	MAP3K10	88	1000
WNK2	WNK2	88	1000
SNRK	SNRK	89	1000
GRK7	GRK7	89	1000
BUB1	BUB1	89	1000
CSNK1A1	CSNK1A1	89	1000
RIOK3	RIOK3	90	1000
PIK3CA(E545A)	PIK3CA	90	1000
ROCK2	ROCK2	90	1000
JAK3(JH1domain-catalytic)	JAK3	90	1000
RIPK5	DSTYK	91	1000
CSF1R	CSF1R	92	1000
JAK1(JH2domain-pseudokinase)	JAK1	92	1000
IRAK3	IRAK3	92	1000

TYRO3	TYRO3	92	1000
PKN1	PKN1	92	1000
RSK3(Kin.Dom.2-C-terminal)	RPS6KA2	92	1000
RSK4(Kin.Dom.2-C-terminal)	RPS6KA6	92	1000
TAK1	MAP3K7	92	1000
PLK3	PLK3	93	1000
PIK3CG	PIK3CG	93	1000
VEGFR2	KDR	93	1000
BRAF(V600E)	BRAF	93	1000
MET(Y1235D)	MET	93	1000
PLK1	PLK1	94	1000
PRKG2	PRKG2	94	1000
RET	RET	94	1000
ABL1(H396P)-phosphorylated	ABL1	94	1000
PRKR	EIF2AK2	94	1000
TIE1	TIE1	94	1000
PRP4	PRPF4B	95	1000
ABL1-phosphorylated	ABL1	95	1000
IRAK4	IRAK4	95	1000
CSNK2A2	CSNK2A2	95	1000
RSK4(Kin.Dom.1-N-terminal)	RPS6KA6	95	1000
PKAC-beta	PRKACB	95	1000
TRKC	NTRK3	96	1000
ABL1(F317I)-phosphorylated	ABL1	96	1000
BMPR1B	BMPR1B	96	1000

ACVR1B	ACVR1B	96	1000
AXL	AXL	96	1000
CAMK4	CAMK4	96	1000
MLK1	MAP3K9	96	1000
MYO3A	MYO3A	96	1000
PDGFRA	PDGFRA	96	1000
PIK3CD	PIK3CD	97	1000
CDC2L5	CDK13	97	1000
CDKL5	CDKL5	97	1000
PIK3CA(E545K)	PIK3CA	97	1000
INSR	INSR	97	1000
CDC2L1	CDK11B	97	1000
FLT3(N841I)	FLT3	97	1000
MKNK2	MKNK2	97	1000
PIK3CB	PIK3CB	97	1000
TTK	TTK	97	1000
MAP3K1	MAP3K1	98	1000
TYK2(JH2domain-pseudokinase)	TYK2	98	1000
CSNK2A1	CSNK2A1	98	1000
IKK-alpha	CHUK	98	1000
SRPK1	SRPK1	98	1000
CDK5	CDK5	98	1000
TNNI3K	TNNI3K	98	1000
TESK1	TESK1	99	1000
FLT3(D835H)	FLT3	99	1000
BLK	BLK	99	1000
CAMK1G	CAMK1G	99	1000

CDK4-cyclinD1	CDK4	99	1000
DRAK2	STK17B	100	1000
MLCK	MYLK3	100	1000
PIK3CA(M1043I)	PIK3CA	100	1000
KIT(V559D,V654A)	KIT	100	1000
DRAK1	STK17A	100	1000
PIK3CA(C420R)	PIK3CA	100	1000
LRRK2	LRRK2	100	1000
ROCK1	ROCK1	100	1000
PIK3CA(Q546K)	PIK3CA	100	1000
HIPK3	HIPK3	100	1000
p38-delta	MAPK13	100	1000
RET(V804M)	RET	100	1000
VPS34	PIK3C3	100	1000
CDK11	CDK19	100	1000
HASPIN	GSG2	100	1000
PIK3CA(I800L)	PIK3CA	100	1000
DDR2	DDR2	100	1000
PIK3C2B	PIK3C2B	100	1000
CDKL3	CDKL3	100	1000
EGFR(E746-A750del)	EGFR	100	1000
NIM1	MGC42105	100	1000
PIK3CA(E542K)	PIK3CA	100	1000
ABL1(T315I)-nonphosphorylated	ABL1	100	1000
CSNK1D	CSNK1D	100	1000
MAK	MAK	100	1000
PFPK5(*P. falciparum*)	MAL13P1.279	100	1000

NEK10	NEK10	100	1000
ERN1	ERN1	100	1000
FLT1	FLT1	100	1000
FLT3-autoinhibited	FLT3	100	1000
PIK3CA	PIK3CA	100	1000
RET(V804L)	RET	100	1000
VRK2	VRK2	100	1000
ABL1(F317L)-phosphorylated	ABL1	100	1000
HIPK4	HIPK4	100	1000
MERTK	MERTK	100	1000
PIK3C2G	PIK3C2G	100	1000
CASK	CASK	100	1000
CDK2	CDK2	100	1000
FLT3(R834Q)	FLT3	100	1000
ABL1(Q252H)-phosphorylated	ABL1	100	1000
ABL1(Y253F)-phosphorylated	ABL1	100	1000
ACVR1	ACVR1	100	1000
CLK4	CLK4	100	1000
EIF2AK1	EIF2AK1	100	1000
GRK2	ADRBK1	100	1000
GSK3B	GSK3B	100	1000
p38-beta	MAPK11	100	1000
PIK4CB	PI4KB	100	1000
RIPK4	RIPK4	100	1000
ZAK	ZAK	100	1000
FAK	PTK2	100	1000

KIT(V559D,T670I)	KIT	100	1000
SBK1	SBK1	100	1000
TSSK1B	TSSK1B	100	1000
WEE1	WEE1	100	1000
ADCK4	ADCK4	100	1000
FGFR3(G697C)	FGFR3	100	1000
KIT(V559D)	KIT	100	1000
OSR1	OXSR1	100	1000
SGK	SGK1	100	1000
SRMS	SRMS	100	1000
TAOK2	TAOK2	100	1000
TGFBR1	TGFBR1	100	1000
AAK1	AAK1	100	1000
ABL1(E255K)-phosphorylated	ABL1	100	1000
ABL1(F317I)-nonphosphorylated	ABL1	100	1000
ABL1(M351T)-phosphorylated	ABL1	100	1000
ABL1(T315I)-phosphorylated	ABL1	100	1000
ABL2	ABL2	100	1000
ACVR2A	ACVR2A	100	1000
ACVR2B	ACVR2B	100	1000
ACVRL1	ACVRL1	100	1000
ADCK3	CABC1	100	1000
AKT1	AKT1	100	1000
AKT2	AKT2	100	1000
ALK(C1156Y)	ALK	100	1000

ALK(L1196M)	ALK	100	1000
BIKE	BMP2K	100	1000
BMPR2	BMPR2	100	1000
BMX	BMX	100	1000
BRAF	BRAF	100	1000
BRK	PTK6	100	1000
BRSK1	BRSK1	100	1000
BRSK2	BRSK2	100	1000
CAMK2B	CAMK2B	100	1000
CAMK2D	CAMK2D	100	1000
CAMK2G	CAMK2G	100	1000
CAMKK1	CAMKK1	100	1000
CAMKK2	CAMKK2	100	1000
CDC2L2	CDC2L2	100	1000
CDK3	CDK3	100	1000
CDK4	CDK4	100	1000
CDK4-cyclinD3	CDK4	100	1000
CDK8	CDK8	100	1000
CDK9	CDK9	100	1000
CDKL1	CDKL1	100	1000
CHEK1	CHEK1	100	1000
CHEK2	CHEK2	100	1000
CIT	CIT	100	1000
CLK1	CLK1	100	1000
CLK2	CLK2	100	1000
CLK3	CLK3	100	1000
CSNK1A1L	CSNK1A1L	100	1000

CSNK1G1	CSNK1G1	100	1000
CSNK1G3	CSNK1G3	100	1000
CTK	MATK	100	1000
DAPK1	DAPK1	100	1000
DAPK2	DAPK2	100	1000
DAPK3	DAPK3	100	1000
DLK	MAP3K12	100	1000
DMPK	DMPK	100	1000
DYRK1A	DYRK1A	100	1000
DYRK2	DYRK2	100	1000
EGFR(G719C)	EGFR	100	1000
EGFR(G719S)	EGFR	100	1000
EGFR(L747-S752del, P753S)	EGFR	100	1000
EGFR(L747-T751del,Sins)	EGFR	100	1000
EGFR(L858R,T790M)	EGFR	100	1000
EGFR(L861Q)	EGFR	100	1000
EGFR(S752-I759del)	EGFR	100	1000
EPHA2	EPHA2	100	1000
EPHA4	EPHA4	100	1000
EPHA5	EPHA5	100	1000
EPHA6	EPHA6	100	1000
EPHA7	EPHA7	100	1000
EPHB1	EPHB1	100	1000
EPHB3	EPHB3	100	1000
EPHB4	EPHB4	100	1000
ERBB2	ERBB2	100	1000

ERBB4	ERBB4	100	1000
ERK3	MAPK6	100	1000
ERK4	MAPK4	100	1000
ERK8	MAPK15	100	1000
FER	FER	100	1000
FGFR1	FGFR1	100	1000
FGFR2	FGFR2	100	1000
FGFR3	FGFR3	100	1000
FGFR4	FGFR4	100	1000
FGR	FGR	100	1000
FLT3	FLT3	100	1000
FLT3(ITD)	FLT3	100	1000
FLT3(K663Q)	FLT3	100	1000
FLT4	FLT4	100	1000
GRK1	GRK1	100	1000
GRK4	GRK4	100	1000
GSK3A	GSK3A	100	1000
HCK	HCK	100	1000
HIPK1	HIPK1	100	1000
HIPK2	HIPK2	100	1000
HUNK	HUNK	100	1000
ICK	ICK	100	1000
IGF1R	IGF1R	100	1000
INSRR	INSRR	100	1000
ITK	ITK	100	1000
JAK1(JH1domain-catalytic)	JAK1	100	1000
KIT	KIT	100	1000

KIT(D816H)	KIT	100	1000
KIT(D816V)	KIT	100	1000
KIT(L576P)	KIT	100	1000
LIMK2	LIMK2	100	1000
LKB1	STK11	100	1000
LRRK2(G2019S)	LRRK2	100	1000
LZK	MAP3K13	100	1000
MAP4K4	MAP4K4	100	1000
MAPKAPK2	MAPKAPK2	100	1000
MAPKAPK5	MAPKAPK5	100	1000
MARK4	MARK4	100	1000
MKNK1	MKNK1	100	1000
MLK3	MAP3K11	100	1000
MUSK	MUSK	100	1000
MYLK4	MYLK4	100	1000
NDR2	STK38L	100	1000
NEK1	NEK1	100	1000
NEK11	NEK11	100	1000
NEK4	NEK4	100	1000
NEK5	NEK5	100	1000
NEK6	NEK6	100	1000
NEK7	NEK7	100	1000
NEK9	NEK9	100	1000
NIK	MAP3K14	100	1000
p38-alpha	MAPK14	100	1000
p38-gamma	MAPK12	100	1000
PAK3	PAK3	100	1000

PCTK1	CDK16	100	1000
PCTK2	CDK17	100	1000
PCTK3	CDK18	100	1000
PFTAIRE2	CDK15	100	1000
PFTK1	CDK14	100	1000
PHKG1	PHKG1	100	1000
PHKG2	PHKG2	100	1000
PIK3CA(H1047L)	PIK3CA	100	1000
PIKFYVE	PIKFYVE	100	1000
PIM1	PIM1	100	1000
PIM2	PIM2	100	1000
PIM3	PIM3	100	1000
PIP5K1C	PIP5K1C	100	1000
PKAC-alpha	PRKACA	100	1000
PKMYT1	PKMYT1	100	1000
PKN2	PKN2	100	1000
PRKCD	PRKCD	100	1000
PRKG1	PRKG1	100	1000
PRKX	PRKX	100	1000
PYK2	PTK2B	100	1000
RAF1	RAF1	100	1000
RET(M918T)	RET	100	1000
RIOK1	RIOK1	100	1000
RIOK2	RIOK2	100	1000
RIPK1	RIPK1	100	1000
ROS1	ROS1	100	1000
RPS6KA4(Kin.Dom.1-N-terminal)	RPS6KA4	100	1000

RPS6KA4(Kin.Dom.2-C-terminal)	RPS6KA4	100	1000
RPS6KA5(Kin.Dom.1-N-terminal)	RPS6KA5	100	1000
RPS6KA5(Kin.Dom.2-C-terminal)	RPS6KA5	100	1000
SGK2	SGK2	100	1000
SRC	SRC	100	1000
SRPK3	SRPK3	100	1000
STK35	STK35	100	1000
STK39	STK39	100	1000
SYK	SYK	100	1000
TAOK3	TAOK3	100	1000
TEC	TEC	100	1000
TGFBR2	TGFBR2	100	1000
TLK1	TLK1	100	1000
TLK2	TLK2	100	1000
TNK1	TNK1	100	1000
TRKB	NTRK2	100	1000
TRPM6	TRPM6	100	1000
TXK	TXK	100	1000
ULK2	ULK2	100	1000
WEE2	WEE2	100	1000
WNK3	WNK3	100	1000
YES	YES1	100	1000
ZAP70	ZAP70	100	1000

Table S3. Selectivity screening results for **7** at 1μM.

DiscoveRx Gene Symbol	Entrez Gene Symbol	Percent Control	Compound Concentration (nM)
KIT(A829P)	KIT	0	1000
MST4	MST4	0	1000
PAK2	PAK2	0	1000
YANK2	STK32B	0	1000
MEK5	MAP2K5	0.2	1000
MEK4	MAP2K4	0.3	1000
CAMK1D	CAMK1D	0.4	1000
SIK	SIK1	0.7	1000
MAP4K5	MAP4K5	0.9	1000
GAK	GAK	1	1000
SIK2	SIK2	1	1000
LOK	STK10	1.2	1000
YANK1	STK32A	1.4	1000
EPHB6	EPHB6	1.6	1000
MST3	STK24	1.7	1000
CAMK1B	PNCK	2.2	1000
LTK	LTK	2.6	1000
TNK2	TNK2	3.5	1000
ARK5	NUAK1	3.9	1000
PAK1	PAK1	3.9	1000
FES	FES	4.7	1000
STK36	STK36	4.7	1000
FER	FER	5.2	1000
SNARK	NUAK2	5.5	1000

FRK	FRK	5.8	1000
DCAMKL2	DCLK2	6	1000
PFCDPK1 (*P. falciparum*)	CDPK1	6.6	1000
FAK	PTK2	7.1	1000
PDGFRB	PDGFRB	8	1000
KIT(V559D)	KIT	8.4	1000
YANK3	STK32C	8.5	1000
PLK4	PLK4	9.1	1000
LCK	LCK	9.3	1000
MAP4K3	MAP4K3	10	1000
MEK1	MAP2K1	11	1000
MRCKB	CDC42BPB	11	1000
NLK	NLK	11	1000
CSF1R	CSF1R	12	1000
PLK3	PLK3	12	1000
PYK2	PTK2B	13	1000
MEK2	MAP2K2	14	1000
MINK	MINK1	14	1000
PRKD3	PRKD3	14	1000
MAP4K4	MAP4K4	15	1000
WNK4	WNK4	15	1000
JNK1	MAPK8	16	1000
KIT(L576P)	KIT	16	1000
MAST1	MAST1	16	1000
CAMK1	CAMK1	17	1000
EGFR(L861Q)	EGFR	17	1000
HPK1	MAP4K1	17	1000

MARK3	MARK3	17	1000
AURKB	AURKB	18	1000
SLK	SLK	18	1000
AURKC	AURKC	19	1000
EGFR(G719C)	EGFR	19	1000
EGFR(L858R)	EGFR	19	1000
ERK5	MAPK7	19	1000
KIT(D816V)	KIT	20	1000
PIP5K2C	PIP4K2C	20	1000
KIT	KIT	22	1000
TNK1	TNK1	22	1000
EPHA1	EPHA1	23	1000
ERBB4	ERBB4	23	1000
TNIK	TNIK	23	1000
MST1	STK4	24	1000
BLK	BLK	25	1000
MEK6	MAP2K6	26	1000
PRKD1	PRKD1	26	1000
MEK3	MAP2K3	28	1000
MST2	STK3	28	1000
DMPK2	CDC42BPG	29	1000
LATS2	LATS2	29	1000
PRKD2	PRKD2	31	1000
PAK3	PAK3	32	1000
MELK	MELK	33	1000
MYO3A	MYO3A	33	1000
AURKA	AURKA	34	1000

MYO3B	MYO3B	34	1000
YSK1	STK25	36	1000
ABL1(F317L)-phosphorylated	ABL1	37	1000
QSK	KIAA0999	38	1000
LIMK1	LIMK1	40	1000
MLK1	MAP3K9	40	1000
HCK	HCK	41	1000
KIT(D816H)	KIT	41	1000
MAP3K3	MAP3K3	42	1000
AMPK-alpha1	PRKAA1	43	1000
DCAMKL3	DCLK3	43	1000
ERBB2	ERBB2	44	1000
SYK	SYK	45	1000
MAP4K2	MAP4K2	46	1000
ABL1(F317L)-nonphosphorylated	ABL1	48	1000
LATS1	LATS1	48	1000
LYN	LYN	48	1000
PDGFRA	PDGFRA	48	1000
EGFR(G719S)	EGFR	50	1000
EGFR(T790M)	EGFR	50	1000
FLT3(D835Y)	FLT3	50	1000
WNK2	WNK2	50	1000
FLT3(K663Q)	FLT3	52	1000
ABL1(H396P)-nonphosphorylated	ABL1	53	1000
DCAMKL1	DCLK1	53	1000
FLT3	FLT3	53	1000

JNK2	MAPK9	53	1000
MAP3K2	MAP3K2	53	1000
MAP3K4	MAP3K4	54	1000
MARK1	MARK1	56	1000
ABL1(F317I)-phosphorylated	ABL1	57	1000
ERK1	MAPK3	57	1000
MKK7	MAP2K7	57	1000
EGFR	EGFR	58	1000
JNK3	MAPK10	58	1000
FLT3(D835V)	FLT3	59	1000
TESK1	TESK1	59	1000
ERK2	MAPK1	60	1000
MARK2	MARK2	60	1000
VEGFR2	KDR	60	1000
DDR2	DDR2	61	1000
TSSK1B	TSSK1B	61	1000
ULK3	ULK3	61	1000
NEK3	NEK3	62	1000
RET	RET	62	1000
CSNK1E	CSNK1E	63	1000
EGFR(L747-S752del, P753S)	EGFR	63	1000
RSK2(Kin.Dom.1-N-terminal)	RPS6KA3	63	1000
TRKA	NTRK1	63	1000
PLK2	PLK2	64	1000
SRPK2	SRPK2	64	1000
STK33	STK33	64	1000

ABL1(Y253F)-phosphorylated	ABL1	65	1000
PKN2	PKN2	65	1000
CDK4	CDK4	66	1000
EGFR(E746-A750del)	EGFR	66	1000
FLT3(ITD,F691L)	FLT3	66	1000
YSK4	MAP3K19	66	1000
TIE2	TEK	68	1000
FGR	FGR	69	1000
PIP5K1A	PIP5K1A	69	1000
LRRK2	LRRK2	70	1000
EGFR(L858R,T790M)	EGFR	71	1000
FLT3(N841I)	FLT3	71	1000
FLT3(R834Q)	FLT3	71	1000
INSR	INSR	71	1000
KIT-autoinhibited	KIT	71	1000
MAP3K15	MAP3K15	71	1000
MARK4	MARK4	71	1000
NDR1	STK38	71	1000
TTK	TTK	71	1000
ADCK4	ADCK4	72	1000
CAMK2A	CAMK2A	72	1000
GRK1	GRK1	72	1000
RSK2(Kin.Dom.2-C-terminal)	RPS6KA3	72	1000
BRK	PTK6	73	1000
BUB1	BUB1	73	1000
FLT3-autoinhibited	FLT3	73	1000

NEK10	NEK10	73	1000
ROCK2	ROCK2	73	1000
WNK1	WNK1	73	1000
ABL1(F317I)-nonphosphorylated	ABL1	74	1000
BTK	BTK	74	1000
NEK2	NEK2	74	1000
PDPK1	PDPK1	74	1000
TSSK3	TSSK3	74	1000
ABL1(Q252H)-nonphosphorylated	ABL1	75	1000
ANKK1	ANKK1	75	1000
DDR1	DDR1	75	1000
JAK1(JH2domain-pseudokinase)	JAK1	75	1000
MKNK2	MKNK2	75	1000
PAK6	PAK6	75	1000
PAK7	PAK7	75	1000
SGK2	SGK2	75	1000
SNRK	SNRK	75	1000
ULK1	ULK1	75	1000
ABL1(M351T)-phosphorylated	ABL1	76	1000
ABL2	ABL2	76	1000
HASPIN	GSG2	76	1000
PIK3CA(Q546K)	PIK3CA	76	1000
RIPK5	DSTYK	76	1000
ROCK1	ROCK1	76	1000
RSK4(Kin.Dom.1-N-terminal)	RPS6KA6	76	1000

WNK3	WNK3	76	1000
AMPK-alpha2	PRKAA2	77	1000
CHEK2	CHEK2	77	1000
EGFR(L747-T751del,Sins)	EGFR	77	1000
IKK-alpha	CHUK	77	1000
PFTAIRE2	CDK15	77	1000
GRK7	GRK7	78	1000
MRCKA	CDC42BPA	78	1000
MYLK	MYLK	78	1000
PCTK2	CDK17	78	1000
ABL1-nonphosphorylated	ABL1	79	1000
CHEK1	CHEK1	79	1000
JAK2(JH1domain-catalytic)	JAK2	79	1000
MTOR	MTOR	79	1000
NEK11	NEK11	79	1000
PHKG2	PHKG2	79	1000
PLK1	PLK1	79	1000
SGK	SGK1	79	1000
STK39	STK39	79	1000
VPS34	PIK3C3	79	1000
ABL1(T315I)-phosphorylated	ABL1	80	1000
CAMK1G	CAMK1G	80	1000
ERBB3	ERBB3	80	1000
RSK3(Kin.Dom.2-C-terminal)	RPS6KA2	80	1000
EPHA8	EPHA8	81	1000

FLT3(D835H)	FLT3	81	1000
PFPK5 (P. *falciparum*)	MAL13P1.279	81	1000
RSK3(Kin.Dom.1-N-terminal)	RPS6KA2	81	1000
BMPR1B	BMPR1B	82	1000
NIM1	MGC42105	82	1000
PRP4	PRPF4B	82	1000
RSK4(Kin.Dom.2-C-terminal)	RPS6KA6	82	1000
SGK3	SGK3	82	1000
TBK1	TBK1	82	1000
VRK2	VRK2	82	1000
ABL1(T315I)-nonphosphorylated	ABL1	83	1000
EIF2AK1	EIF2AK1	83	1000
PAK4	PAK4	83	1000
PIK3CA(E545K)	PIK3CA	83	1000
PIK3CB	PIK3CB	83	1000
ABL1-phosphorylated	ABL1	84	1000
AXL	AXL	84	1000
ERK4	MAPK4	84	1000
NDR2	STK38L	84	1000
S6K1	RPS6KB1	84	1000
TXK	TXK	84	1000
ULK2	ULK2	84	1000
YES	YES1	84	1000
CSF1R-autoinhibited	CSF1R	85	1000
CSNK1A1L	CSNK1A1L	85	1000
TRKC	NTRK3	85	1000

TYRO3	TYRO3	85	1000
CDC2L5	CDK13	86	1000
CDK9	CDK9	86	1000
IRAK1	IRAK1	86	1000
PIP5K1C	PIP5K1C	86	1000
TYK2(JH1domain-catalytic)	TYK2	86	1000
ABL1(Q252H)-phosphorylated	ABL1	87	1000
CSK	CSK	87	1000
MLCK	MYLK3	87	1000
CDKL5	CDKL5	88	1000
CSNK2A1	CSNK2A1	88	1000
ERN1	ERN1	88	1000
FLT3(ITD,D835V)	FLT3	88	1000
GCN2(Kin.Dom.2,S808G)	EIF2AK4	88	1000
OSR1	OXSR1	88	1000
PRKG2	PRKG2	88	1000
RIOK3	RIOK3	88	1000
RSK1(Kin.Dom.2-C-terminal)	RPS6KA1	88	1000
TRPM6	TRPM6	88	1000
IGF1R	IGF1R	89	1000
PHKG1	PHKG1	89	1000
PIK3CG	PIK3CG	89	1000
RET(M918T)	RET	89	1000
TEC	TEC	89	1000
DAPK2	DAPK2	90	1000
IRAK4	IRAK4	90	1000

JAK3(JH1domain-catalytic)	JAK3	90	1000
MLK3	MAP3K11	90	1000
PIK3CA(I800L)	PIK3CA	90	1000
ABL1(E255K)-phosphorylated	ABL1	91	1000
ABL1(H396P)-phosphorylated	ABL1	91	1000
CDC2L1	CDK11B	91	1000
EGFR(S752-I759del)	EGFR	91	1000
HIPK2	HIPK2	91	1000
IKK-beta	IKBKB	91	1000
ITK	ITK	91	1000
KIT(V559D,V654A)	KIT	91	1000
LRRK2(G2019S)	LRRK2	91	1000
MET	MET	91	1000
MUSK	MUSK	91	1000
TIE1	TIE1	91	1000
CLK1	CLK1	92	1000
DYRK1A	DYRK1A	92	1000
EPHB1	EPHB1	92	1000
GRK3	ADRBK2	92	1000
PIK3CA(E542K)	PIK3CA	92	1000
CSNK1G2	CSNK1G2	93	1000
DAPK3	DAPK3	93	1000
FLT4	FLT4	93	1000
MST1R	MST1R	93	1000
PRKCI	PRKCI	93	1000
TYK2(JH2domain-	TYK2	93	1000

pseudokinase)			
CAMK2D	CAMK2D	94	1000
CAMK2G	CAMK2G	94	1000
CAMKK2	CAMKK2	94	1000
LZK	MAP3K13	94	1000
PIK3CA(H1047L)	PIK3CA	94	1000
PRKCE	PRKCE	94	1000
RSK1(Kin.Dom.1-N-terminal)	RPS6KA1	94	1000
STK16	STK16	94	1000
TLK1	TLK1	94	1000
CDK7	CDK7	95	1000
DAPK1	DAPK1	95	1000
MET(M1250T)	MET	95	1000
NEK7	NEK7	95	1000
PIK3C2B	PIK3C2B	95	1000
RPS6KA5(Kin.Dom.2-C-terminal)	RPS6KA5	95	1000
CSNK2A2	CSNK2A2	96	1000
DRAK2	STK17B	96	1000
PRKX	PRKX	96	1000
RIPK4	RIPK4	96	1000
BMPR2	BMPR2	97	1000
CDK8	CDK8	97	1000
CSNK1A1	CSNK1A1	97	1000
DLK	MAP3K12	97	1000
GRK2	ADRBK1	97	1000
IKK-epsilon	IKBKE	97	1000

INSRR	INSRR	97	1000
PIK3CA	PIK3CA	97	1000
RPS6KA4(Kin.Dom.2-C-terminal)	RPS6KA4	97	1000
CAMKK1	CAMKK1	98	1000
FYN	FYN	98	1000
NEK6	NEK6	98	1000
p38-delta	MAPK13	98	1000
SgK110	SgK110	98	1000
WEE2	WEE2	98	1000
CAMK2B	CAMK2B	99	1000
HIPK4	HIPK4	99	1000
LIMK2	LIMK2	99	1000
MAPKAPK5	MAPKAPK5	99	1000
PIK3CA(C420R)	PIK3CA	99	1000
PKMYT1	PKMYT1	99	1000
SRC	SRC	99	1000
AAK1	AAK1	100	1000
ACVR1	ACVR1	100	1000
ACVR1B	ACVR1B	100	1000
ACVR2A	ACVR2A	100	1000
ACVR2B	ACVR2B	100	1000
ACVRL1	ACVRL1	100	1000
ADCK3	CABC1	100	1000
AKT1	AKT1	100	1000
AKT2	AKT2	100	1000
AKT3	AKT3	100	1000
ALK	ALK	100	1000

ALK(C1156Y)	ALK	100	1000
ALK(L1196M)	ALK	100	1000
ASK1	MAP3K5	100	1000
ASK2	MAP3K6	100	1000
BIKE	BMP2K	100	1000
BMPR1A	BMPR1A	100	1000
BMX	BMX	100	1000
BRAF	BRAF	100	1000
BRAF(V600E)	BRAF	100	1000
BRSK1	BRSK1	100	1000
BRSK2	BRSK2	100	1000
CAMK4	CAMK4	100	1000
CASK	CASK	100	1000
CDC2L2	CDC2L2	100	1000
CDK11	CDK19	100	1000
CDK2	CDK2	100	1000
CDK3	CDK3	100	1000
CDK4-cyclinD1	CDK4	100	1000
CDK4-cyclinD3	CDK4	100	1000
CDK5	CDK5	100	1000
CDKL1	CDKL1	100	1000
CDKL2	CDKL2	100	1000
CDKL3	CDKL3	100	1000
CIT	CIT	100	1000
CLK2	CLK2	100	1000
CLK3	CLK3	100	1000
CLK4	CLK4	100	1000

CSNK1D	CSNK1D	100	1000
CSNK1G1	CSNK1G1	100	1000
CSNK1G3	CSNK1G3	100	1000
CTK	MATK	100	1000
DMPK	DMPK	100	1000
DRAK1	STK17A	100	1000
DYRK1B	DYRK1B	100	1000
DYRK2	DYRK2	100	1000
EGFR(L747-E749del, A750P)	EGFR	100	1000
EPHA2	EPHA2	100	1000
EPHA3	EPHA3	100	1000
EPHA4	EPHA4	100	1000
EPHA5	EPHA5	100	1000
EPHA6	EPHA6	100	1000
EPHA7	EPHA7	100	1000
EPHB2	EPHB2	100	1000
EPHB3	EPHB3	100	1000
EPHB4	EPHB4	100	1000
ERK3	MAPK6	100	1000
ERK8	MAPK15	100	1000
FGFR1	FGFR1	100	1000
FGFR2	FGFR2	100	1000
FGFR3	FGFR3	100	1000
FGFR3(G697C)	FGFR3	100	1000
FGFR4	FGFR4	100	1000
FLT1	FLT1	100	1000
FLT3(ITD)	FLT3	100	1000

GRK4	GRK4	100	1000
GSK3A	GSK3A	100	1000
GSK3B	GSK3B	100	1000
HIPK1	HIPK1	100	1000
HIPK3	HIPK3	100	1000
HUNK	HUNK	100	1000
ICK	ICK	100	1000
IRAK3	IRAK3	100	1000
JAK1(JH1domain-catalytic)	JAK1	100	1000
KIT(V559D,T670I)	KIT	100	1000
LKB1	STK11	100	1000
MAK	MAK	100	1000
MAP3K1	MAP3K1	100	1000
MAPKAPK2	MAPKAPK2	100	1000
MERTK	MERTK	100	1000
MET(Y1235D)	MET	100	1000
MKNK1	MKNK1	100	1000
MLK2	MAP3K10	100	1000
MYLK2	MYLK2	100	1000
MYLK4	MYLK4	100	1000
NEK1	NEK1	100	1000
NEK4	NEK4	100	1000
NEK5	NEK5	100	1000
NEK9	NEK9	100	1000
NIK	MAP3K14	100	1000
p38-alpha	MAPK14	100	1000
p38-beta	MAPK11	100	1000

p38-gamma	MAPK12	100	1000
PCTK1	CDK16	100	1000
PCTK3	CDK18	100	1000
PFTK1	CDK14	100	1000
PIK3C2G	PIK3C2G	100	1000
PIK3CA(E545A)	PIK3CA	100	1000
PIK3CA(H1047Y)	PIK3CA	100	1000
PIK3CA(M1043I)	PIK3CA	100	1000
PIK3CD	PIK3CD	100	1000
PIK4CB	PI4KB	100	1000
PIKFYVE	PIKFYVE	100	1000
PIM1	PIM1	100	1000
PIM2	PIM2	100	1000
PIM3	PIM3	100	1000
PIP5K2B	PIP4K2B	100	1000
PKAC-alpha	PRKACA	100	1000
PKAC-beta	PRKACB	100	1000
PKN1	PKN1	100	1000
PKNB (*M. tuberculosis*)	pknB	100	1000
PRKCD	PRKCD	100	1000
PRKCH	PRKCH	100	1000
PRKCQ	PRKCQ	100	1000
PRKG1	PRKG1	100	1000
PRKR	EIF2AK2	100	1000
RAF1	RAF1	100	1000
RET(V804L)	RET	100	1000
RET(V804M)	RET	100	1000

RIOK1	RIOK1	100	1000
RIOK2	RIOK2	100	1000
RIPK1	RIPK1	100	1000
RIPK2	RIPK2	100	1000
ROS1	ROS1	100	1000
RPS6KA4(Kin.Dom.1-N-terminal)	RPS6KA4	100	1000
RPS6KA5(Kin.Dom.1-N-terminal)	RPS6KA5	100	1000
SBK1	SBK1	100	1000
SRMS	SRMS	100	1000
SRPK1	SRPK1	100	1000
SRPK3	SRPK3	100	1000
STK35	STK35	100	1000
TAK1	MAP3K7	100	1000
TAOK1	TAOK1	100	1000
TAOK2	TAOK2	100	1000
TAOK3	TAOK3	100	1000
TGFBR1	TGFBR1	100	1000
TGFBR2	TGFBR2	100	1000
TLK2	TLK2	100	1000
TNNI3K	TNNI3K	100	1000
TRKB	NTRK2	100	1000
WEE1	WEE1	100	1000
ZAK	ZAK	100	1000
ZAP70	ZAP70	100	1000

Table S4. Selectivity screening results for compound **9** at 1μM.

DiscoveRx Gene Symbol	Entrez Gene Symbol	Percent Control	Compound Concentration (nM)
MEK5	MAP2K5	0	1000
MST4	MST4	0	1000
PFCDPK1 (*P. falciparum*)	CDPK1	0	1000
SIK2	SIK2	0	1000
SIK	SIK1	0.3	1000
DCAMKL3	DCLK3	0.4	1000
GAK	GAK	0.7	1000
LOK	STK10	1	1000
MEK1	MAP2K1	1.1	1000
MAP4K5	MAP4K5	1.4	1000
STK36	STK36	1.4	1000
YANK2	STK32B	1.4	1000
MEK2	MAP2K2	1.6	1000
YANK1	STK32A	2.2	1000
SNARK	NUAK2	2.3	1000
LTK	LTK	2.5	1000
QSK	KIAA0999	3.4	1000
PAK2	PAK2	3.8	1000
MST3	STK24	4	1000
PAK1	PAK1	4.3	1000
CAMK1D	CAMK1D	4.8	1000
LCK	LCK	4.9	1000
MRCKB	CDC42BPB	6.3	1000
MEK4	MAP2K4	7.1	1000
EPHB6	EPHB6	7.8	1000

PRKD2	PRKD2	8.4	1000
PRKD3	PRKD3	8.8	1000
DMPK2	CDC42BPG	9.2	1000
NLK	NLK	10	1000
MST2	STK3	12	1000
MAST1	MAST1	14	1000
SLK	SLK	14	1000
MELK	MELK	15	1000
AURKC	AURKC	16	1000
DDR1	DDR1	16	1000
FLT3(ITD,F691L)	FLT3	17	1000
CSNK1E	CSNK1E	20	1000
MINK	MINK1	20	1000
AKT3	AKT3	21	1000
ARK5	NUAK1	22	1000
PKN2	PKN2	22	1000
PRKD1	PRKD1	22	1000
YANK3	STK32C	23	1000
ERK5	MAPK7	25	1000
MET(M1250T)	MET	25	1000
MAP4K3	MAP4K3	26	1000
MET	MET	28	1000
PIP5K2C	PIP4K2C	28	1000
AURKB	AURKB	29	1000
LIMK1	LIMK1	29	1000
AURKA	AURKA	31	1000
LATS2	LATS2	34	1000

EPHA8	EPHA8	35	1000
MARK3	MARK3	36	1000
STK33	STK33	36	1000
TNIK	TNIK	37	1000
WNK4	WNK4	37	1000
YSK4	MAP3K19	37	1000
MKNK2	MKNK2	38	1000
RIPK2	RIPK2	38	1000
HPK1	MAP4K1	39	1000
MST1R	MST1R	39	1000
YSK1	STK25	39	1000
EPHA1	EPHA1	40	1000
RSK1(Kin.Dom.2-C-terminal)	RPS6KA1	40	1000
AMPK-alpha1	PRKAA1	41	1000
KIT(A829P)	KIT	41	1000
PDPK1	PDPK1	41	1000
DDR2	DDR2	42	1000
ERK2	MAPK1	42	1000
ERK1	MAPK3	43	1000
WNK1	WNK1	43	1000
AMPK-alpha2	PRKAA2	44	1000
CAMK1B	PNCK	44	1000
MAP4K2	MAP4K2	45	1000
MAP4K4	MAP4K4	46	1000
TRKA	NTRK1	46	1000
ABL1(H396P)-nonphosphorylated	ABL1	47	1000

IRAK1	IRAK1	47	1000
TIE2	TEK	47	1000
PRKCI	PRKCI	48	1000
MAP3K3	MAP3K3	49	1000
JNK1	MAPK8	50	1000
PKNB (*M. tuberculosis*)	pknB	50	1000
RSK4(Kin.Dom.2-C-terminal)	RPS6KA6	50	1000
JNK2	MAPK9	51	1000
MARK2	MARK2	51	1000
RSK2(Kin.Dom.2-C-terminal)	RPS6KA3	51	1000
FRK	FRK	52	1000
ULK3	ULK3	53	1000
CDKL2	CDKL2	57	1000
TESK1	TESK1	57	1000
MEK6	MAP2K6	58	1000
SGK3	SGK3	59	1000
MRCKA	CDC42BPA	60	1000
NEK2	NEK2	60	1000
LATS1	LATS1	61	1000
MKK7	MAP2K7	61	1000
FLT3(ITD,D835V)	FLT3	62	1000
MET(Y1235D)	MET	63	1000
RSK3(Kin.Dom.1-N-terminal)	RPS6KA2	63	1000
S6K1	RPS6KB1	63	1000
PDGFRB	PDGFRB	64	1000
WNK2	WNK2	64	1000

ABL1(F317L)-phosphorylated	ABL1	65	1000
CAMK2A	CAMK2A	65	1000
FLT3(K663Q)	FLT3	65	1000
MYO3A	MYO3A	65	1000
PFTAIRE2	CDK15	65	1000
PIP5K1A	PIP5K1A	65	1000
RSK4(Kin.Dom.1-N-terminal)	RPS6KA6	65	1000
CDK7	CDK7	66	1000
FLT3 (D835V)	FLT3	66	1000
MAP3K4	MAP3K4	66	1000
NEK3	NEK3	66	1000
PAK6	PAK6	66	1000
RSK2 (Kin.Dom.1-N-terminal)	RPS6KA3	66	1000
MAP3K2	MAP3K2	67	1000
MARK1	MARK1	67	1000
PFPK5 (*P. falciparum)*	MAL13P1.279	67	1000
TAOK1	TAOK1	67	1000
BRAF(V600E)	BRAF	68	1000
MYO3B	MYO3B	68	1000
AKT1	AKT1	69	1000
FLT3(D835Y)	FLT3	69	1000
MST1	STK4	69	1000
EPHA3	EPHA3	70	1000
ERBB3	ERBB3	70	1000
HASPIN	GSG2	70	1000
ROCK2	ROCK2	70	1000

KIT(L576P)	KIT	71	1000
MYLK	MYLK	71	1000
CDC2L5	CDK13	72	1000
CSK	CSK	72	1000
PYK2	PTK2B	72	1000
SGK	SGK1	72	1000
SNRK	SNRK	72	1000
ABL1(Q252H)-nonphosphorylated	ABL1	73	1000
ABL1(Y253F)-phosphorylated	ABL1	73	1000
BMPR1B	BMPR1B	73	1000
DCAMKL2	DCLK2	73	1000
EIF2AK1	EIF2AK1	73	1000
PKN1	PKN1	73	1000
PRKCQ	PRKCQ	73	1000
TRKC	NTRK3	73	1000
TYK2(JH1domain-catalytic)	TYK2	73	1000
LZK	MAP3K13	74	1000
MLK2	MAP3K10	74	1000
TSSK3	TSSK3	74	1000
LYN	LYN	75	1000
NEK10	NEK10	75	1000
RSK1(Kin.Dom.1-N-terminal)	RPS6KA1	75	1000
ANKK1	ANKK1	76	1000
ERBB2	ERBB2	76	1000
IKK-epsilon	IKBKE	76	1000

JNK3	MAPK10	76	1000
PIK3CD	PIK3CD	76	1000
SGK2	SGK2	76	1000
CHEK2	CHEK2	77	1000
CSNK1A1L	CSNK1A1L	77	1000
FLT3(R834Q)	FLT3	77	1000
ROCK1	ROCK1	77	1000
VPS34	PIK3C3	77	1000
CHEK1	CHEK1	78	1000
IKK-alpha	CHUK	78	1000
PIK3C2B	PIK3C2B	78	1000
IKK-beta	IKBKB	79	1000
IRAK3	IRAK3	79	1000
MTOR	MTOR	79	1000
ABL1(Q252H)-phosphorylated	ABL1	80	1000
BLK	BLK	80	1000
PLK2	PLK2	80	1000
BRSK1	BRSK1	81	1000
BTK	BTK	81	1000
CDK4	CDK4	81	1000
GRK3	ADRBK2	81	1000
GRK7	GRK7	81	1000
JAK3(JH1domain-catalytic)	JAK3	81	1000
PIK3CA	PIK3CA	81	1000
PLK4	PLK4	81	1000
PRKCH	PRKCH	81	1000

RSK3(Kin.Dom.2-C-terminal)	RPS6KA2	81	1000
TNNI3K	TNNI3K	81	1000
ABL1(F317I)-phosphorylated	ABL1	82	1000
ABL1(M351T)-phosphorylated	ABL1	82	1000
ABL1-nonphosphorylated	ABL1	82	1000
EGFR(T790M)	EGFR	82	1000
JAK2(JH1domain-catalytic)	JAK2	82	1000
NDR1	STK38	82	1000
PAK4	PAK4	82	1000
PLK1	PLK1	82	1000
WNK3	WNK3	82	1000
ABL1-phosphorylated	ABL1	83	1000
ERN1	ERN1	83	1000
NEK11	NEK11	83	1000
PIK3CG	PIK3CG	83	1000
PRKG2	PRKG2	83	1000
RIOK3	RIOK3	83	1000
ABL1(F317L)-nonphosphorylated	ABL1	84	1000
DCAMKL1	DCLK1	84	1000
FYN	FYN	84	1000
PAK7	PAK7	84	1000
PIK3CA(Q546K)	PIK3CA	84	1000
RET(V804M)	RET	84	1000
WEE2	WEE2	84	1000
EPHA4	EPHA4	85	1000

FLT1	FLT1	85	1000
FLT3(D835H)	FLT3	85	1000
LIMK2	LIMK2	85	1000
NIM1	MGC42105	85	1000
PIK3CA(E545K)	PIK3CA	85	1000
RIPK5	DSTYK	85	1000
STK39	STK39	85	1000
TBK1	TBK1	85	1000
TYRO3	TYRO3	85	1000
VRK2	VRK2	85	1000
ABL1(T315I)-phosphorylated	ABL1	86	1000
BMX	BMX	86	1000
CDKL5	CDKL5	86	1000
KIT(D816V)	KIT	86	1000
MYLK2	MYLK2	86	1000
SgK110	SgK110	86	1000
STK16	STK16	86	1000
ABL1(T315I)-nonphosphorylated	ABL1	87	1000
AKT2	AKT2	87	1000
CTK	MATK	87	1000
EGFR(E746-A750del)	EGFR	87	1000
EPHA6	EPHA6	87	1000
FLT3(ITD)	FLT3	87	1000
GCN2(Kin.Dom.2,S808G)	EIF2AK4	87	1000
NEK9	NEK9	87	1000
PIP5K2B	PIP4K2B	87	1000

TAOK3	TAOK3	87	1000
ABL1(H396P)-phosphorylated	ABL1	88	1000
BUB1	BUB1	88	1000
FES	FES	88	1000
MEK3	MAP2K3	88	1000
PIP5K1C	PIP5K1C	88	1000
TIE1	TIE1	88	1000
TRKB	NTRK2	88	1000
ACVR1B	ACVR1B	89	1000
BRK	PTK6	89	1000
CDK5	CDK5	89	1000
INSR	INSR	89	1000
RIPK4	RIPK4	89	1000
CLK1	CLK1	90	1000
EPHA5	EPHA5	90	1000
MAP3K1	MAP3K1	90	1000
SRC	SRC	90	1000
BMPR1A	BMPR1A	91	1000
CDK8	CDK8	91	1000
ERBB4	ERBB4	91	1000
GSK3A	GSK3A	91	1000
ICK	ICK	91	1000
KIT(V559D)	KIT	91	1000
LKB1	STK11	91	1000
PHKG1	PHKG1	91	1000
PIK3CA(E542K)	PIK3CA	91	1000
PIK3CA(I800L)	PIK3CA	91	1000

PRKX	PRKX	91	1000
CSNK1G2	CSNK1G2	92	1000
DLK	MAP3K12	92	1000
EGFR(G719C)	EGFR	92	1000
EGFR(L858R,T790M)	EGFR	92	1000
EPHB2	EPHB2	92	1000
FLT3-autoinhibited	FLT3	92	1000
KIT(D816H)	KIT	92	1000
PIK4CB	PI4KB	92	1000
PLK3	PLK3	92	1000
BRAF	BRAF	93	1000
LRRK2	LRRK2	93	1000
PDGFRA	PDGFRA	93	1000
RAF1	RAF1	93	1000
RET	RET	93	1000
RPS6KA4(Kin.Dom.2-C-terminal)	RPS6KA4	93	1000
SYK	SYK	93	1000
AXL	AXL	94	1000
CDC2L2	CDC2L2	94	1000
CSNK2A2	CSNK2A2	94	1000
EGFR(L861Q)	EGFR	94	1000
IGF1R	IGF1R	94	1000
MLK1	MAP3K9	94	1000
NDR2	STK38L	94	1000
PKAC-beta	PRKACB	94	1000
RPS6KA5(Kin.Dom.1-N-terminal)	RPS6KA5	94	1000

SRPK2	SRPK2	94	1000
ALK	ALK	95	1000
CAMK1	CAMK1	95	1000
CDK9	CDK9	95	1000
FGR	FGR	95	1000
HCK	HCK	95	1000
IRAK4	IRAK4	95	1000
KIT	KIT	95	1000
PIK3CB	PIK3CB	95	1000
ABL1(E255K)-phosphorylated	ABL1	96	1000
CDC2L1	CDK11B	96	1000
CSF1R	CSF1R	96	1000
DYRK2	DYRK2	96	1000
EGFR(G719S)	EGFR	96	1000
PCTK2	CDK17	96	1000
RPS6KA5(Kin.Dom.2-C-terminal)	RPS6KA5	96	1000
TNK2	TNK2	96	1000
ULK1	ULK1	96	1000
ULK2	ULK2	96	1000
CLK2	CLK2	97	1000
DAPK1	DAPK1	97	1000
DAPK2	DAPK2	97	1000
DYRK1A	DYRK1A	97	1000
FLT3(N841I)	FLT3	97	1000
MLCK	MYLK3	97	1000
p38-beta	MAPK11	97	1000

ACVRL1	ACVRL1	98	1000
ERK4	MAPK4	98	1000
JAK1(JH1domain-catalytic)	JAK1	98	1000
MAK	MAK	98	1000
MAPKAPK5	MAPKAPK5	98	1000
NEK6	NEK6	98	1000
PKAC-alpha	PRKACA	98	1000
PRKCE	PRKCE	98	1000
PRP4	PRPF4B	98	1000
BIKE	BMP2K	99	1000
CAMK1G	CAMK1G	99	1000
CAMK4	CAMK4	99	1000
CLK3	CLK3	99	1000
EGFR(L858R)	EGFR	99	1000
EPHA2	EPHA2	99	1000
FER	FER	99	1000
HIPK2	HIPK2	99	1000
MAP3K15	MAP3K15	99	1000
MARK4	MARK4	99	1000
TGFBR2	TGFBR2	99	1000
TLK1	TLK1	99	1000
AAK1	AAK1	100	1000
ABL1(F317I)-nonphosphorylated	ABL1	100	1000
ABL2	ABL2	100	1000
ACVR1	ACVR1	100	1000
ACVR2A	ACVR2A	100	1000

ACVR2B	ACVR2B	100	1000
ADCK3	CABC1	100	1000
ADCK4	ADCK4	100	1000
ALK(C1156Y)	ALK	100	1000
ALK(L1196M)	ALK	100	1000
ASK1	MAP3K5	100	1000
ASK2	MAP3K6	100	1000
BMPR2	BMPR2	100	1000
BRSK2	BRSK2	100	1000
CAMK2B	CAMK2B	100	1000
CAMK2D	CAMK2D	100	1000
CAMK2G	CAMK2G	100	1000
CAMKK1	CAMKK1	100	1000
CAMKK2	CAMKK2	100	1000
CASK	CASK	100	1000
CDK11	CDK19	100	1000
CDK2	CDK2	100	1000
CDK3	CDK3	100	1000
CDK4-cyclinD1	CDK4	100	1000
CDK4-cyclinD3	CDK4	100	1000
CDKL1	CDKL1	100	1000
CDKL3	CDKL3	100	1000
CIT	CIT	100	1000
CLK4	CLK4	100	1000
CSF1R-autoinhibited	CSF1R	100	1000
CSNK1A1	CSNK1A1	100	1000
CSNK1D	CSNK1D	100	1000

CSNK1G1	CSNK1G1	100	1000
CSNK1G3	CSNK1G3	100	1000
CSNK2A1	CSNK2A1	100	1000
DAPK3	DAPK3	100	1000
DMPK	DMPK	100	1000
DRAK1	STK17A	100	1000
DRAK2	STK17B	100	1000
DYRK1B	DYRK1B	100	1000
EGFR	EGFR	100	1000
EGFR(L747-E749del, A750P)	EGFR	100	1000
EGFR(L747-S752del, P753S)	EGFR	100	1000
EGFR(L747-T751del,Sins)	EGFR	100	1000
EGFR(S752-I759del)	EGFR	100	1000
EPHA7	EPHA7	100	1000
EPHB1	EPHB1	100	1000
EPHB3	EPHB3	100	1000
EPHB4	EPHB4	100	1000
ERK3	MAPK6	100	1000
ERK8	MAPK15	100	1000
FAK	PTK2	100	1000
FGFR1	FGFR1	100	1000
FGFR2	FGFR2	100	1000
FGFR3	FGFR3	100	1000
FGFR3(G697C)	FGFR3	100	1000
FGFR4	FGFR4	100	1000
FLT3	FLT3	100	1000

FLT4	FLT4	100	1000
GRK1	GRK1	100	1000
GRK2	ADRBK1	100	1000
GRK4	GRK4	100	1000
GSK3B	GSK3B	100	1000
HIPK1	HIPK1	100	1000
HIPK3	HIPK3	100	1000
HIPK4	HIPK4	100	1000
HUNK	HUNK	100	1000
INSRR	INSRR	100	1000
ITK	ITK	100	1000
JAK1(JH2domain-pseudokinase)	JAK1	100	1000
KIT(V559D,T670I)	KIT	100	1000
KIT(V559D,V654A)	KIT	100	1000
KIT-autoinhibited	KIT	100	1000
LRRK2(G2019S)	LRRK2	100	1000
MAPKAPK2	MAPKAPK2	100	1000
MERTK	MERTK	100	1000
MKNK1	MKNK1	100	1000
MLK3	MAP3K11	100	1000
MUSK	MUSK	100	1000
MYLK4	MYLK4	100	1000
NEK1	NEK1	100	1000
NEK4	NEK4	100	1000
NEK5	NEK5	100	1000
NEK7	NEK7	100	1000
NIK	MAP3K14	100	1000

OSR1	OXSR1	100	1000
p38-alpha	MAPK14	100	1000
p38-delta	MAPK13	100	1000
p38-gamma	MAPK12	100	1000
PAK3	PAK3	100	1000
PCTK1	CDK16	100	1000
PCTK3	CDK18	100	1000
PFTK1	CDK14	100	1000
PHKG2	PHKG2	100	1000
PIK3C2G	PIK3C2G	100	1000
PIK3CA(C420R)	PIK3CA	100	1000
PIK3CA(E545A)	PIK3CA	100	1000
PIK3CA(H1047L)	PIK3CA	100	1000
PIK3CA(H1047Y)	PIK3CA	100	1000
PIK3CA(M1043I)	PIK3CA	100	1000
PIKFYVE	PIKFYVE	100	1000
PIM1	PIM1	100	1000
PIM2	PIM2	100	1000
PIM3	PIM3	100	1000
PKMYT1	PKMYT1	100	1000
PRKCD	PRKCD	100	1000
PRKG1	PRKG1	100	1000
PRKR	EIF2AK2	100	1000
RET(M918T)	RET	100	1000
RET(V804L)	RET	100	1000
RIOK1	RIOK1	100	1000
RIOK2	RIOK2	100	1000

RIPK1	RIPK1	100	1000
ROS1	ROS1	100	1000
RPS6KA4(Kin.Dom.1-N-terminal)	RPS6KA4	100	1000
SBK1	SBK1	100	1000
SRMS	SRMS	100	1000
SRPK1	SRPK1	100	1000
SRPK3	SRPK3	100	1000
STK35	STK35	100	1000
TAK1	MAP3K7	100	1000
TAOK2	TAOK2	100	1000
TEC	TEC	100	1000
TGFBR1	TGFBR1	100	1000
TLK2	TLK2	100	1000
TNK1	TNK1	100	1000
TRPM6	TRPM6	100	1000
TSSK1B	TSSK1B	100	1000
TTK	TTK	100	1000
TXK	TXK	100	1000
TYK2(JH2domain-pseudokinase)	TYK2	100	1000
VEGFR2	KDR	100	1000
WEE1	WEE1	100	1000
YES	YES1	100	1000
ZAK	ZAK	100	1000
ZAP70	ZAP70	100	1000

Table S5. Selectivity screening results compound **10** (MRIA9) at 1µM.

Kinase Name	Mutant/ Wild type	Residual activity	Compound Concentration (nM)
SIK2	Wild type	1	1000
SIK3	Wild type	2	1000
SIK1	Wild type	4	1000
MAP4K5	Wild type	8	1000
PAK3	Wild type	9	1000
PAK2	Wild type	10	1000
NLK	Wild type	13	1000
PKN3	Wild type	35	1000
PAK1	Wild type	36	1000
MKK4	Wild type	37	1000
TIE2	Wild type	39	1000
KIT D816V	Mutant	41	1000
MST4	Wild type	45	1000
RAF1 YDYD	Const. active variant	47	1000
MELK	Wild type	48	1000
PRKD2	Wild type	51	1000
RET S891A	Mutant	52	1000
PKCmu	Wild type	53	1000
EPHA1	Wild type	53	1000
EPHA6	Wild type	54	1000
STK25	Wild type	56	1000
TYRO3	Wild type	56	1000
ERK2	Wild type	58	1000
TIE2 Y1108F	Mutant	58	1000

BMX	Wild type	60	1000
LCK	Wild type	61	1000
CAMK1D	Wild type	62	1000
RON	Wild type	63	1000
MAP3K10	Wild type	64	1000
WNK2	Wild type	65	1000
TIE2 R849W	Mutant	65	1000
MET D1228H	Mutant	67	1000
MKK6 SDTD	Const. active variant	68	1000
MEK1 F53L	Mutant	68	1000
KIT V560G	Mutant	68	1000
RIPK2	Wild type	69	1000
RPS6KA4	Wild type	69	1000
RET R749T	Mutant	69	1000
KIT D816H	Mutant	70	1000
KIT V559D/T670I	Mutant	71	1000
TRKA G667C	Mutant	71	1000
AuroraB	Wild type	72	1000
FGFR3 K650M	Mutant	72	1000
EGFR G719C	Mutant	72	1000
MINK1	Wild type	75	1000
BRK	Wild type	75	1000
MET F1200I	Mutant	75	1000
KIT V559D	Mutant	75	1000
MYLK	Wild type	76	1000
RPS6KA5	Wild type	77	1000
MET D1228N	Mutant	77	1000

MET Y1230D	Mutant	77	1000
KIT V654A	Mutant	77	1000
MEK1	Wild type	77	1000
CSK	Wild type	77	1000
SLK	Wild type	77	1000
DDR2	Wild type	77	1000
JNK2	Wild type	78	1000
WNK1	Wild type	78	1000
MEK2	Wild type	78	1000
RET R813Q	Mutant	78	1000
EGFR d747-752/P753S	Mutant	78	1000
ALK L1196M	Mutant	78	1000
RET E762Q	Mutant	78	1000
MET Y1230H	Mutant	79	1000
RET V804L	Mutant	79	1000
TSF1	Wild type	79	1000
p38beta	Wild type	79	1000
ACVR1B	Wild type	79	1000
MAP3K11	Wild type	79	1000
RET Y791F	Mutant	79	1000
TGFBR2	Wild type	79	1000
CAMKK1	Wild type	79	1000
KIT	Wild type	80	1000
AMPKalpha1	Wild type	80	1000
MET Y1230C	Mutant	80	1000
EGFR d747-749/A750P	Mutant	81	1000
VEGFR2	Wild type	81	1000

PDGFRalpha D842V	Mutant	81	1000
ACK1	Wild type	82	1000
MET Y1230A	Mutant	82	1000
MLK4	Wild type	82	1000
FGFR2	Wild type	82	1000
MAP3K9	Wild type	82	1000
MAP4K4	Wild type	83	1000
MET M1250T	Mutant	83	1000
PKCnu	Wild type	83	1000
PYK2	Wild type	83	1000
EGFR L858R	Mutant	84	1000
EPHA3	Wild type	84	1000
FGFR3 K650E	Mutant	84	1000
EGFR C797S/L858R	Mutant	84	1000
ACVR2B	Wild type	84	1000
EIF2AK2	Wild type	84	1000
TAOK3	Wild type	84	1000
PDGFRalpha V561D	Mutant	84	1000
RPS6KA6	Wild type	84	1000
RET M918T	Mutant	84	1000
FLT3 ITD	Mutant	84	1000
MST1	Wild type	84	1000
MYLK2	Wild type	84	1000
ABL1 H396P	Mutant	85	1000
MET	Wild type	85	1000
KIT V559D/V654A	Mutant	85	1000
VEGFR3	Wild type	85	1000

EPHA4	Wild type	85	1000
PKCdelta	Wild type	85	1000
RET G691S	Mutant	85	1000
AKT2	Wild type	85	1000
TIE2 Y897S	Mutant	85	1000
EGFR G719S	Mutant	86	1000
FGFR1 V561M	Mutant	86	1000
FGFR1	Wild type	86	1000
PAK7	Wild type	86	1000
RET V804E	Mutant	86	1000
MET Y1235D	Mutant	86	1000
EPHA5	Wild type	87	1000
PKCbeta2	Wild type	87	1000
COT	Wild type	87	1000
NPM1 ALK F1174L	Mutant	87	1000
CDK3/CycC	Wild type	87	1000
RET V804M	Mutant	87	1000
EGFR C797S	Mutant	87	1000
MAP3K7/MAP3K7IP1	Wild type	87	1000
TAOK2	Wild type	87	1000
AuroraA	Wild type	88	1000
PIM1	Wild type	88	1000
RET G810C	Mutant	88	1000
FYN Y531F	Mutant	88	1000
CDK4/CycD3	Wild type	88	1000
RPS6KA2	Wild type	88	1000
KIT T670I	Mutant	88	1000

ERK1	Wild type	88	1000
EGFR L861Q	Mutant	88	1000
RPS6KA1	Wild type	89	1000
STK33	Wild type	89	1000
BLK	Wild type	89	1000
BMPR1B	Wild type	89	1000
CHK2	Wild type	89	1000
PI4K2A	Wild type	89	1000
SGK1	Wild type	89	1000
NEK9	Wild type	89	1000
p38gamma	Wild type	89	1000
CDK19/CycC	Wild type	89	1000
EPHB2	Wild type	89	1000
CDK2/CycA2	Wild type	89	1000
BRAF	Wild type	90	1000
p38alpha	Wild type	90	1000
MARK1	Wild type	90	1000
NEK2	Wild type	90	1000
ALK R1275Q	Mutant	90	1000
ERBB2 775YVMA776	Mutant	90	1000
RET Y806H	Mutant	90	1000
TGFBR1	Wild type	91	1000
FGFR3 G697C	Mutant	91	1000
IRAK1	Wild type	91	1000
ALK F1174S	Mutant	91	1000
RET G810S	Mutant	91	1000
EIF2AK3	Wild type	91	1000

CAMKK2	Wild type	91	1000
PLK1	Wild type	91	1000
PKA	Wild type	91	1000
DYRK2	Wild type	91	1000
ROS	Wild type	91	1000
IRAK4	Wild type	92	1000
EGFR d752-759	Mutant	92	1000
PKMzeta	Wild type	92	1000
KIT A829P	Mutant	92	1000
MUSK	Wild type	92	1000
RPS6KA3	Wild type	92	1000
CDK1/CycA2	Wild type	92	1000
PKCepsilon	Wild type	92	1000
PHKG1	Wild type	92	1000
ASK1	Wild type	93	1000
PKCgamma	Wild type	93	1000
S6Kbeta	Wild type	93	1000
STK23	Wild type	93	1000
ARK5	Wild type	93	1000
RET	Wild type	93	1000
FLT3 D835Y	Mutant	93	1000
MTOR	Wild type	93	1000
STK39	Wild type	93	1000
CDK1/CycE1	Wild type	93	1000
MAP4K2	Wild type	93	1000
MYLK3	Wild type	93	1000
PDGFRbeta	Wild type	93	1000

ABL1 T315I	Mutant	94	1000
MET L1195V	Mutant	94	1000
PAK4	Wild type	94	1000
SNARK	Wild type	94	1000
DDR2 N456S	Mutant	94	1000
JAK1 S729C	Mutant	94	1000
ABL1 F317I	Mutant	94	1000
JNK1	Wild type	94	1000
CCDC6 RET	Mutant	94	1000
CAMK4	Wild type	94	1000
CK1epsilon	Wild type	94	1000
NPM1 ALK	Mutant	94	1000
PKMYT1	Wild type	94	1000
CSF1R	Wild type	94	1000
AuroraC	Wild type	95	1000
TRKA	Wild type	95	1000
MKNK1	Wild type	95	1000
CDK1/CycB1	Wild type	95	1000
DYRK3	Wild type	95	1000
MST2	Wild type	95	1000
TNK1	Wild type	95	1000
SRPK1	Wild type	95	1000
p38delta	Wild type	95	1000
RIPK5	Wild type	95	1000
ROCK2	Wild type	95	1000
ZAK	Wild type	96	1000
EPHB3	Wild type	96	1000

CDK4/CycD1	Wild type	96	1000
JAK1	Wild type	96	1000
AXL	Wild type	96	1000
ACVRL1	Wild type	96	1000
IKKepsilon	Wild type	96	1000
EEF2K	Wild type	96	1000
PBK	Wild type	96	1000
CDK2/CycD1	Wild type	96	1000
CDK6/CycD2	Wild type	96	1000
GSK3beta	Wild type	96	1000
EGFR T790M/L858R	Mutant	96	1000
PDGFRalpha T674I	Mutant	96	1000
PAK6	Wild type	96	1000
PIP5K1C	Wild type	96	1000
FYN	Wild type	97	1000
CDK9/CycK	Wild type	97	1000
EML4 ALK F1174L	Mutant	97	1000
CK1alpha1	Wild type	97	1000
HIPK4	Wild type	97	1000
CDK3/CycE1	Wild type	97	1000
IKKbeta	Wild type	97	1000
ALK	Wild type	97	1000
IKKalpha	Wild type	97	1000
ERK7	Wild type	97	1000
VRK1	Wild type	97	1000
ITK	Wild type	97	1000
ABL1 Q252H	Mutant	97	1000

NEK1	Wild type	98	1000
DNAPK	Wild type	98	1000
PKCiota	Wild type	98	1000
ZAP70	Wild type	98	1000
EGFR T790M/C797S/L858R	Mutant	98	1000
S6K	Wild type	98	1000
MERTK	Wild type	98	1000
PI4KB	Wild type	98	1000
GSG2	Wild type	98	1000
EPHA2	Wild type	98	1000
TRKC	Wild type	98	1000
SYK	Wild type	98	1000
FER	Wild type	98	1000
CDK8/CycC	Wild type	98	1000
ERBB2	Wild type	98	1000
INSR	Wild type	98	1000
DYRK1B	Wild type	98	1000
MATK	Wild type	98	1000
ULK2	Wild type	98	1000
WNK3	Wild type	99	1000
LRRK2 I2020T	Mutant	99	1000
LRRK2 G2019S	Mutant	99	1000
ABL1 M351T	Mutant	99	1000
SGK3	Wild type	99	1000
TEC	Wild type	99	1000
ABL1 G250E	Mutant	99	1000
CDK5/p25NCK	Wild type	99	1000

CDK20/CycT1	Wild type	99	1000
EML4 ALK	Mutant	99	1000
AKT3	Wild type	99	1000
EPHB1	Wild type	99	1000
ABL2	Wild type	99	1000
MEK5	Wild type	99	1000
PIK3CA/PIK3R1	Wild type	99	1000
ABL1 E255K	Mutant	99	1000
TYK2	Wild type	99	1000
HIPK1	Wild type	99	1000
LYN	Wild type	100	1000
PRKG2	Wild type	100	1000
ALK F1174L	Mutant	100	1000
PRKG1	Wild type	100	1000
MAPKAPK3	Wild type	100	1000
ABL1 Y253F	Mutant	100	1000
NEK4	Wild type	100	1000
ALK C1156Y	Mutant	100	1000
CDK7/CycH/MAT1	Wild type	100	1000
MKNK2	Wild type	100	1000
CDK16/CycY	Wild type	100	1000
ERBB4	Wild type	100	1000
CDK5/p35NCK	Wild type	100	1000
FGFR3	Wild type	100	1000
PIP5K1B	Wild type	100	1000
PIP5K1A	Wild type	100	1000
ACVR2A	Wild type	101	1000

CAMK2D	Wild type	101	1000
PIK3CG	Wild type	101	1000
TBK1	Wild type	101	1000
PIK3C2A	Wild type	101	1000
BRSK1	Wild type	101	1000
CDK6/CycD3	Wild type	101	1000
EGFR d746-750/T790M/C797S	Mutant	101	1000
CDK9/CycT1	Wild type	101	1000
EPHA8	Wild type	101	1000
CDK20/CycH	Wild type	101	1000
HIPK3	Wild type	101	1000
TSK2	Wild type	101	1000
PIK3CB/PIK3R1	Wild type	102	1000
ACVR1	Wild type	102	1000
SRPK2	Wild type	102	1000
AKT1	Wild type	102	1000
BMPR1A	Wild type	102	1000
PKCzeta	Wild type	102	1000
ABL1	Wild type	102	1000
EGFR T790M	Mutant	102	1000
TTK	Wild type	102	1000
MET G1163R	Mutant	102	1000
CHK1	Wild type	103	1000
INSRR	Wild type	103	1000
CDC7/DBF4	Wild type	103	1000
GRK7	Wild type	103	1000
MARK2	Wild type	103	1000

PDK1	Wild type	103	1000
PIK3C3	Wild type	103	1000
EPHA7	Wild type	103	1000
FES	Wild type	103	1000
ROCK1	Wild type	103	1000
CAMK2A	Wild type	103	1000
CDK13/CycK	Wild type	103	1000
MST3	Wild type	103	1000
CAMK2G	Wild type	103	1000
PIK3CD/PIK3R1	Wild type	104	1000
FRK	Wild type	104	1000
CDC42BPA	Wild type	104	1000
SNK	Wild type	104	1000
CDK12/CycK	Wild type	104	1000
NEK11	Wild type	104	1000
MAP3K1	Wild type	104	1000
PRK2	Wild type	104	1000
LIMK2	Wild type	104	1000
DMPK	Wild type	104	1000
JNK3	Wild type	104	1000
DYRK1A	Wild type	104	1000
CDK6/CycD1	Wild type	104	1000
CDK18/CycY	Wild type	105	1000
LTK	Wild type	105	1000
TTBK2	Wild type	105	1000
PIM2	Wild type	105	1000
EGFR d746-750	Mutant	105	1000

HIPK2	Wild type	105	1000
EPHB4	Wild type	105	1000
EGFR	Wild type	105	1000
EGFR d746-750/C797S	Mutant	105	1000
DYRK4	Wild type	105	1000
CK1delta	Wild type	105	1000
CDK17/p35NCK	Wild type	105	1000
PDGFRalpha	Wild type	105	1000
FGR	Wild type	106	1000
PI4K2B	Wild type	106	1000
CDK12 R722C/CycK	Mutant	106	1000
PKCbeta1	Wild type	106	1000
VEGFR1	Wild type	106	1000
WEE1	Wild type	106	1000
PASK	Wild type	106	1000
PIM3	Wild type	106	1000
LRRK2	Wild type	106	1000
JAK2	Wild type	106	1000
MARK4	Wild type	107	1000
SGK2	Wild type	107	1000
DDR2 T654M	Mutant	107	1000
GRK3	Wild type	107	1000
TLK1	Wild type	107	1000
PRK1	Wild type	107	1000
TRKB	Wild type	107	1000
MEKK3	Wild type	107	1000
CDC42BPB	Wild type	107	1000

NEK6	Wild type	107	1000
TXK	Wild type	107	1000
CDK2/CycE1	Wild type	107	1000
PKCalpha	Wild type	107	1000
BRAF V600E	Mutant	107	1000
RET G810R	Mutant	108	1000
SRC	Wild type	108	1000
YES	Wild type	108	1000
NEK3	Wild type	108	1000
PHKG2	Wild type	108	1000
JAK3	Wild type	108	1000
FAK	Wild type	108	1000
GSK3alpha	Wild type	108	1000
ALK G1202R	Mutant	109	1000
HRI	Wild type	109	1000
CDK4/CycD2	Wild type	109	1000
FGFR4	Wild type	109	1000
BTK	Wild type	109	1000
IGF1R	Wild type	109	1000
EGFR d746-750/T790M/C797S/L858R	Mutant	109	1000
EGFR L718Q	Mutant	109	1000
CK2alpha2	Wild type	110	1000
CLK2	Wild type	110	1000
PIK3C2G	Wild type	110	1000
PKCtheta	Wild type	110	1000
GRK2	Wild type	111	1000

MKK7	Wild type	111	1000
BRSK2	Wild type	111	1000
STK17A	Wild type	111	1000
GRK6	Wild type	111	1000
ERK5	Wild type	111	1000
HCK	Wild type	111	1000
MAPKAPK5	Wild type	112	1000
DAPK2	Wild type	112	1000
MARK3	Wild type	112	1000
DCAMKL2	Wild type	112	1000
CK1gamma3	Wild type	113	1000
LIMK1	Wild type	113	1000
FLT3	Wild type	113	1000
SRMS	Wild type	114	1000
MASTL	Wild type	114	1000
PIK3C2B	Wild type	115	1000
PLK3	Wild type	116	1000
CK2alpha1	Wild type	116	1000
DAPK3	Wild type	116	1000
VRK2	Wild type	117	1000
SAK	Wild type	117	1000
PRKX	Wild type	117	1000
CAMK2B	Wild type	117	1000
CLK1	Wild type	118	1000
PKCeta	Wild type	119	1000
CLK4	Wild type	119	1000
RIPK4	Wild type	120	1000

MEKK2	Wild type	120	1000
DAPK1	Wild type	121	1000
GRK5	Wild type	122	1000
CK1gamma2	Wild type	123	1000
BUB1B	Wild type	123	1000
TLK2	Wild type	123	1000
MAPKAPK2	Wild type	124	1000
LRRK2 R1441C	Mutant	125	1000
CK1gamma1	Wild type	127	1000
GRK4	Wild type	127	1000
TSSK1	Wild type	127	1000
NEK7	Wild type	131	1000
TTBK1	Wild type	131	1000
CLK3	Wild type	132	1000
NIK	Wild type	140	1000

Table S6. NanoBRET™ assay information.

Protein Kinase	Alias	Catalog #/ CAS #	NanoLuc orientation	Tracer K10 IC_{50}, [nM]	Tracer K10, used [nM]
SIK1		NV2031	N	120	150
SNF1LK2	SIK2	NV2061	N	30	50
SIK3		NV2041	N	250	250
STK24	MST3	CS1810C243	C	260	300
STK26	MST4	CS1810C245	C	270	300
MAP4K5		CS1810C270	C	2000	1000
NLK		CS1810C222	C	750	500
PKN3		CS181023	C	260	300
TIE2		NV2151	C	145	150

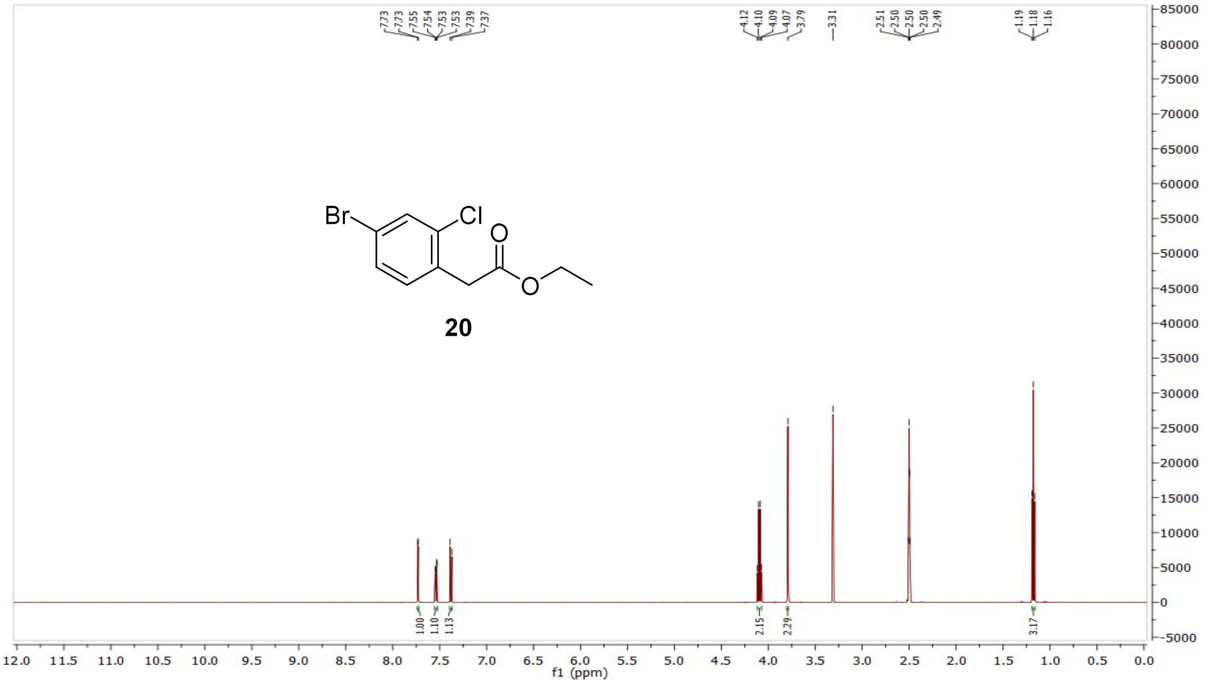
Table S7. Data collection and refinement statistics.

Complex	MST3- **6** (G-5555)	MST3-**10** (MRIA9)	MST3- **7** (MRIA7)	MST3-**16** (MRIA11)	MST3-**9** (MRIA12)	MST3-**14** (MRIA13)	MST4- **6** (G-5555)
PDB code	7B30	7B31	7B32	7B33	7B34	7B35	7B36
Data Collection							
Resolution range (Å)^a	39.64 - 2.10 (2.16 - 2.10)	39.86 - 1.80 (1.84 - 1.80)	49.90 - 1.75 (1.78 - 1.75)	49.41 - 1.90 (1.94 - 1.90)	39.73 - 2.10 (2.16 - 2.10)	47.89 - 2.40 (2.49 - 2.40)	46-47 - 2.11 (2.17 - 2.11)
Space group	*C*2	*C*2	*C*2	*C*2	*C*2	*P*2$_1$	*P*2$_1$
No. molecules/asymmetric unit	1	1	1	1	1	2	2
Cell dimensions a, b, c (Å)	99.00, 58.85, 61.84	99.43, 59.07, 61.73	100.04, 59.21, 61.55	98.97, 58.95, 61.44	99.26, 59.07, 61.79	55.88, 93.21, 61.30	63.75, 53.19, 93.52
α, β, γ (°C)	89.96, 92.92, 89.98	90.00, 93.52, 90.00	90.00, 93.95, 90.00	90.00, 93.13, 90.00	90.00, 93.05, 90.00	90.00, 92.19, 90.00	90.00, 96.36, 90.00
No. unique observations ^{a}	20236 (1341)	33013 (1926)	36097 (1989)	27657 (1776)	20791 (1732)	24436 (2563)	35855 (2756)
Completeness (%)^a	97.0 (79.3)	99.4 (99.6)	99.5 (99.9)	98.9 (99.5)	99.1 (99.9)	99.2 (99.1)	98.7 (94.0)
Mean ((*I*)/σ(*I*)) ^{a}	12.6 (3.6)	16.7 (2.2)	18.4 (3.6)	10.5 (2.6)	12.1 (2.1)	9.2 (2.3)	13.3 (2.1)
R$_{pim}$ ^{a}	0.030 (0.190)	0.024 (0.352)	0.024 (0.209)	0.045 (0.307)	0.042 (0.477)	0.059 (0.353)	0.029 (0.348)
CC(1/2) ^{a}	0.997 (0.881)	0.999 (0.742)	0.999 (0.905)	0.997 (0.813)	0.997 (0.518)	0.995 (0.823)	0.999 (0.886)
Multiplicity ^{a}	6.0 (4.7)	6.1 (6.3)	6.9 (7.1)	5.0 (5.3)	5.4 (5.6)	5.6 (5.4)	5.0 (4.5)
Refinement							
No. atoms in refinement (P/L/O)	2035 / 35 / 108	2109 / 35 / 116	2070 / 42 / 125	2069 / 37 / 119	2056 / 36 / 102	4009 / 37 / 49	4157 / 35 / 96
B factor (Å^2) (P/L/O)	46.0 / 39.2 / 45.4	42.1 / 27.3 / 37.1	32.2 / 20.9 / 29.4	43.1 / 30.0 / 40.8	51.5 / 34.0 / 50.4	49.9 / 37.3 / 40.8	54.4 / 43.5 / 48.5
R$_{work}$ (%)	17.7	17.7	17.4	18.1	18.9	20.5	20.1
R$_{free}$ (%)	19.6	21.2	20.3	20.8	21.5	26.3	24.4
r.m.s. deviation bond length (Å)	0.007	0.006	0.006	0.007	0.008	0.004	0.008
r.m.s deviation bond angle (°)	0.99	0.82	0.79	0.85	0.88	0.67	0.85
Molprobity Ramachandran							
Favoured (%)	96	96	96	97	95	96	96
Outliers (%)	0	0	0	0	0	0	0
Crystallization conditions	10% PEG 6000, 0.1M HEPES pH 7.0	16% PEG 6000, 0.1M HEPES pH 7.0	20% PEG 3350, 0.1M Bis-tris pH 6.5	19% PEG 3350, 0.1M Bis-tris pH 6.8	14% PEG 6000, 0.1M HEPES pH 7.2	24% PEG 3350, 0.1M citrate pH 5.6	28% PEG 6000, 0.1M HEPES pH 7.5

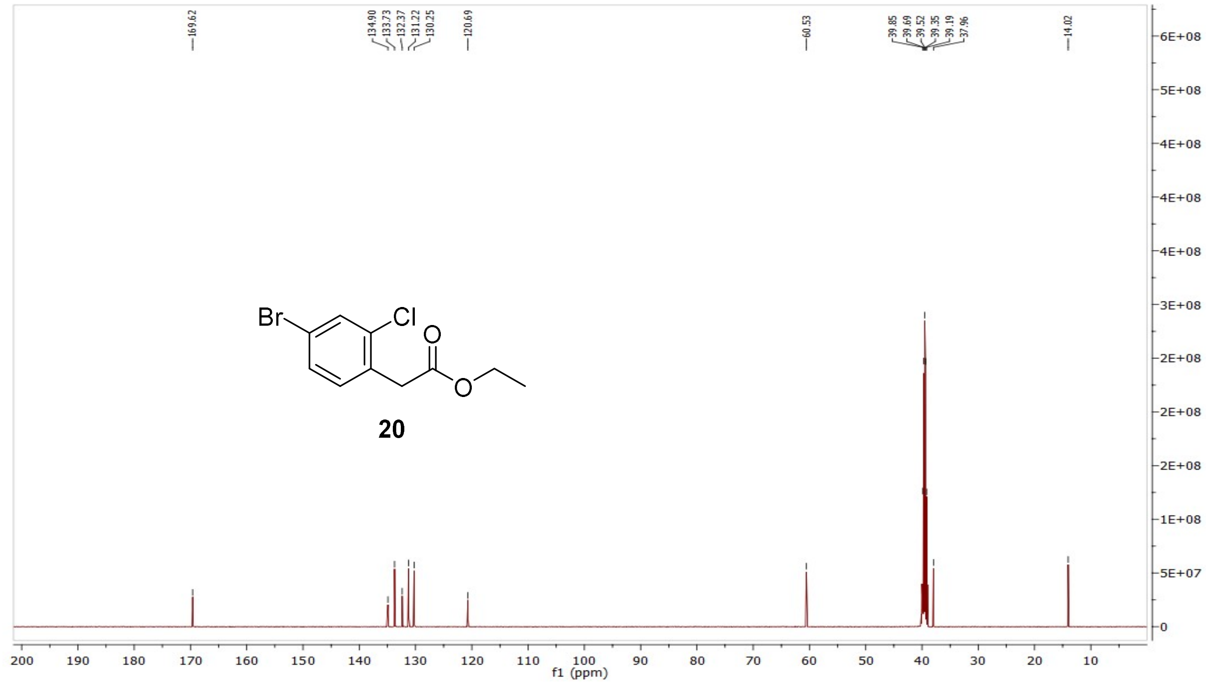
[a] Numbers in parenthesis refer to the highest-resolution shell.

Analytical data for compounds 7-38.

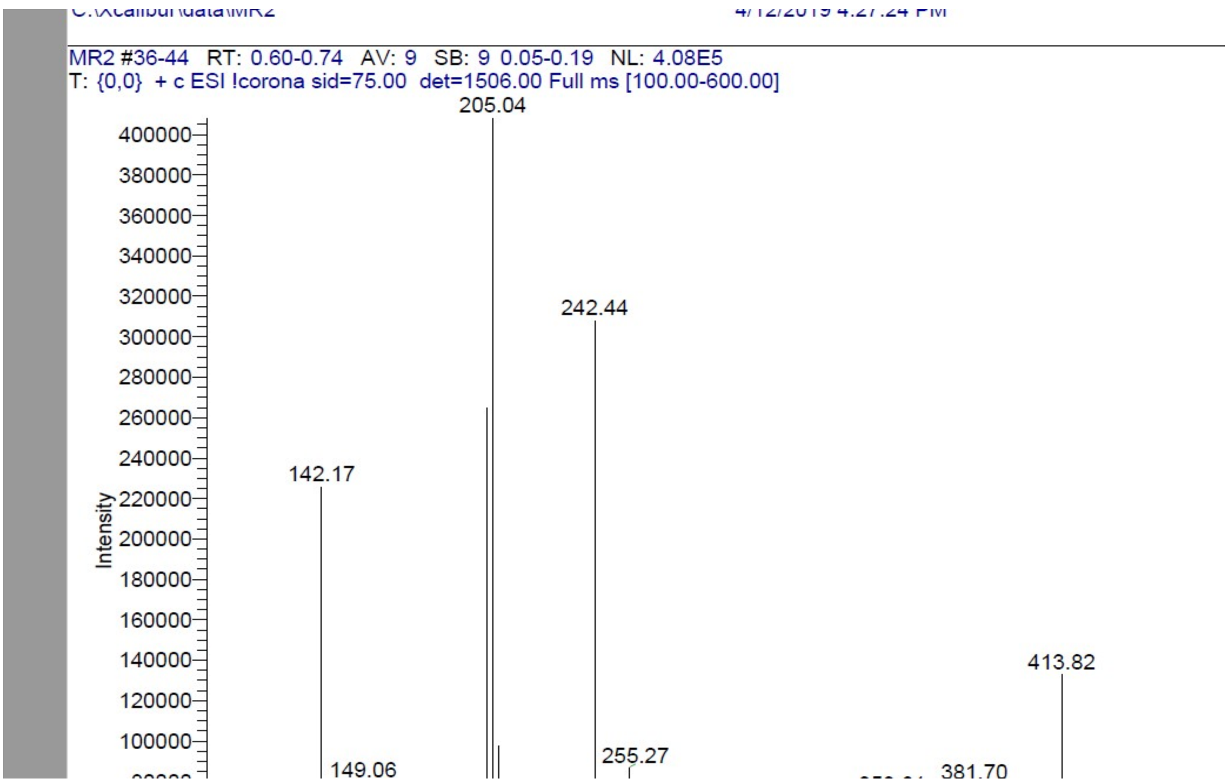
^{1}H NMR compound **21**:



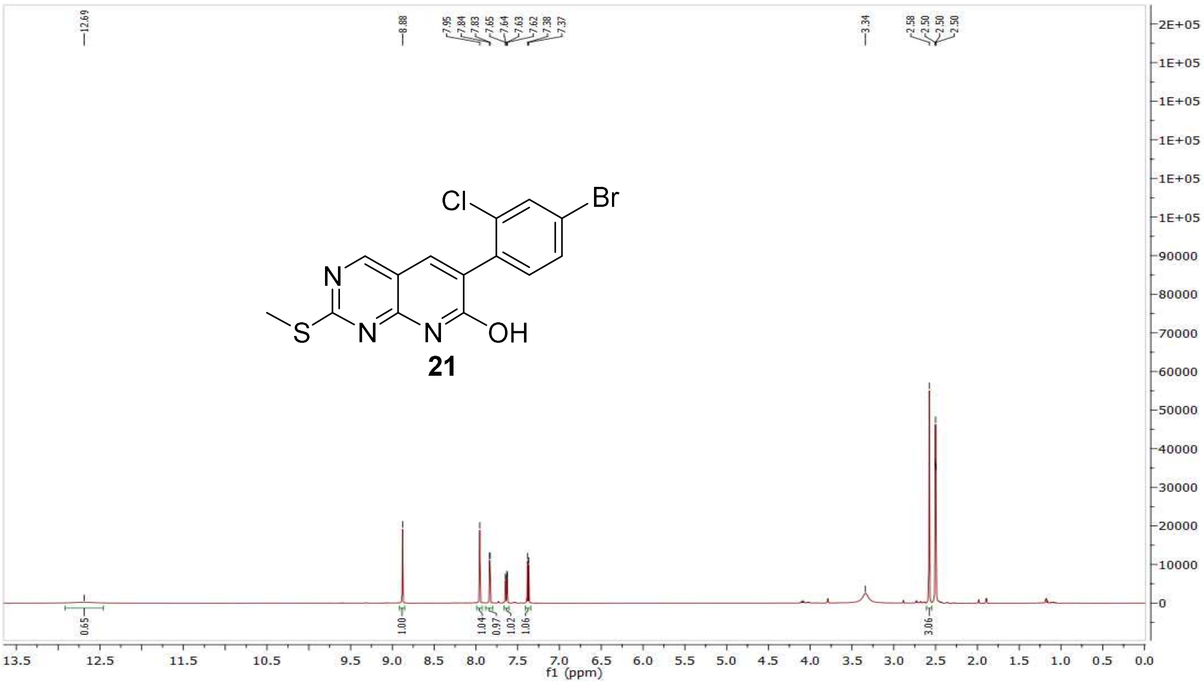
^{13}C NMR compound **21**:



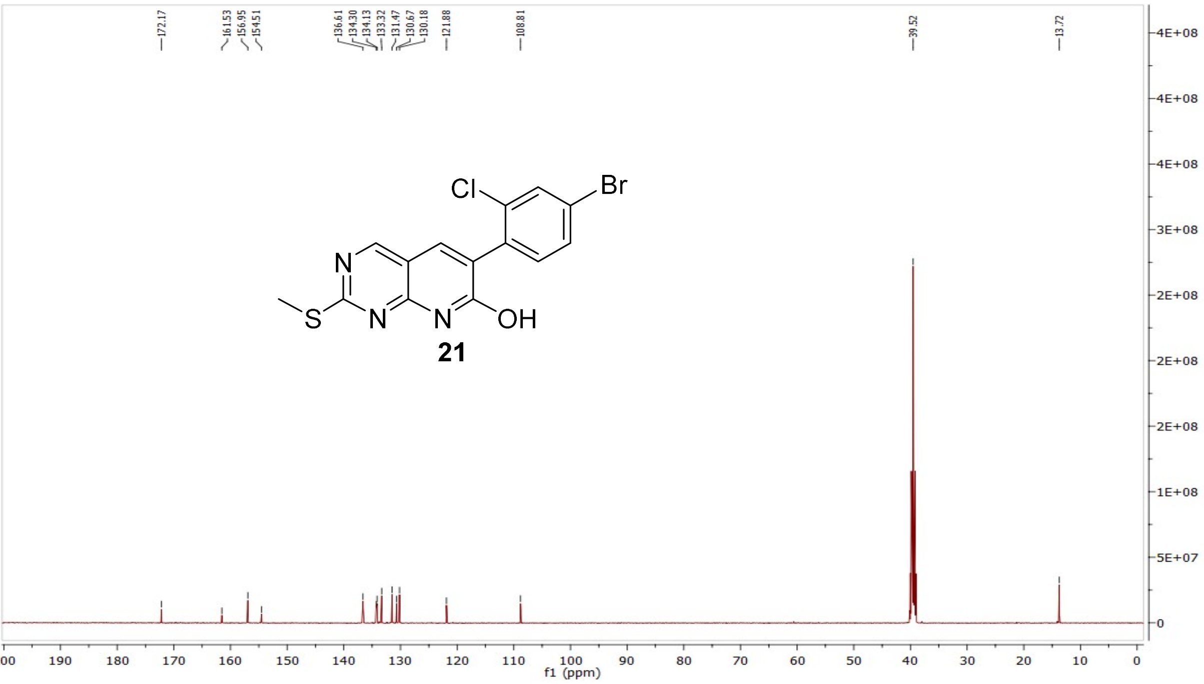
MS (ESI+) compound **21**:



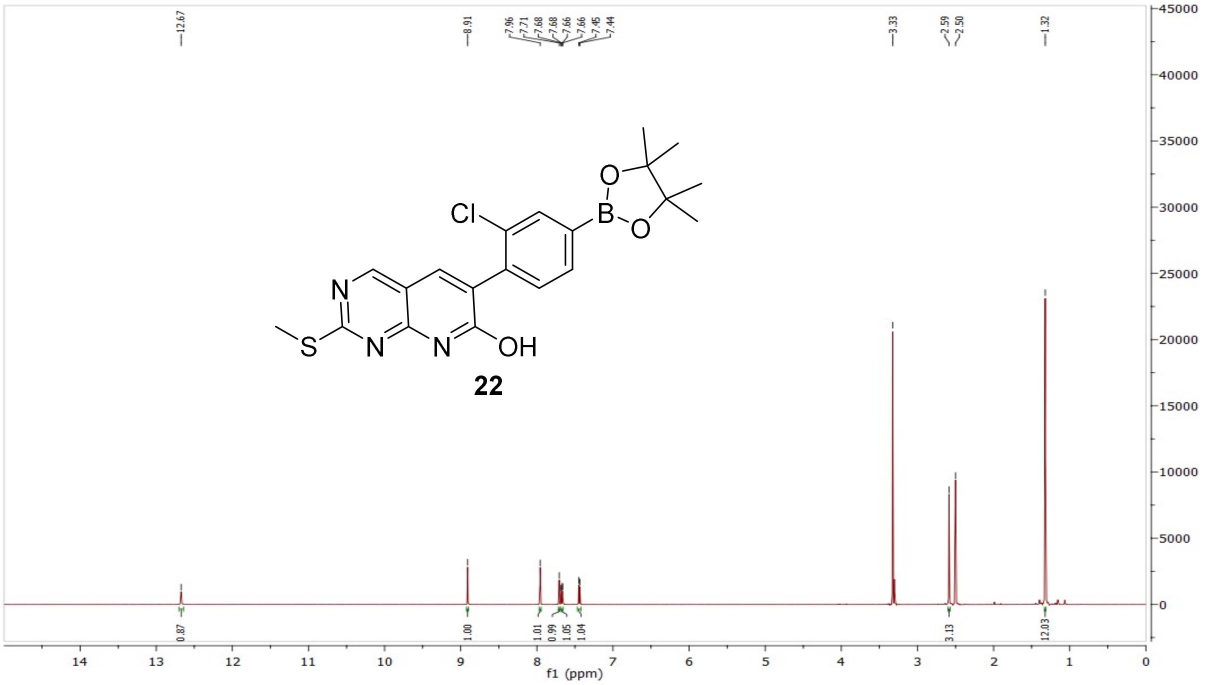
^{1}H NMR compound **22**:



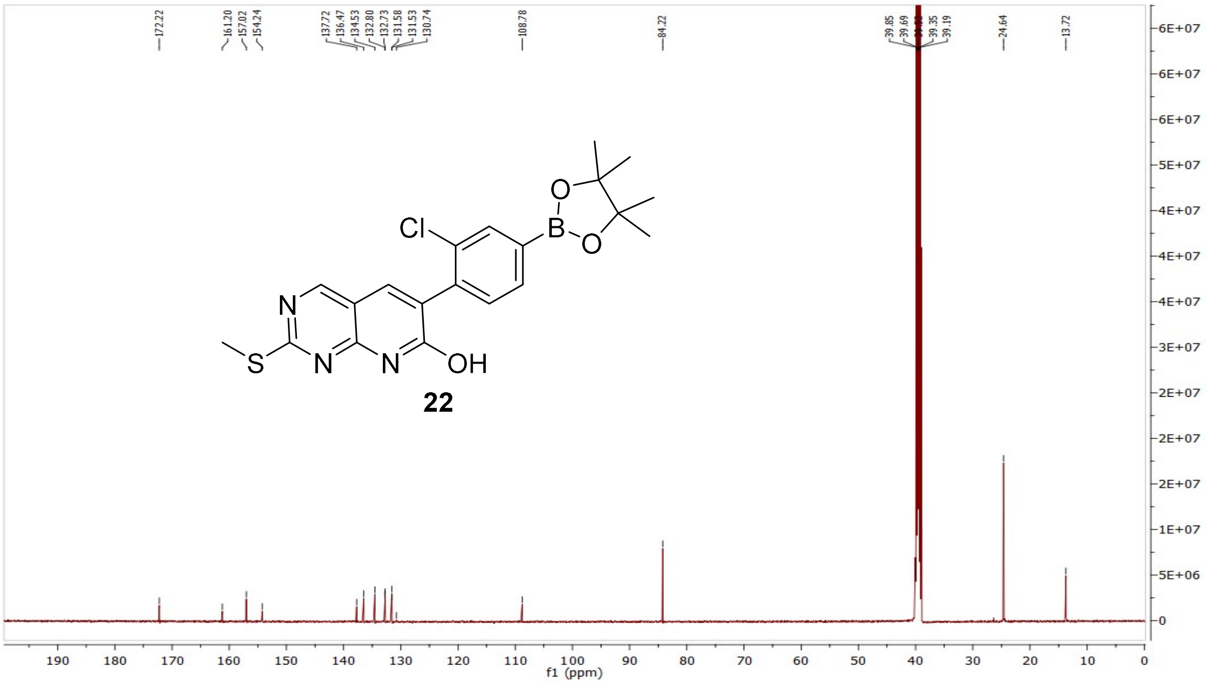
^{13}C NMR compound **22**:



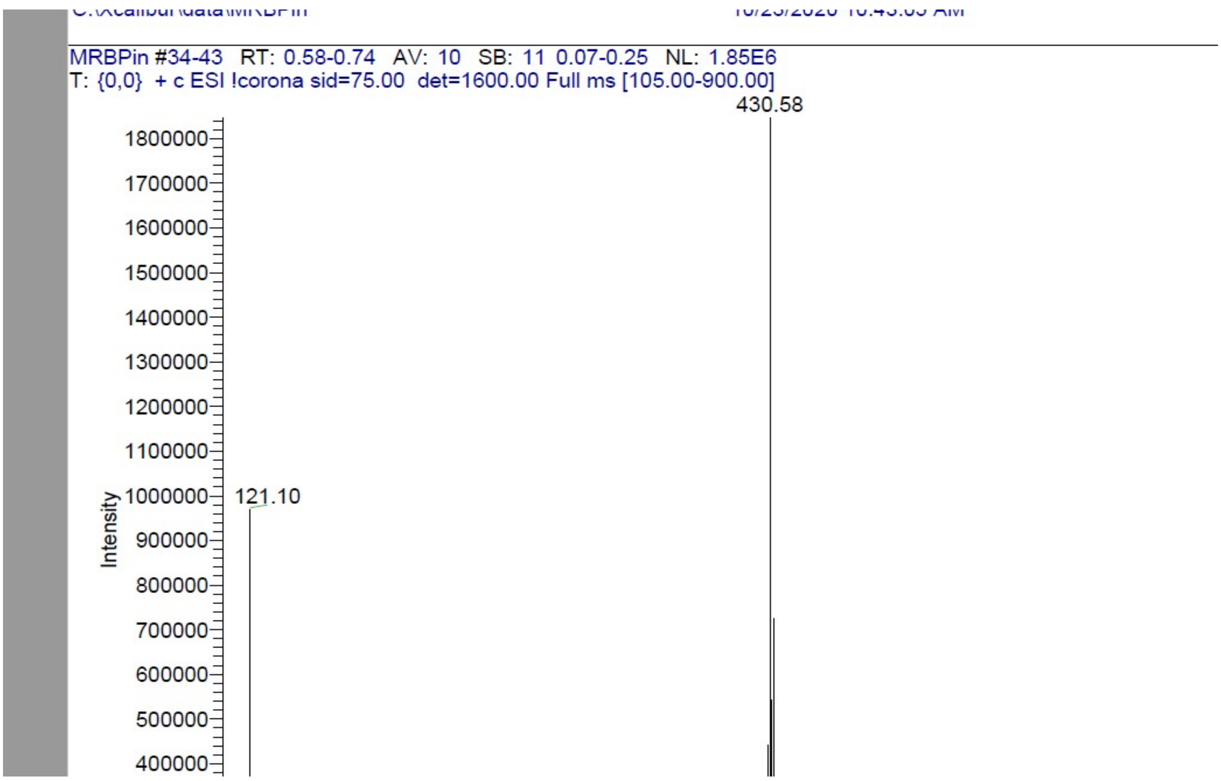
^{1}H NMR compound **23**:



^{13}C NMR compound **23**:

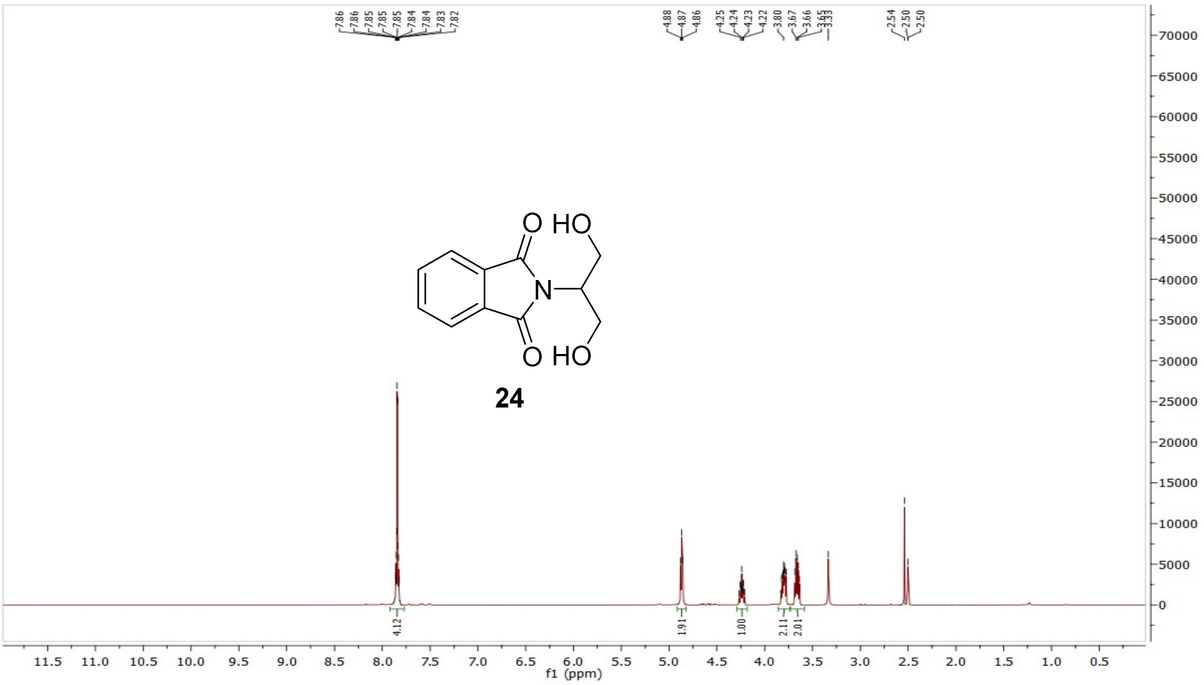


MS (ESI+) compound **23**:

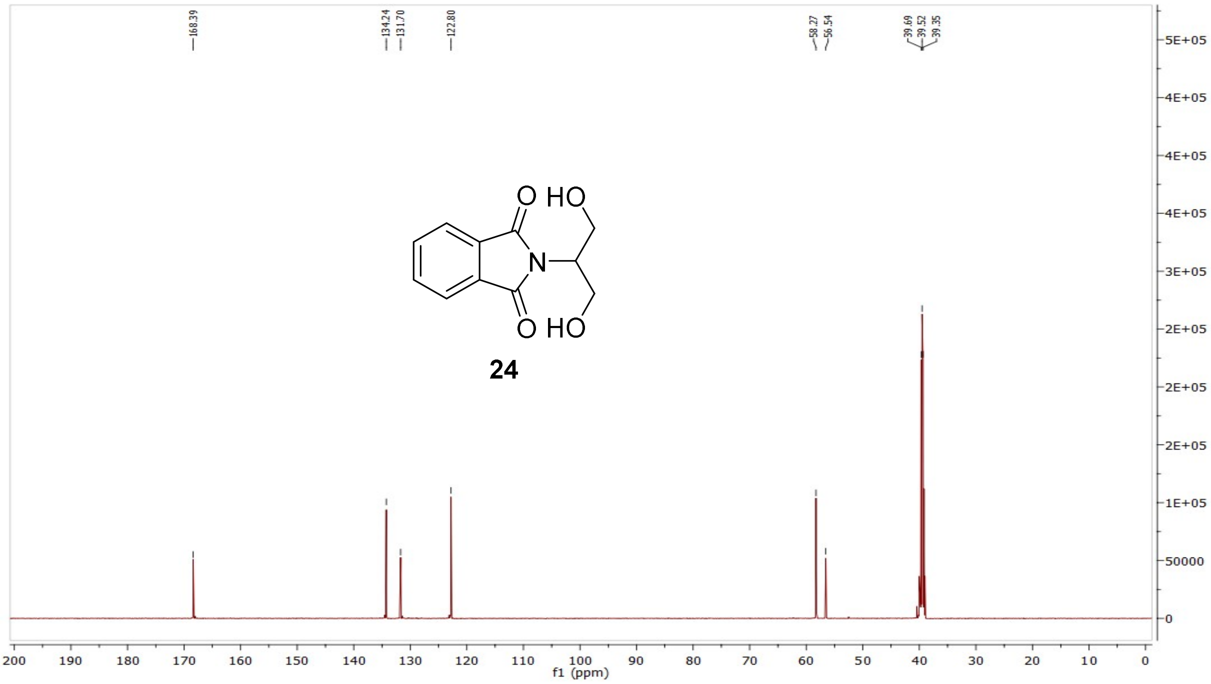


MRBPin #34-43 RT: 0.58-0.74 AV: 10 SB: 11 0.07-0.25 NL: 1.85E6
T: {0,0} + c ESI !corona sid=75.00 det=1600.00 Full ms [105.00-900.00]

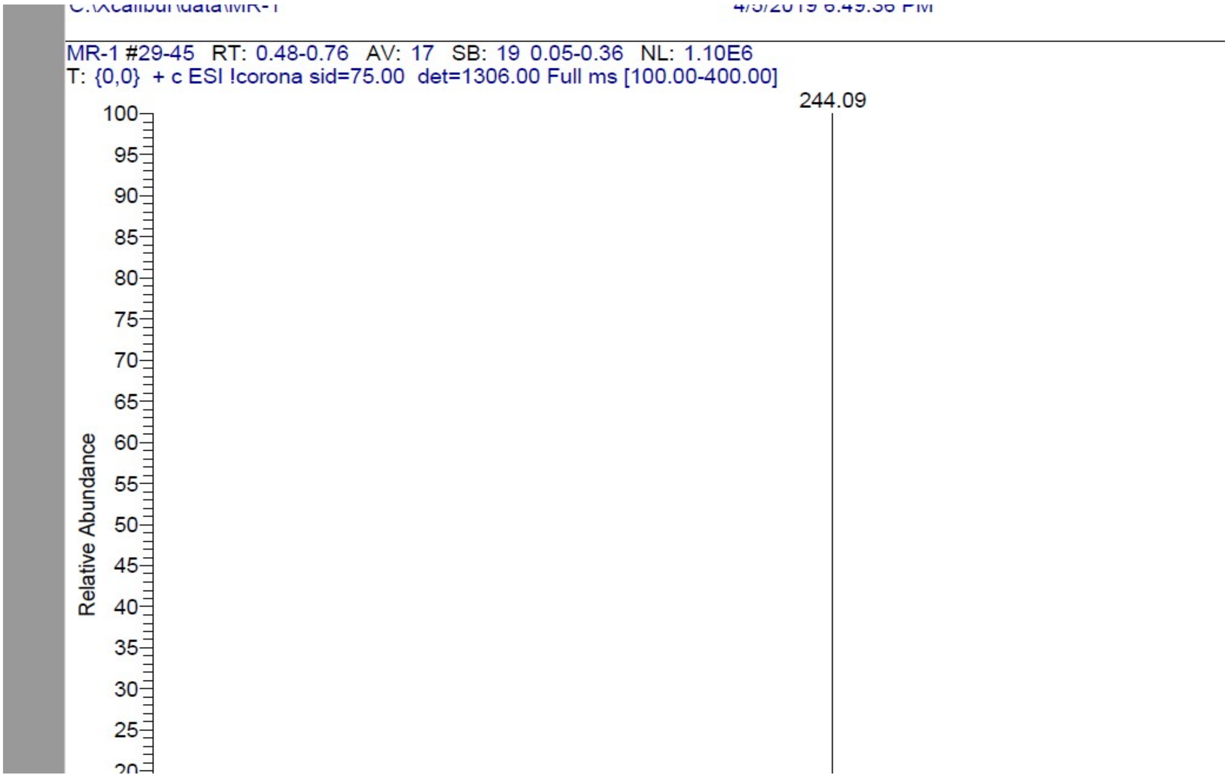
^{1}H NMR compound **25**:



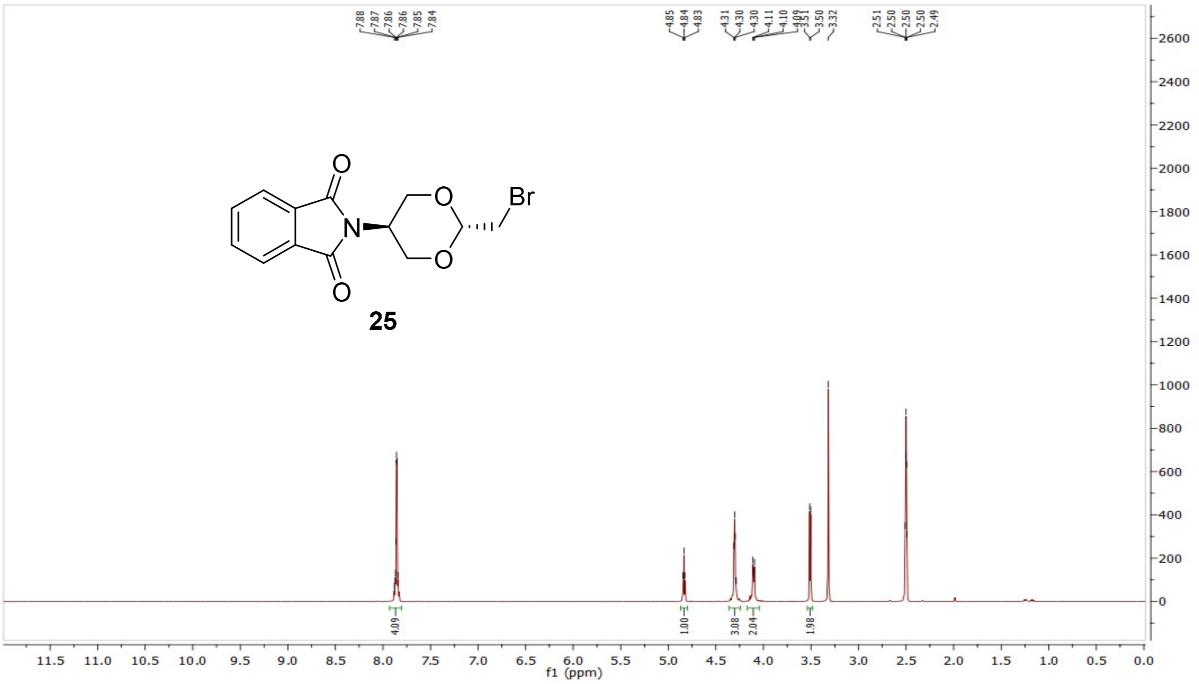
^{13}C NMR compound **25**:



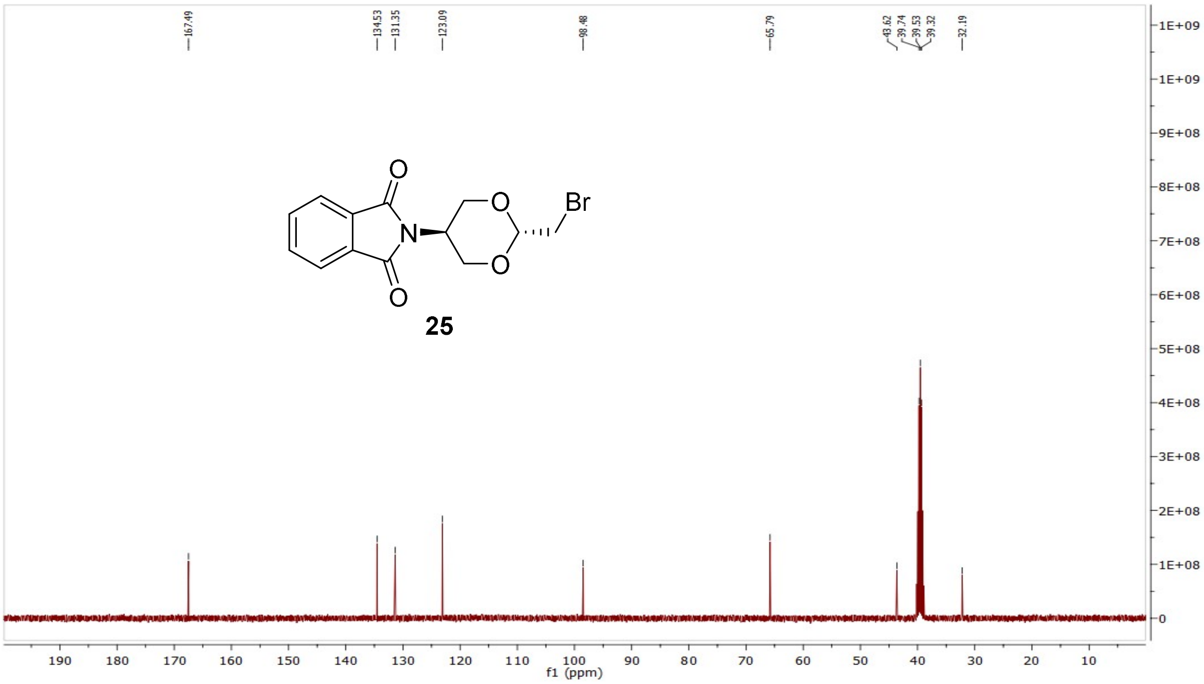
MS (ESI+) compound **25**:


MR-1 #29-45 RT: 0.48-0.76 AV: 17 SB: 19 0.05-0.36 NL: 1.10E6
T: {0,0} + c ESI !corona sid=75.00 det=1306.00 Full ms [100.00-400.00]

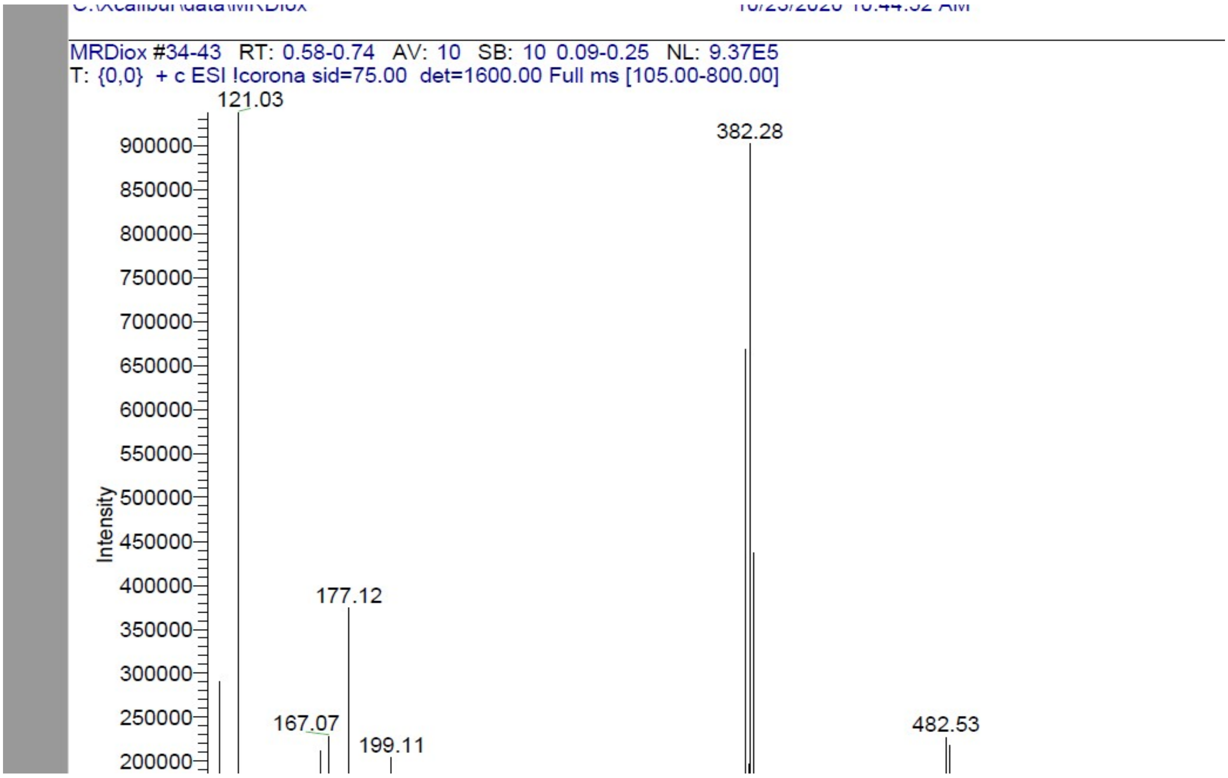
^{1}H NMR compound **26**:



^{13}C NMR compound **26**:

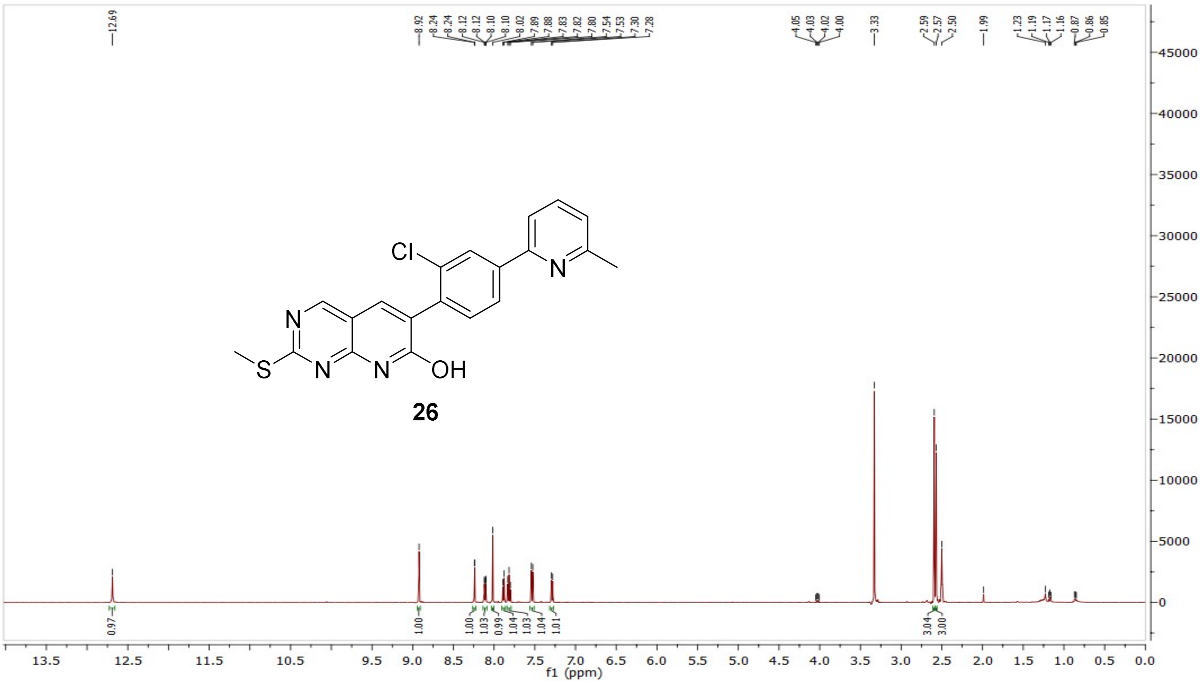


MS (ESI+) compound **26**:

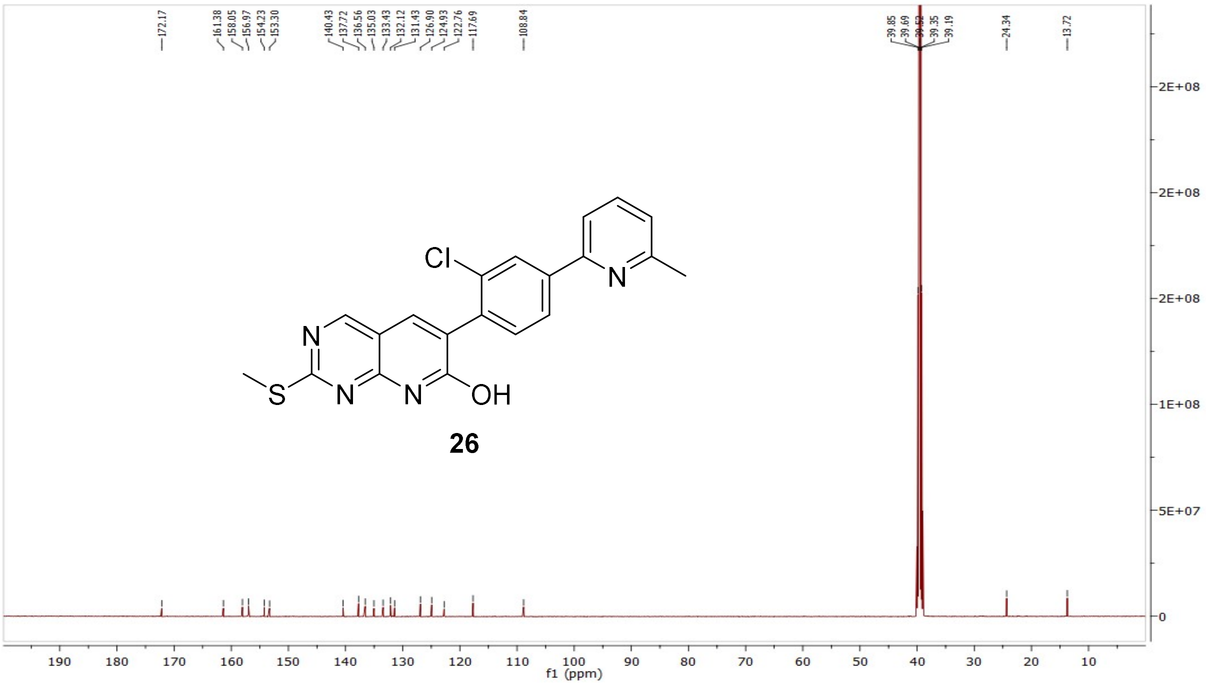


MRDiox #34-43 RT: 0.58-0.74 AV: 10 SB: 10 0.09-0.25 NL: 9.37E5
T: {0,0} + c ESI !corona sid=75.00 det=1600.00 Full ms [105.00-800.00]

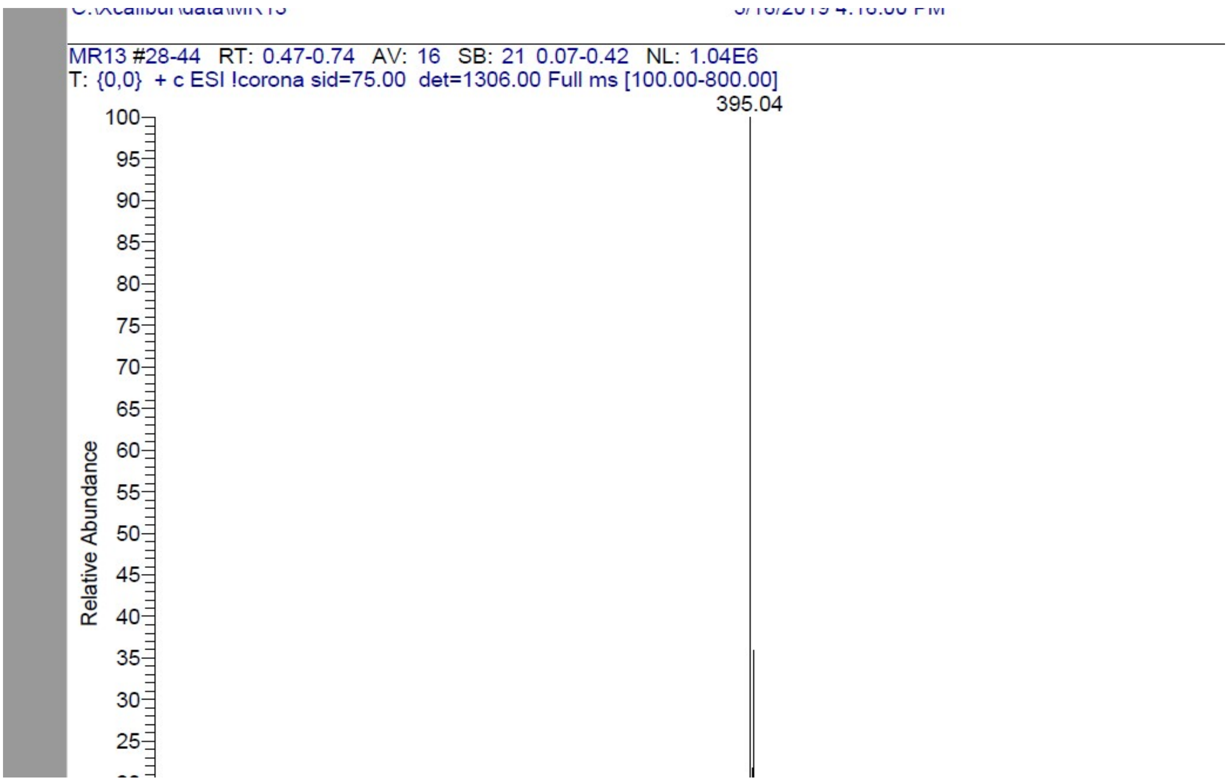
^{1}H NMR compound **27**:



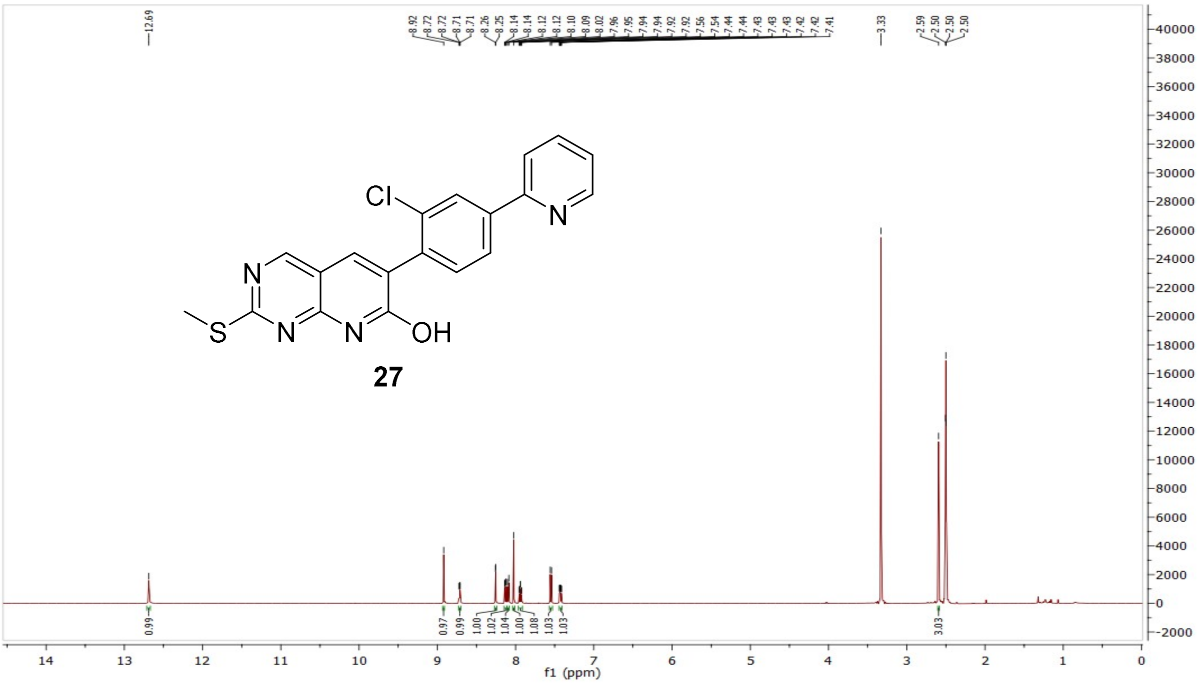
^{13}C NMR compound **27**:



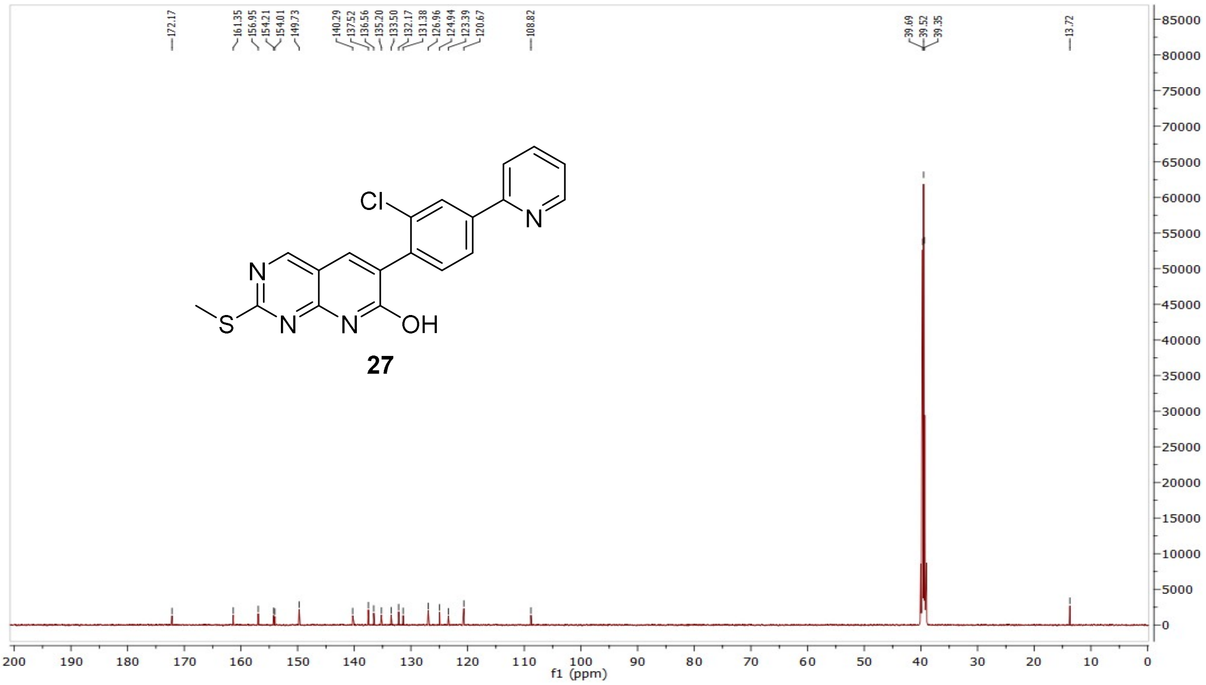
MS (ESI+) compound **27**:



^{1}H NMR compound **28**:



^{13}C NMR compound **28**:

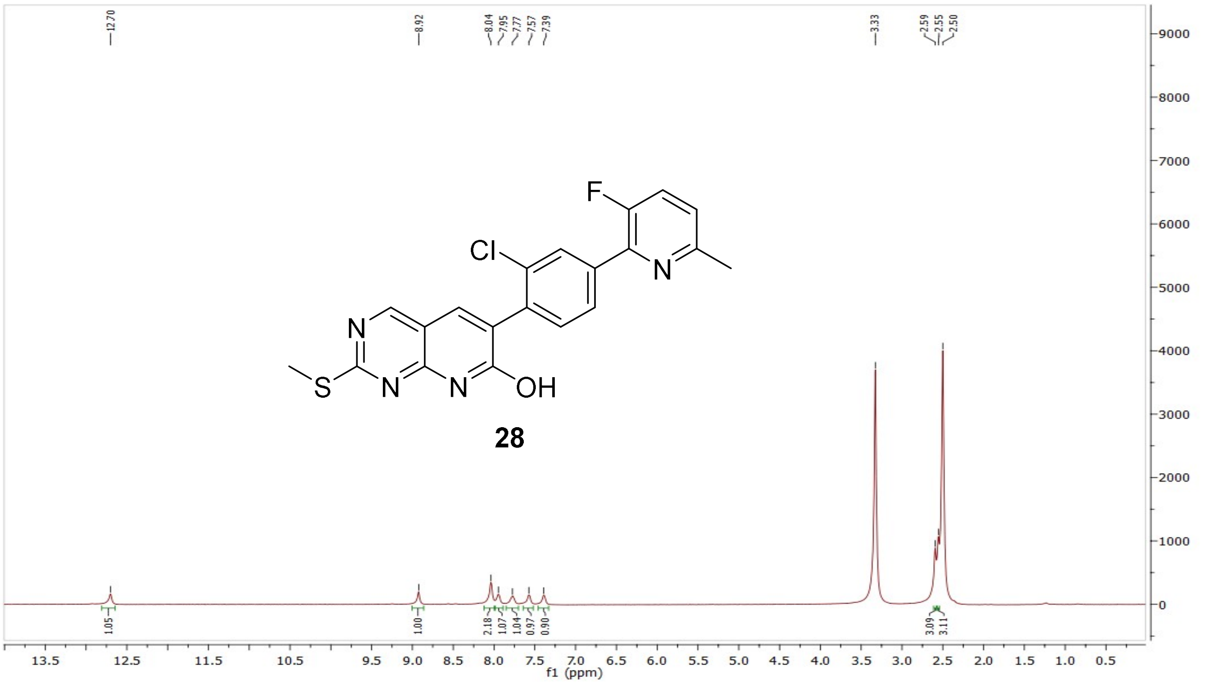


MS (ESI+) compound **28**:

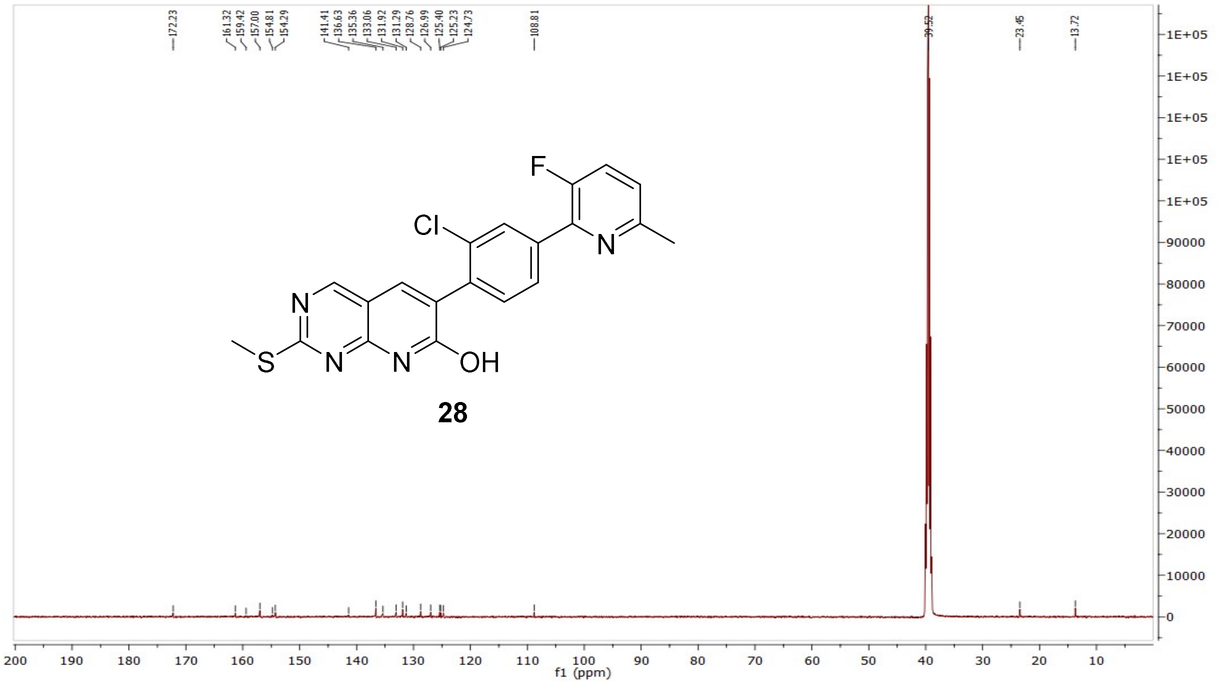
MR18_oben #31-42 RT: 0.53-0.72 AV: 12 SB: 9 0.12-0.26 NL: 1.18E6

T: {0,0} + c ESI !corona sid=75.00 det=1306.00 Full ms [105.00-800.00]

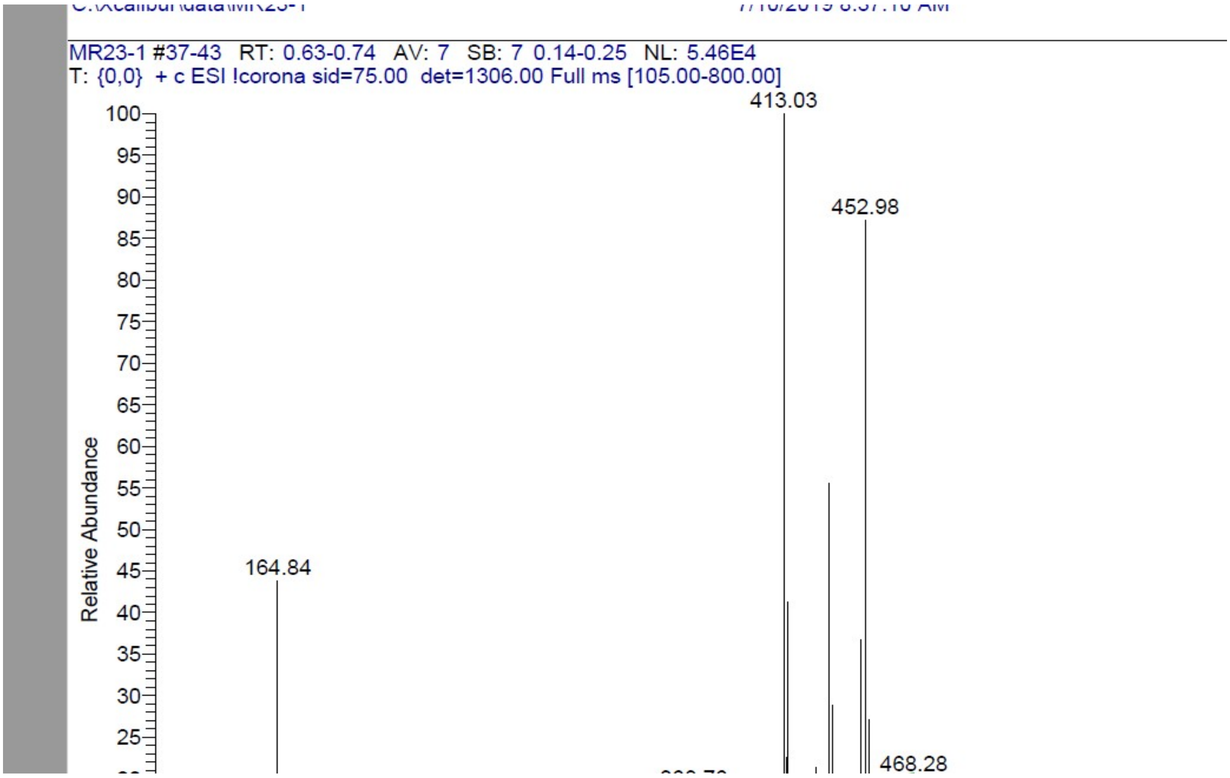
^{1}H NMR compound **29**:



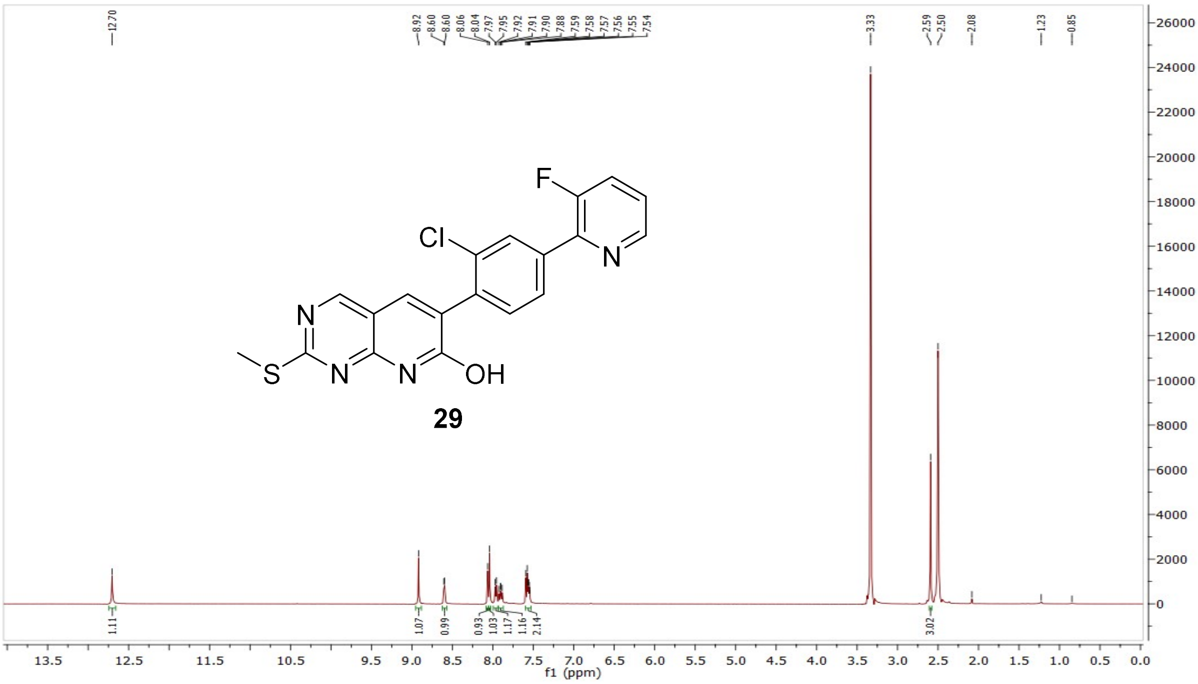
^{13}C NMR compound **29**:



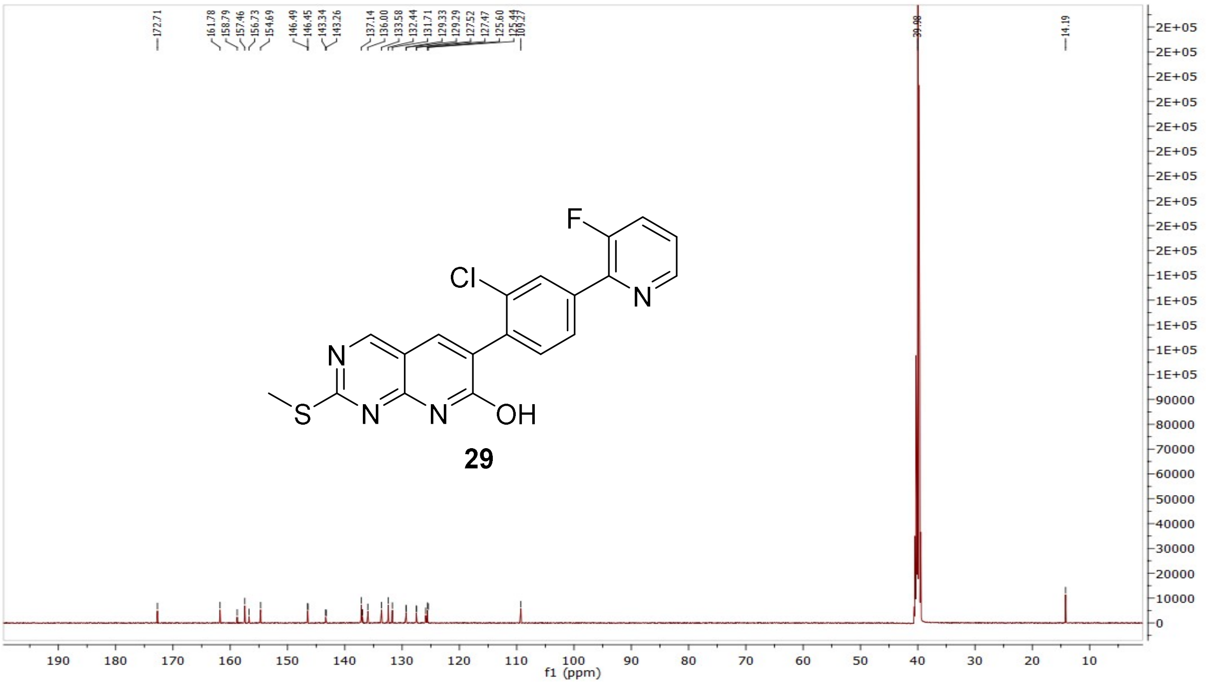
MS (ESI+) compound **29**:



¹H NMR compound **30**:

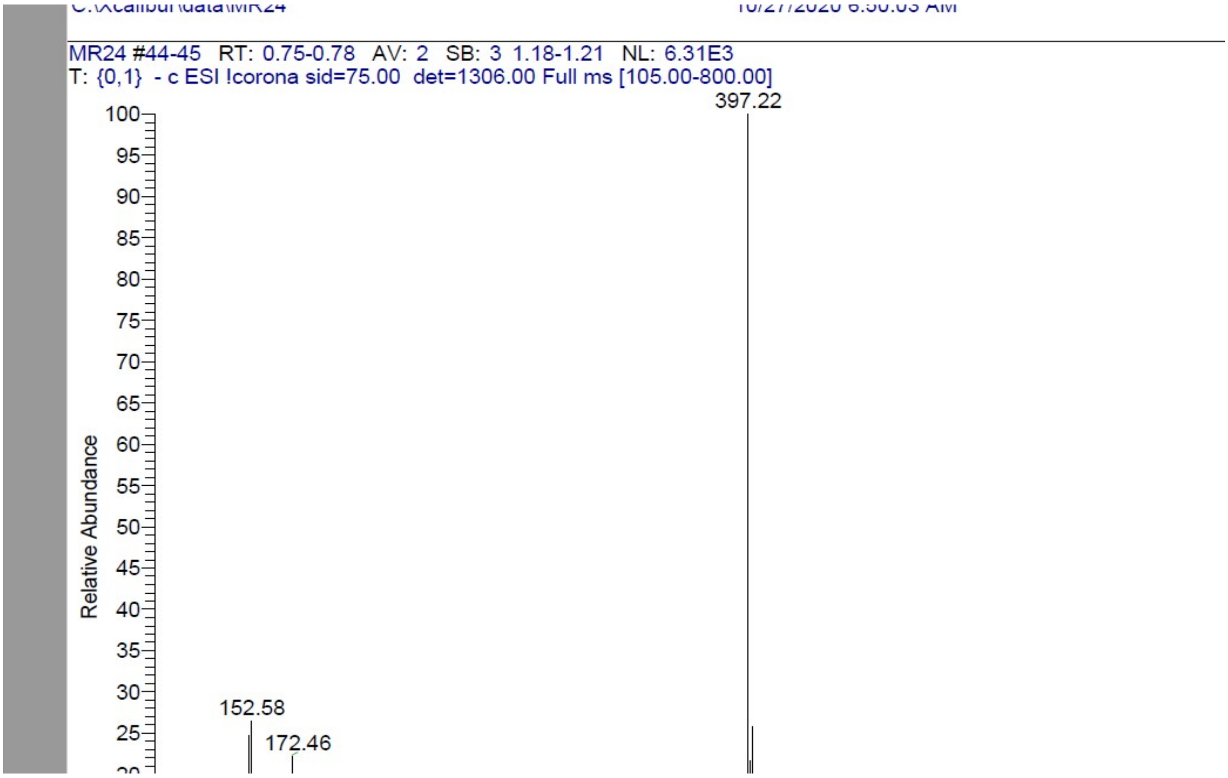


^{13}C NMR compound **30**:



29

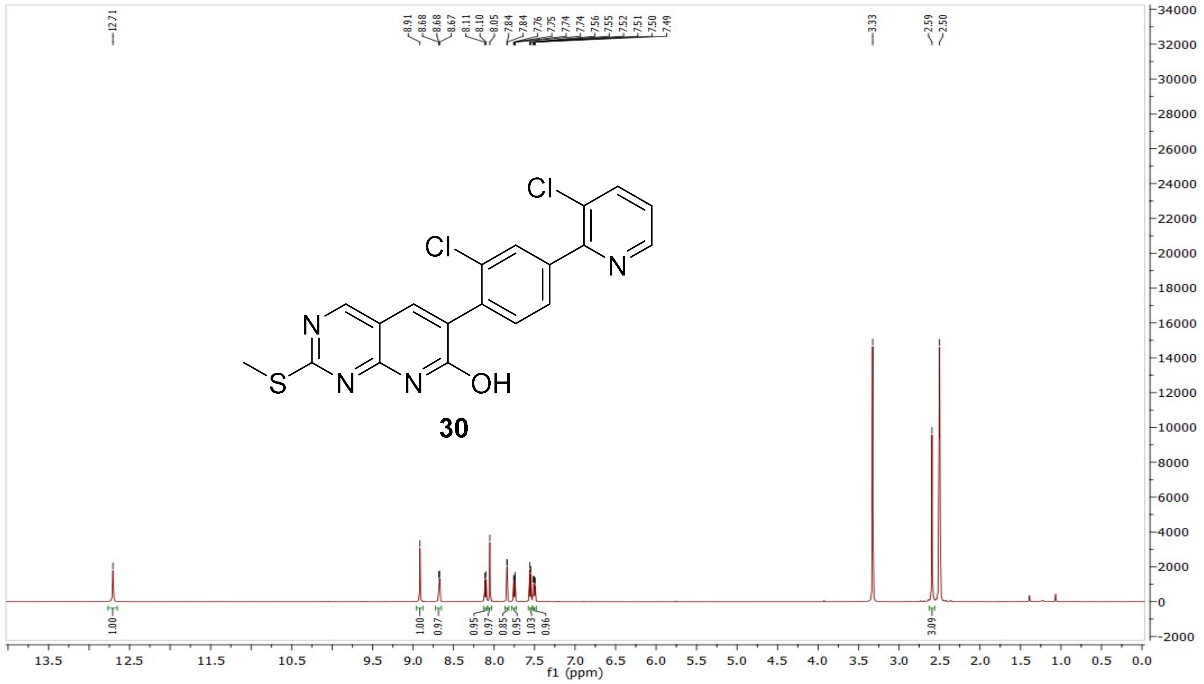
MS (ESI-) compound **30**:



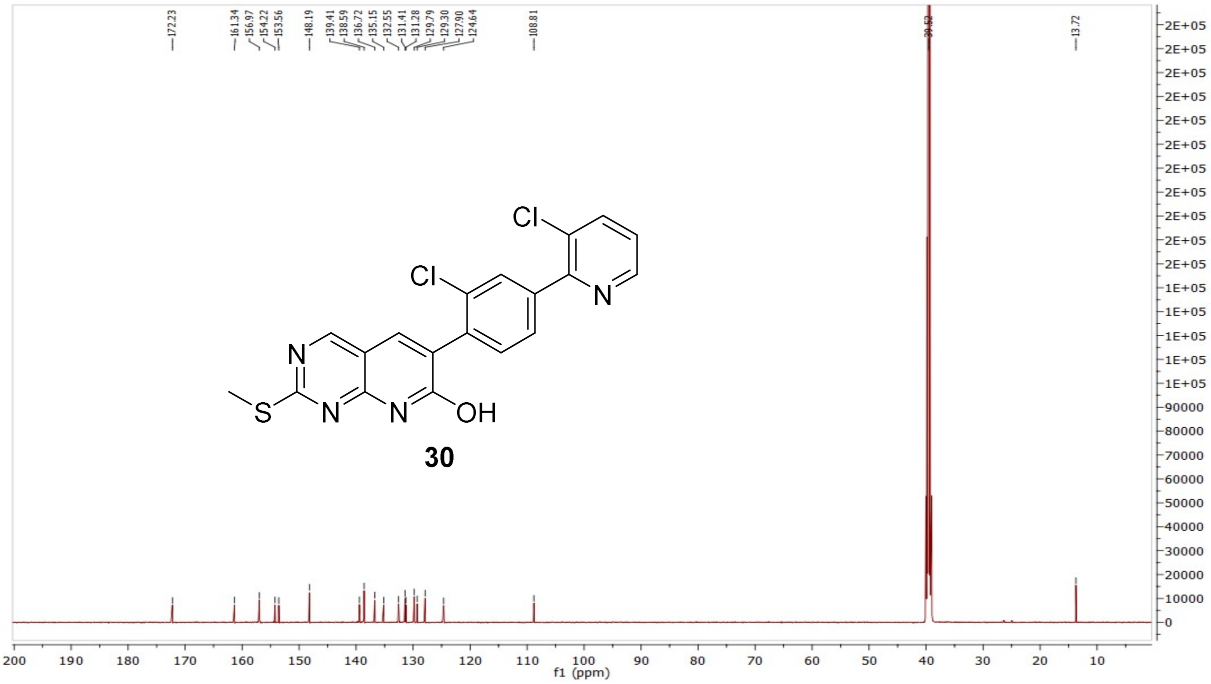
C:\Xcalibur\data\MR24 10/27/2020 6:50:03 AM

MR24 #44-45 RT: 0.75-0.78 AV: 2 SB: 3 1.18-1.21 NL: 6.31E3
T: {0,1} - c ESI !corona sid=75.00 det=1306.00 Full ms [105.00-800.00]

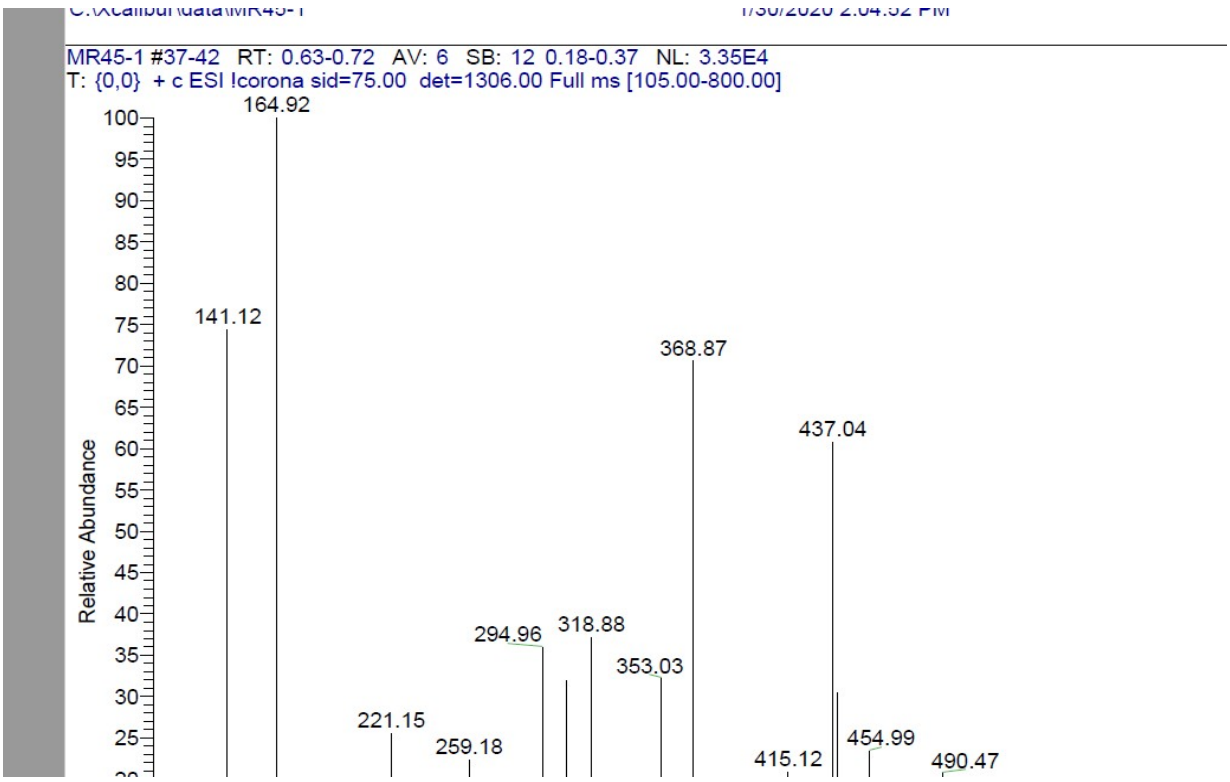
^{1}H NMR compound **31**:



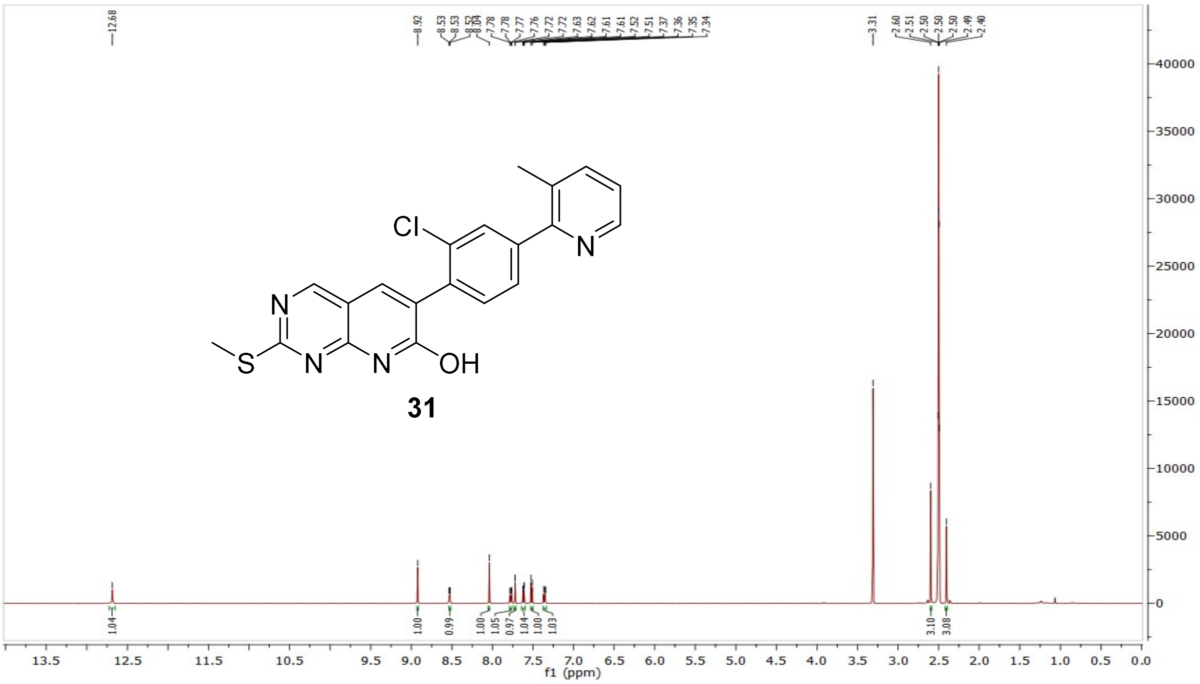
^{13}C NMR compound **31**:



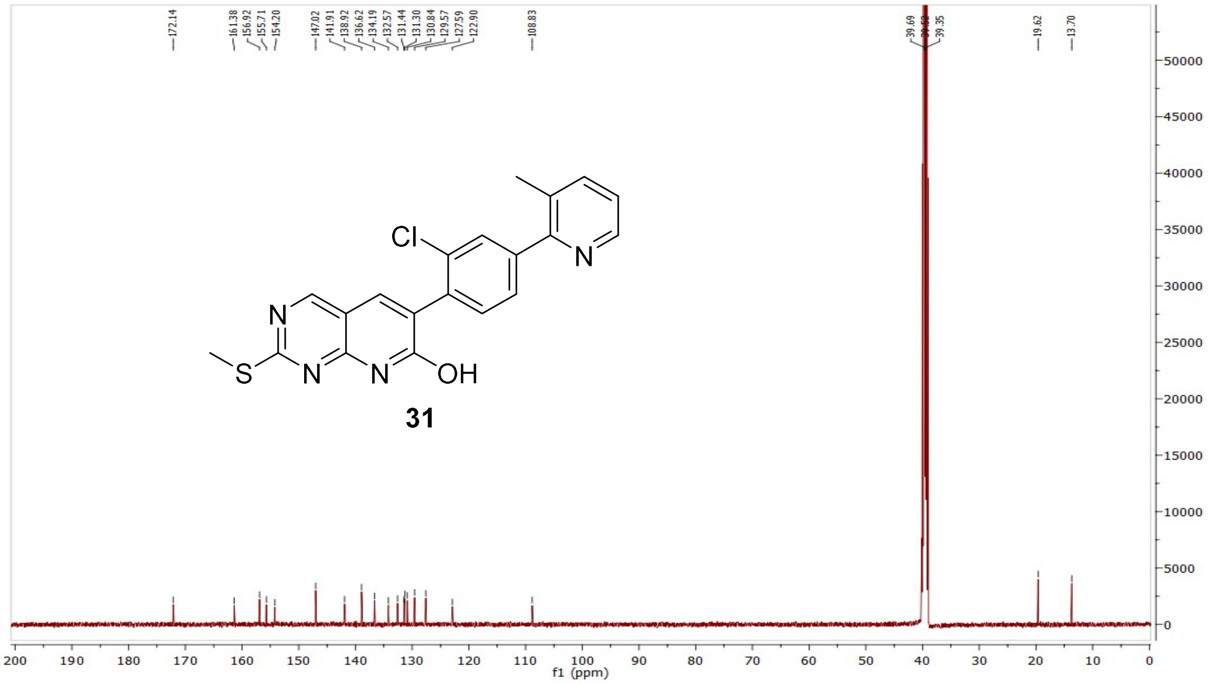
MS (ESI+) compound **31**:



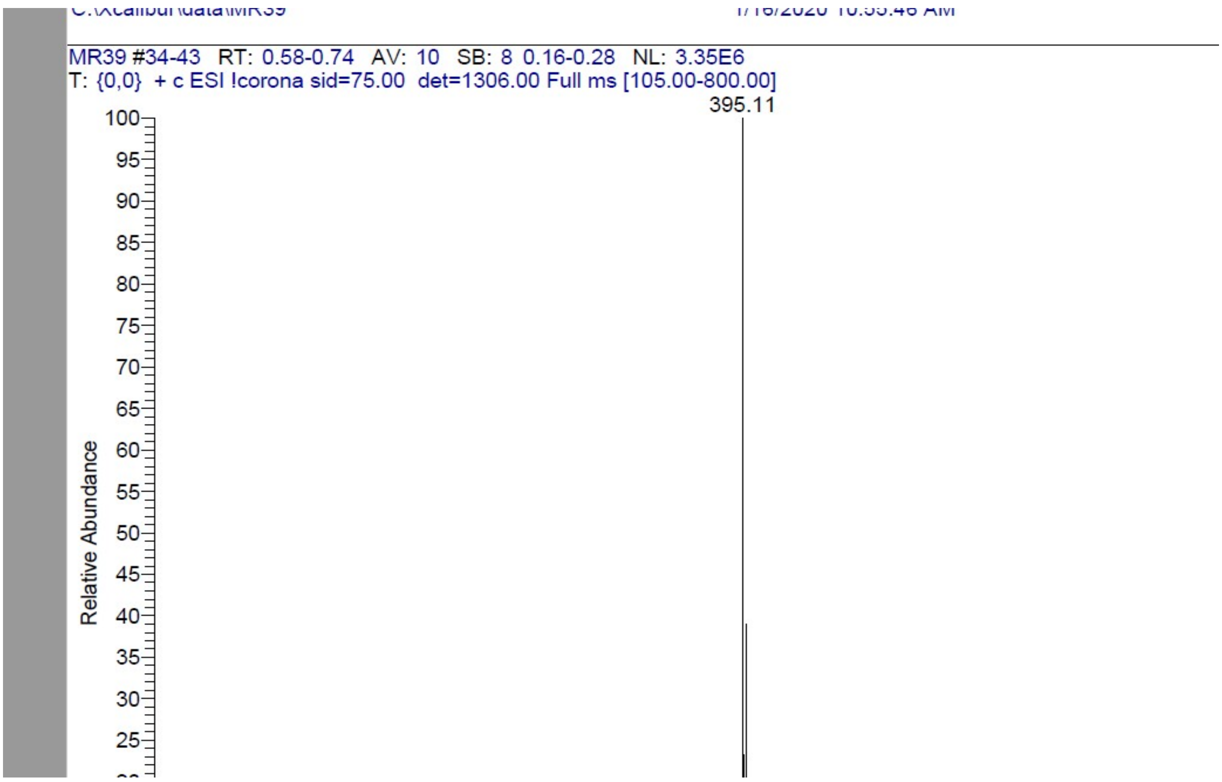
^{1}H NMR compound **32**:



^{13}C NMR compound **32**:

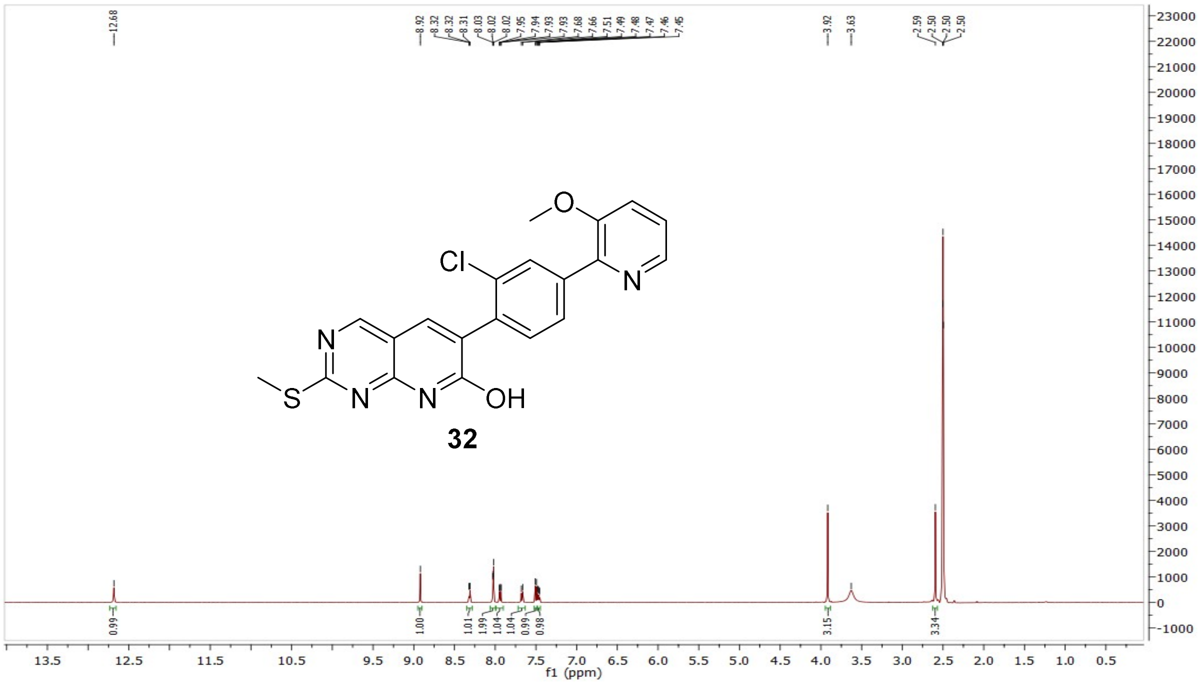


MS (ESI+) compound **32**:

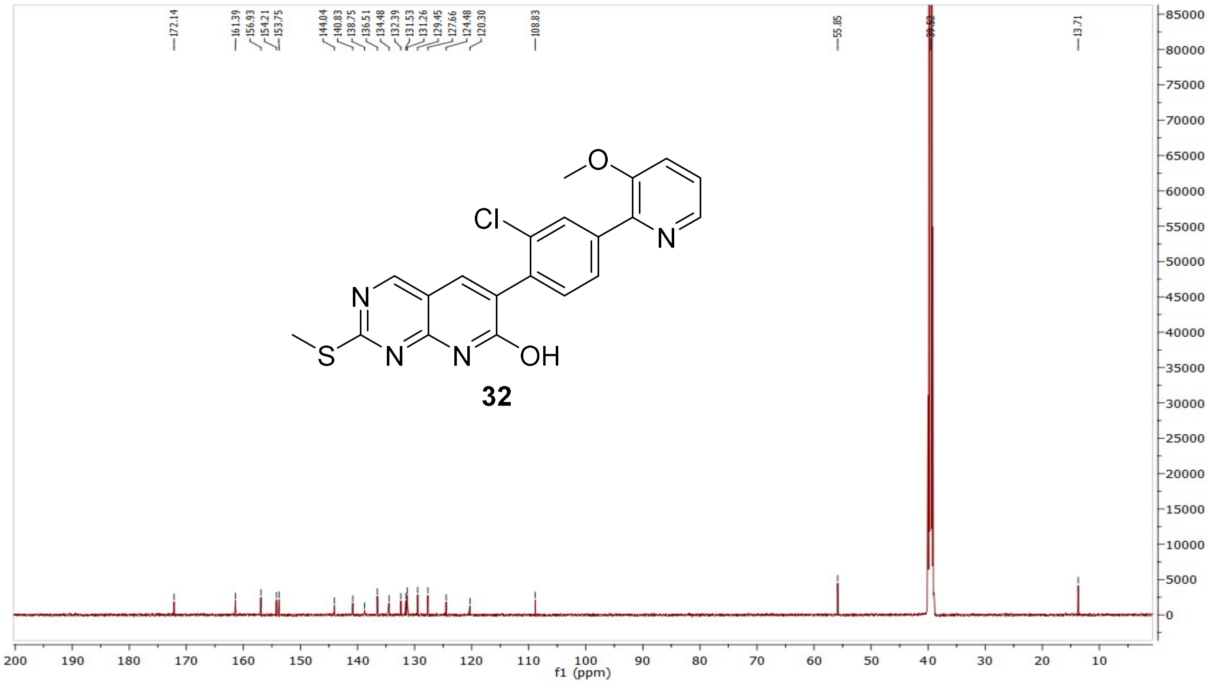

C:\Xcalibur\data\MR39 1/16/2020 10:55:46 AM

MR39 #34-43 RT: 0.58-0.74 AV: 10 SB: 8 0.16-0.28 NL: 3.35E6
T: {0,0} + c ESI !corona sid=75.00 det=1306.00 Full ms [105.00-800.00]

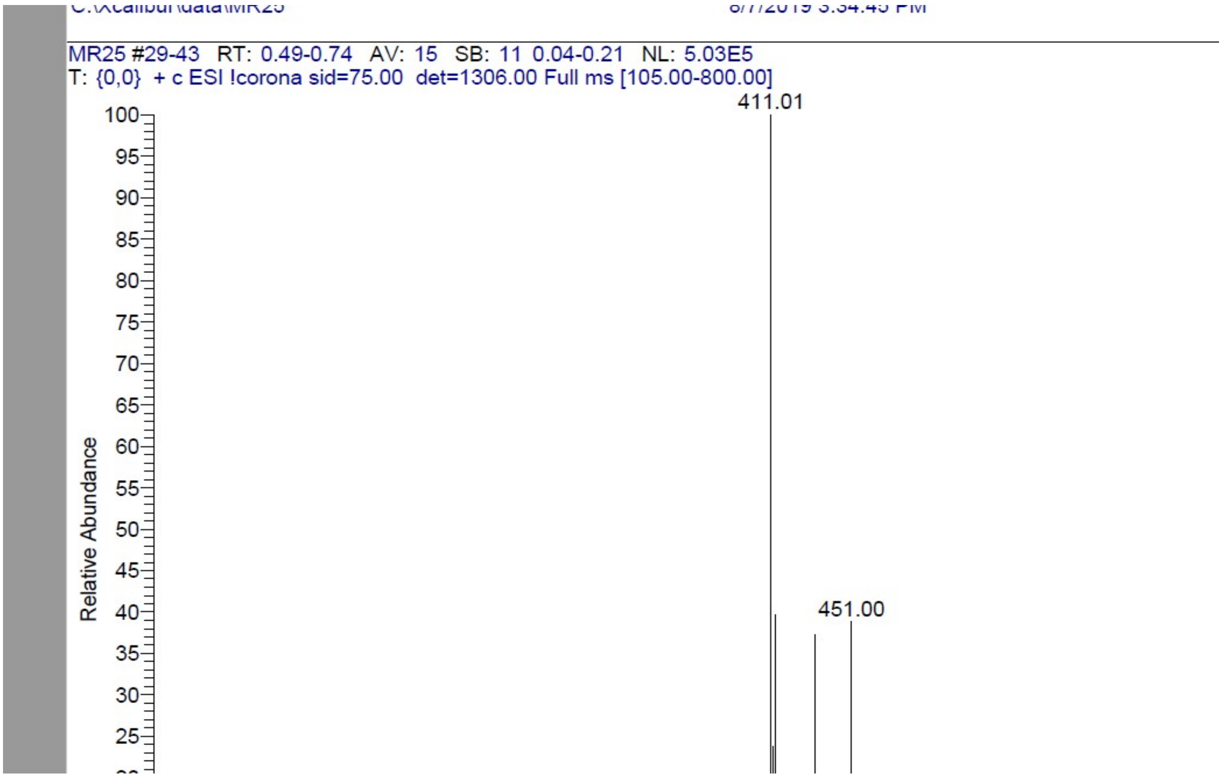
^{1}H NMR compound **33**:



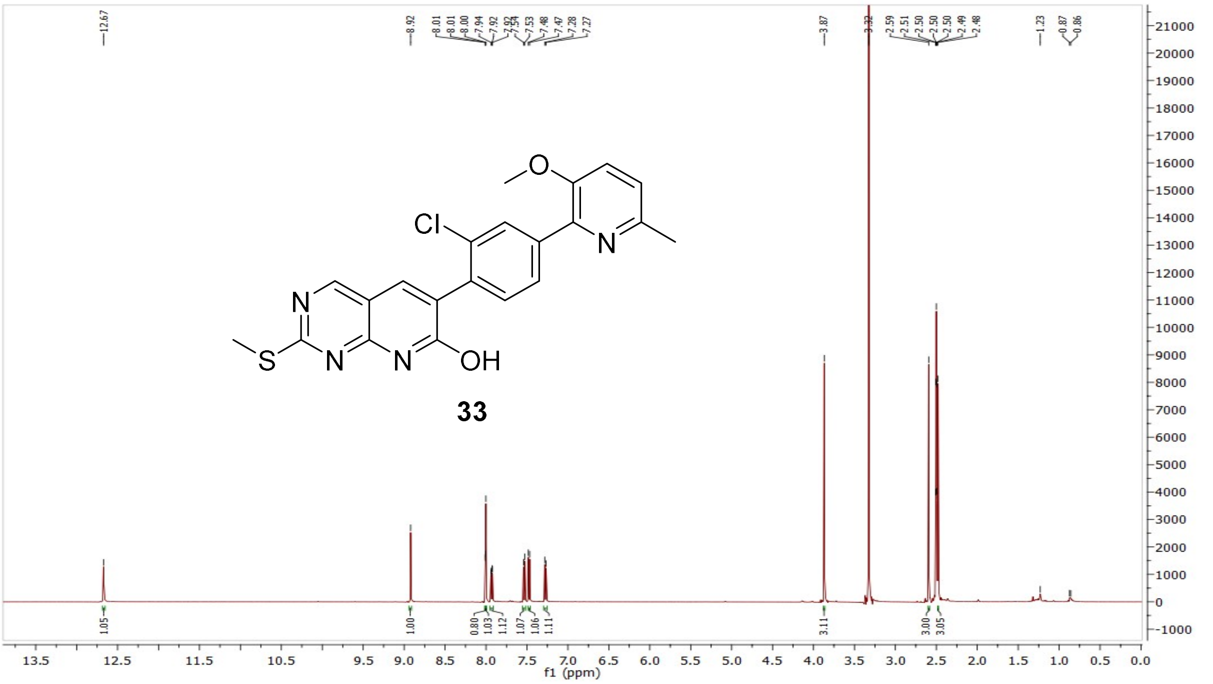
^{13}C NMR compound **33**:



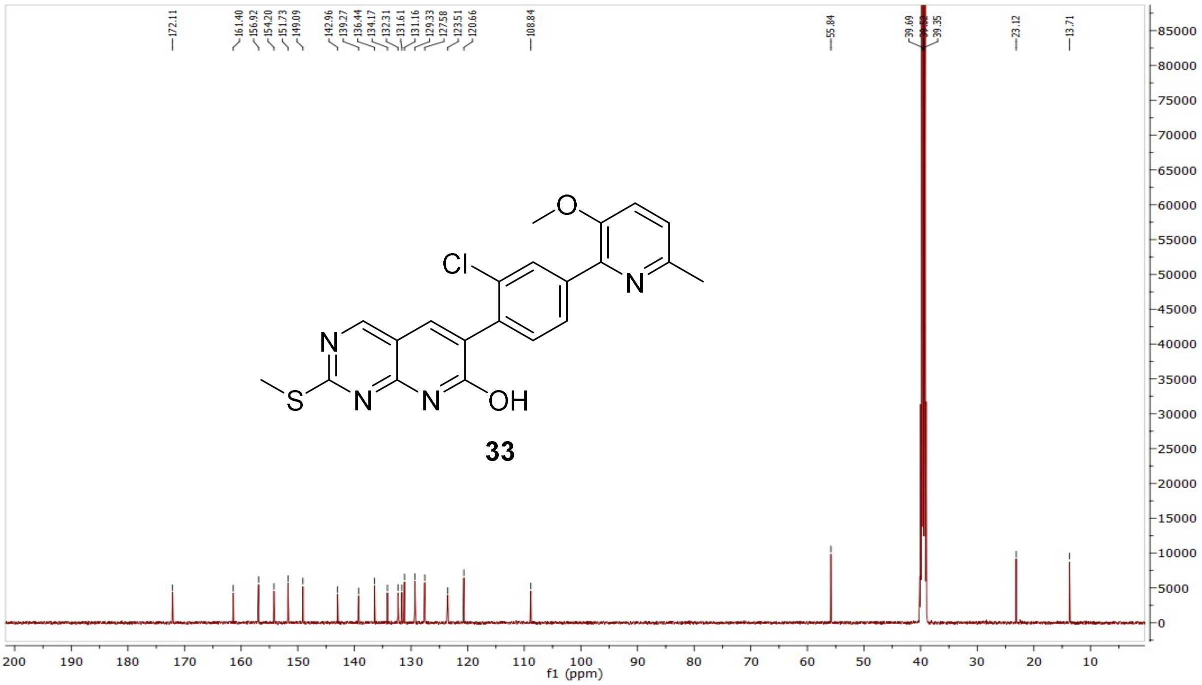
MS (ESI+) compound **33**:



^{1}H NMR compound **34**:

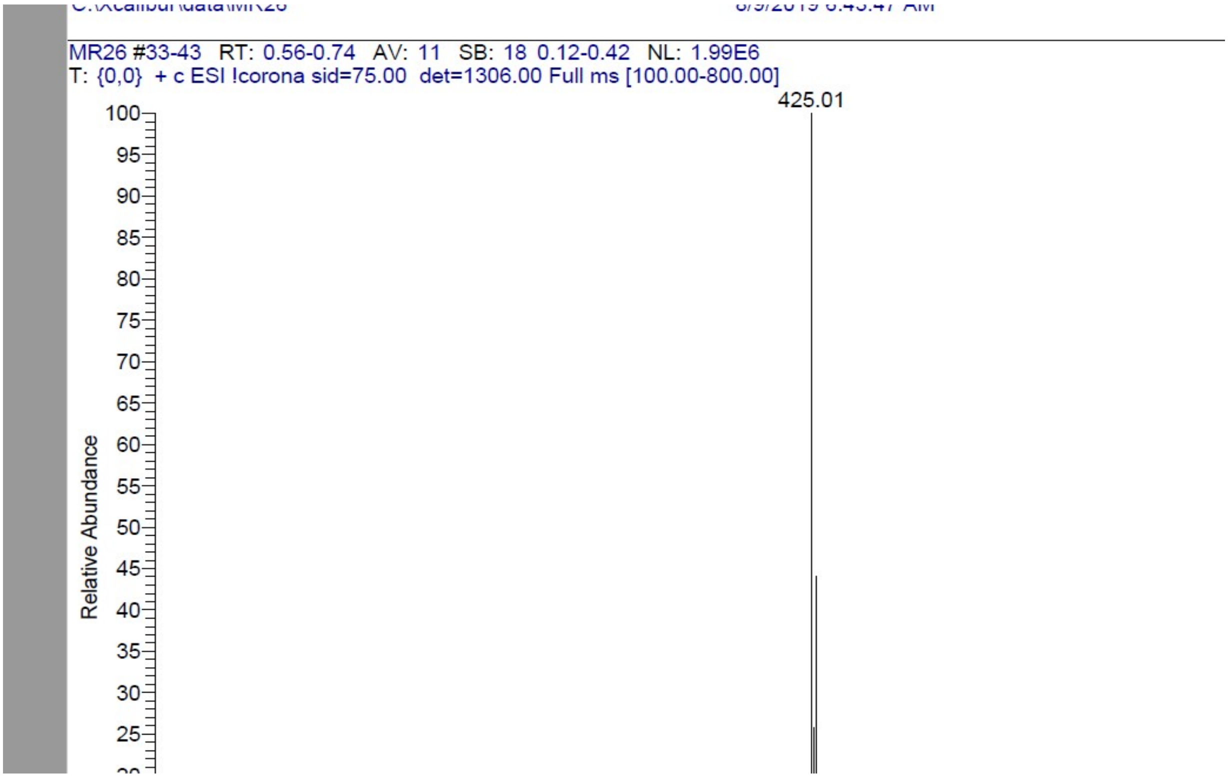


^{13}C NMR compound **34**:

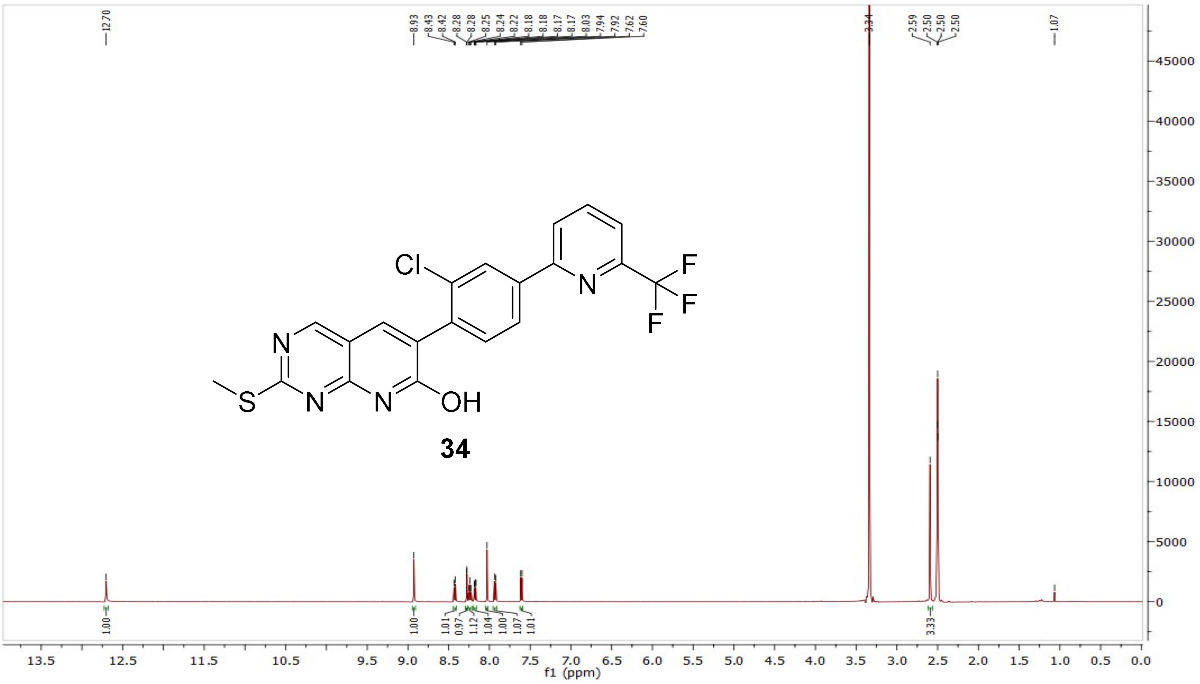


33

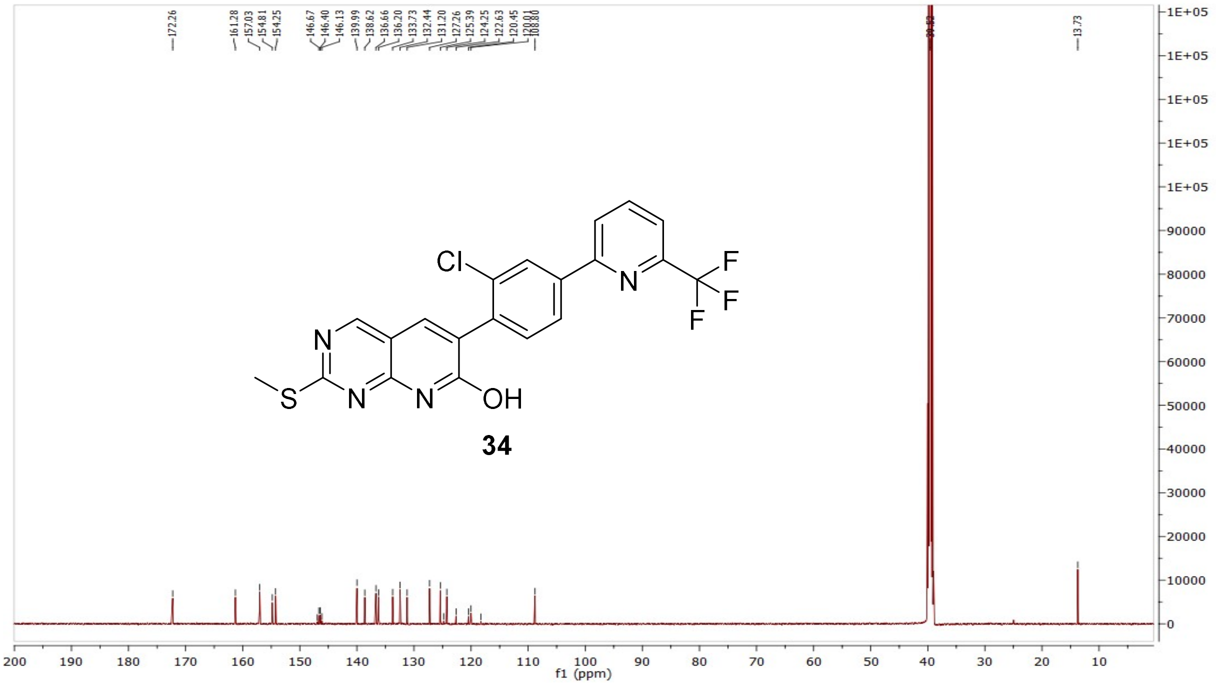
MS (ESI+) compound **34**:


MR26 #33-43 RT: 0.56-0.74 AV: 11 SB: 18 0.12-0.42 NL: 1.99E6
T: {0,0} + c ESI !corona sid=75.00 det=1306.00 Full ms [100.00-800.00]

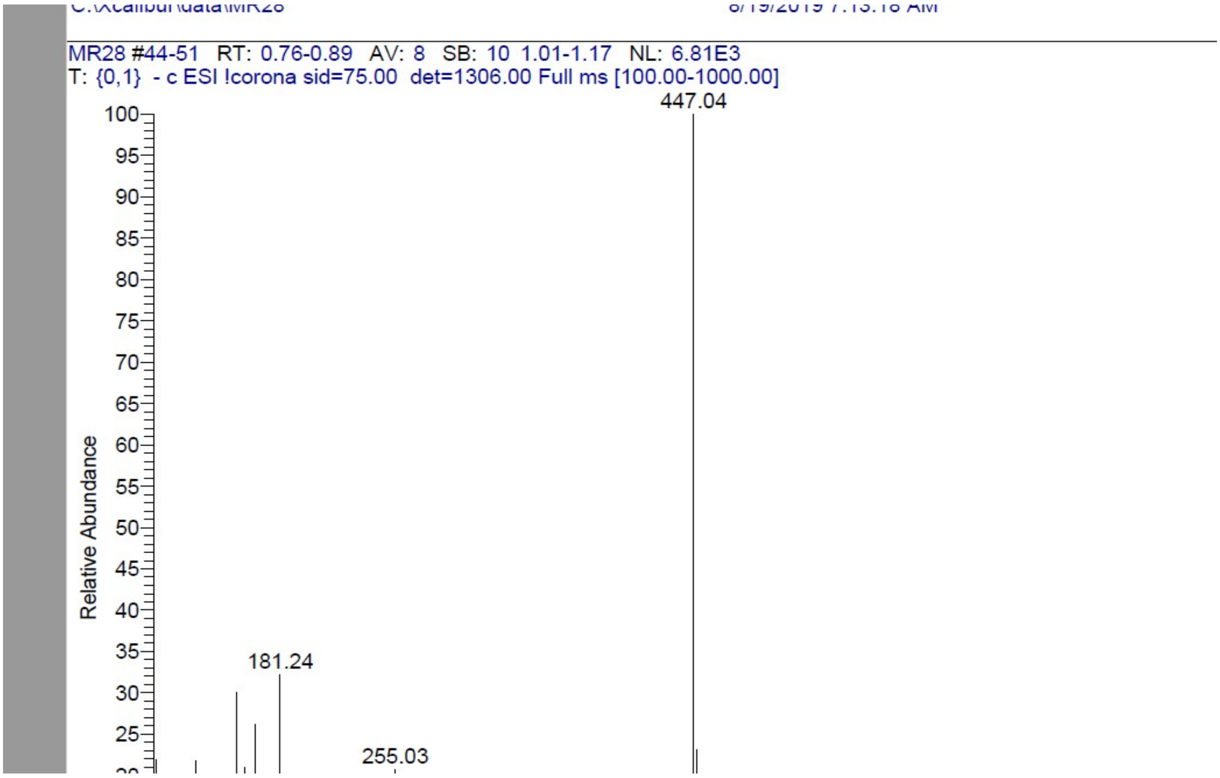
^{1}H NMR compound **35**:



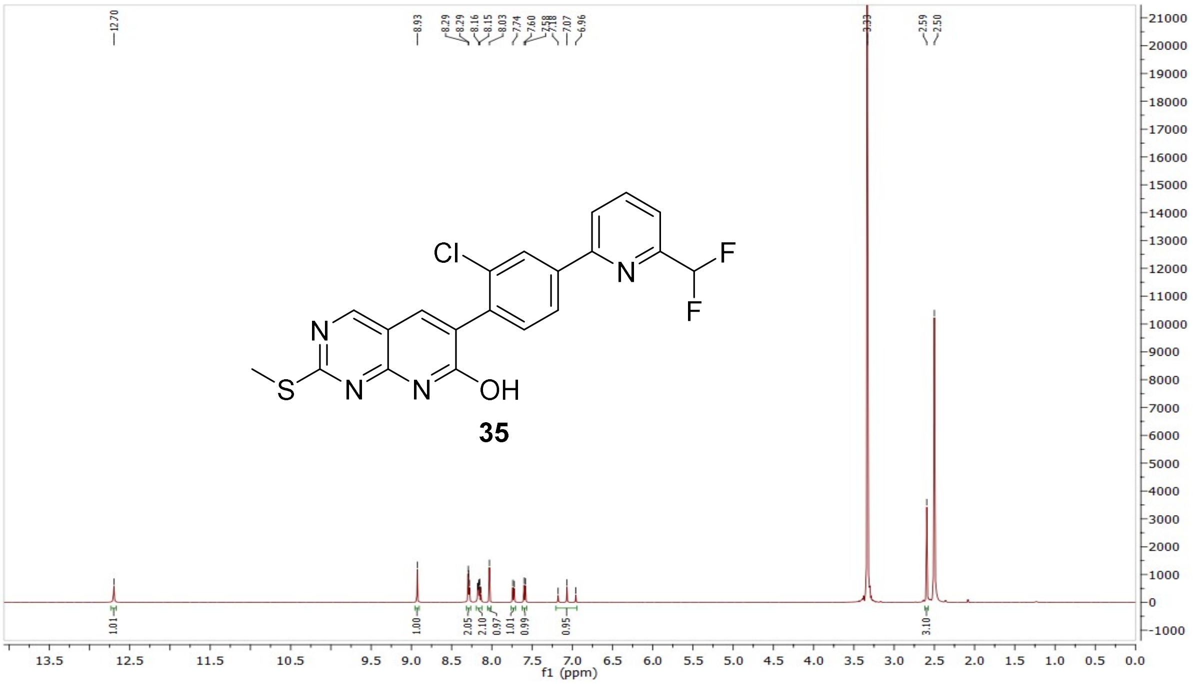
^{13}C NMR compound **35**:



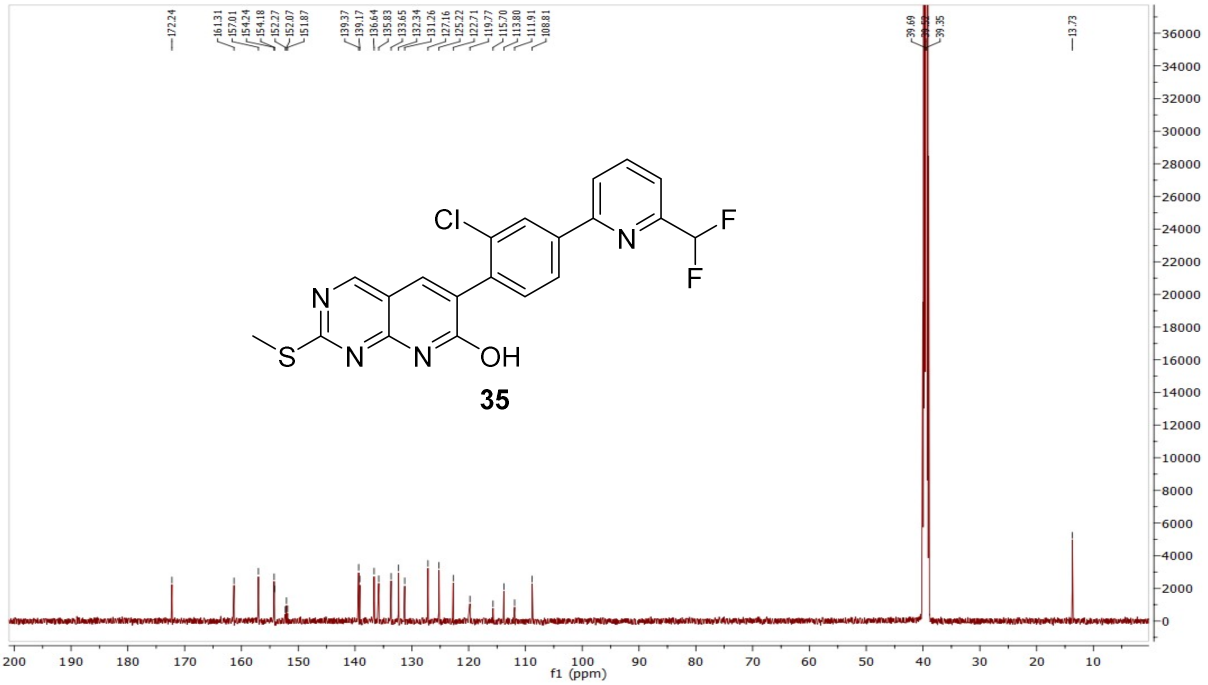
MS (ESI-) compound **35**:



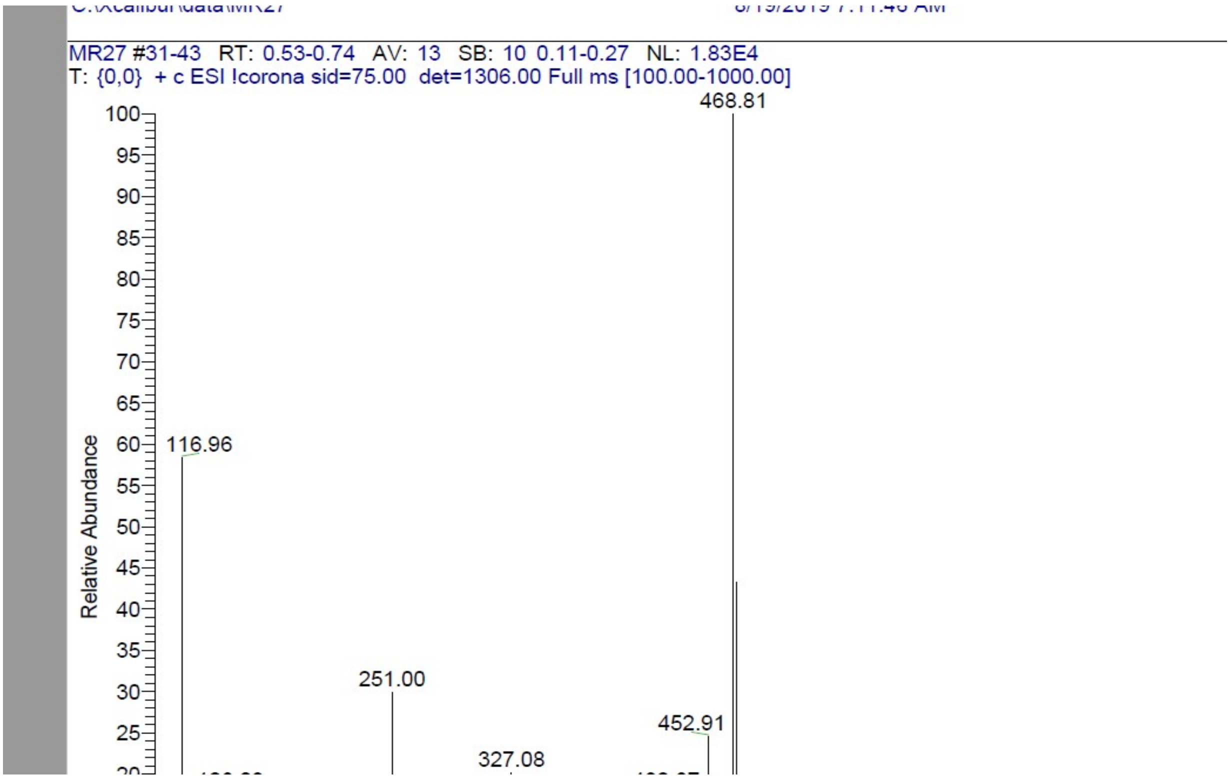
^{1}H NMR compound **36**:



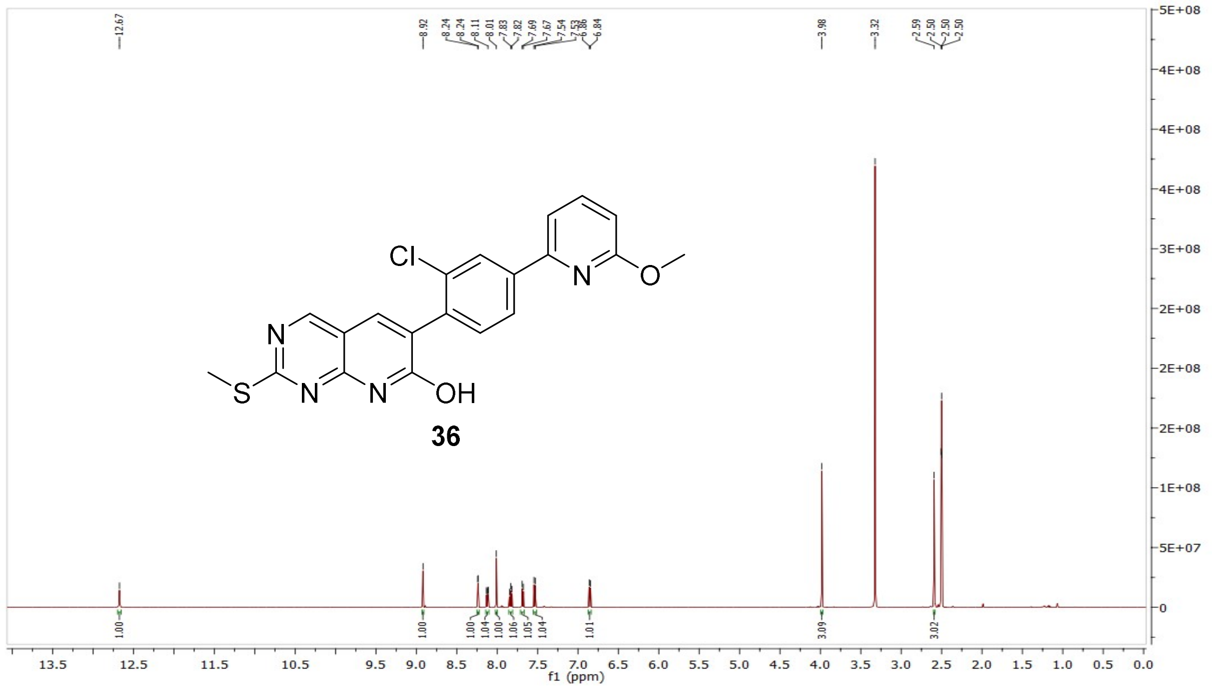
^{13}C NMR compound **36**:



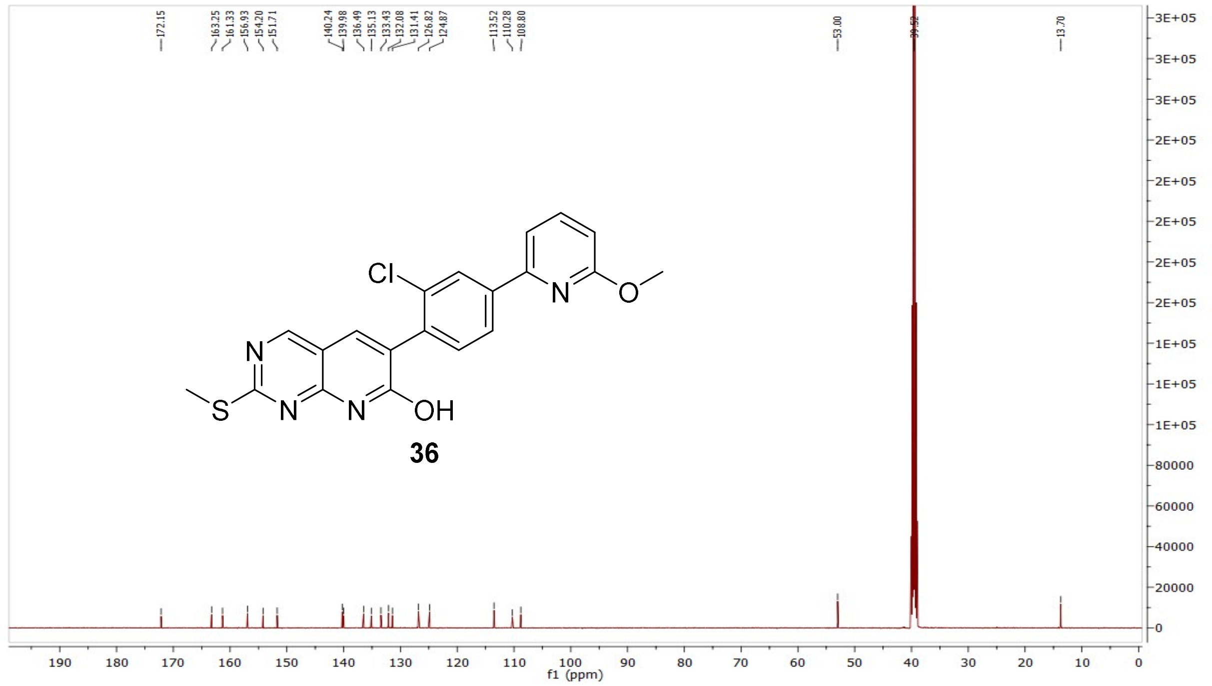
MS (ESI+) compound **36**:



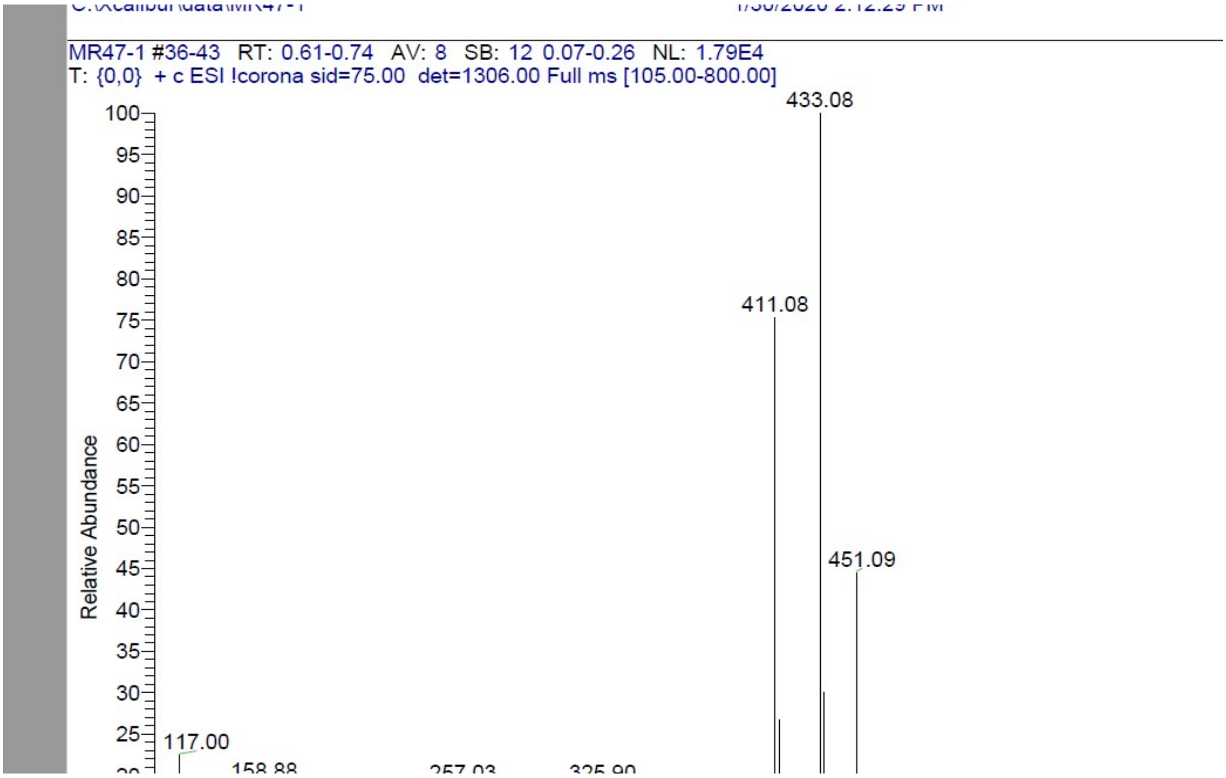
^{1}H NMR compound **37**:



^{13}C NMR compound **37**:

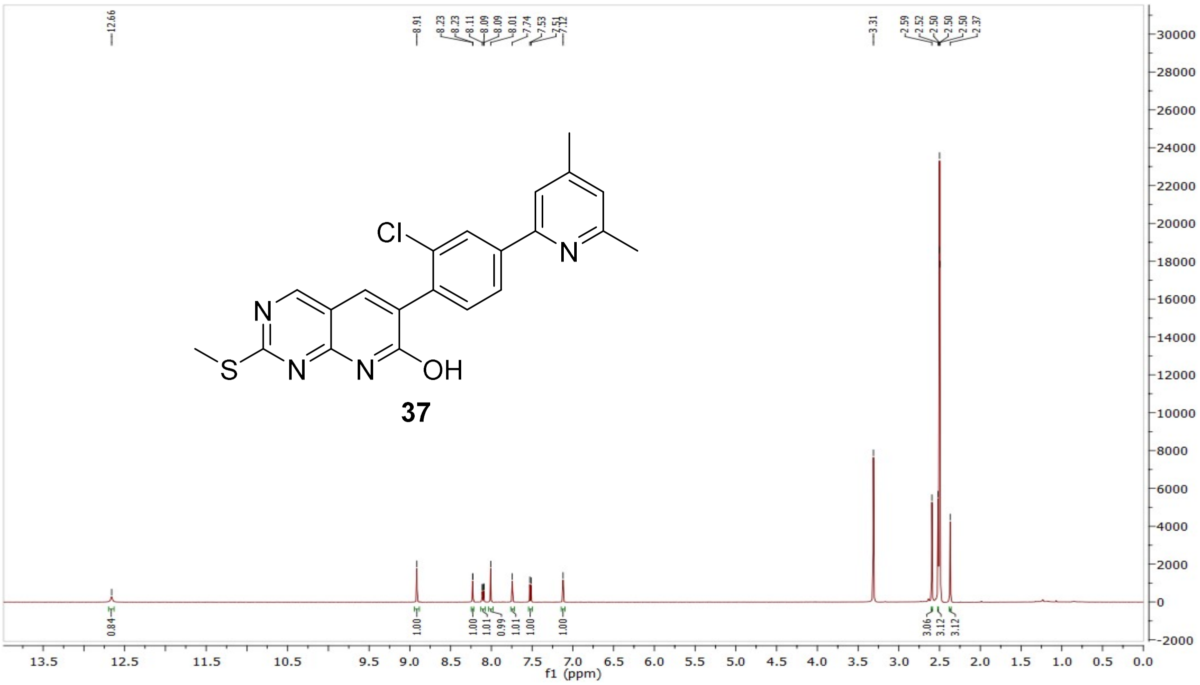


MS (ESI+) compound **37**:

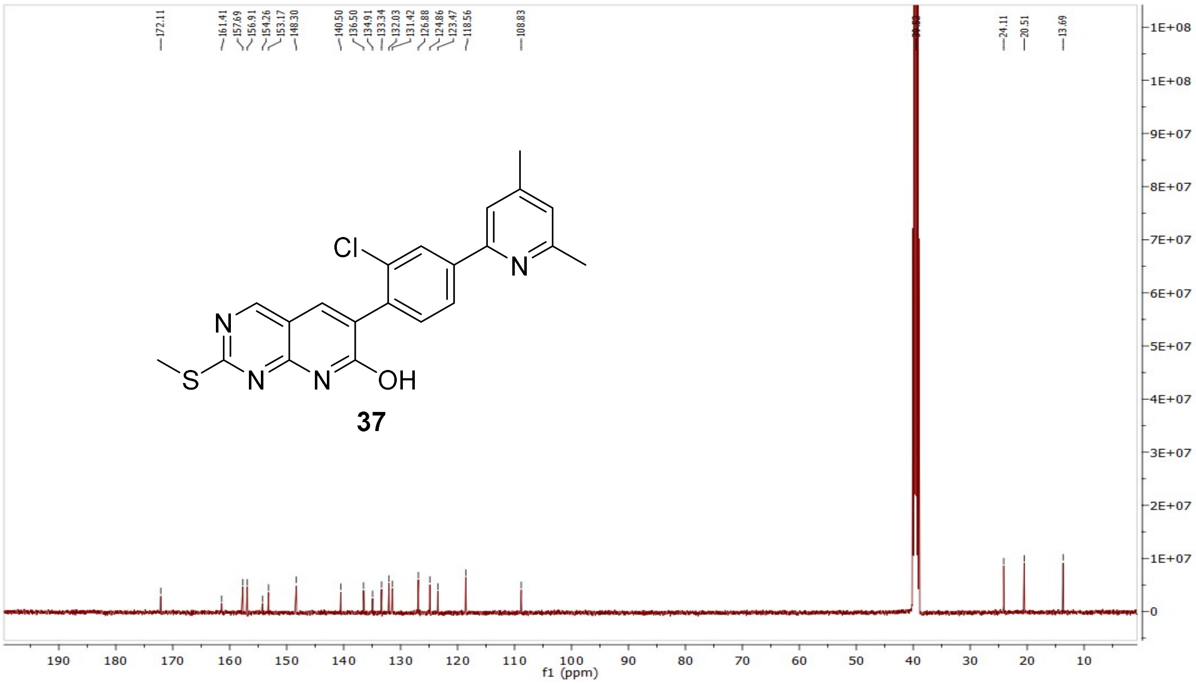


MR47-1 #36-43 RT: 0.61-0.74 AV: 8 SB: 12 0.07-0.26 NL: 1.79E4
T: {0,0} + c ESI !corona sid=75.00 det=1306.00 Full ms [105.00-800.00]

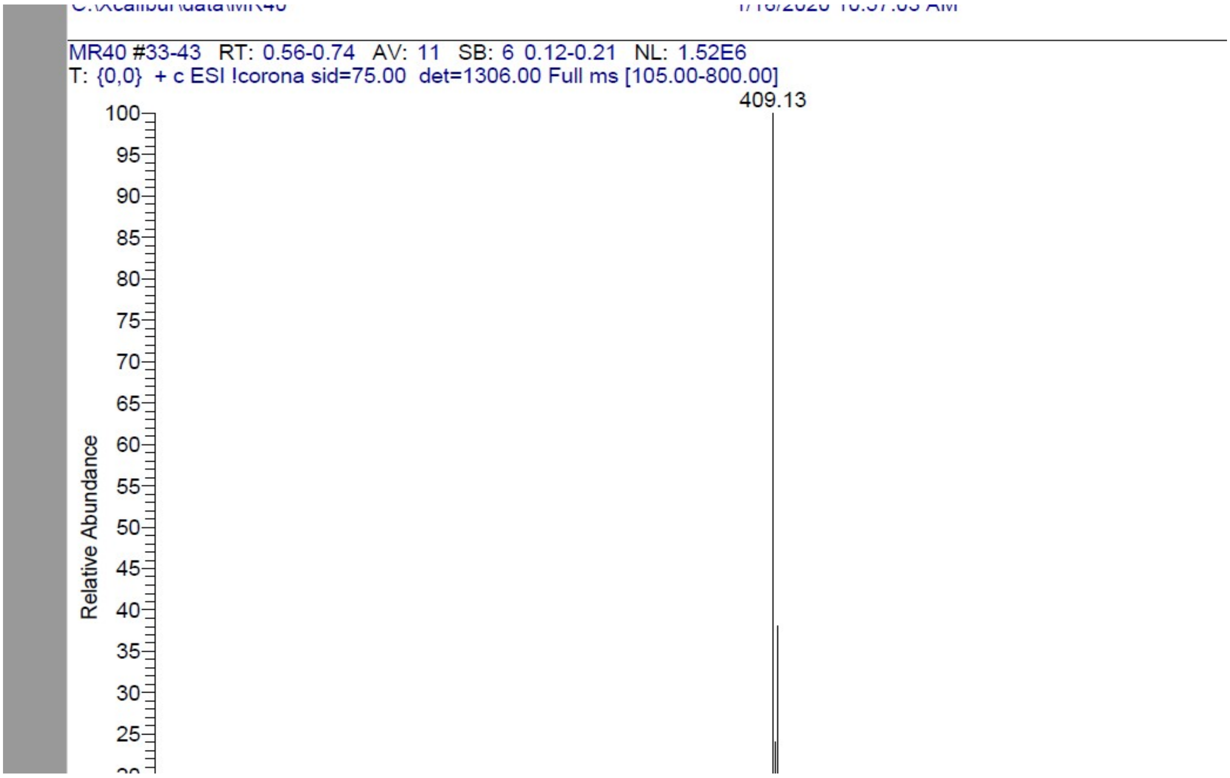
^{1}H NMR compound **38**:



^{13}C NMR compound **38**:

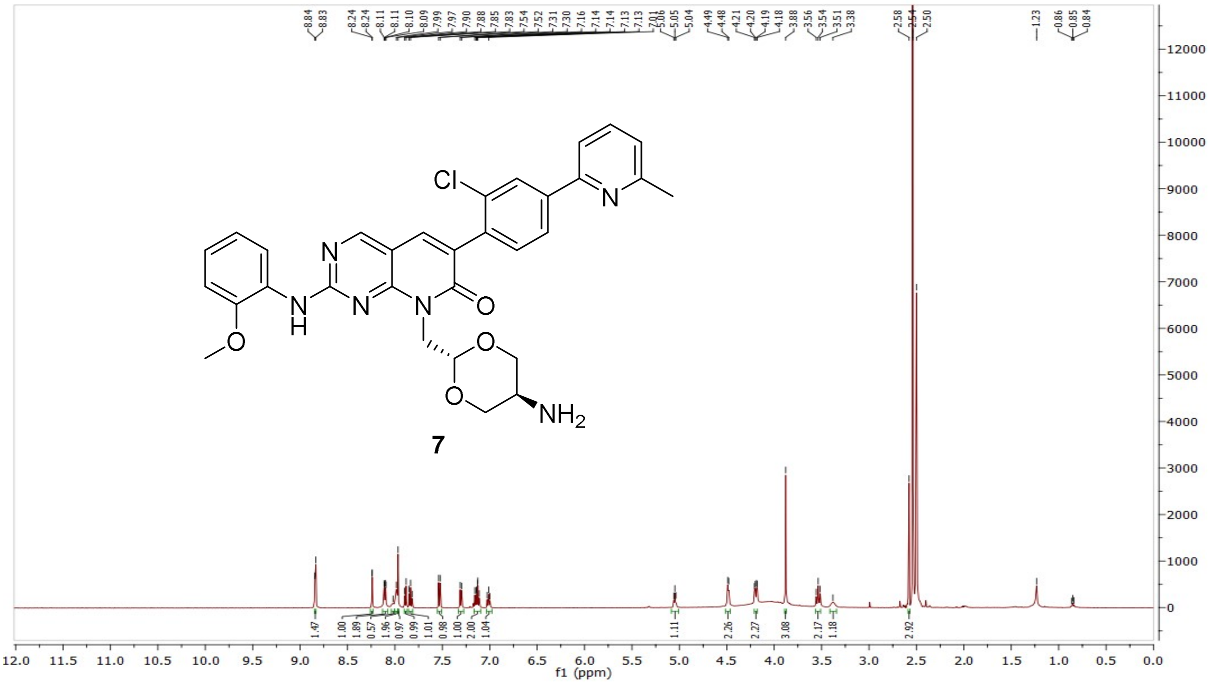


MS (ESI+) compound **38**:

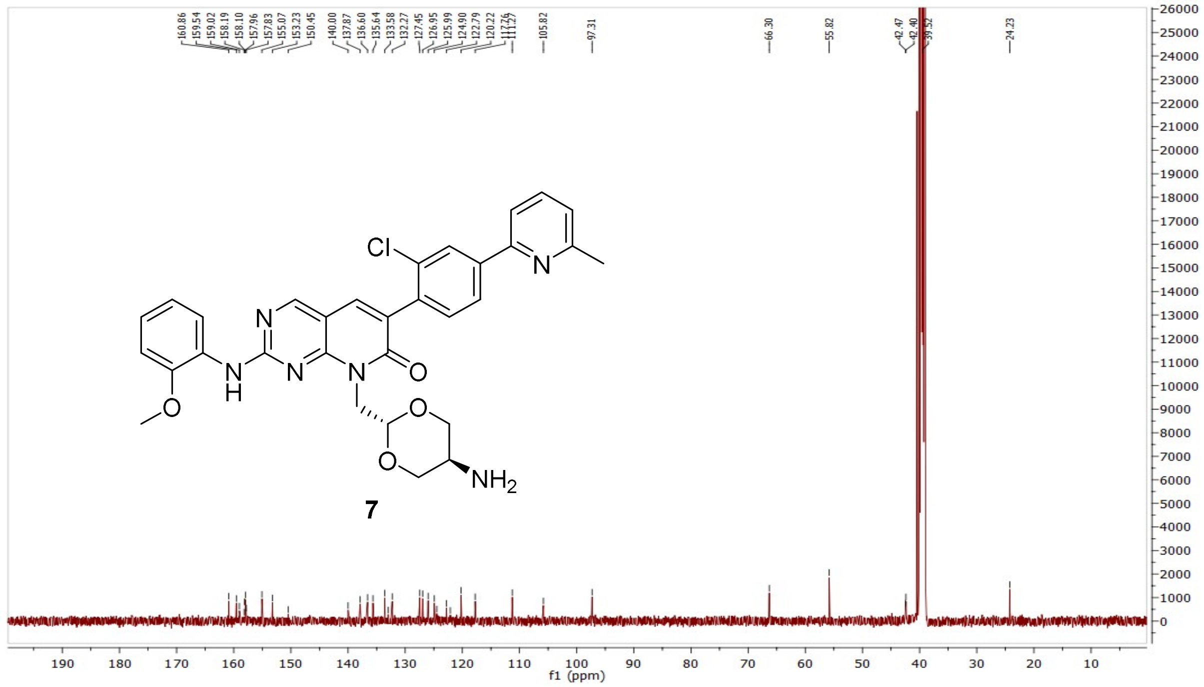


MR40 #33-43 RT: 0.56-0.74 AV: 11 SB: 6 0.12-0.21 NL: 1.52E6
T: {0,0} + c ESI !corona sid=75.00 det=1306.00 Full ms [105.00-800.00]

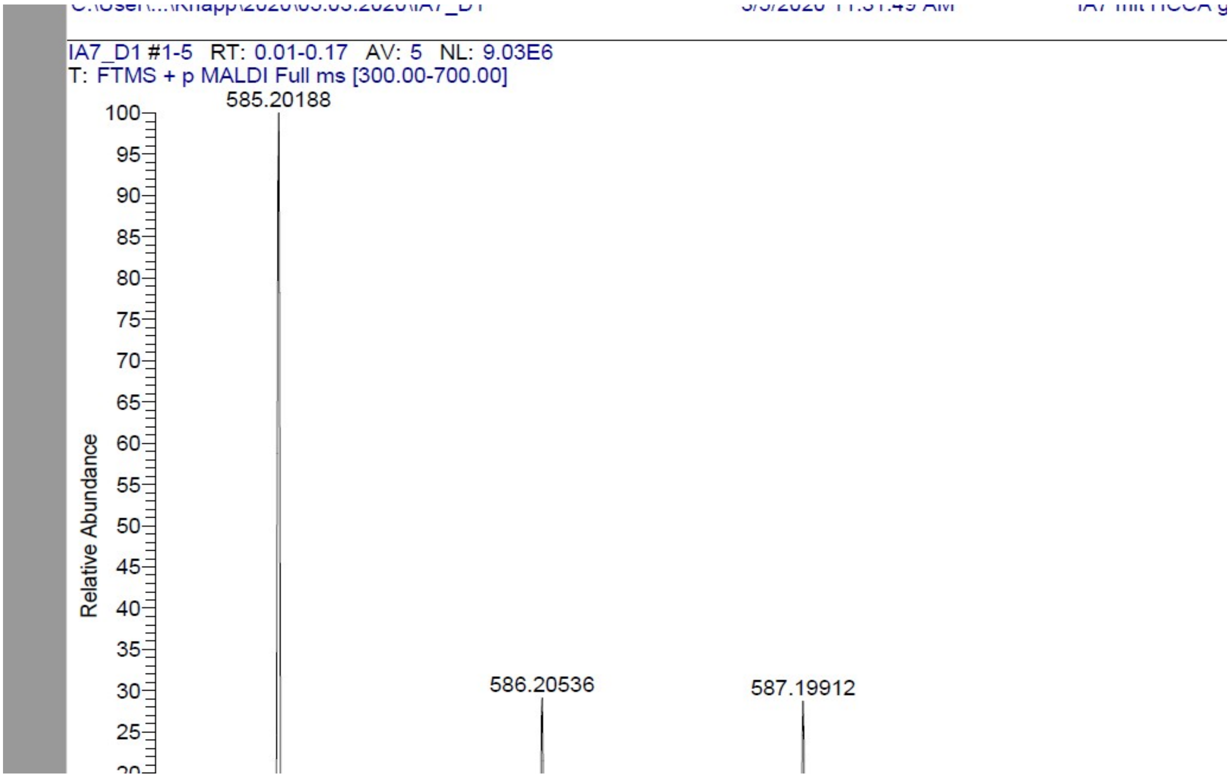
^{1}H NMR compound **7**:



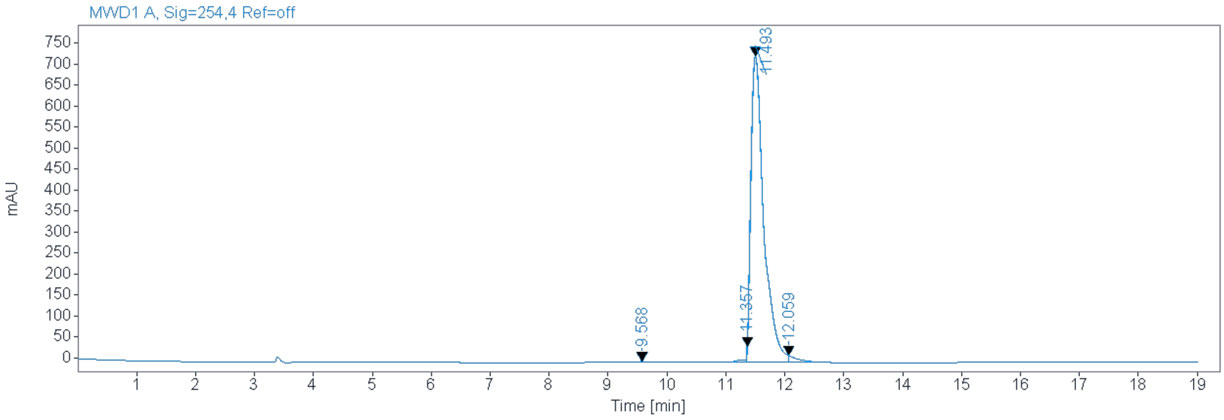
^{13}C NMR compound **7**:

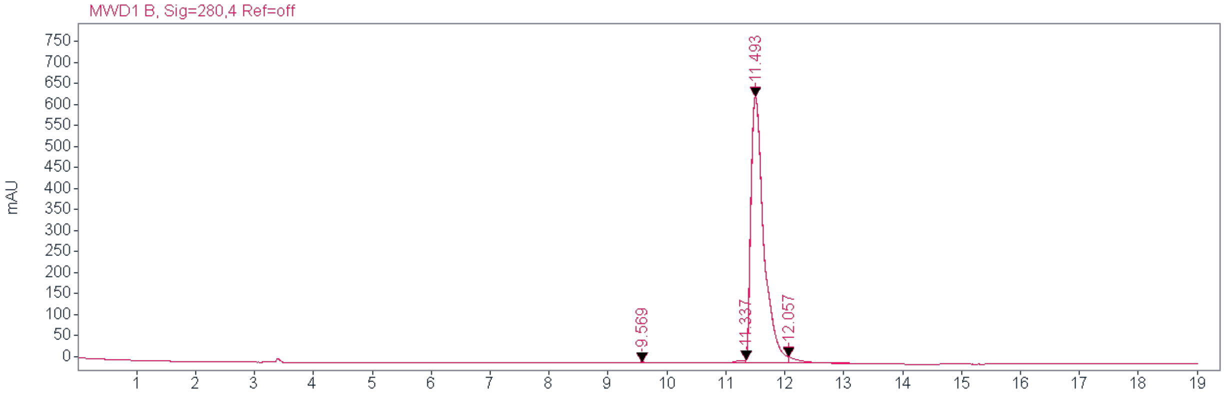


HRMS (FTMS +p MALDI) compound **7**:



HPLC-chromatograms compound **7**:



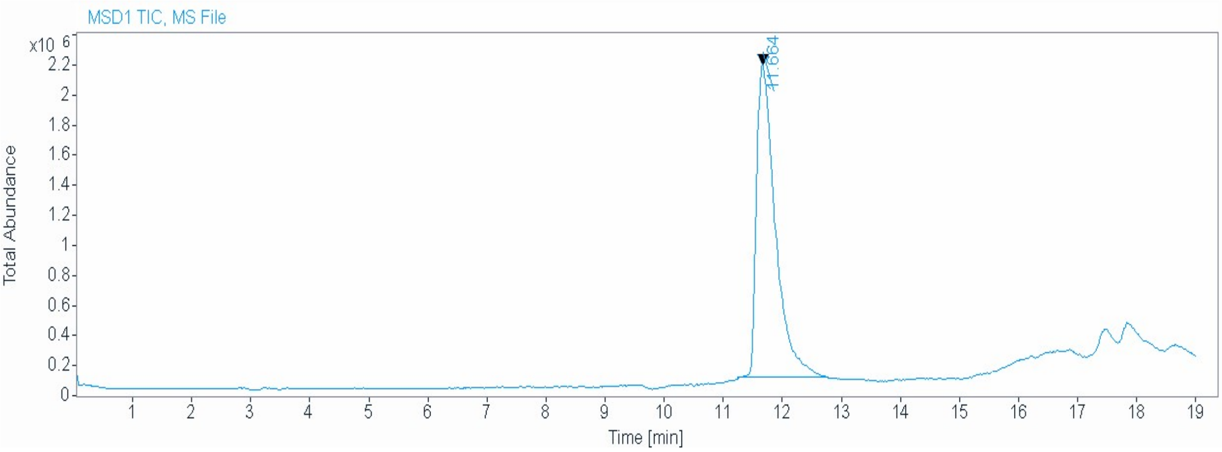


Signal: MWD1 A, Sig=254,4 Ref=off

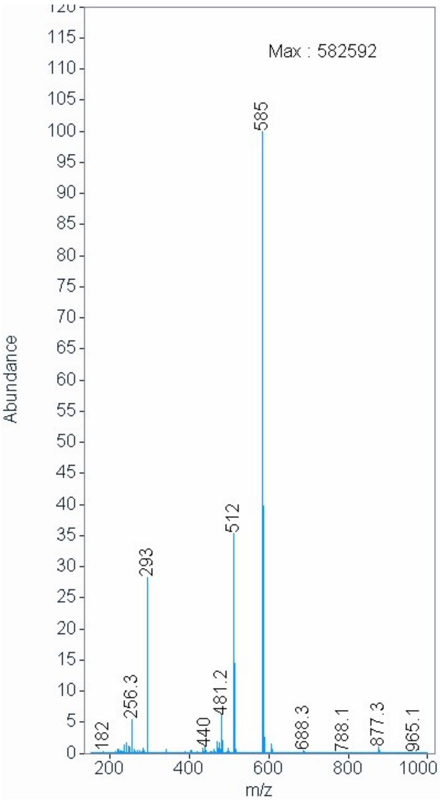
RT [min]	Type	Width [min]	Area	Height	Area%	Name
9.568	MM	0.8038	110.8189	2.2979	0.9661	
11.357	MM	0.0392	89.1243	37.8772	0.7769	
11.493	MM	0.2533	11085.0762	729.4694	96.6346	
12.059	MM	0.1912	186.1067	16.2195	1.6224	
		Sum	11471.1261			

Signal: MWD1 B, Sig=280,4 Ref=off

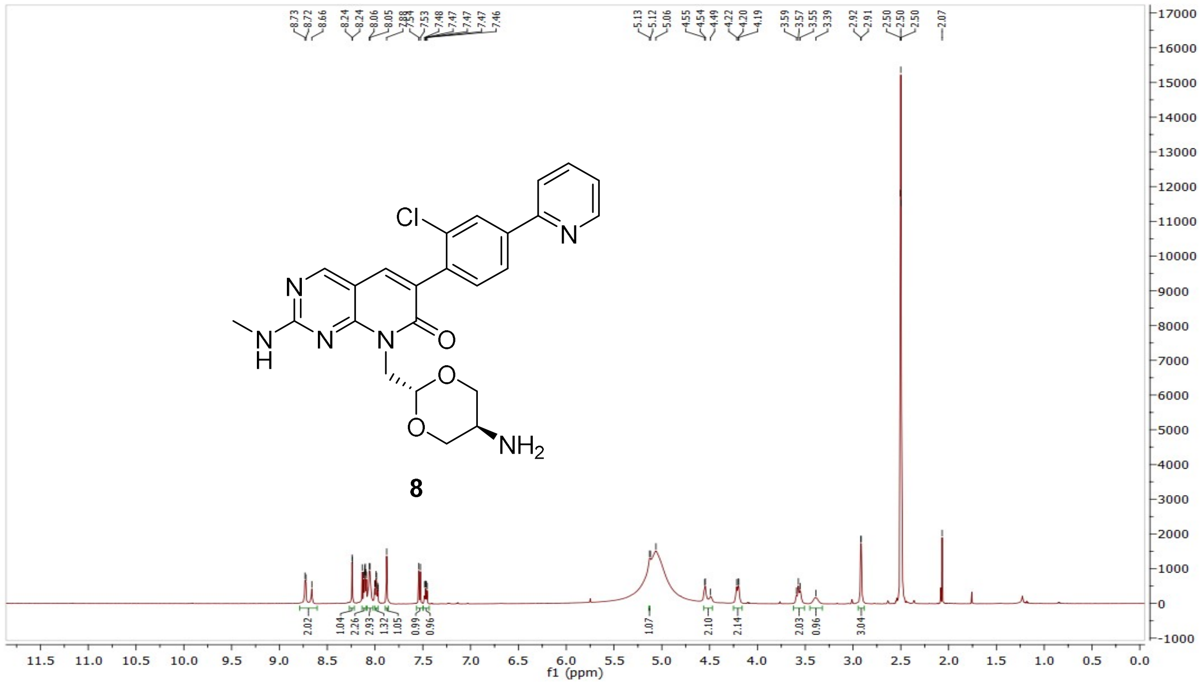
RT [min]	Type	Width [min]	Area	Height	Area%	Name
9.569	MM	0.7332	109.5441	2.4901	1.0867	
11.337	MM	0.2213	93.9797	7.0787	0.9323	
11.493	MM	0.2543	9672.0059	633.9951	95.9459	
12.057	MM	0.1576	205.1585	15.2968	2.0352	
		Sum	0080.882			



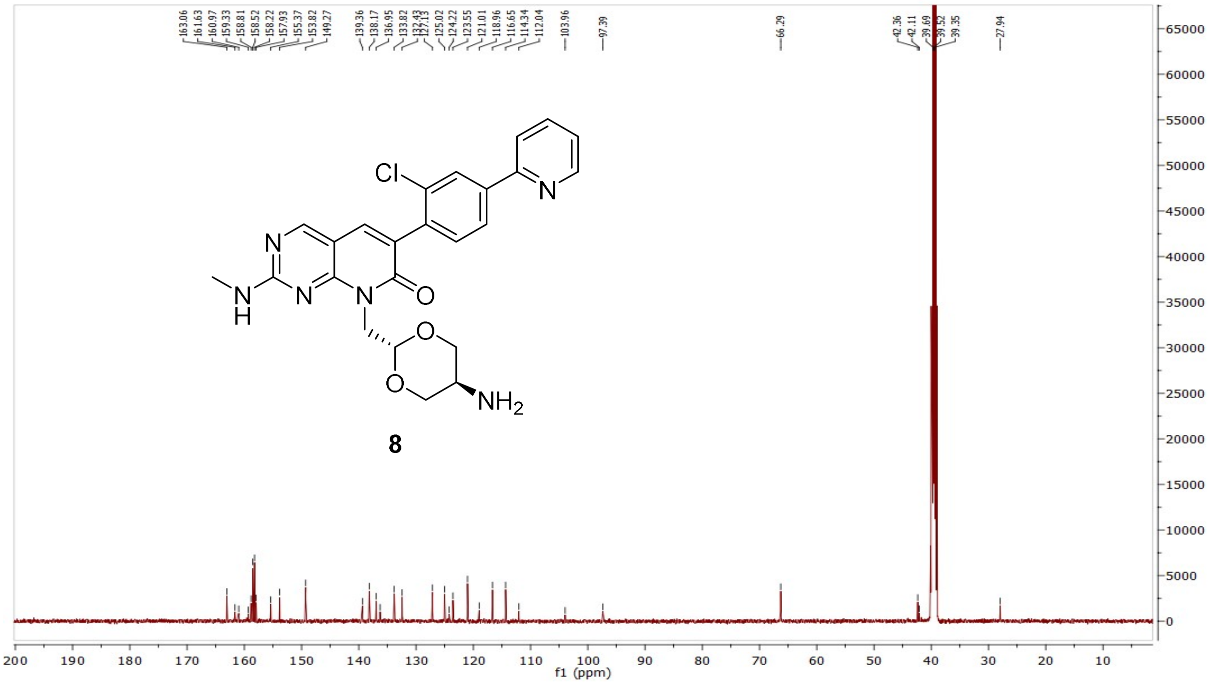
Signal	MSD1 TIC, MS File
Peak RT	11.664



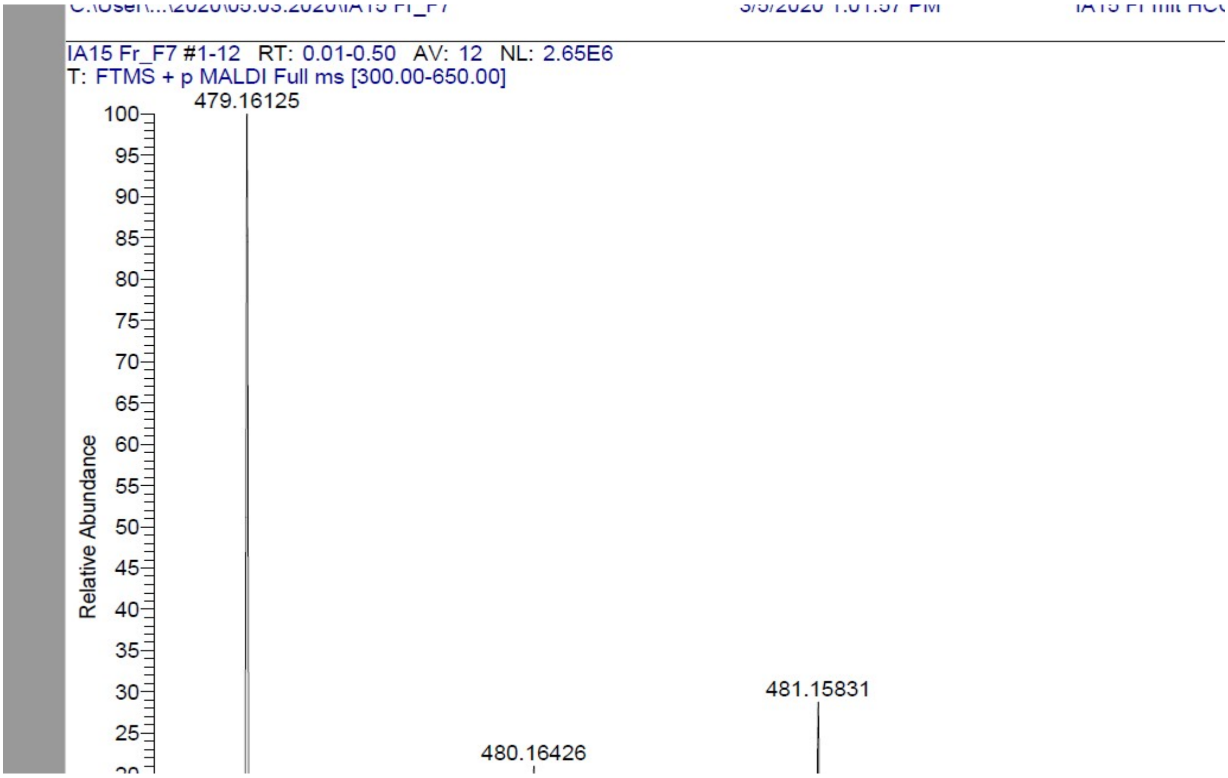
^{1}H NMR compound **8**:



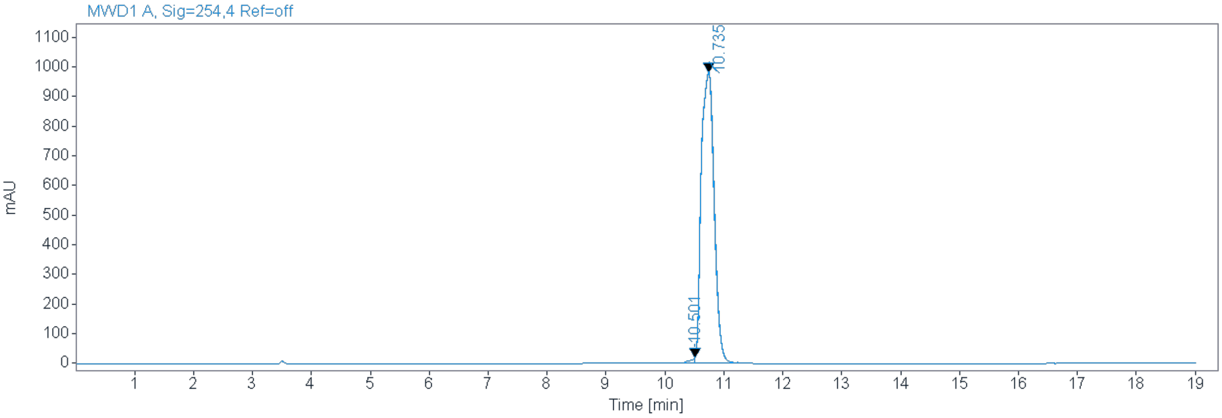
^{13}C NMR compound **8**:

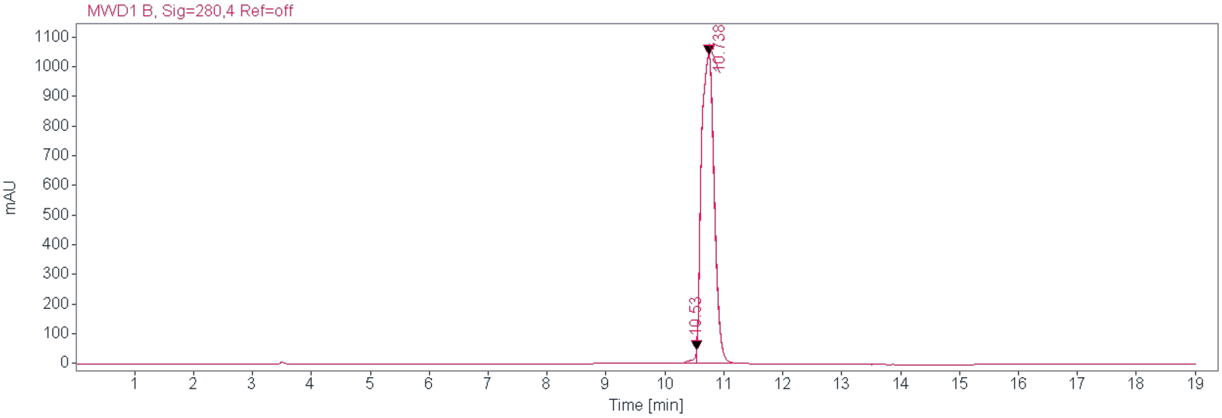


HRMS (FTMS +p MALDI) compound **8**:



HPLC-chromatograms compound **8**:



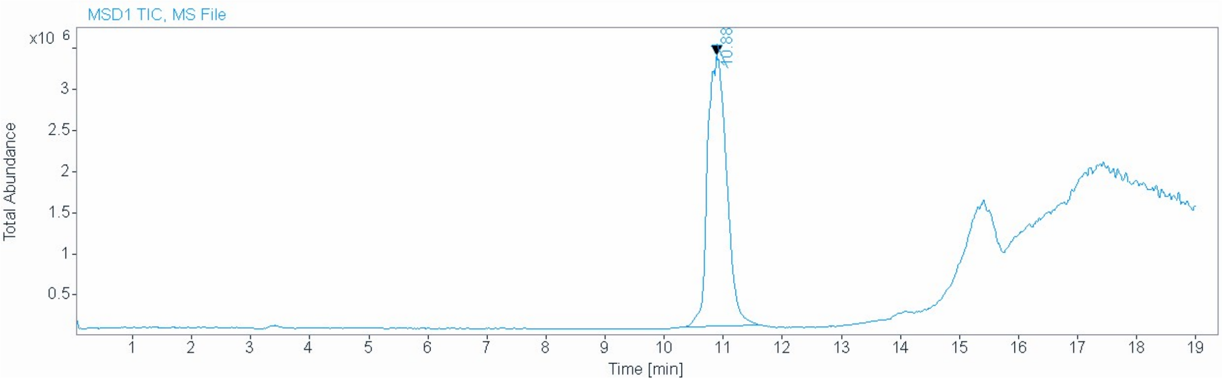


Signal: MWD1 A, Sig=254,4 Ref=off

RT [min]	Type	Width [min]	Area	Height	Area%	Name
10.501	MM	0.1003	120.8871	20.0778	0.8036	
10.735	MM	0.2533	14922.7129	981.7443	99.1964	
		Sum	15043.5999			

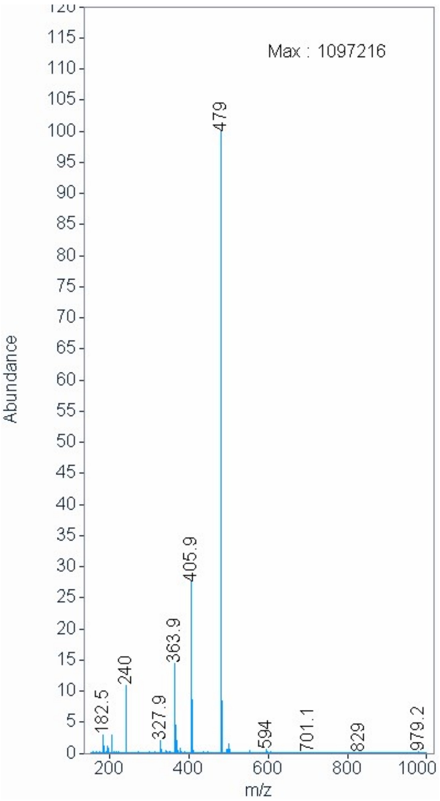
Signal: MWD1 B, Sig=280,4 Ref=off

RT [min]	Type	Width [min]	Area	Height	Area%	Name
10.530	MM	0.0641	177.3867	46.1568	1.1163	
10.738	MM	0.2515	15713.6553	1041.1525	98.8837	
		Sum	15891.0419			

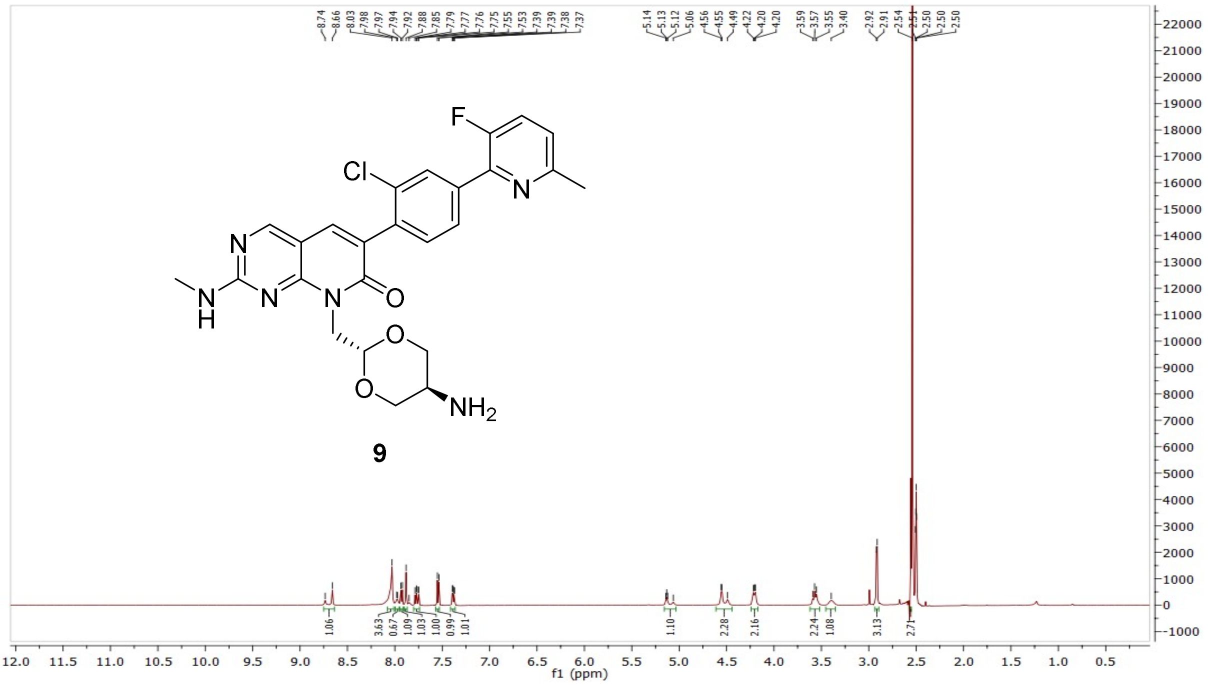


Signal MSD1 TIC, MS File

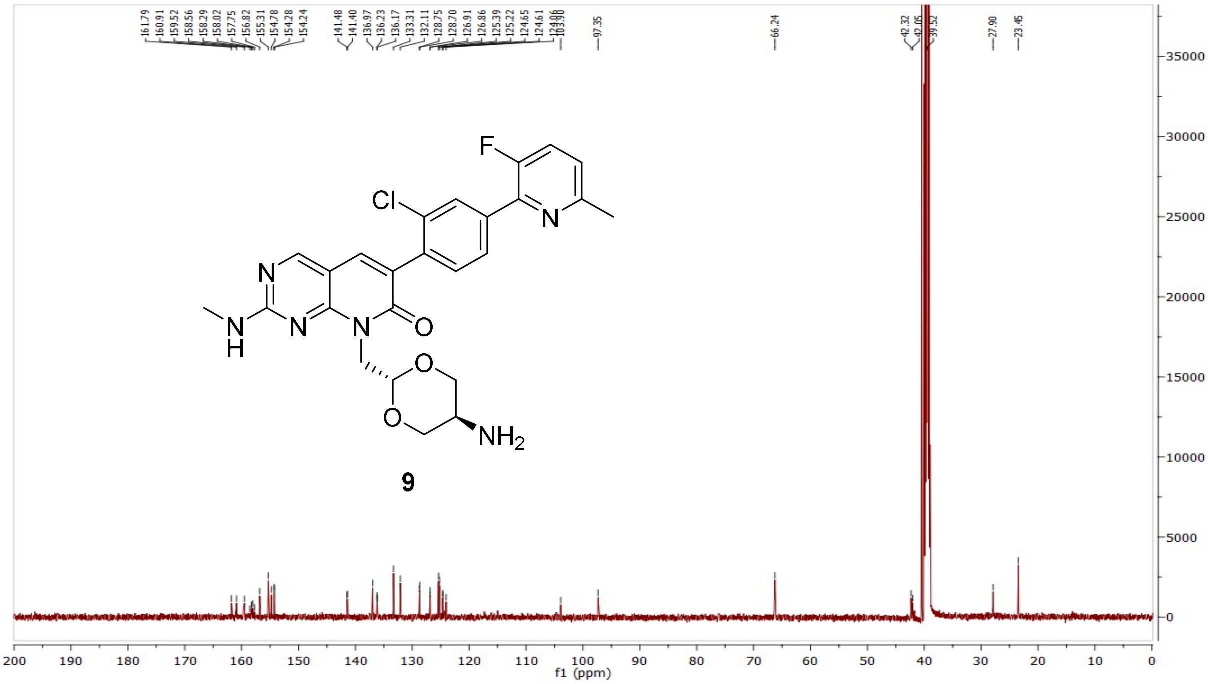
Peak RT 10.880



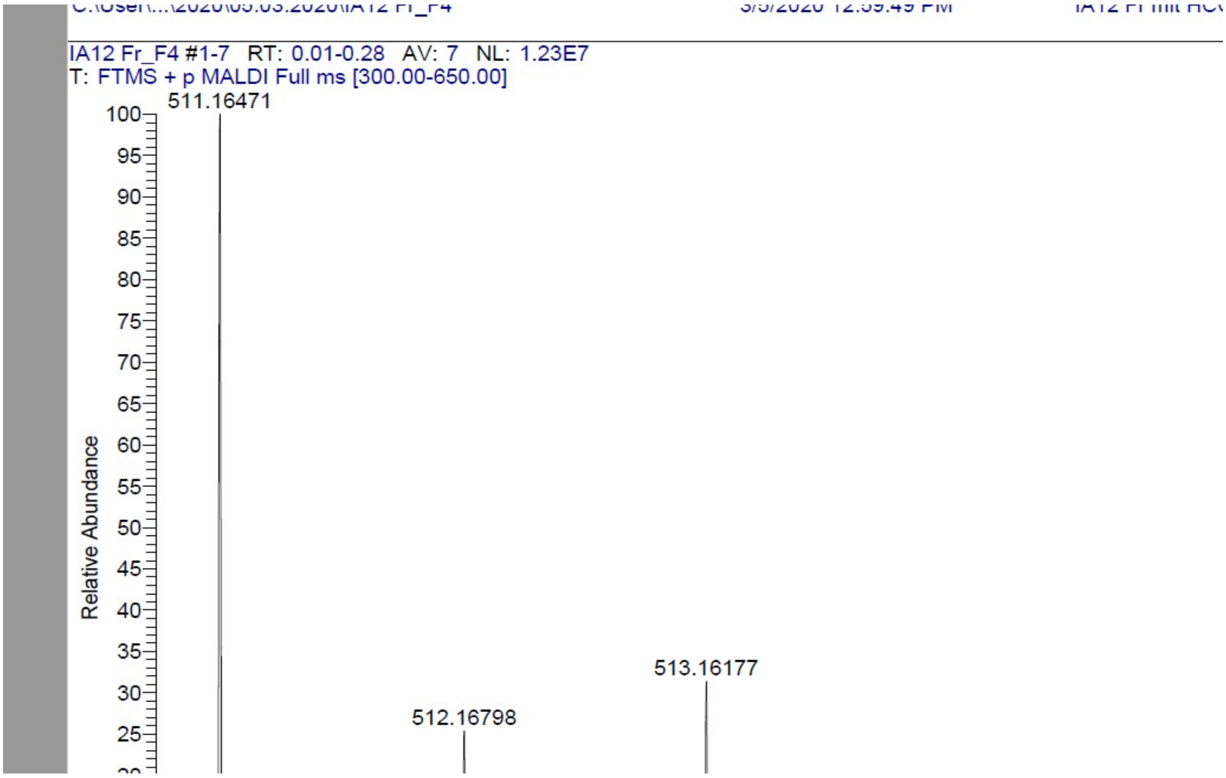
^{1}H NMR compound **9**:



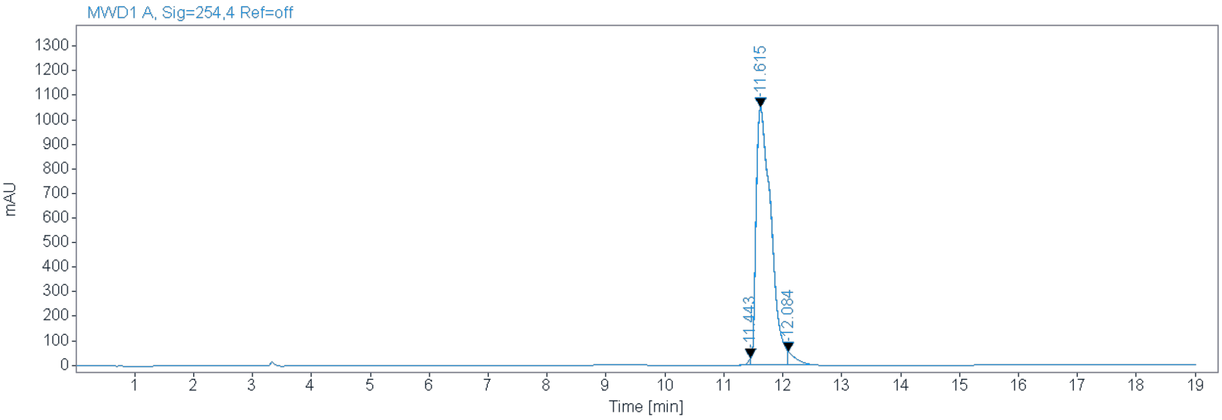
^{13}C NMR compound **9**:

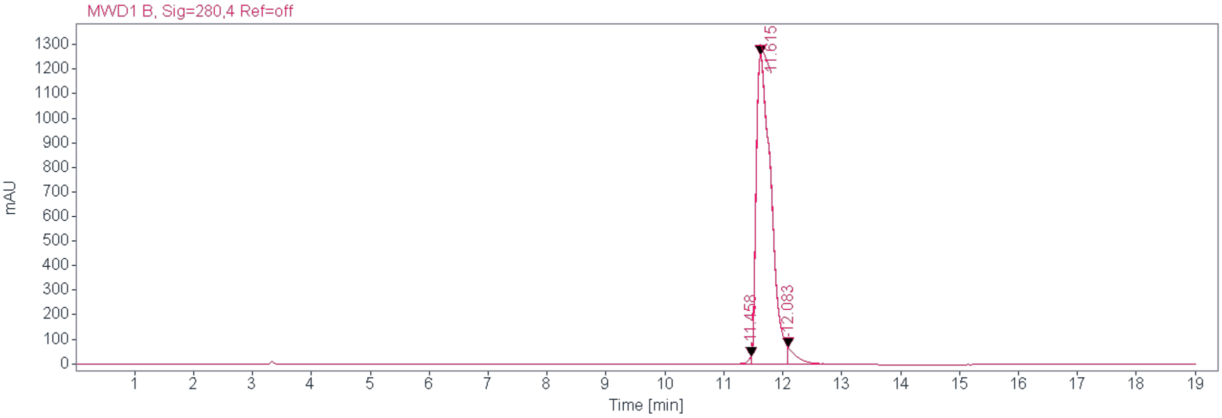


HRMS (FTMS +p MALDI) compound **9**:



HPLC-chromatograms compound **9**:



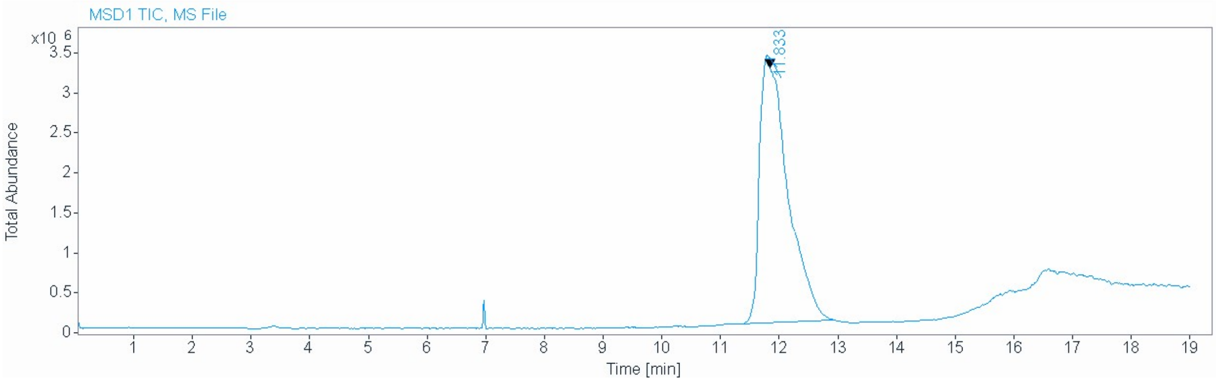


Signal: MWD1 B, Sig=280,4 Ref=off

RT [min]	Type	Width [min]	Area	Height	Area%	Name
11.443	MM	0.0502	85.6657	28.4422	0.4551	
11.615	MM	0.2890	18216.6621	1050.6274	96.7666	
12.084	MM	0.1218	523.0377	55.6911	2.7784	
		Sum	18825.3655			

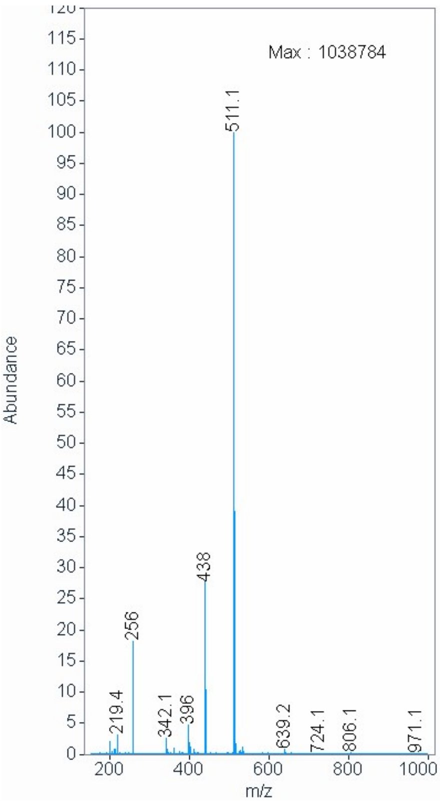
Signal: MWD1 B, Sig=280,4 Ref=off

RT [min]	Type	Width [min]	Area	Height	Area%	Name
11.458	MM	0.0683	123.5502	30.1602	0.5462	
11.615	MM	0.2885	21807.9980	1259.8616	96.4134	
12.083	MM	0.1291	687.7219	68.4209	3.0404	
		Sum	22619.2702			

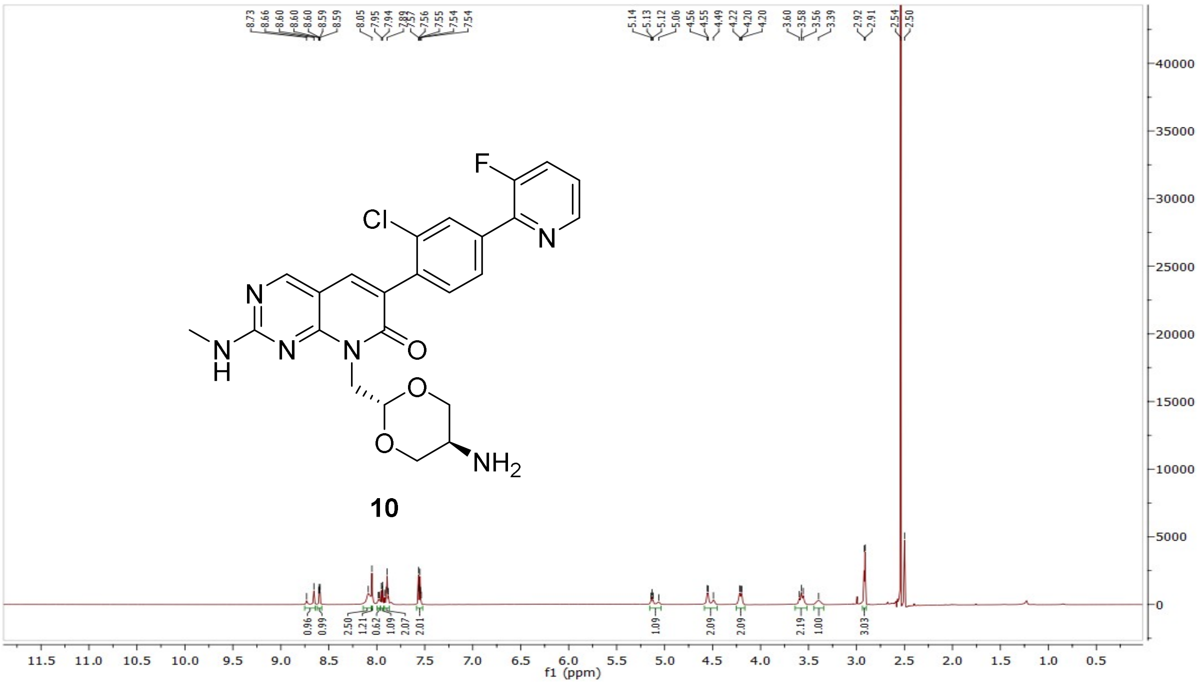


Signal MSD1 TIC, MS File

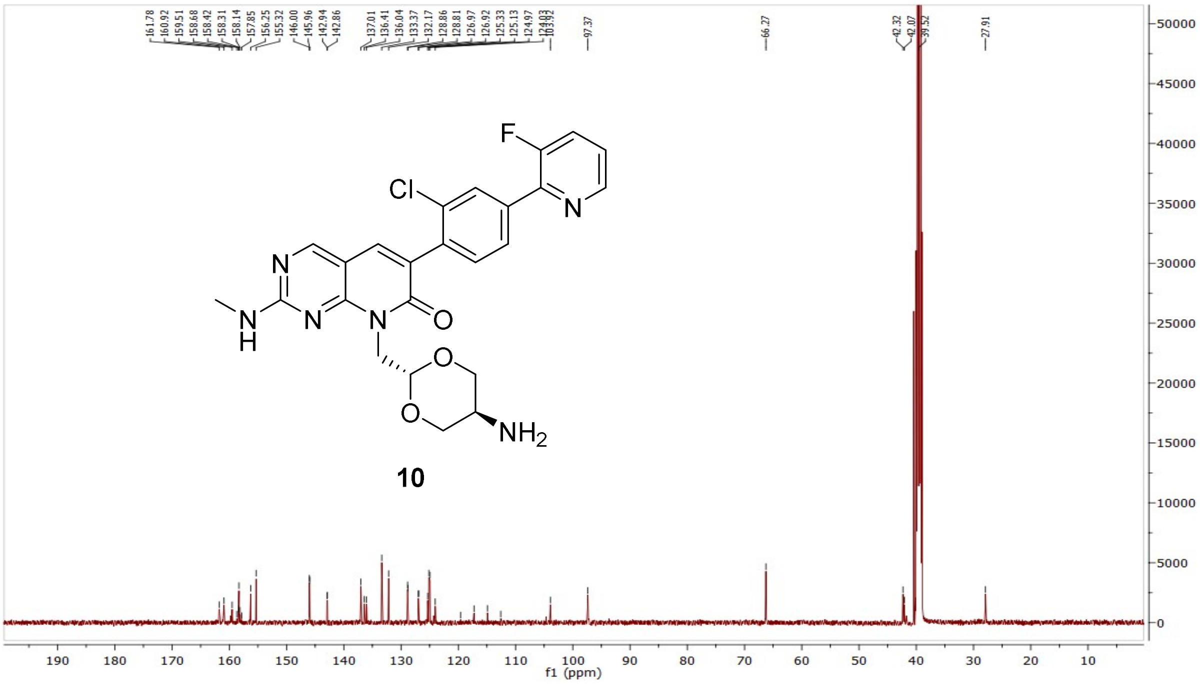
Peak RT 11.833



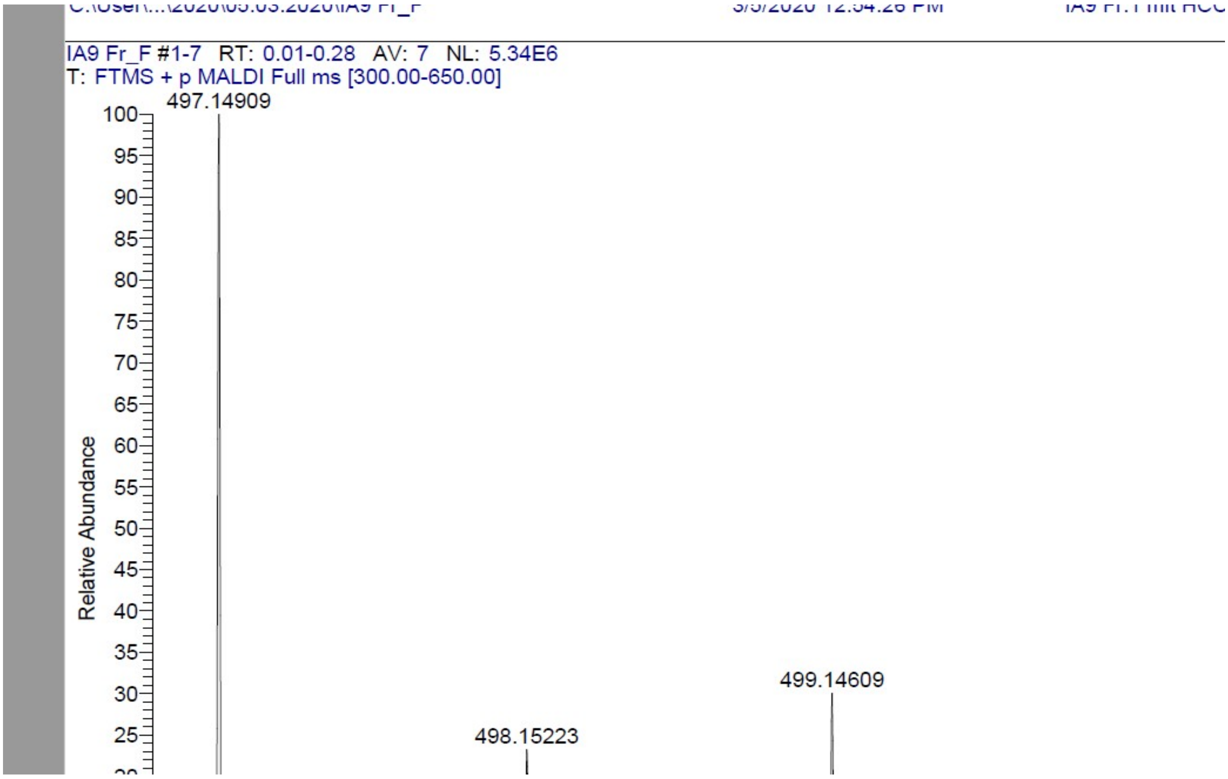
^{1}H NMR compound **10**:



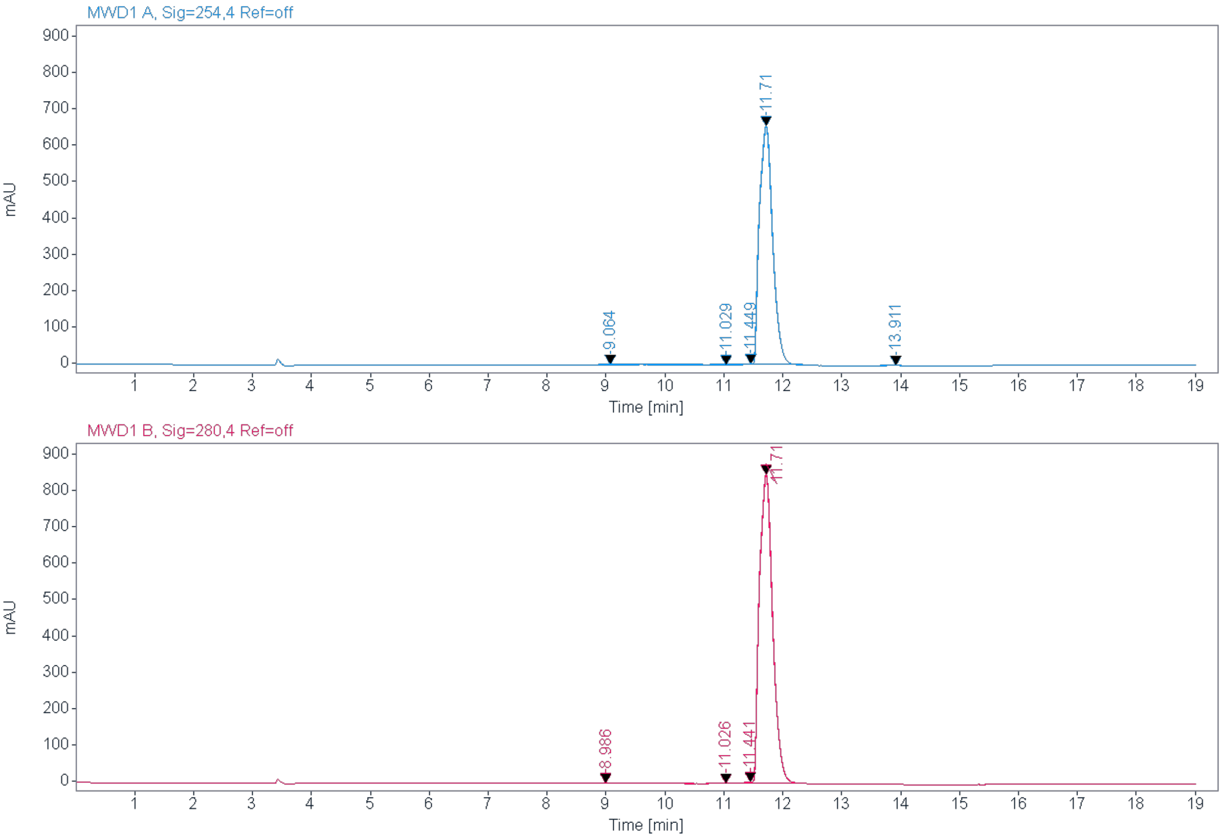
^{13}C NMR compound **10**:



HRMS (FTMS +p MALDI) compound **10**:



HPLC-chromatograms compound **10**:

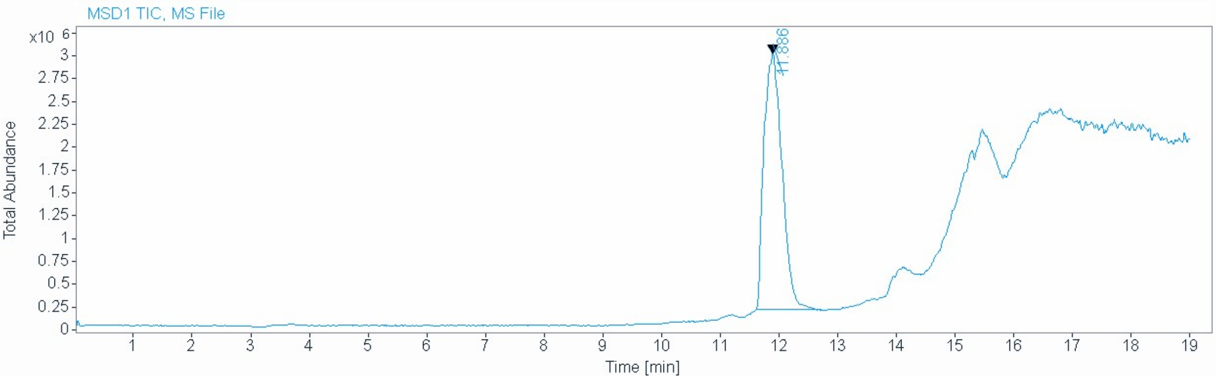


Signal: MWD1 B, Sig=254,4 Ref=off

RT [min]	Type	Width [min]	Area	Height	Area%	Name
9.064	MM	1.0205	122.5904	2.0021	1.1764	
11.029	MM	0.2613	7.2988	0.4655	0.0700	
11.449	MM	0.1052	21.5046	3.4072	0.2064	
11.710	MM	0.2597	10239.5293	657.1000	98.2597	
13.911	MM	0.2819	29.9574	1.7710	0.2875	
		Sum	10420.8806			

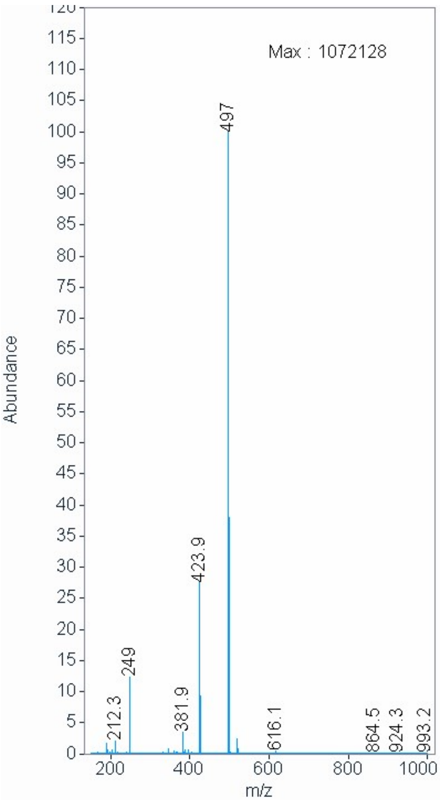
Signal: MWD1 B, Sig=280,4 Ref=off

RT [min]	Type	Width [min]	Area	Height	Area%	Name
8.986	MM	0.9499	74.7159	1.3109	0.5594	
11.026	MM	0.2749	7.0301	0.4262	0.0526	
11.441	MM	0.1003	27.4708	4.5632	0.2057	
11.710	MM	0.2600	13247.0850	849.1813	99.1823	
		Sum	3356.3018			

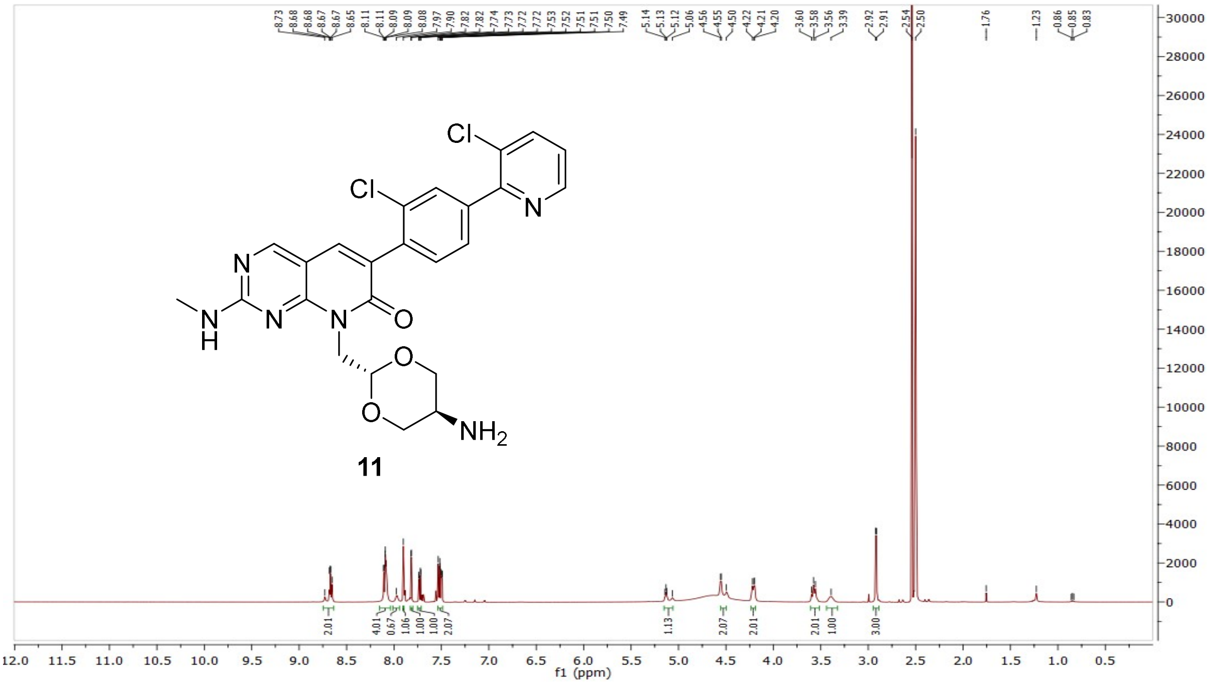


Signal MSD1 TIC, MS File

Peak RT 11.886

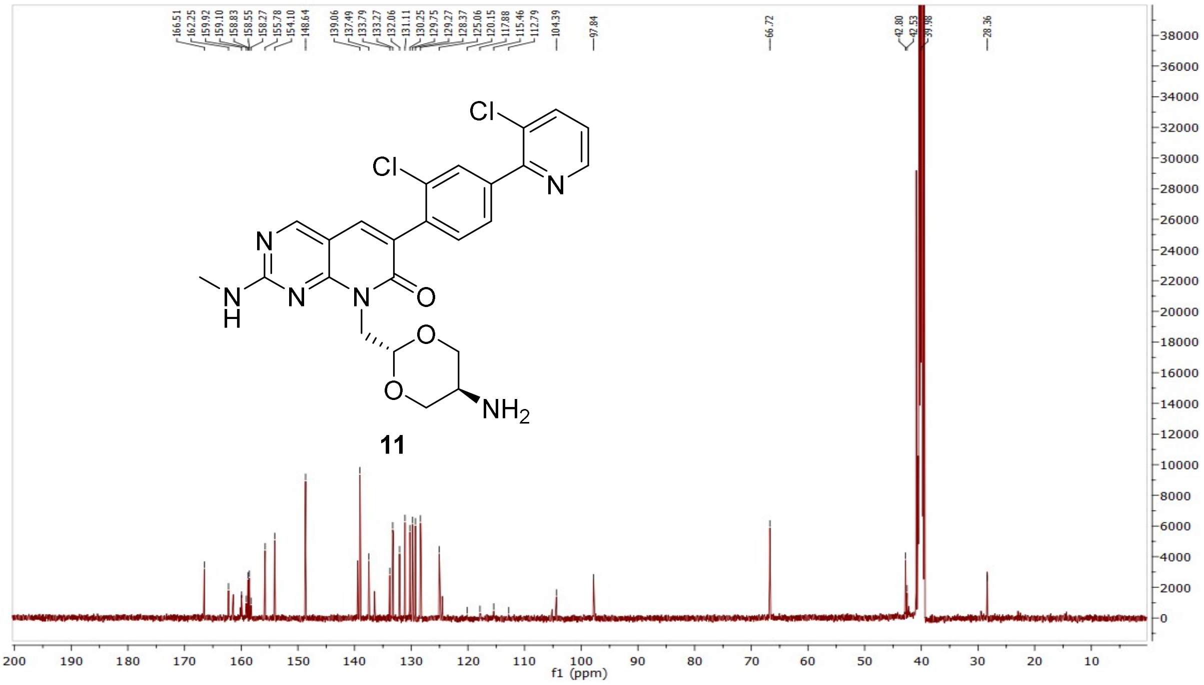


^{1}H NMR compound **11**:



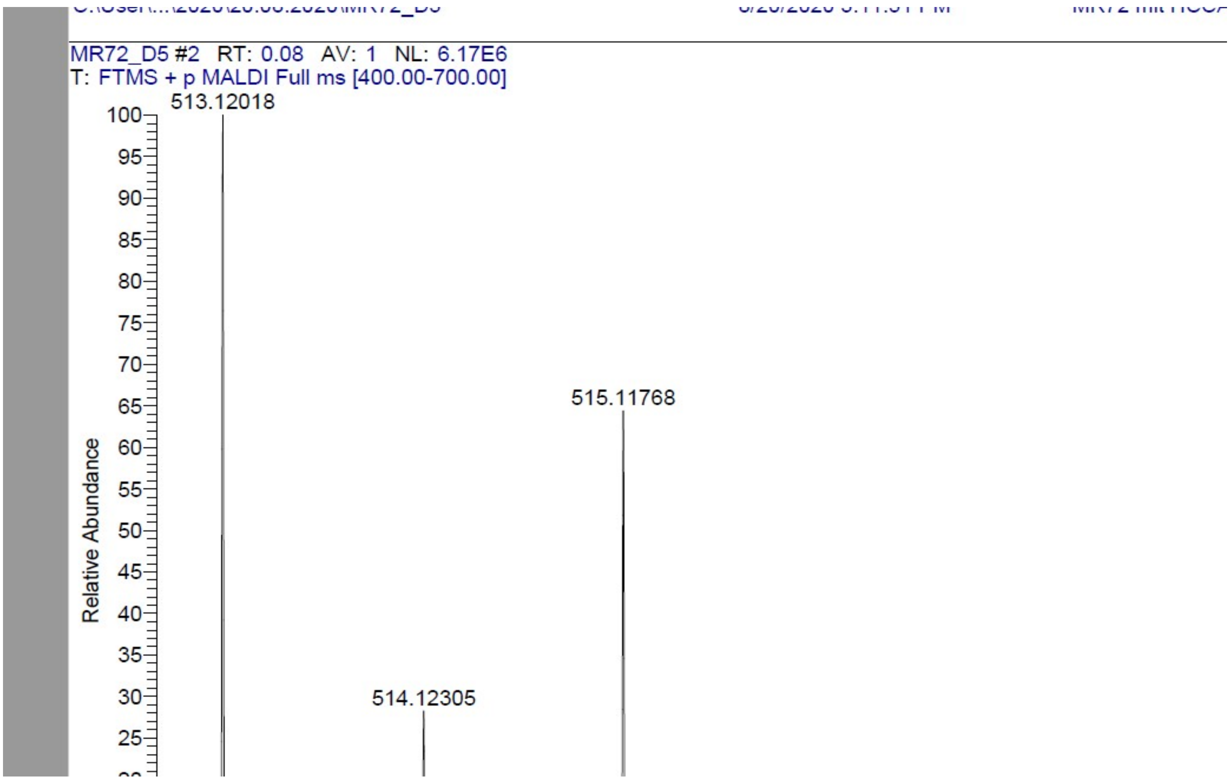
11

^{13}C NMR compound **11**:

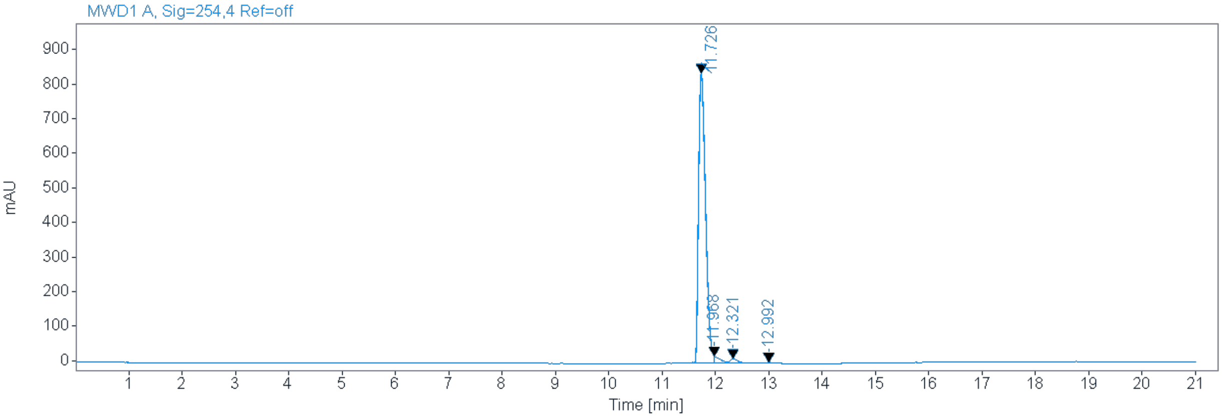


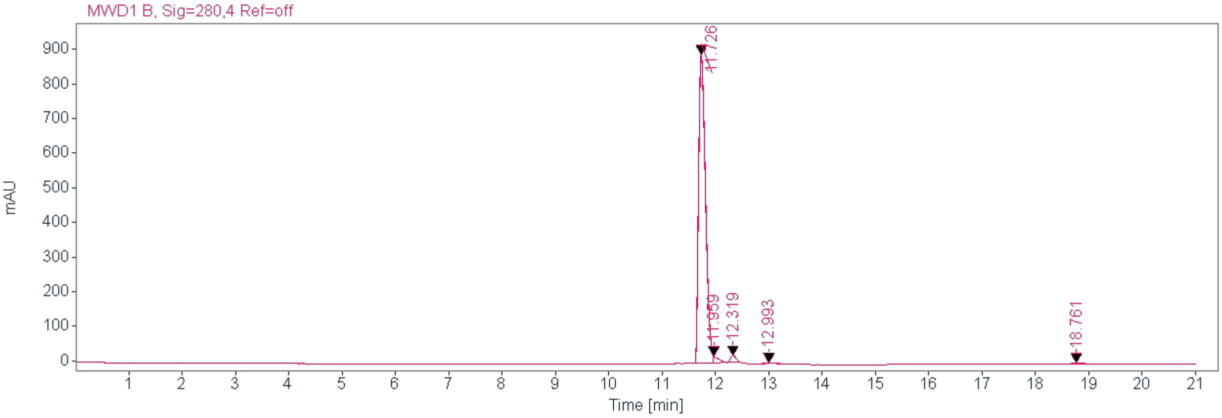
11

HRMS (FTMS +p MALDI) compound **11**:



HPLC-chromatograms compound **11**:



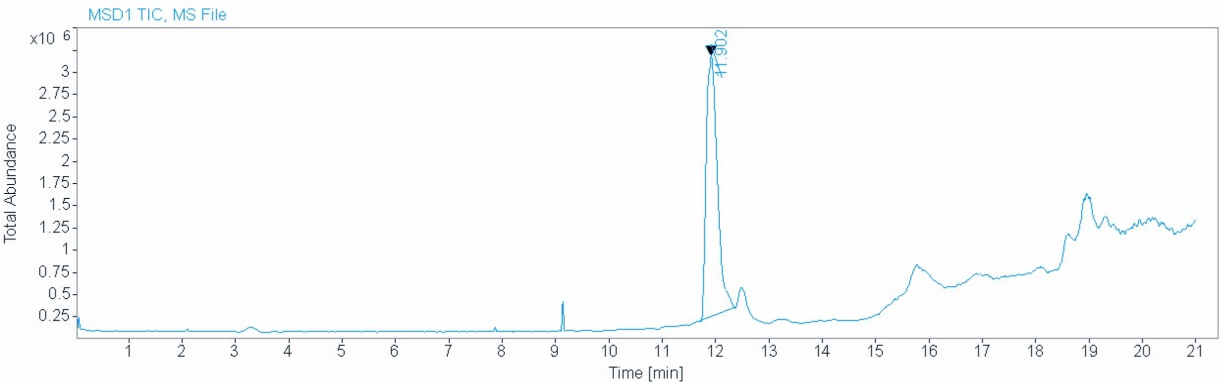


Signal: MWD1 A, Sig=254,4 Ref=off

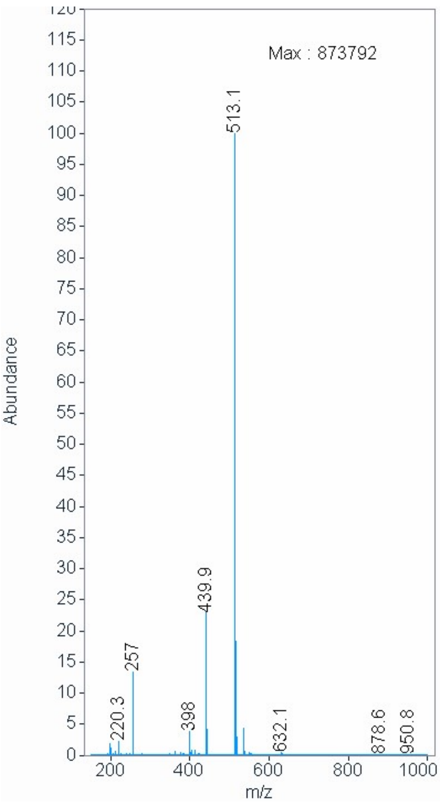
RT [min]	Type	Width [min]	Area	Height	Area%	Name
11.726	MM	0.1512	7596.8838	837.4711	96.2666	
11.968	MM	0.0944	137.5973	18.7323	1.7436	
12.321	MM	0.1568	114.3046	12.1498	1.4485	
12.992	MM	0.2028	42.7236	3.5116	0.5414	
		Sum	7891.5093			

Signal: MWD1 B, Sig=280,4 Ref=off

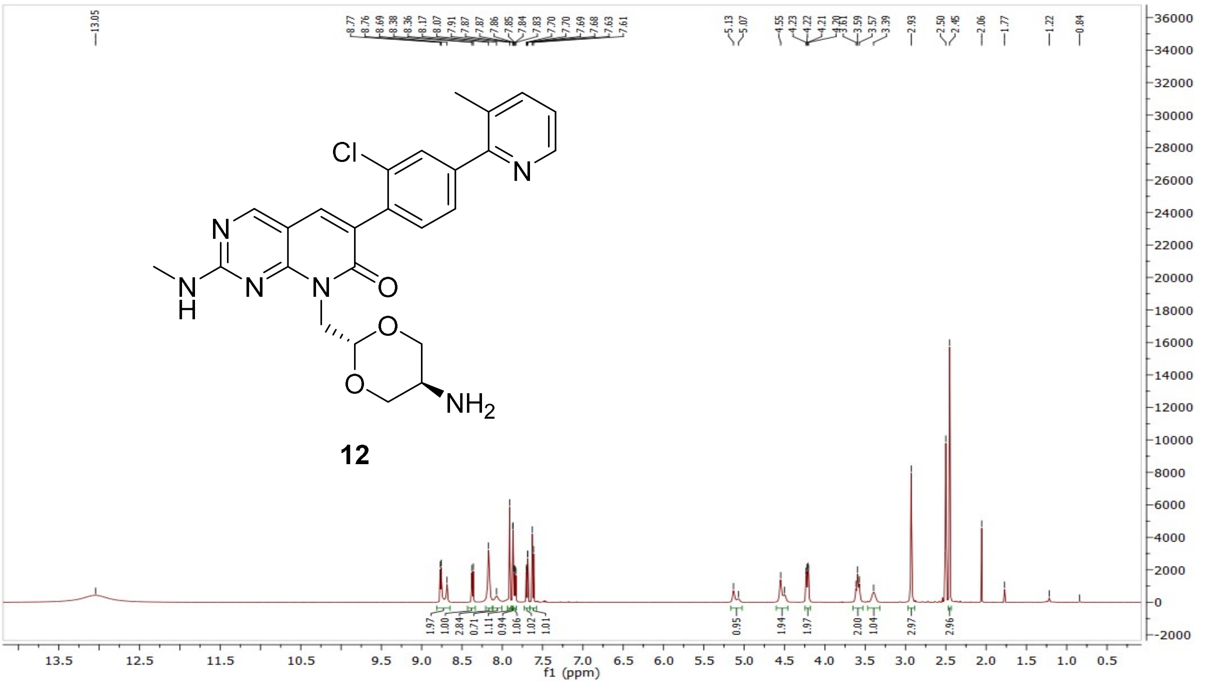
RT [min]	Type	Width [min]	Area	Height	Area%	Name
11.726	MM	0.1506	8061.8169	892.2730	95.0987	
11.959	MM	0.0843	136.8278	21.4267	1.6140	
12.319	MM	0.1287	165.3623	21.4181	1.9506	
12.993	MM	0.1497	38.6249	4.2991	0.4556	
18.761	MM	0.2741	74.6817	4.5410	0.8810	
		Sum	8477.3136			



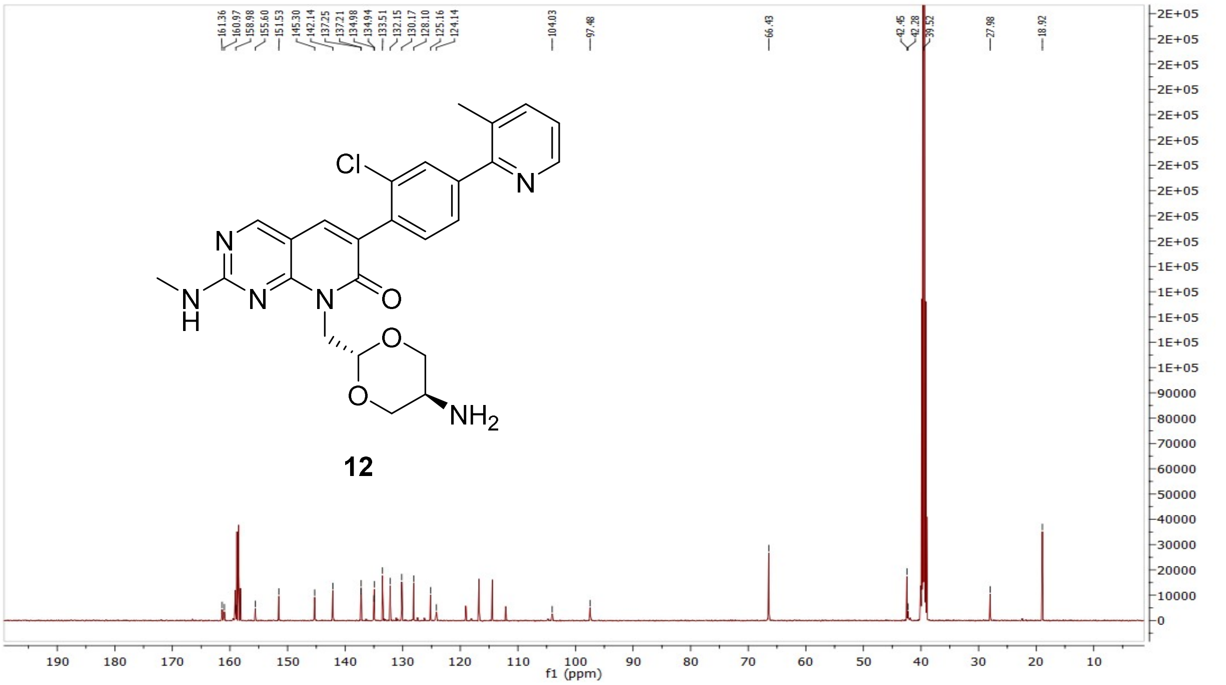
Signal	MSD1 TIC, MS File
Peak RT	11.902



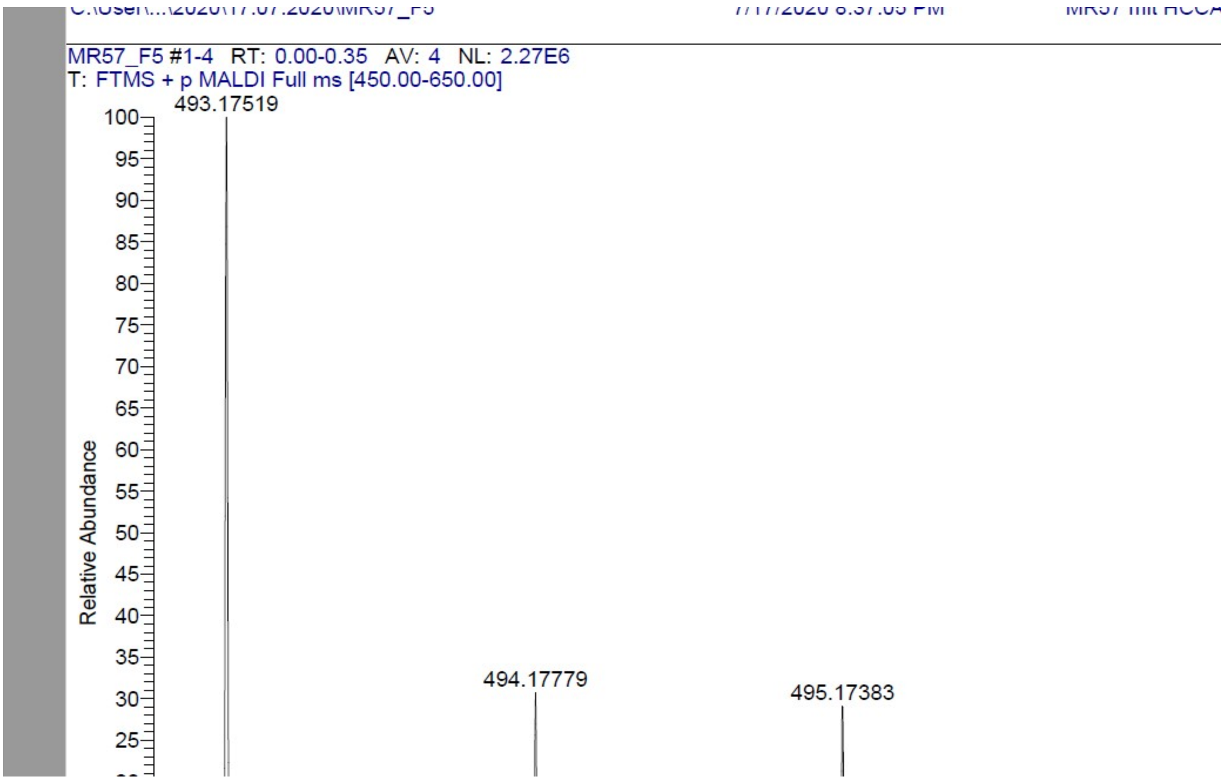
^{1}H NMR compound **12**:



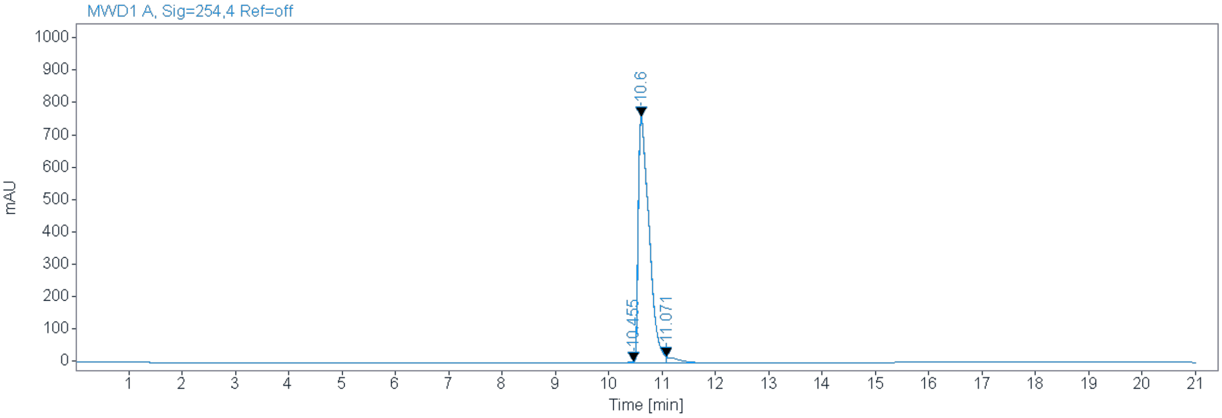
^{13}C NMR compound **12**:

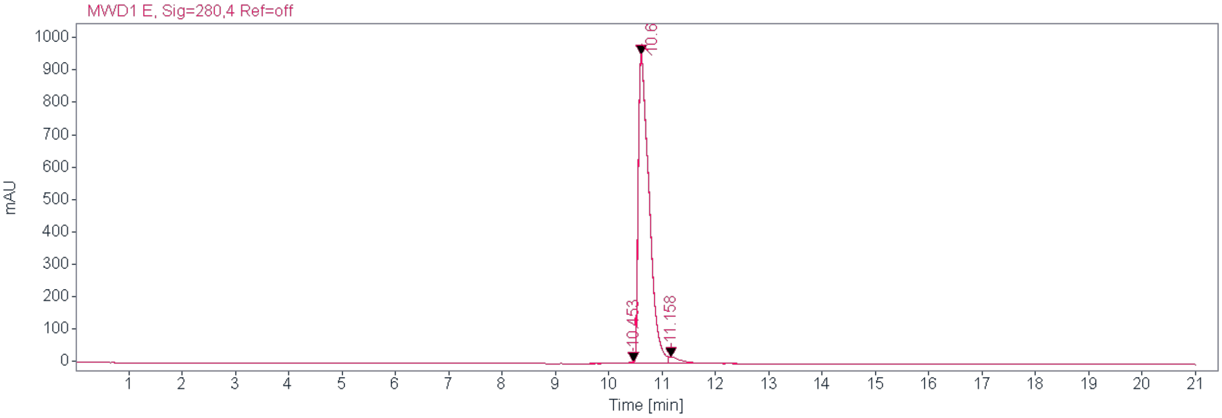


HRMS (FTMS +p MALDI) compound **12**:



HPLC-chromatograms compound **12**:



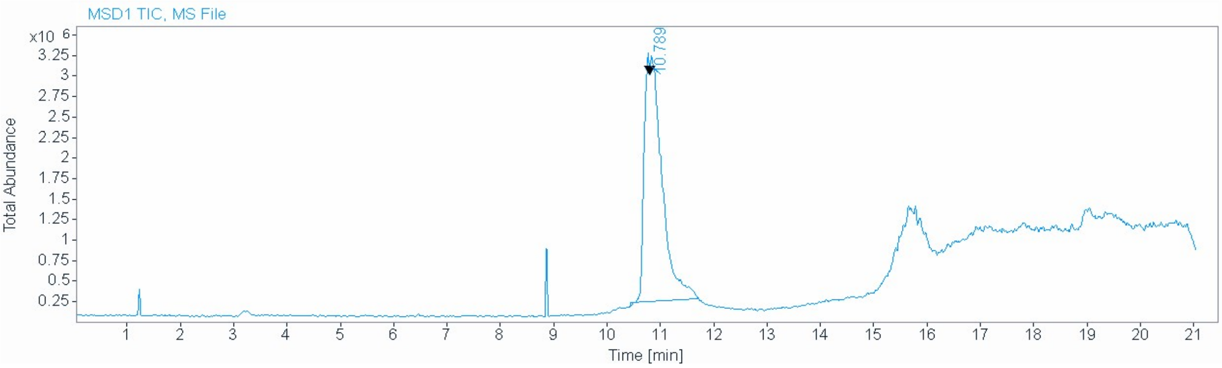


Signal: MWD1 A, Sig=254,4 Ref=off

RT [min]	Type	Width [min]	Area	Height	Area%	Name
10.455	MM	0.1863	51.0844	4.5689	0.4567	
10.600	MM	0.2358	10794.9180	762.9228	96.5067	
11.071	MM	0.2201	339.6660	19.0116	3.0366	
		Sum	11185.6684			

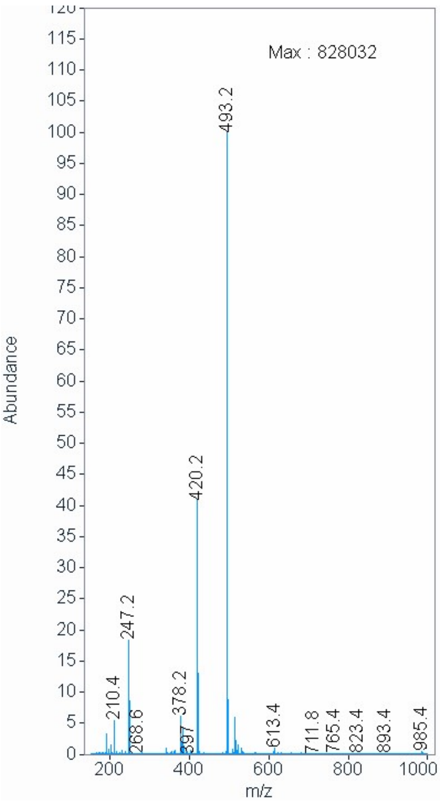
Signal: MWD1 E, Sig=280,4 Ref=off

RT [min]	Type	Width [min]	Area	Height	Area%	Name
10.453	MM	0.2230	75.3987	5.6364	0.5394	
10.600	MM	0.2364	13542.0771	954.7060	96.8774	
11.158	MM	0.2917	361.0904	20.6307	2.5832	
		Sum	13978.5663			

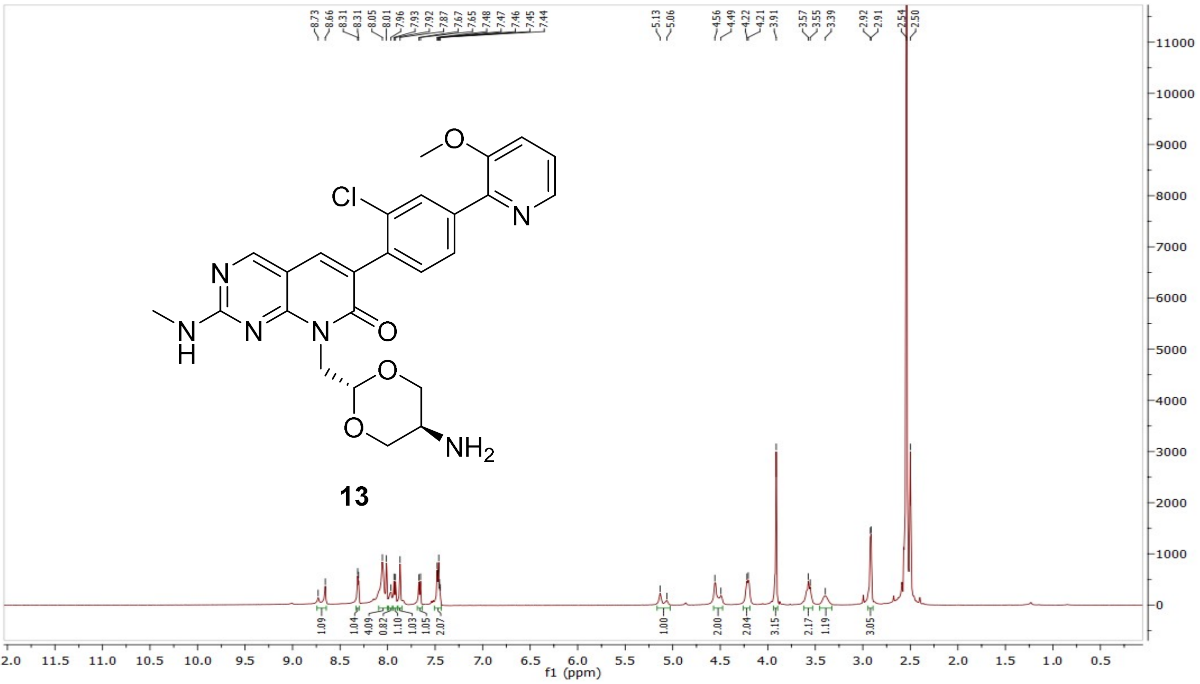


Signal MSD1 TIC, MS File

Peak RT 10.789

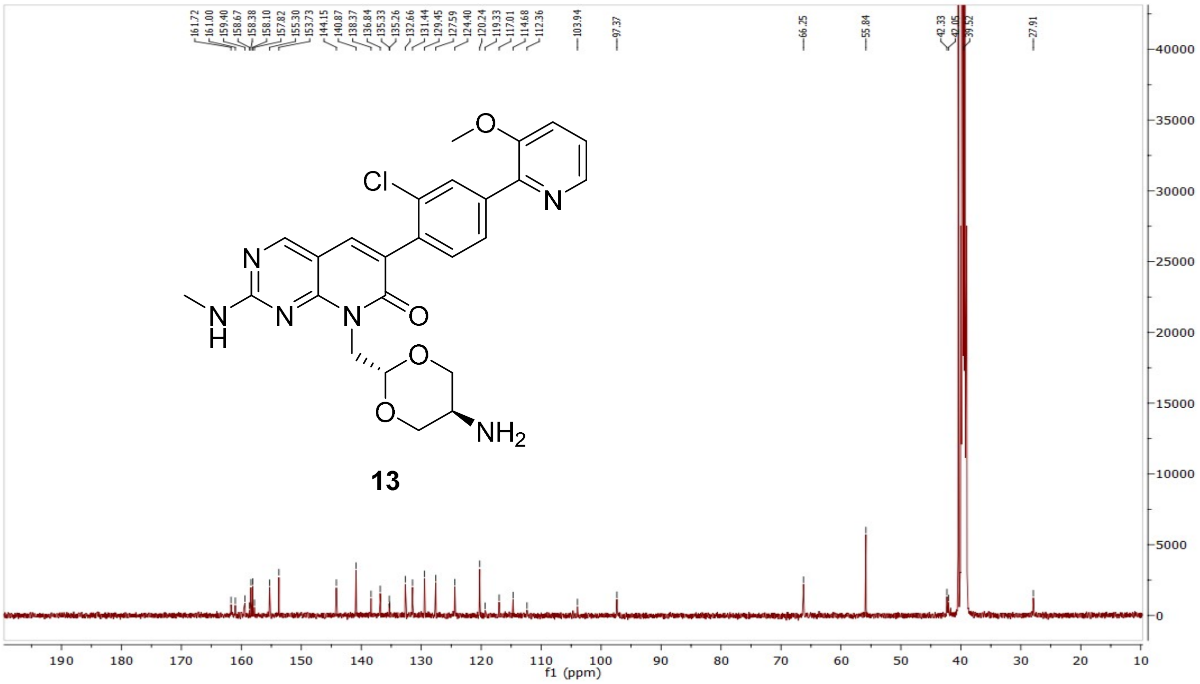


^{1}H NMR compound **13**:



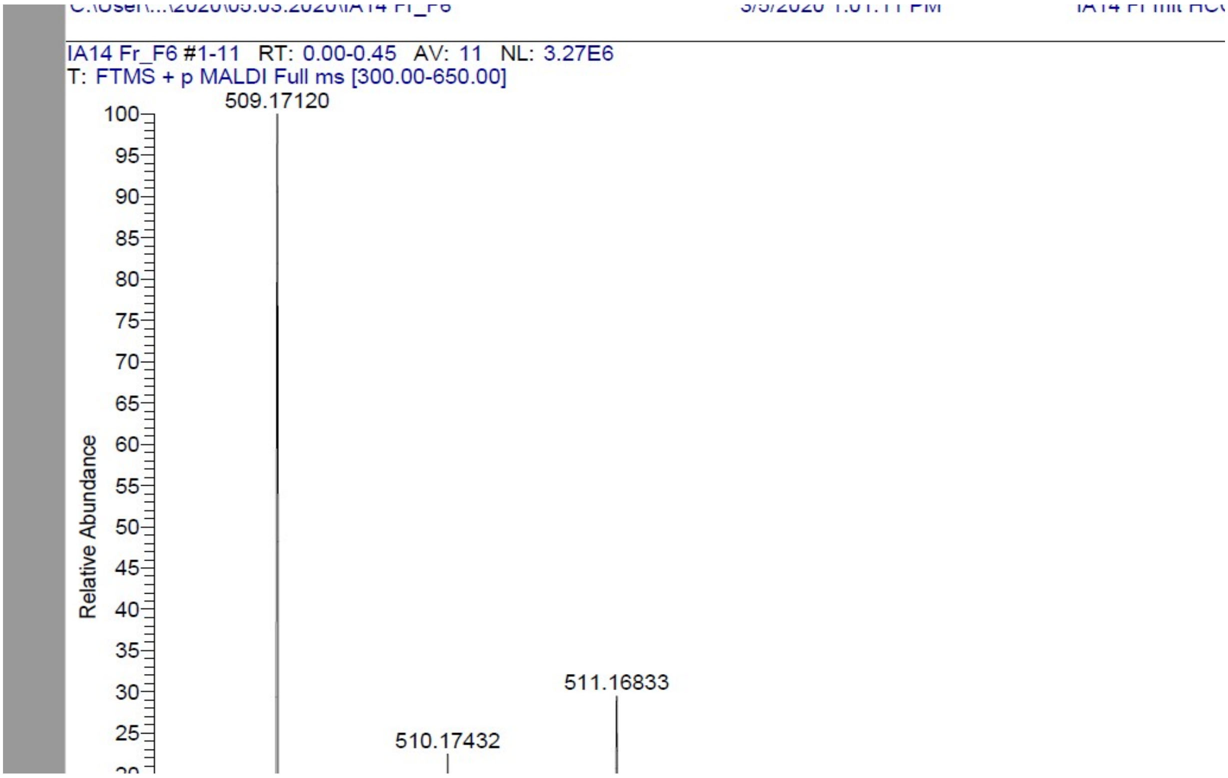
13

^{13}C NMR compound **13**:

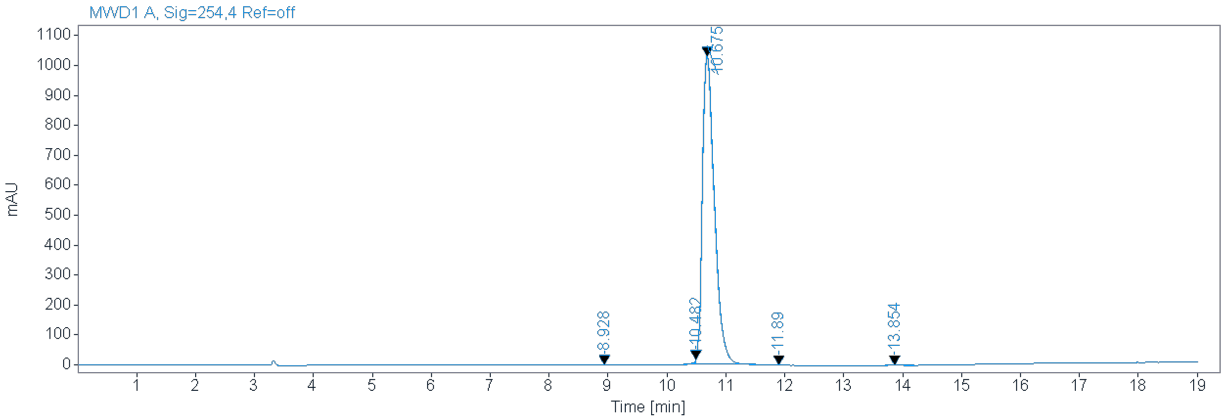


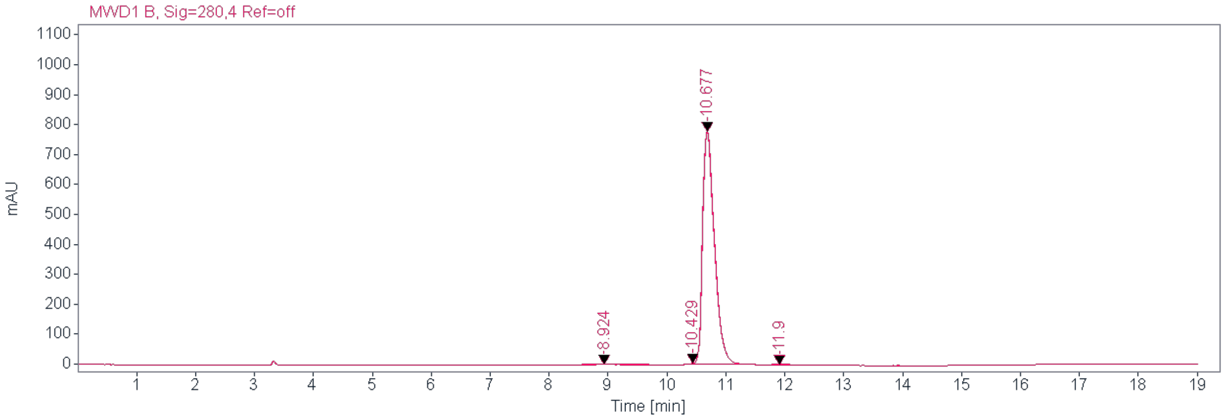
13

HRMS (FTMS +p MALDI) compound **13**:



HPLC-chromatograms compound **13**:



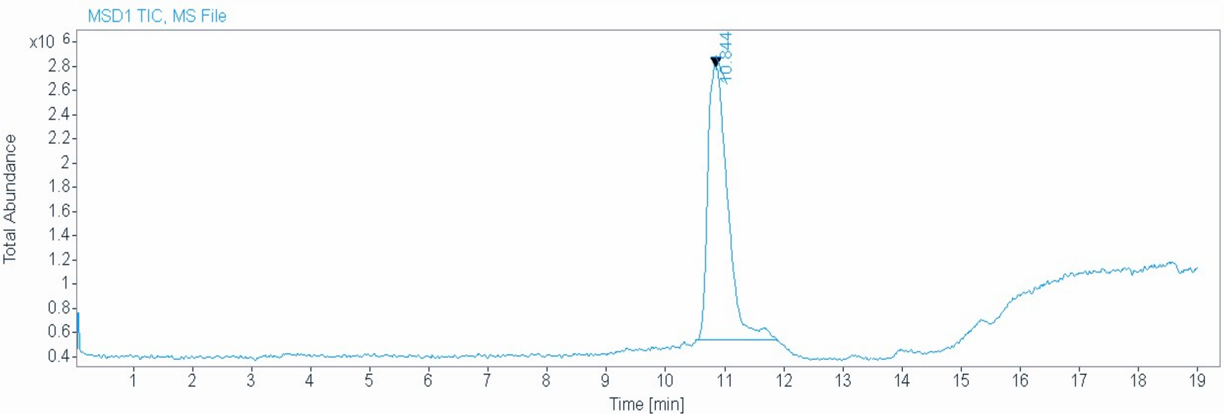


Signal: MWD1 B, Sig=254,4 Ref=off

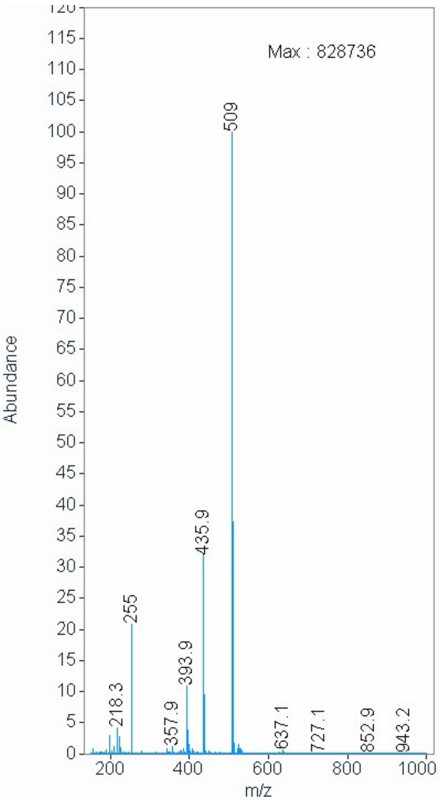
RT [min]	Type	Width [min]	Area	Height	Area%	Name
8.928	MM	0.7858	78.3781	1.6623	0.5283	
0.482	MM	0.0530	54.7126	17.2084	0.3688	
10.675	MM	0.237	114668.0869	1030.8914	98.8728	
11.890	MM	0.1731	11.7460	1.1311	0.0792	
13.8541	MM	0.2388	22.3856	1.5621	0.1509	
		Sum	14835.3092			

Signal: MWD1 B, Sig=280,4 Ref=off

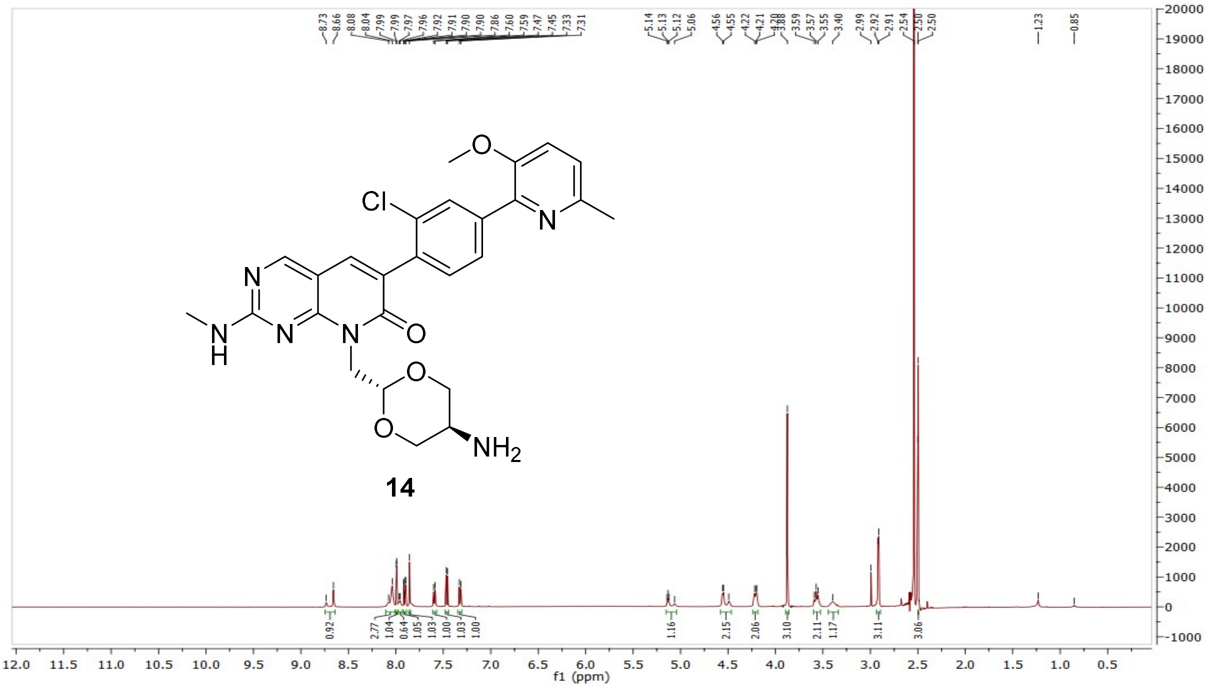
RT [min]	Type	Width [min]	Area	Height	Area%	Name
8.924	MM	0.5921	35.1620	0.9898	0.3194	
10.429	MM	0.0679	16.9301	4.1544	0.1538	
10.677	MM	0.2343	10946.5010	778.5373	99.4392	
11.900	MM	0.1744	9.6435	0.9218	0.0876	
		Sum	11008.2365			



Signal	MSD1 TIC, MS File
Peak RT	10.844

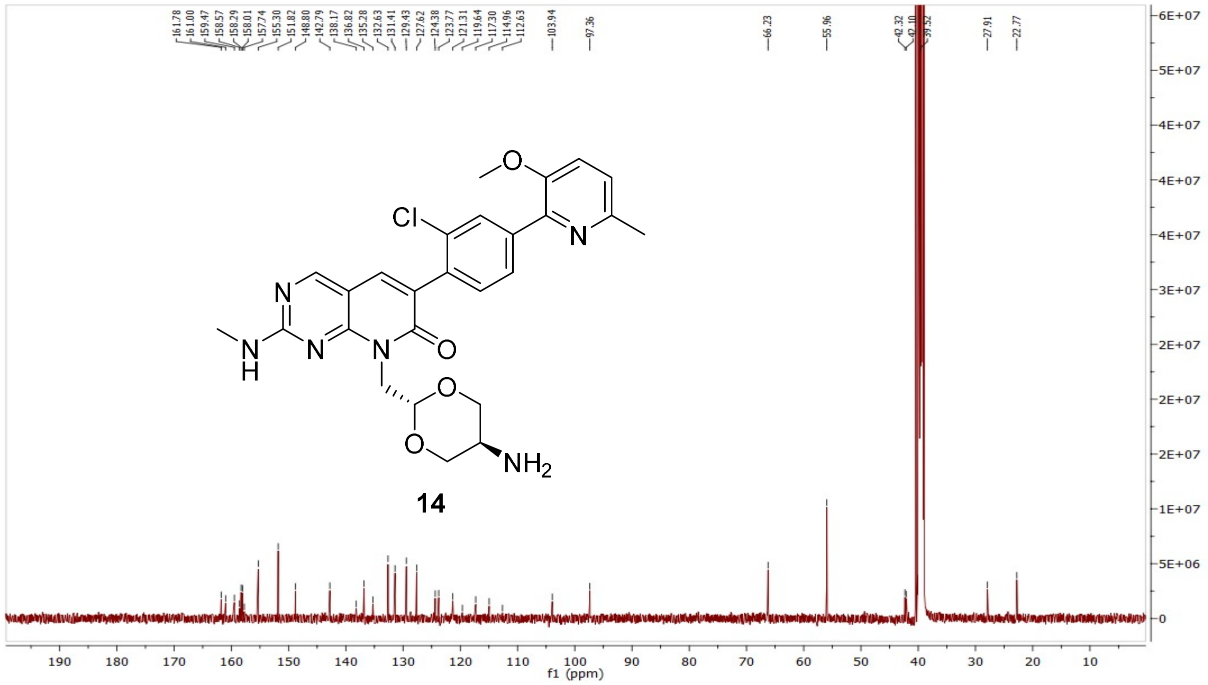


^{1}H NMR compound **14**:



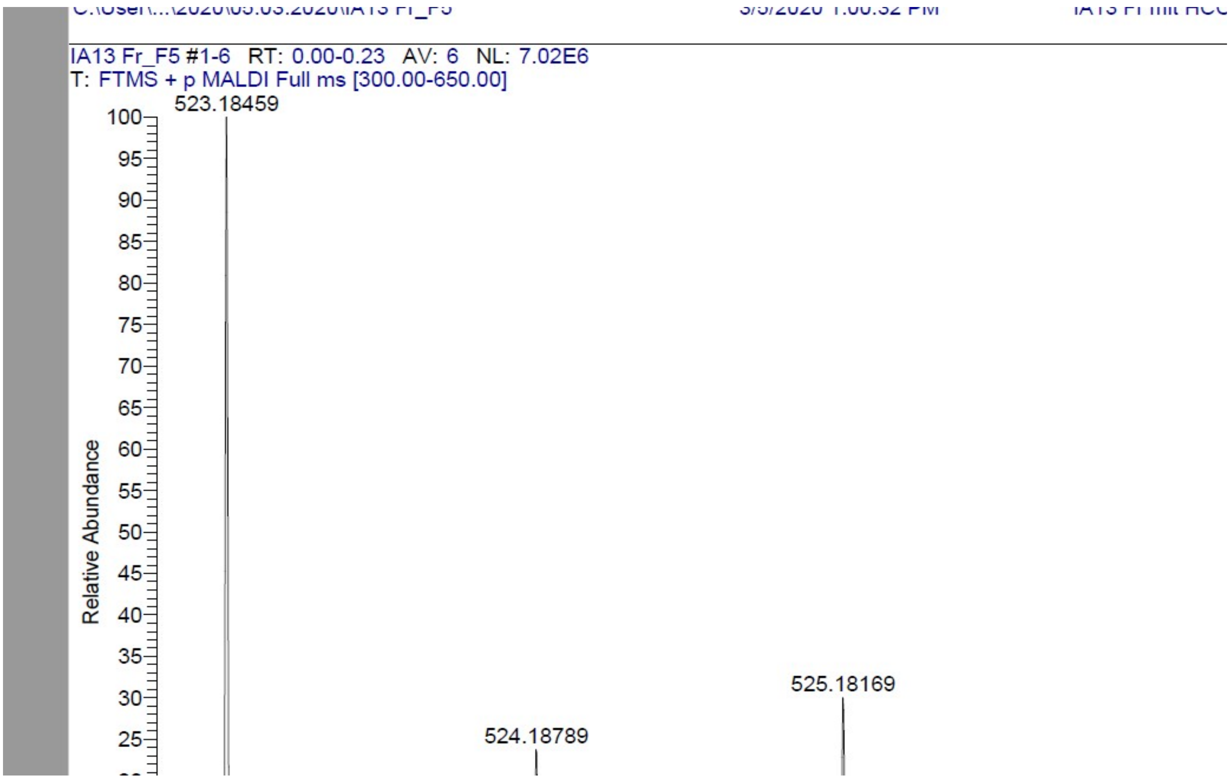
14

^{13}C NMR compound **14**:

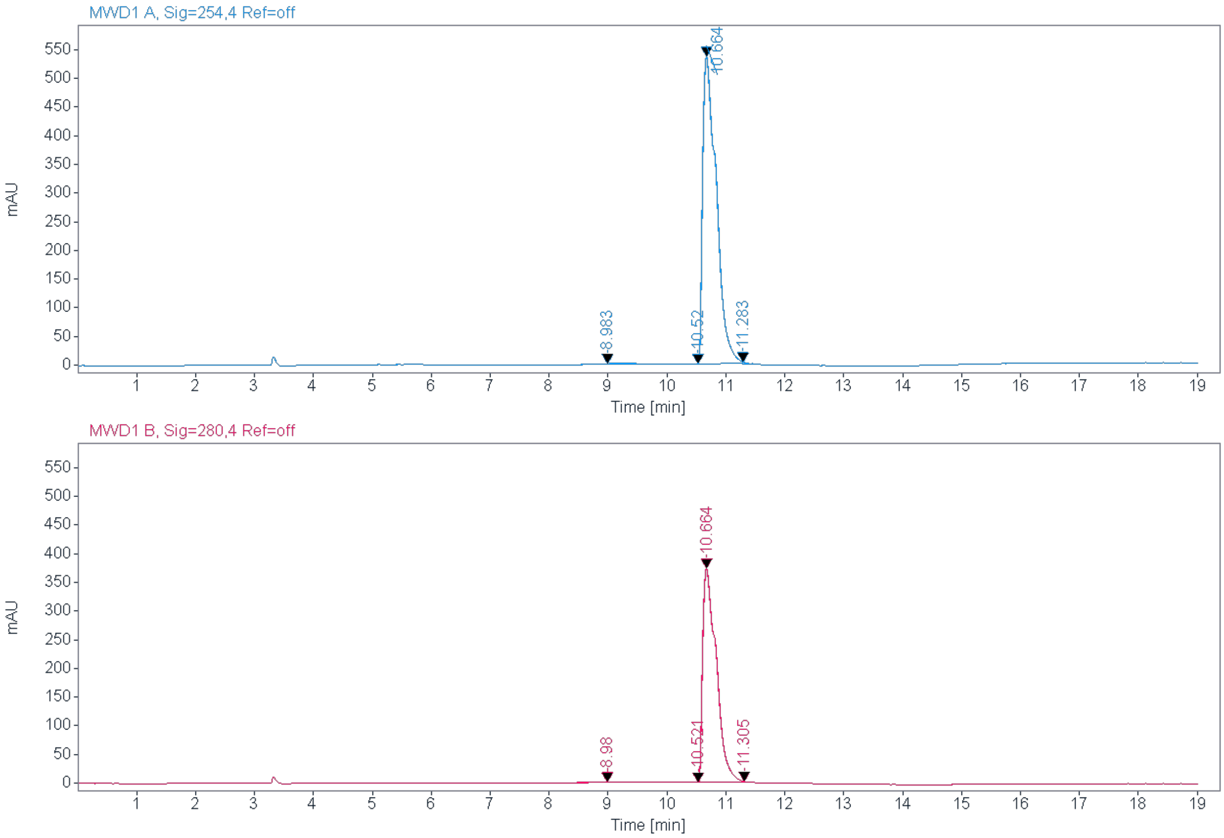


14

HRMS (FTMS +p MALDI) compound **14**:



HPLC-chromatograms compound **14**:

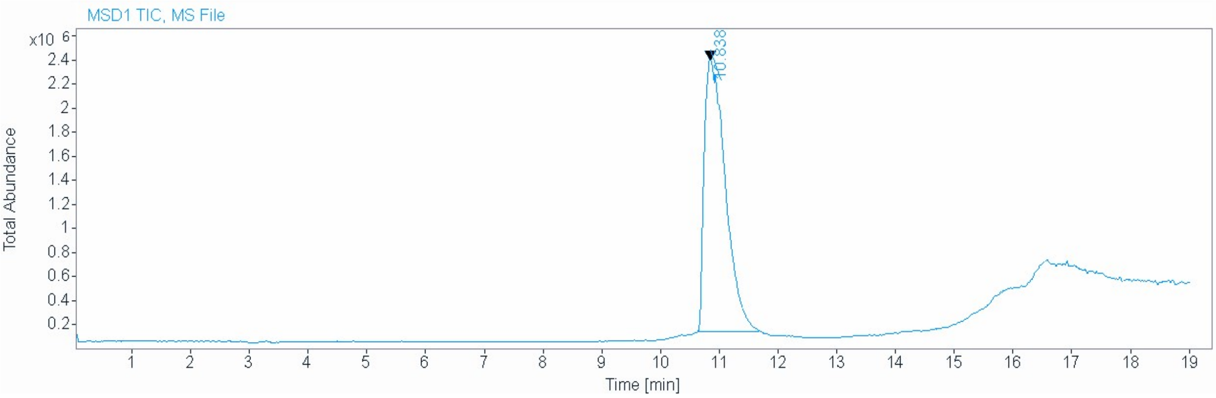


Signal: MWD1 B, Sig=254,4 Ref=off

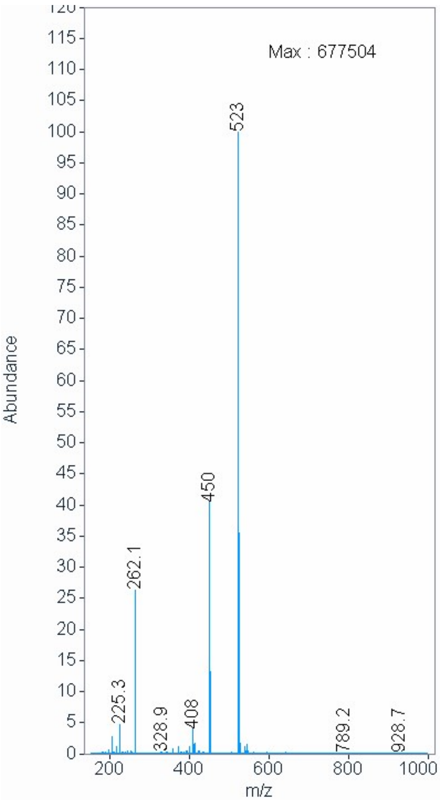
RT [min]	Type	Width [min]	Area	Height	Area%	Name
8.983	MM	0.5270	40.0456	1.2665	0.4618	
10.520	MM	0.0872	4.0174	0.7682	0.0463	
10.664	MM	0.2675	8613.9375	536.6498	99.3355	
11.283	MM	0.0454	13.5567	3.5621	0.1563	
		Sum	8671.5573			

Signal: MWD1 B, Sig=280,4 Ref=off

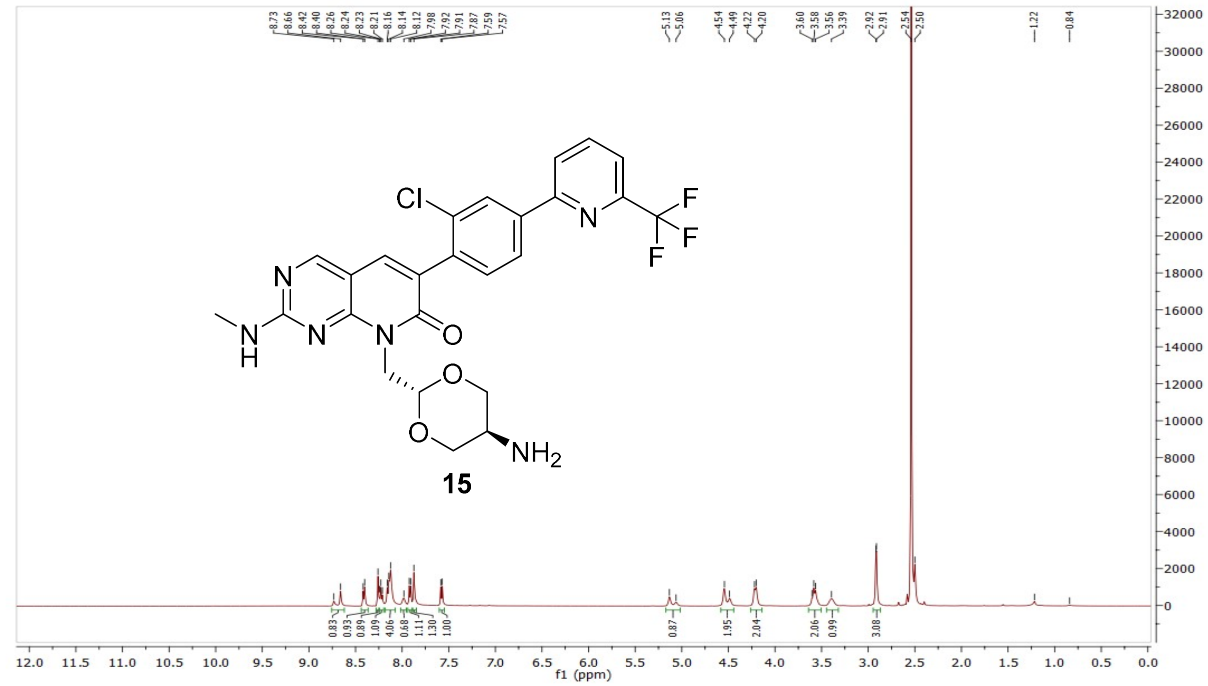
RT [min]	Type	Width [min]	Area	Height	Area%	Name
8.980	MM	0.4528	23.3658	0.8601	0.3876	
10.521	MM	0.1583	8.0296	0.8453	0.1332	
10.664	MM	0.2669	5988.4331	373.9075	99.3269	
11.305	MM	0.0718	9.1867	2.1336	0.1524	
		Sum	6029.0152			



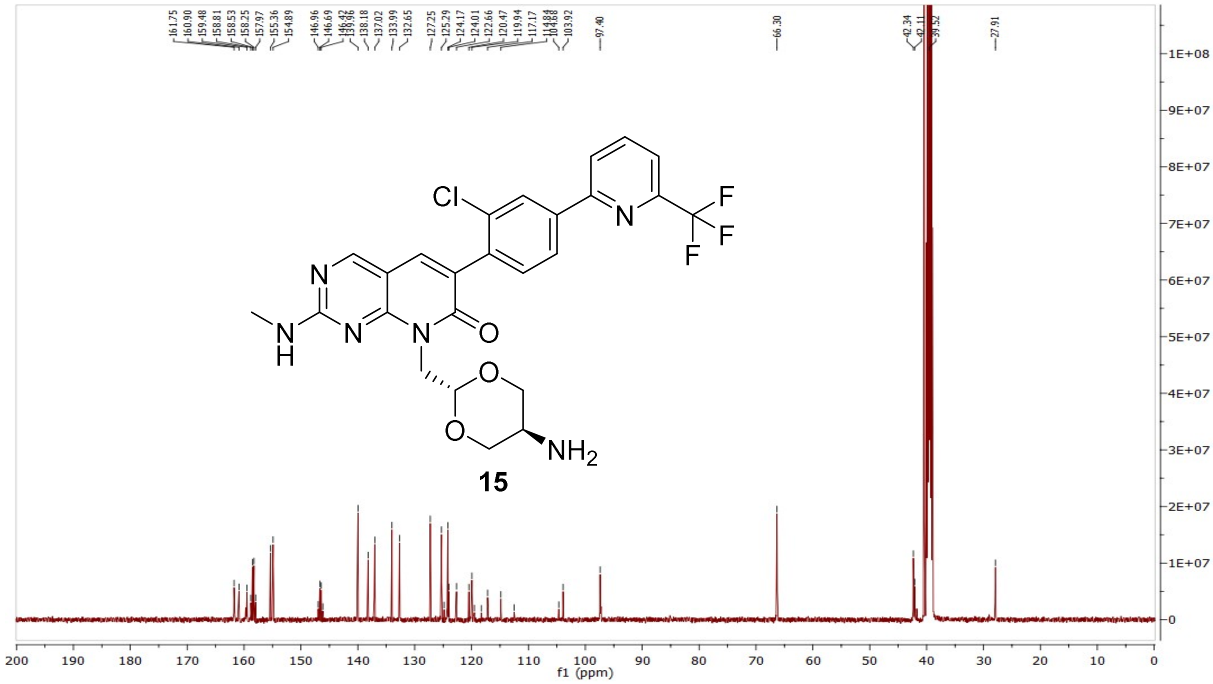
Signal	MSD1 TIC, MS File
Peak RT	10.838



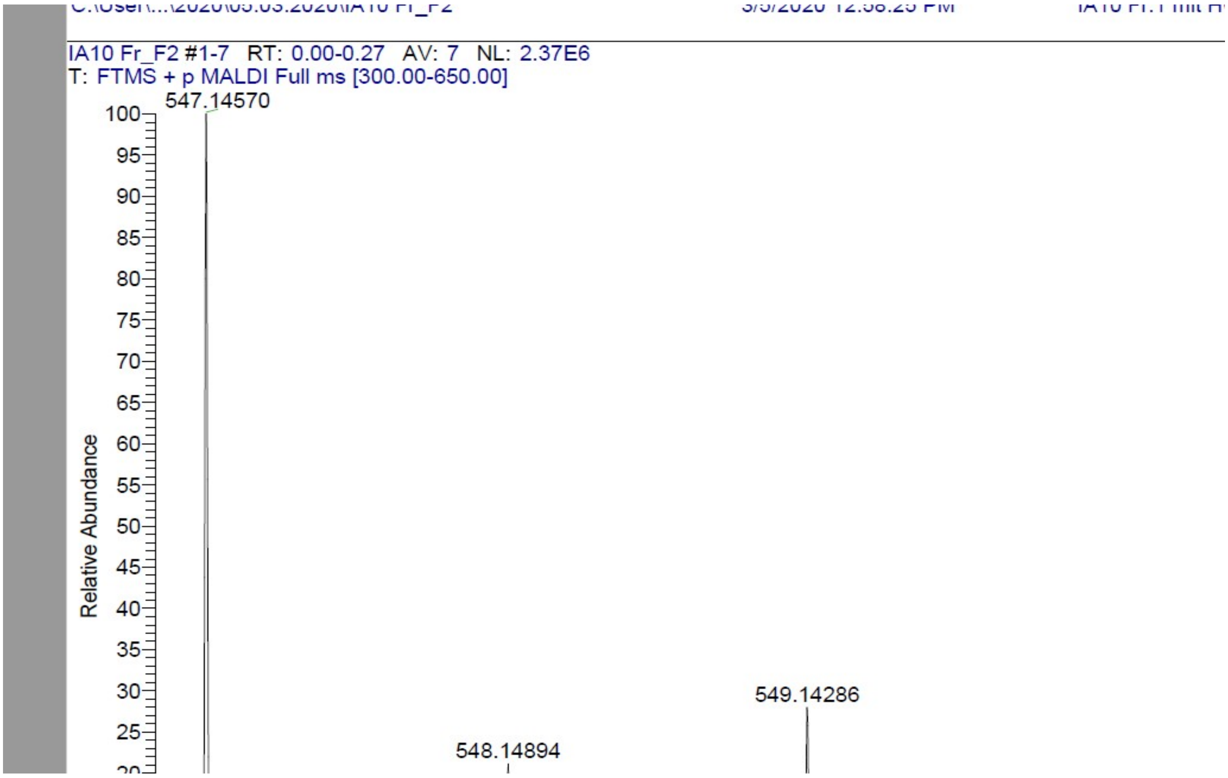
^{1}H NMR compound **15**:



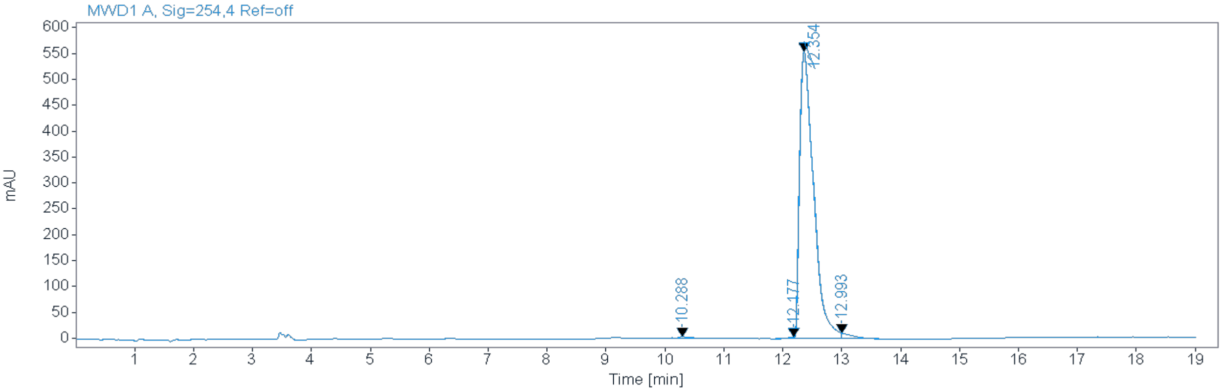
^{13}C NMR compound **15**:

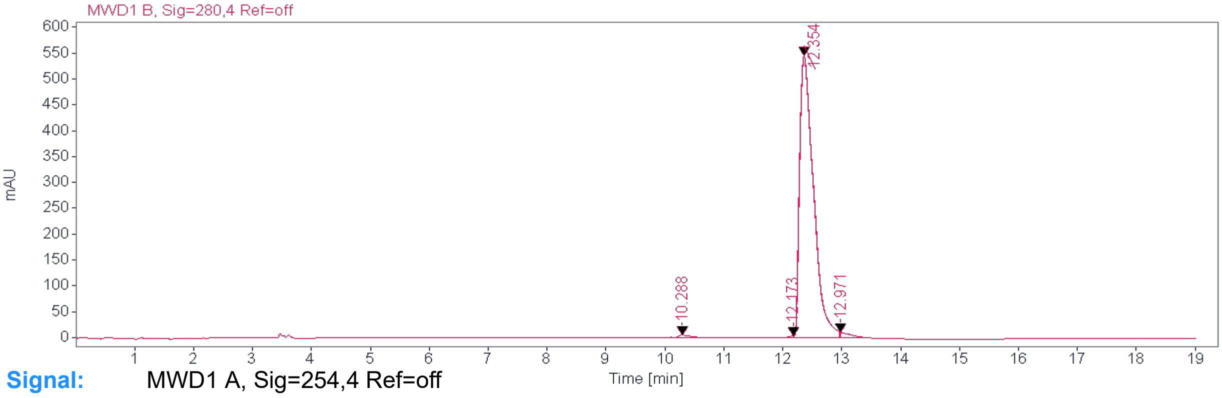


HRMS (FTMS +p MALDI) compound **15**:



HPLC-chromatograms compound **15**:



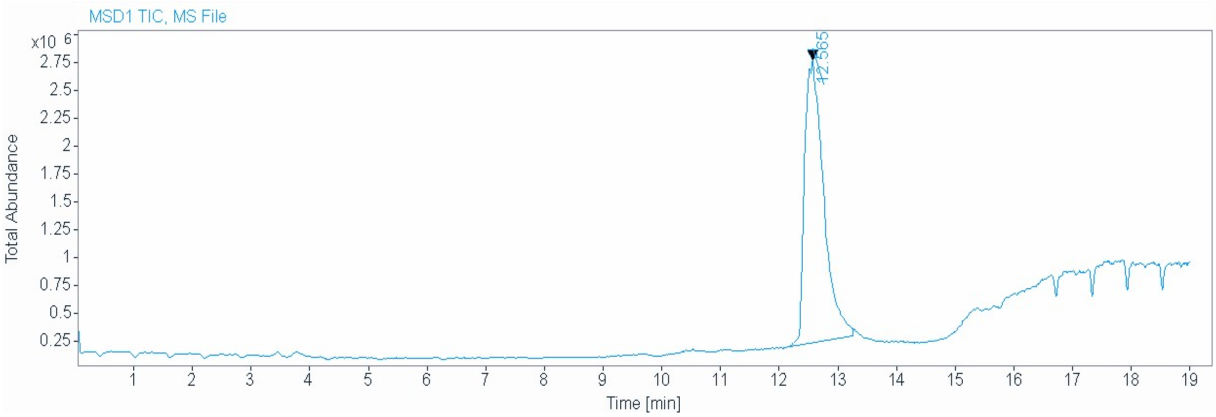


Signal: MWD1 A, Sig=254,4 Ref=off

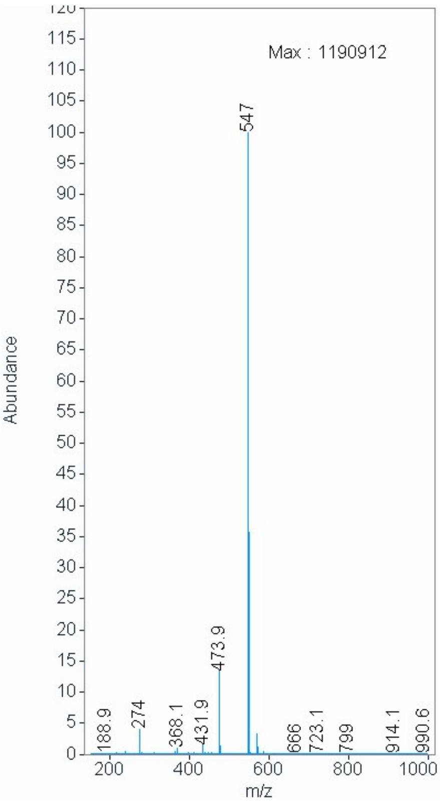
RT [min]	Type	Width [min]	Area	Height	Area%	Name
10.288	MM	0.2572	47.9928	3.1098	0.5090	
12.177	MM	0.1312	31.8189	4.0426	0.3375	
12.354	MM	0.2757	9188.1260	555.4003	97.4454	
12.993	MM	0.1682	161.0629	11.3575	1.7082	
		Sum	9429.0006			

Signal: MWD1 B, Sig=280,4 Ref=off

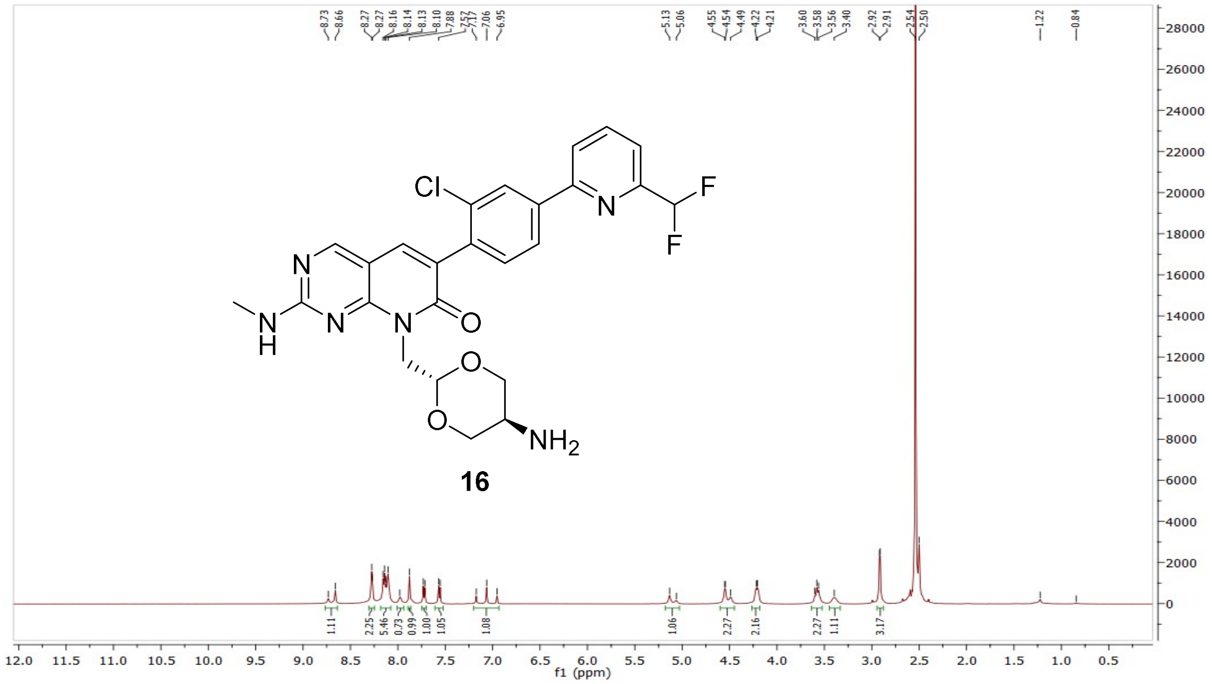
RT [min]	Type	Width [min]	Area	Height	Area%	Name
10.288	MM	0.2357	68.5422	4.8457	0.7445	
12.173	MM	0.1164	27.3388	3.9133	0.2969	
12.354	MM	0.2739	8973.6221	545.9641	97.4655	
12.971	MM	0.1468	137.4744	11.1369	1.4932	
		Sum	9206.9775			



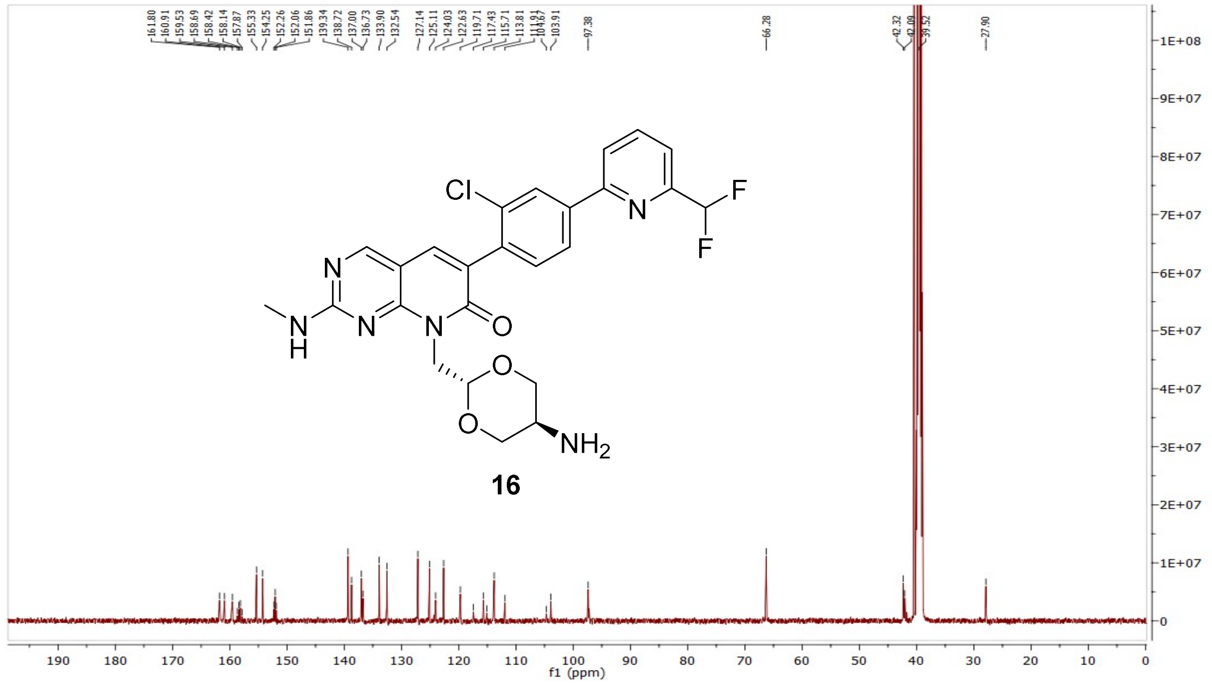
Signal	MSD1 TIC, MS File
Peak RT	12.565



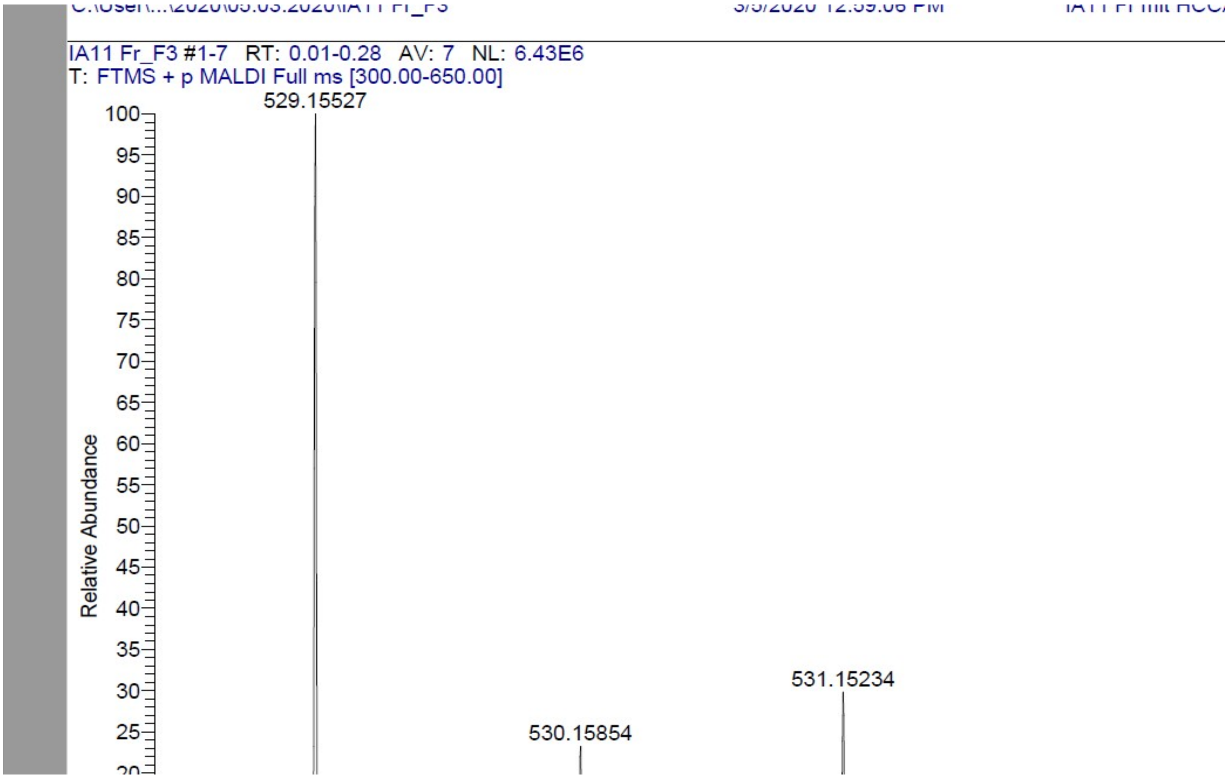
^{1}H NMR compound **16**:



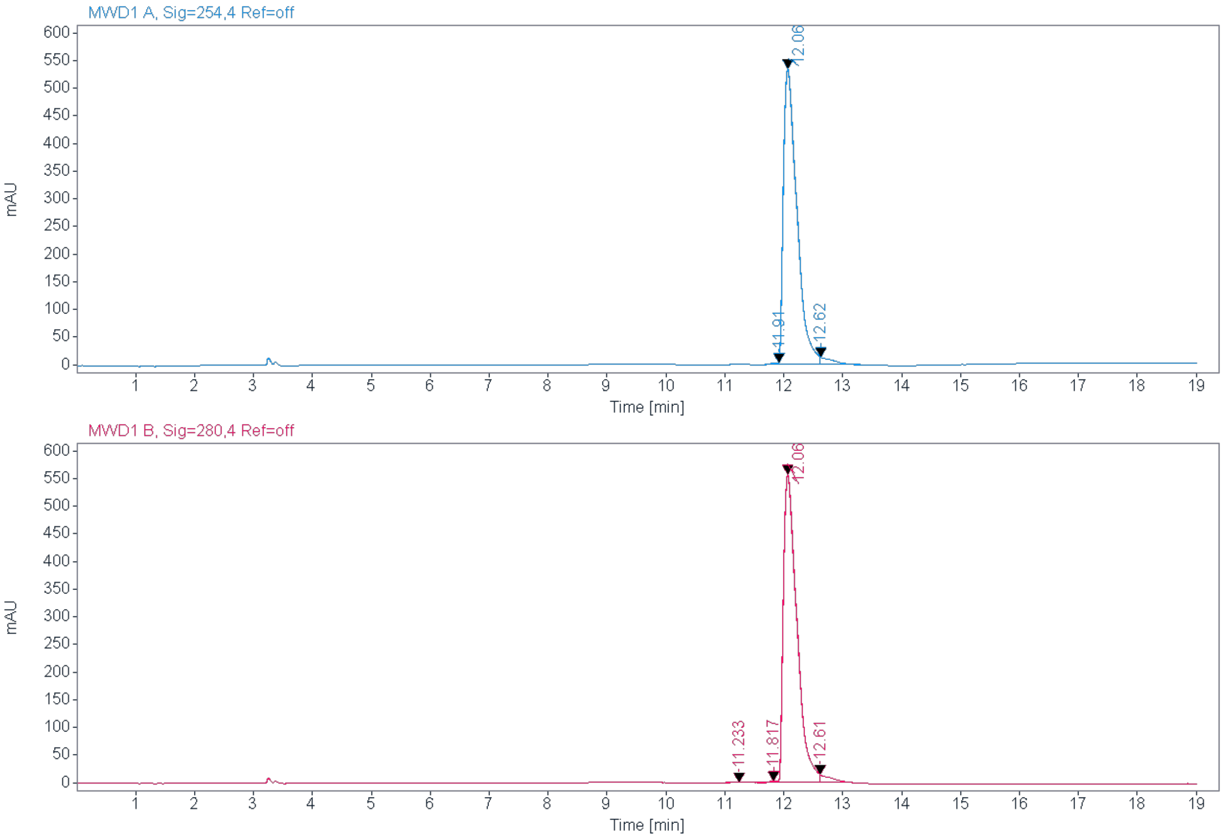
^{13}C NMR compound **16**:



HRMS (FTMS +p MALDI) compound **16**:



HPLC-chromatograms compound **16**:

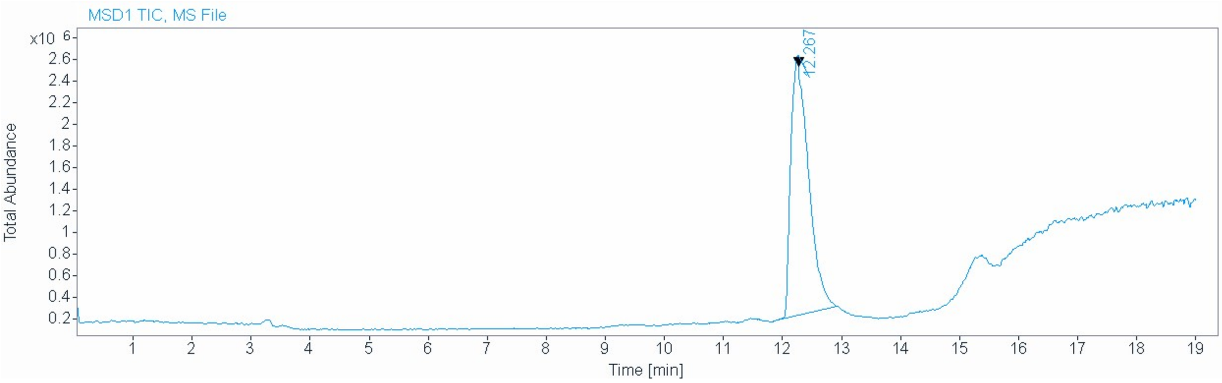


Signal: MWD1 B, Sig=254,4 Ref=off

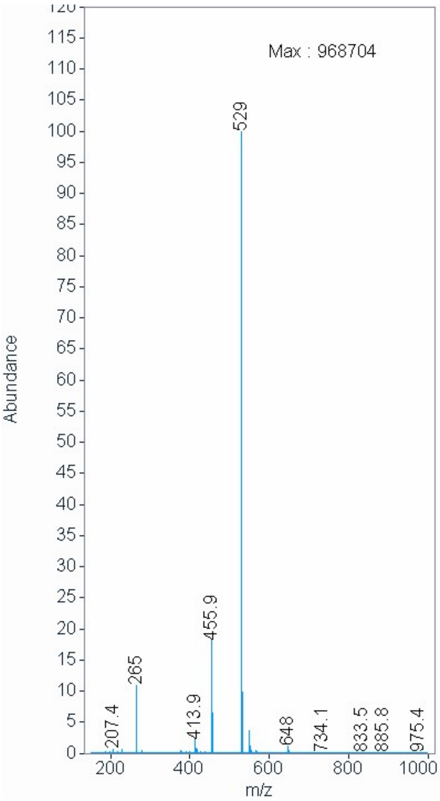
RT [min]	Type	Width [min]	Area	Height	Area%	Name
11.910	MM	0.1333	31.7624	3.9714	0.3618	
12.060	MM	0.2657	8540.8691	535.7968	97.2979	
12.620	MM	0.2482	205.4298	13.7930	2.3403	
		Sum	8778.0613			

Signal: MWD1 B, Sig=280,4 Ref=off

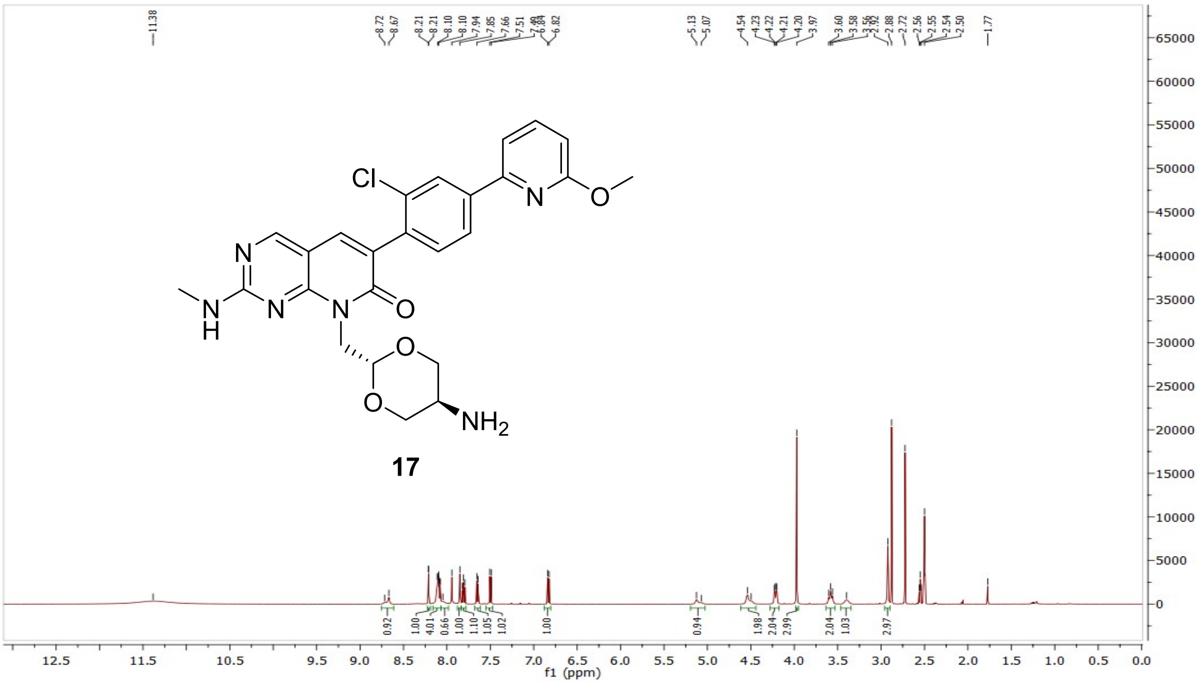
RT [min]	Type	Width [min]	Area	Height	Area%	Name
11.233	MM	0.3910	17.4154	0.7424	0.1915	
11.817	MM	0.1473	25.8467	2.9238	0.2843	
12.060	MM	0.2646	8852.8828	557.6185	97.3696	
12.610	MM	0.1574	195.8993	14.5508	2.1546	
		Sum	9092.0442			



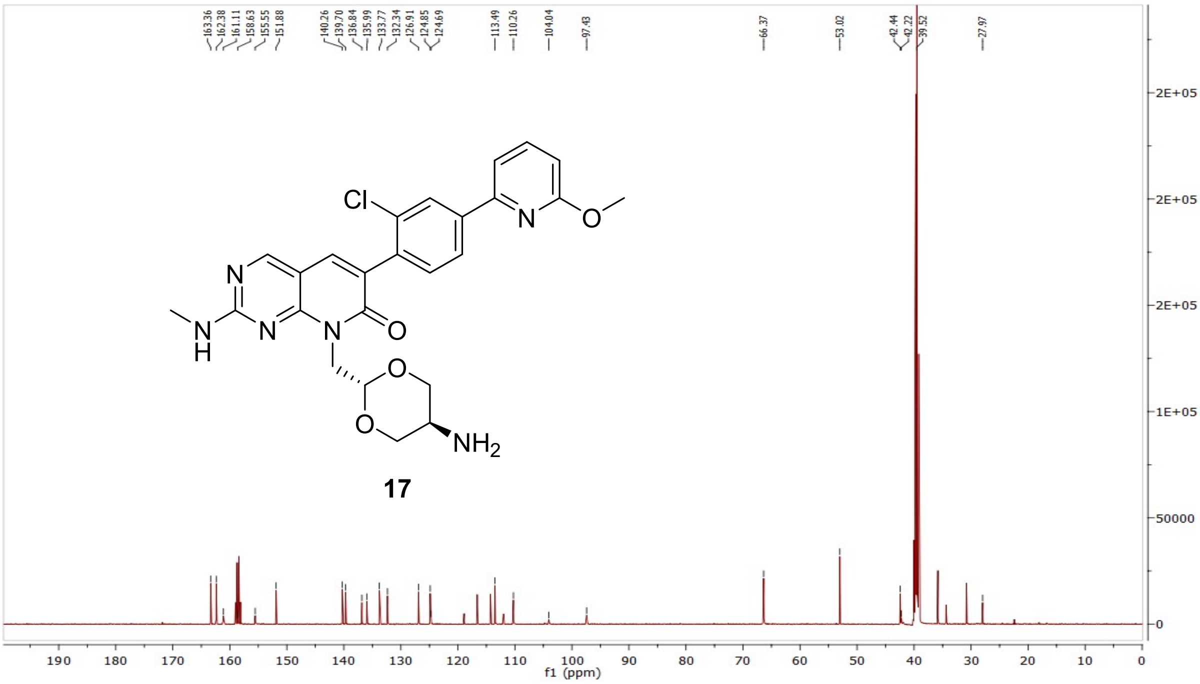
Signal	MSD1 TIC, MS File
Peak RT	12.267



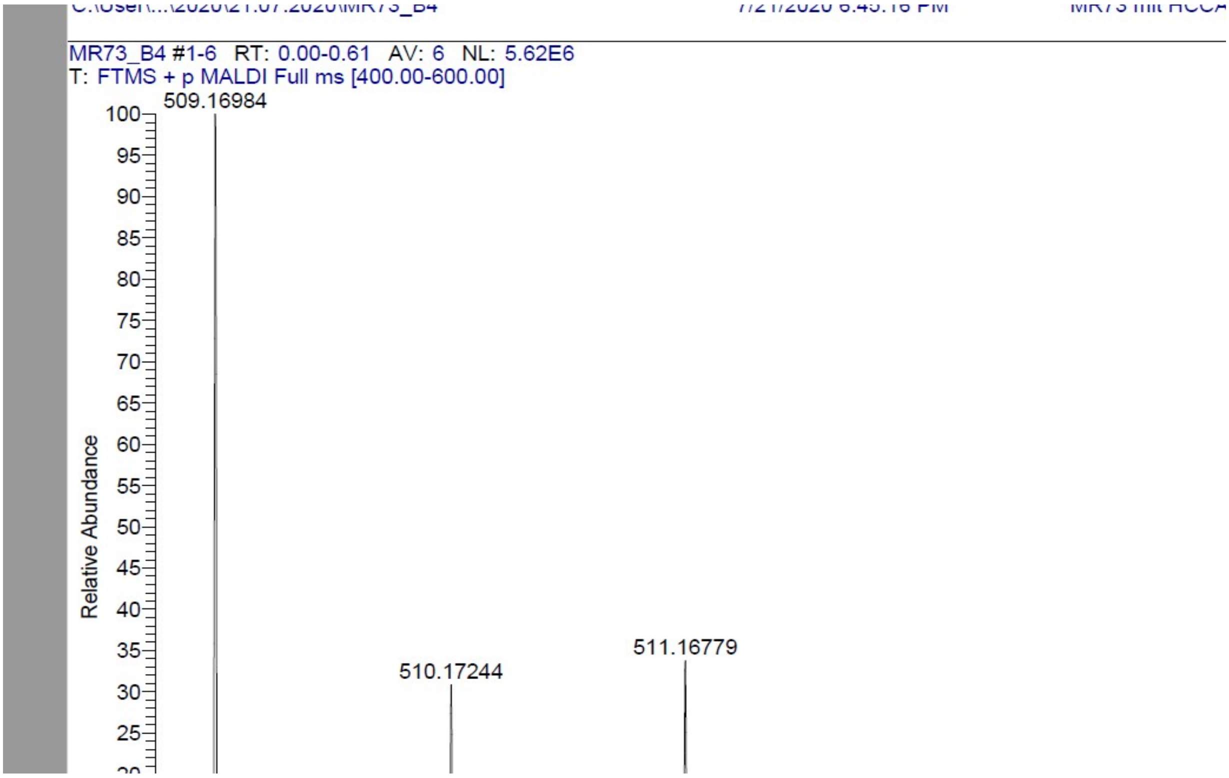
^{1}H NMR compound **17**:



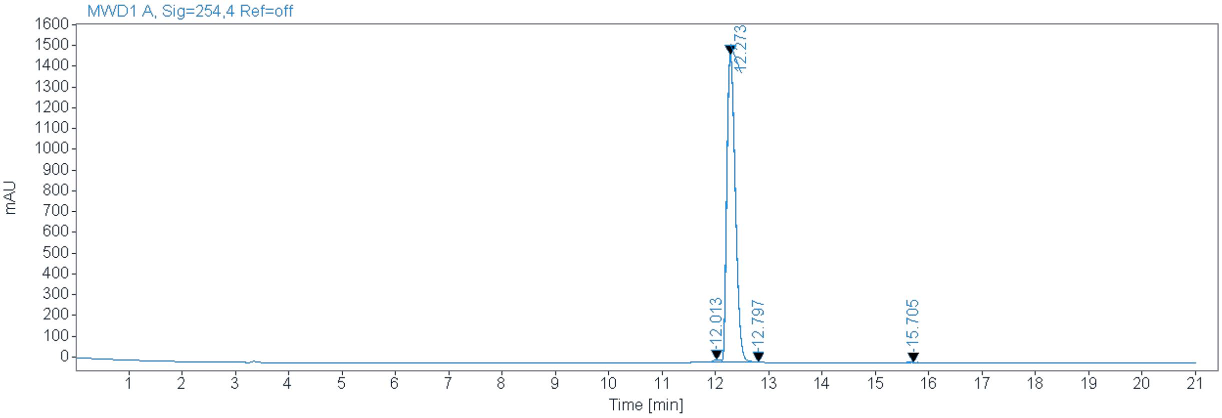
^{13}C NMR compound **17**:

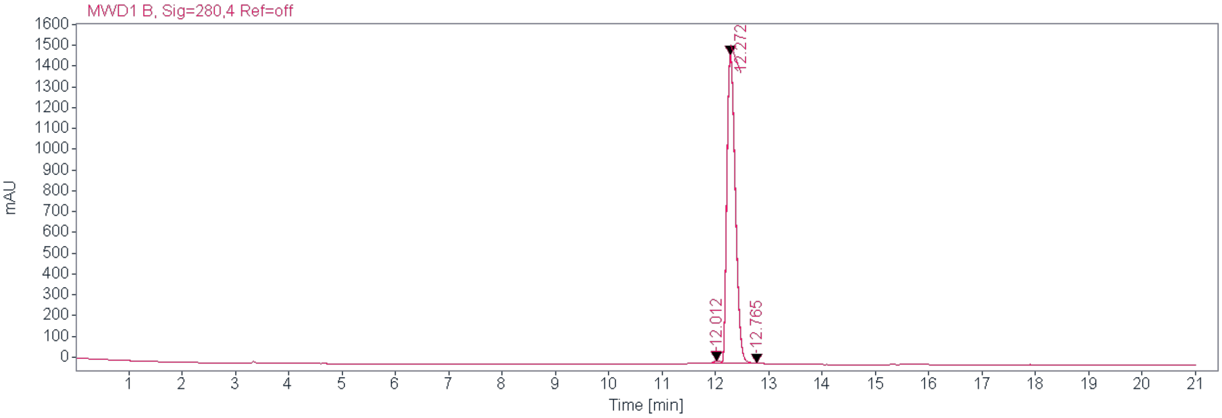


HRMS (FTMS +p MALDI) compound **17**:



HPLC-chromatograms compound **17**:



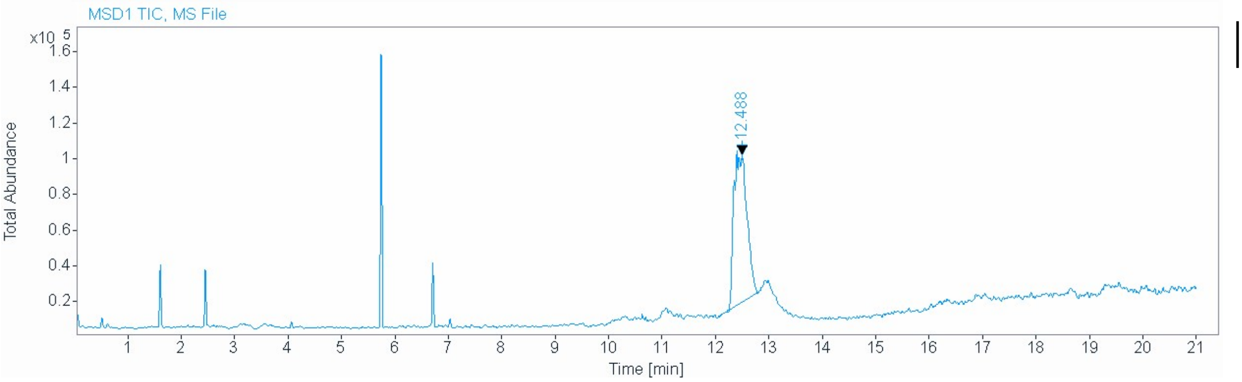


Signal: MWD1 A, Sig=254,4 Ref=off

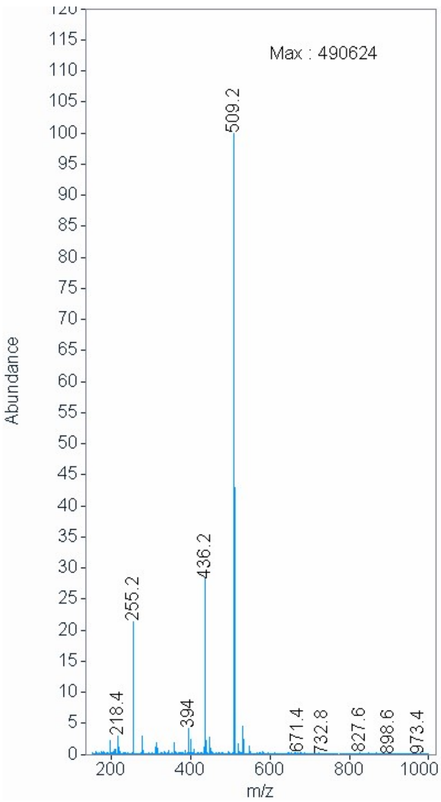
RT [min]	Type	Width [min]	Area	Height	Area%	Name
12.013	MM	0.2048	179.2532	14.5895	1.0797	
12.273	MM	0.1842	16380.1162	1482.1260	98.6652	
12.797	MM	0.0800	17.5503	2.6820	0.1057	
15.705	MM	0.1394	24.7923	2.9645	0.1493	
		Sum	16601.7119			

Signal: MWD1 B, Sig=280,4 Ref=off

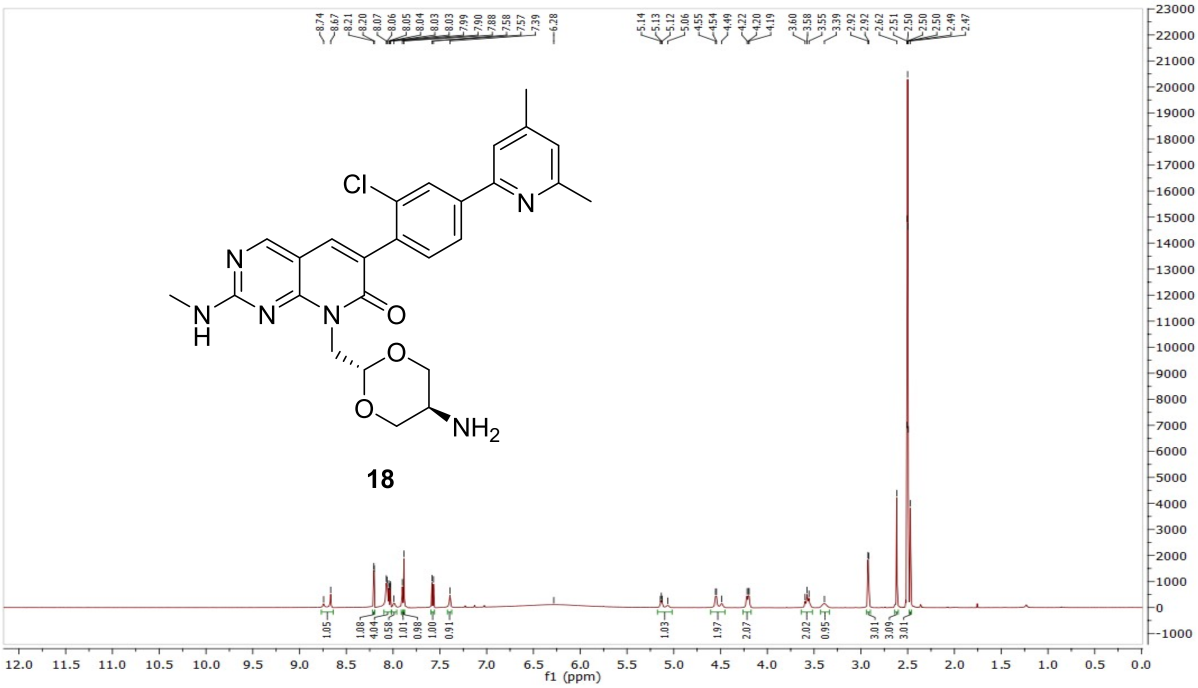
RT [min]	Type	Width [min]	Area	Height	Area%	Name
12.012	MM	0.2251	178.3978	13.2059	1.0702	
12.272	MM	0.1848	16472.2617	1485.4857	98.8137	
12.765	MM	0.0750	19.3637	3.1213	0.1162	
		Sum	16670.0232			



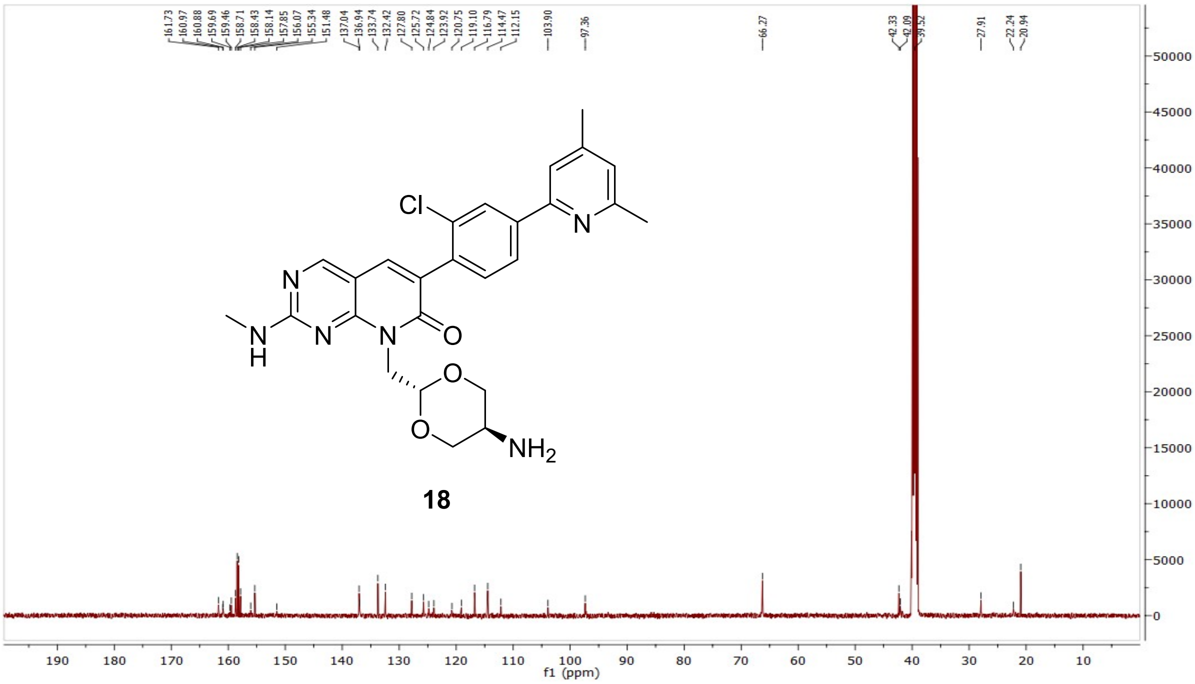
Signal	MSD1 TIC, MS File
Peak RT	12.488



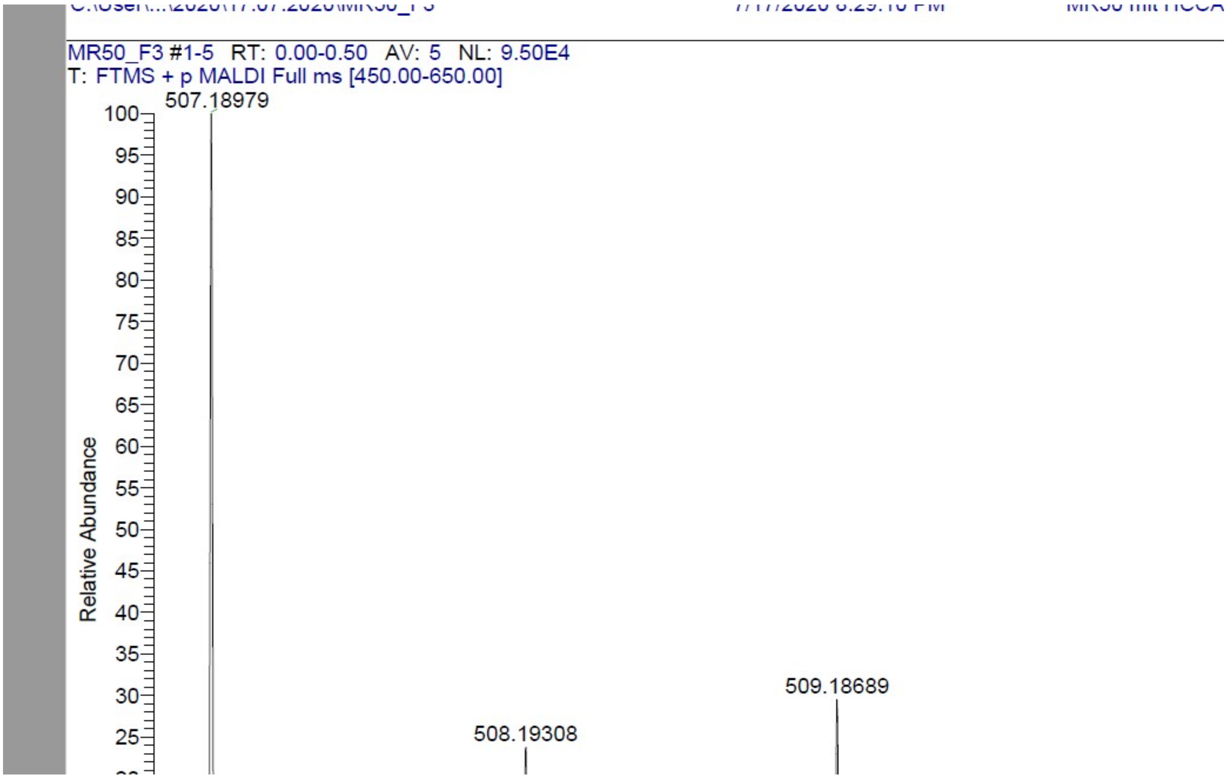
^{1}H NMR compound **18**:



^{13}C NMR compound **18**:

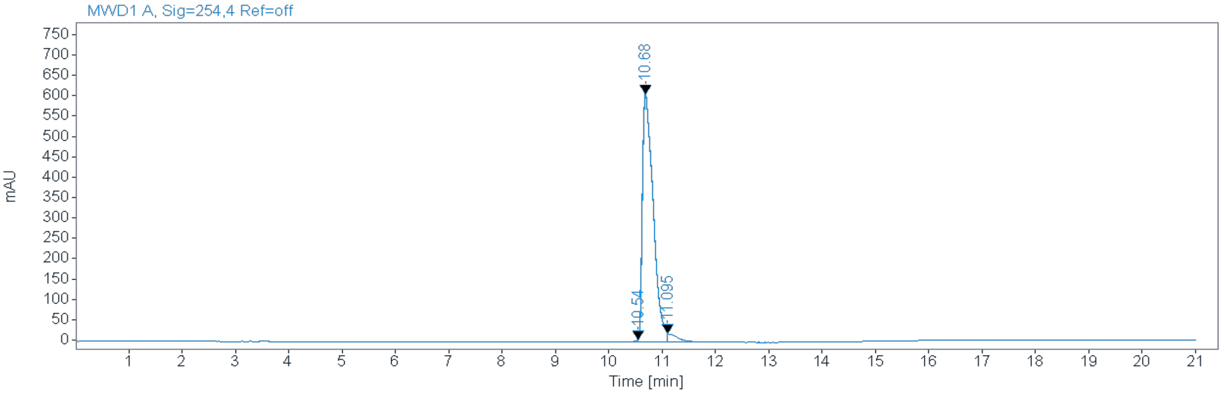


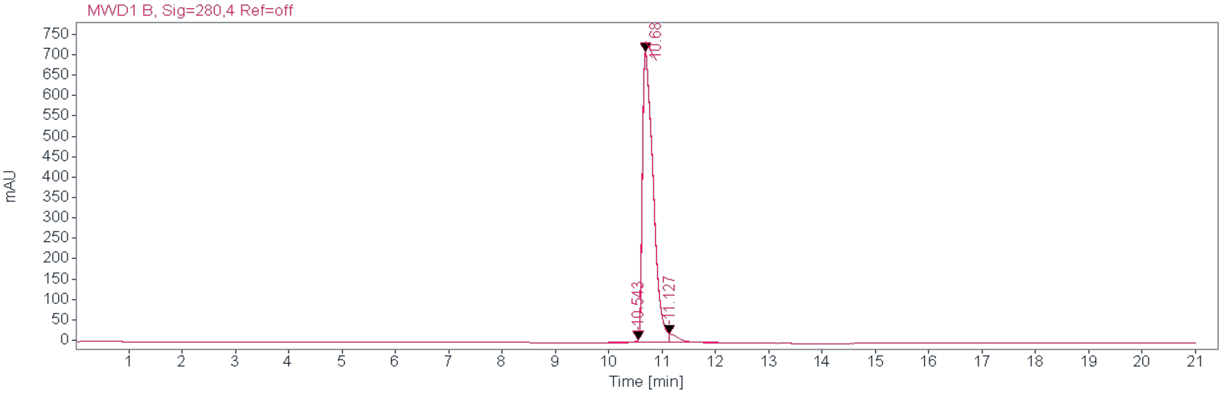
HRMS (FTMS +p MALDI) compound **18**:



MR50_F3 #1-5 RT: 0.00-0.50 AV: 5 NL: 9.50E4
T: FTMS + p MALDI Full ms [450.00-650.00]

HPLC-chromatograms compound **18**:



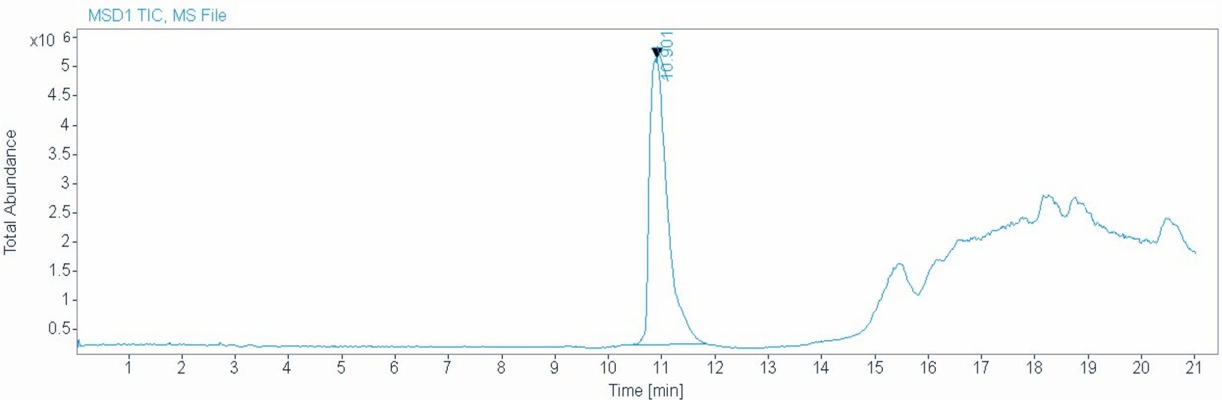


Signal: MWD1 A, Sig=254,4 Ref=off

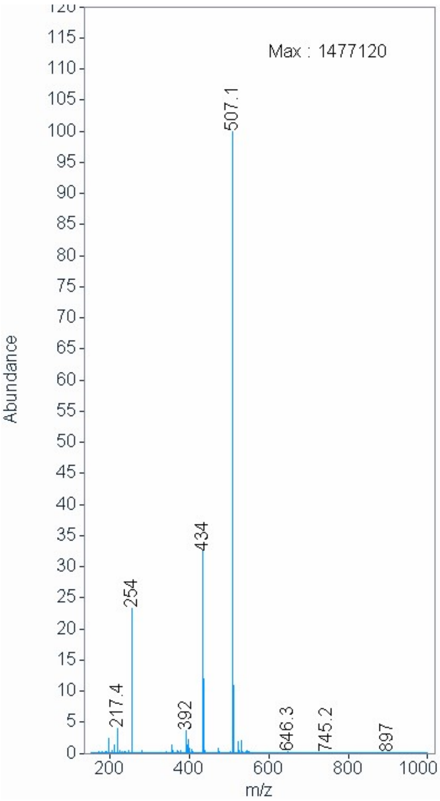
RT [min]	Type	Width [min]	Area	Height	Area%	Name
10.540	MM	0.0698	24.7134	5.9042	0.2805	
10.680	MM	0.2329	8514.1914	609.2924	96.6284	
11.095	MM	0.1652	272.3693	21.4063	3.0911	
		Sum	8811.2740			

Signal: MWD1 B, Sig=280,4 Ref=off

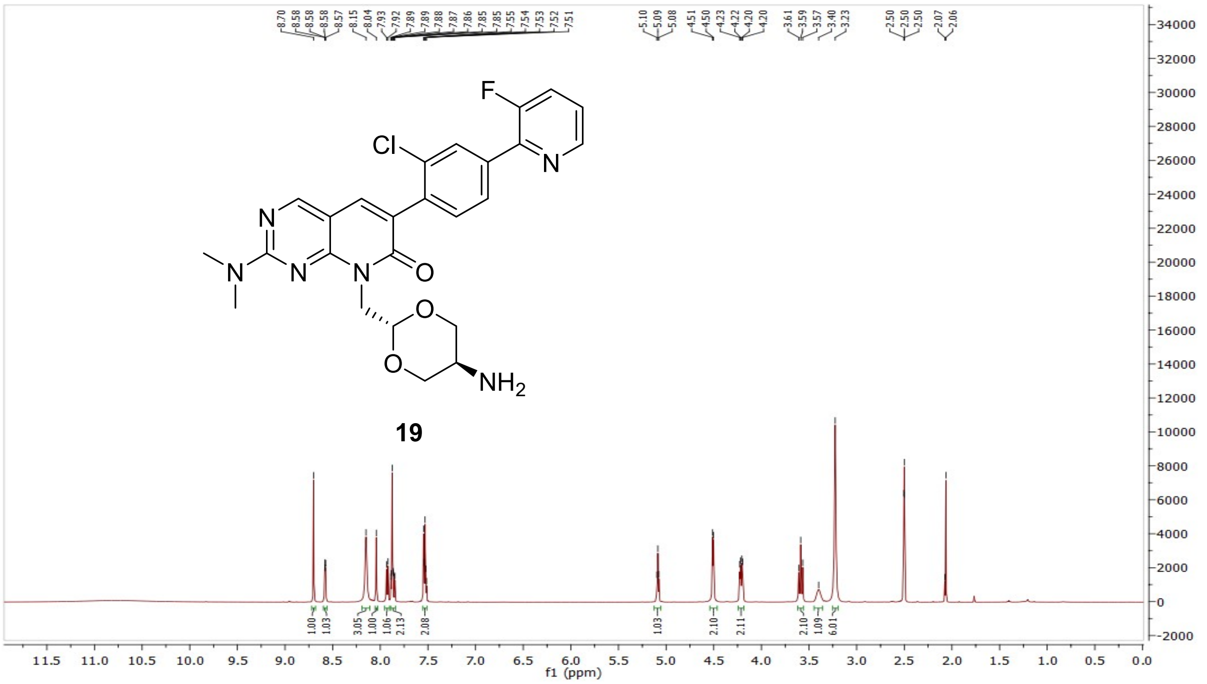
RT [min]	Type	Width [min]	Area	Height	Area%	Name
10.543	MM	0.0942	37.4948	6.6360	0.3629	
10.680	MM	0.2338	10014.0166	713.7814	96.9262	
11.127	MM	0.1574	280.0792	21.8666	2.7109	
		Sum	10331.5906			



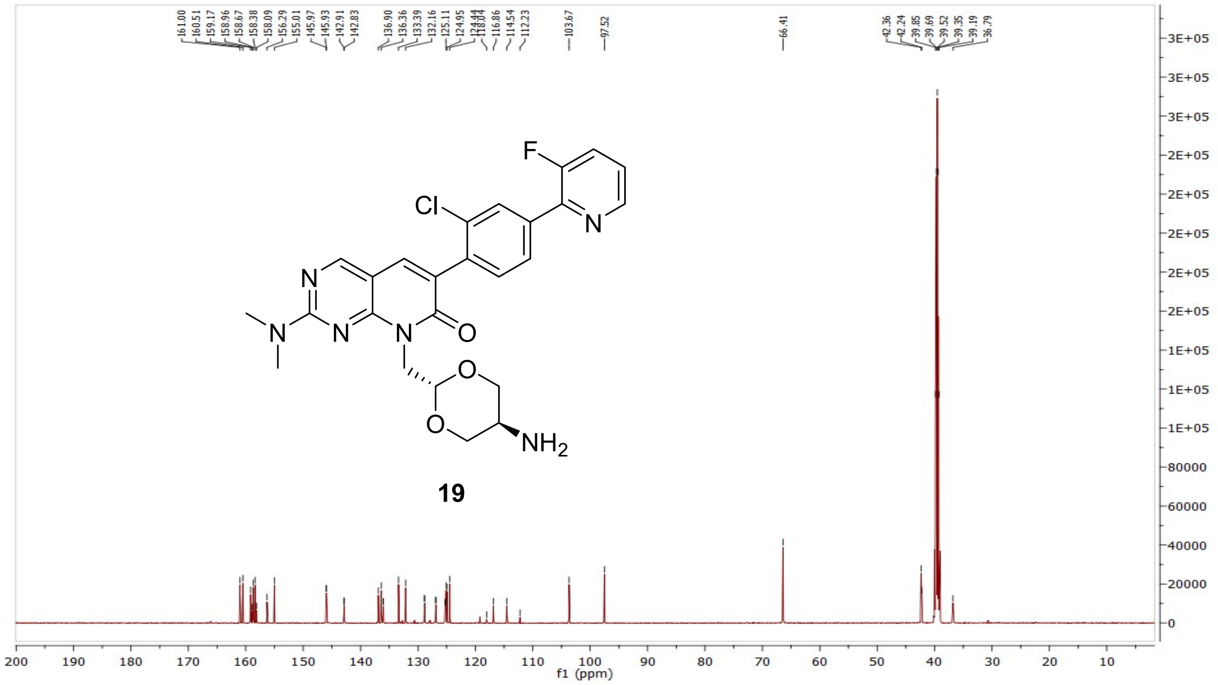
Signal	MSD1 TIC, MS File
Peak RT	10.901



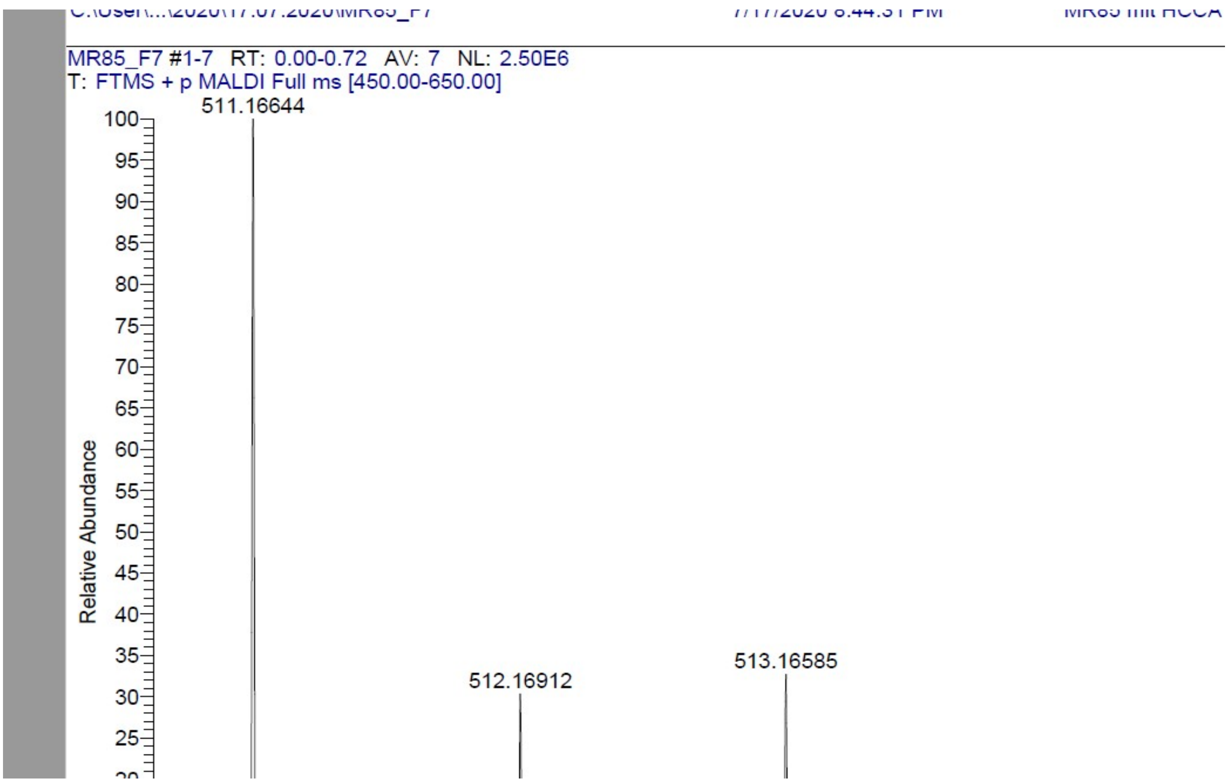
^{1}H NMR compound **19**:



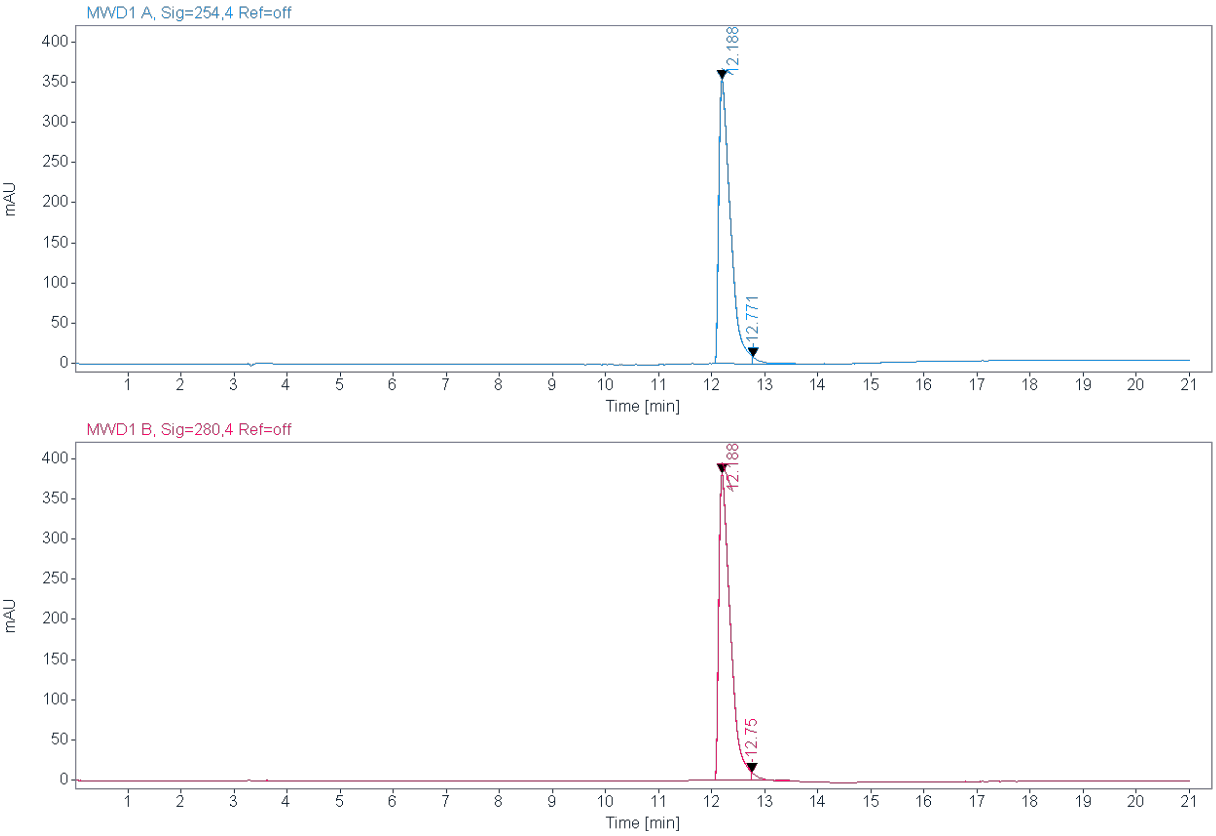
^{13}C NMR compound **19**:



HRMS (FTMS +p MALDI) compound **19**:



HPLC-chromatograms compound **19**:

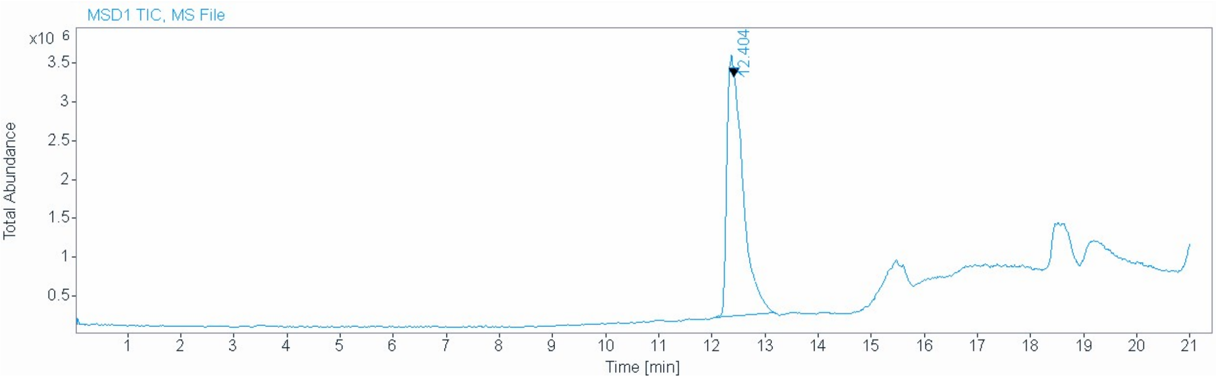


Signal: MWD1 A, Sig=254,4 Ref=off

RT [min]	Type	Width [min]	Area	Height	Area%	Name
12.188	MM	0.2522	5368.8589	354.7678	97.7154	
12.771	MM	0.1685	125.5265	8.9348	2.2846	
		Sum	5494.3854			

Signal: MWD1 B, Sig=280,4 Ref=off

RT [min]	Type	Width [min]	Area	Height	Area%	Name
12.188	MM	0.2509	5768.1577	383.2370	98.0186	
12.750	MM	0.1898	116.5990	10.2369	1.9814	
		Sum	5884.7567			



Signal MSD1 TIC, MS File

Peak RT 12.404