## **Supporting Information**

# Novel Benzohydroxamate-Based Potent and Selective Histone Deacetylase 6 (HDAC6) Inhibitors Bearing a Pentaheterocyclic Scaffold: Design, Synthesis and Biological Evaluation

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## **Table of Contents**

In vitro determination of specific HDAC6 inhibitory activity (data related to Figure 8)	S3
In vivo determination of specific HDAC6 inhibitory activity (data related to Figure 9)	S4
Six-membered heteroaromatic central scaffold compounds	S5
Repeats of enzyme assay IC50 determination (for key compounds) and standard deviations	S6
Repeats of cytotoxicity on PBMC and on 697 B-precursor acute lymphoblastic leukemia (B-ALL) cell line experiments (on key compounds) and standard deviations	
Homology model protocol	S11
Docking protocol	S11
Comparison between the best docking poses of compound 35 (Figure 7), Bavarostat and A 1083 into HDAC6 active site	
HPLC chromatograms of key compounds	S14

## *In vitro* determination of specific HDAC6 inhibitory activity (data related to Figure 8)

**Table S1** - Tubulin and H3 acetylation in human 697 B-precursor acute lymphoblastic leukemia(B-Pre-ALL) cell line.

	α-tubulin <sup>a</sup> H3 <sup>a</sup>				H3 <sup>a</sup>			
		Conc (	nM)		C	onc (nM)		
compd	1000	333	111	37	1000	333	111	
13	16±2	13±1	7±1	3±1	2±1	1±1	1±1	
29	7±1	6±1	4±1	2±1	8±3	n.a.	n.a.	
34	6±1	4±1	3±1	2±1	1±1	1±1	1±1	
35	11±1	8±1	3±1	2±1	3±1	n.a.	n.a.	
39	22±1	20±1	19±1	10±1	2±1	3±1	1±1	
42	14±3	9±2	3±1	2±1	3±1	2±1	1±1	
43	12±2	9±1	4±1	3±1	1±1	1±1	1±1	
44	10±2	9±2	8±1	3±1	2±1	2±1	1±1	
45	17±1	21±1	15±1	7±1	1±1	1±1	1±1	
47	14±1	10±1	11±1	6±1	1±1	n.a.	n.a.	
48	7 ±1	5±1	2±1	2±1	2±1	1±1	1±1	
49	19±1	15±1	7±1	2±1	1±1	n.a.	n.a.	
Givinostat	13±1	9±1	3±1	2±1	23±7	17±5	8±3	

a. *fold increase* of the ratio of acetylated tubulin and total tubulin and of acetylated H3 and total H3 ratio towards control. The test has been carried out in dose/response (4-points for tubulin and 3-points for histone H3) starting from 1  $\mu$ M with 3-fold serial dilution (3 technical replicates).

n.a. not available.

## *In vivo* determination of specific HDAC6 inhibitory activity (data related to Figure 9)

**Table S2** - Levels of tubulin and histone H3 acetylation and concentrations of compound 42 in the spleen and in plasma of mice following oral administration of the inhibitor (data presented in Figure 9A).

Time (hrs)	Ac-tubulin	Ac-H3	Compound 42 concentration	Compound 42 plasma concentration
	Fold increase (a	average ± sem)	(ng/g spleen)	(ng/ml)
1	$10.54 \pm 0.97$	$2.03 \pm 0.38$	$1357 \pm 492$	958 ± 362
4	$1.68 \pm 0.21$	$0.83 \pm 0.07$	$106.1 \pm 26.6$	$17.8 \pm 3.3$
24	$0.84 \pm 0.02$	$0.72 \pm 0.05$	$17.1 \pm 2.6$	0.7 ± 0.4

**Table S3** - Levels of tubulin and histone H3 acetylation and concentrations of compound 13 in the spleen and in plasma of mice following oral administration of the inhibitor (data presented in Figure 9B).

Time (hrs)	Ac-tubulin	Ac-H3	Compound 13 concentration	Compound 13 plasma concentration
	Fold increase (a	verage ± sem)	(ng/g spleen)	(ng/ml)
1	$11.04 \pm 1.25$	$3.12 \pm 0.59$	$6140 \pm 1583$	$1989 \pm 638$
4	$1.94 \pm 0.21$	$1.14 \pm 0.04$	$109.2 \pm 24.1$	$16.0 \pm 4.8$
24	$0.80 \pm 0.04$	$0.85 \pm 0.05$	$17.5 \pm 3.3$	$1.3 \pm 0.1$

## Six-membered heteroaromatic central scaffold compounds

Some compounds bearing a six-membered heteroaromatic ring as a central scaffold were synthesized and tested. These compounds show quite low potency in HDAC6 inhibitory activity compared to compounds with five-membered heteroaromatic ring core, even if they retain a certain selectivity toward HDAC3.

Compd code	Structure	HDAC6 IC <sub>50</sub> (nM) <sup>a</sup>	HDAC3 IC <sub>50</sub> (nM) <sup>a</sup>	Selectivity (HDAC3 IC <sub>50</sub> /HDAC6 IC <sub>50</sub> )
ITF3858	O N S O H H H	621±16	5414±95	8.7
ITF3857	O N S O H O H	701±8	6691±154	9.5
ITF3743		129±2	1558±31	12.1

 Table S4 – Enzymatic activity of some Six-membered heteroaromatic central scaffold compounds

a - Enzymatic data (IC<sub>50</sub>) in nM unit were obtained from curve-fitting of a 5-point enzymatic assay starting from 100, 30 or 10  $\mu$ M with 10-fold serial dilution. Experiments were done in triplicate (single experiment). SDs were calculated on technical replicates.

## Repeats of enzyme assay IC<sub>50</sub> determination (for key compounds) and standard deviations.

Enzyme	Compd		IC <sub>50</sub>	(nM)		Mean	Std Dev	repeats
	13	9	8	8		8	1	3
	29	8	8	5		7	1	3
	33	8	7	7		7	1	3
	34	6	5	5		5	1	3
	35	3	5	2		3	2	3
	39	6	8	4		6	2	3
HDAC6	42	27	15	15	9	17	8	4
IIDACO	43	9	8	9		9	1	3
	44	4	4	1		3	2	3
	45	4	2	6		4	2	3
	46	5	4	6		5	1	3
	47	5	6	6		6	1	3
	48	6	9	15		10	4	3
	49	11	13	16		13	3	3
	13	487	532	493		504	24	3
	29	974	1026	681	804	871	158	4
	33	6510	7831	6680	6357	6845	671	4
HDAC3	34	5988	5243	4306		5179	843	3
	35	641	750	617		669	71	3
	39	2470	2803	2450		2574	198	3
	42	979	794	712	975	865	134	4

Table S5 – IC<sub>50</sub> calculation - Single experiments results

		1	1	1				
	43	2827	2074	1871	1606	2095	524	4
	44	2635	2273	2348		2419	191	3
	45	1776	1870	1885	1584	1779	138	4
	46	2608	2729	1887		2408	455	3
	47	3005	2661	2669		2778	196	3
	48	2936	3635	3741	3851	3541	413	4
	49	13717	10953	10382	8614	10917	2116	4
	13	1015	1004			1010	8	2
	29	812	1047			929	166	2
	33	7512	6768			7140	526	2
	34	4447	3472			3960	689	2
	35	1425	700			1063	513	2
	39	2898	2436			2667	327	2
HDAC1	42	1094	953	829	820	924	129	4
	43	3991	4288			4140	210	2
	44	2517	2107			2312	290	2
	45	2878	2983			2931	74	2
	46	3659	4677			4168	720	2
	47	3182	3452			3317	191	2
	48	5162	5269			5216	76	2
	49	7377	8838			8107	1033	2

## Repeats of cytotoxicity on PBMC and on 697 B-precursor acute lymphoblastic leukemia (B-Pre-ALL) cell line experiments (on key compounds) and standard deviations

Compd	PBMC cytotoxicity (nM)	Standard deviation	repeats
13	5857	4230	6
29	4274	3507	6
33	>10000	-	2
34	7387	7608	4
35	5524	6334	2
39	>10000	-	2
42	5387	5128	5
43	>10000	-	3
44	>10000	-	3
45	>10000	-	1
46	>10000	-	3
47	5987	3892	3
48	7445	6210	3
49	3963	4108	5
Givinostat	313		

**Table S6** – Cytotoxicity on PBMC

Compd	697 cell line cytotoxicity (nM)	Standard deviations	repeats
13	>10000	-	3
29	3634	2271	6
33	>10000	-	5
34	>10000	-	7
35	6489	2603	6
39	>10000	-	3
42	8934	5531	6
43	5506	3031	4
44	2749	1865	7
45	>10000	-	6
46	5983	2844	5
47	>10000	-	5
48	>10000	-	4
49	>10000	-	3
Givinostat	100		

Table S7 – Cytotxicity on 697 B-precursor acute lymphoblastic leukemia (B-Pre-ALL) cell line

Both cytotoxicity test on 697 (B-Pre-AL) and hPBMC were performed in a concentration range between 10 and 10000 nM (Higher concentrations lead to phenomena which could compromise the assay, such as inhibitor precipitation). The IC<sub>50</sub> of the majority of tested compounds could not be determined, being higher than 10000 nM. The high standard deviations of the other compounds are due to the closeness of the  $IC_{50}$  value to the experiment highest dose. These data state that all the tested compounds are not cytotoxic.

**Cell cytotoxicity assay.** Cytotoxic activities of the compounds were evaluated in the human 697 promyelocytic B leukemia cell line (ACC 42, DSMZ- Deutsche Sammlung von Mikroorganismen und Zellkulturen) and on human peripheral blood mononuclear cells (PBMCs) using a commercial viability assay which measures the mitochondrial activity. 697 cells were plated at 2x10<sup>4</sup> cells per well, and the compounds were added in concentrations ranging from 10 to 10000 nM. After 48 h of incubation, cell viability was evaluated with CellTiter 96® Aqueous One Solution Cell Proliferation Assay (Promega) according to the manufacturer's instructions.

hPBMC from healthy donors were separated by density gradient on Ficoll Hypaque.

PBMCs were plated at  $5x10^5$  cell per well and compounds were added in a concentration range from 10 to 10000 nM. After 72 h of incubation, cell viability was evaluated as described before.

## Homology model protocol

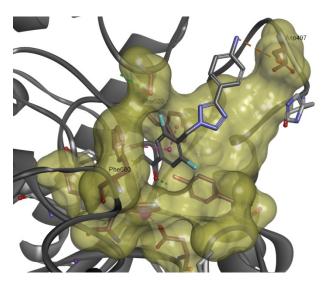
The homology model h-HDAC6-CD2.pdb was prepared using "Build Homology Model" protocols available in Discovery Studio, and based on MODELER (Sali, A.; Blundell, T.L., *J. Mol. Biol.* **1993**, *234*(3), 779-815.). Parameters are set to the default values suggested by supplier. Sequences of templates (h-HDAC8: PDB code 1T64, h-HDAC2: PDB code 4LXZ and h-HDAC3: PDB code 4A69) and the portion of h-HDAC6 target of homology modeling (h-HDAC6-CD2, residues from 485 to 835, GenBank: AAH69243.1 - Ref. Strausberg et al., *Proc. Natl. Acad. Sci.* **2002**, *99*, 16899-16903). Water molecules available in templates were removed, whereas all ligands coprecipitated with template were conserved and transferred to the model. Optimization level was set to the highest level.

## **Docking protocol**

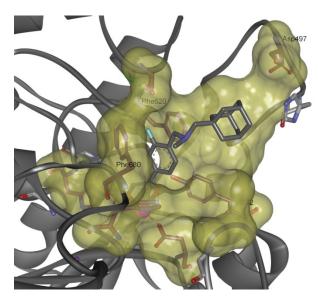
Docking calculation were performed using libdoc protocol of Discovery Studio (DS) Suite, focusing the conformational search of candidates in a sphere centered in the center of mass of aligned inhibitors and having radius equal to 8.0 A. The volume includes both L1 and L2 loops, the catalytic core, the zinc cation and its residue directly bound to the metal ion.

The best score function for poses ranking was detected in the preliminary calculation, where a training set of HDAC6 selective and pan inhibitors are mixed with compounds exhibiting low isoform 6 potency (at least 10-fold).

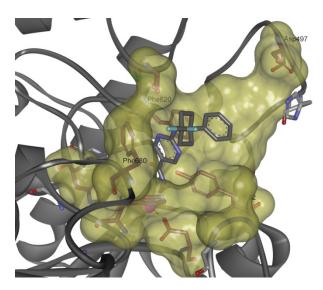
Final Receiving Operator Curves (ROC) were based on the Dreiding scores, which exhibited the highest number of true positive hits, on the basis of the top scoring function value. Comparison between the best docking poses of compound 35 (related to Figure 7), Bavarostat and ACY-1083 into HDAC6 active site.



**Figure S1.1 (related to Figure 7)**. Compound 35 h-CD-HDAC6 complex: conformer detected in the docking experiment. Protein PDB code: 5EDU



**Figure S1.2**. Bavarostat h-CD-HDAC6 virtual complex: the "binding" conformer was extracted from Bavarostat-z-CD2-HDAC6 complex (PDB code 6DVO), preliminary superimposed to h-CD2-HDAC6 (PDB code 5EDU) by using sequences alignment.

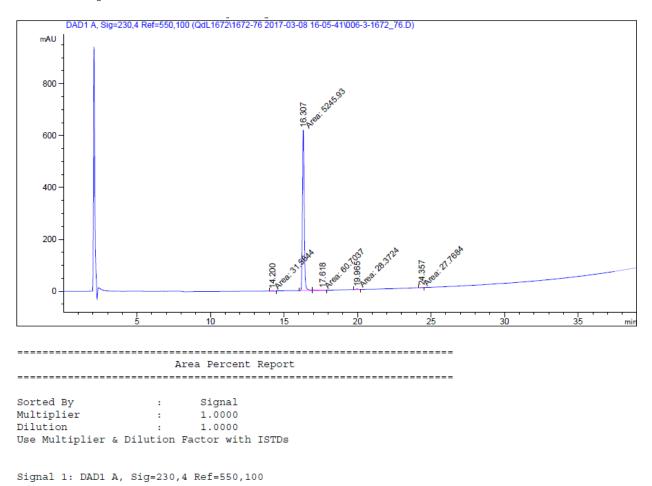


**Figure S1.3.** ACY-1083 h-CD-HDAC6 virtual complex: the "binding" conformer was extracted from ACY-1083-z-CD2-HDAC6 complex (PDB code 5WGM), preliminary superimposed to h-CD2-HDAC6 (PDB code 5EDU) by using sequences alignment.

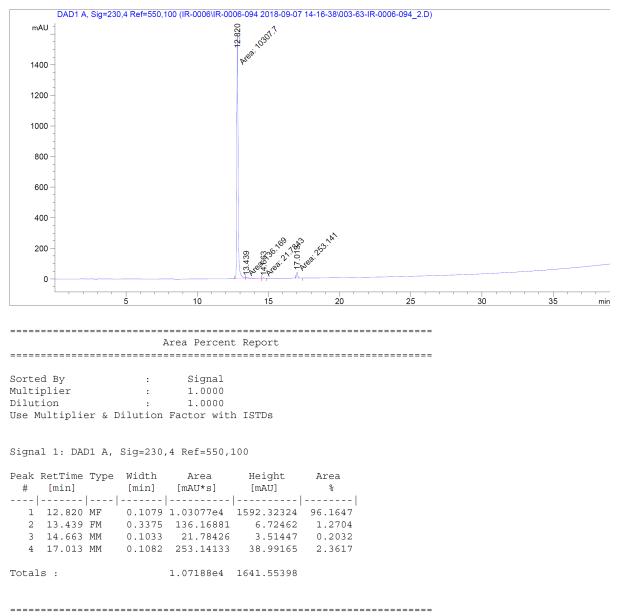
## HPLC chromatograms of key compounds

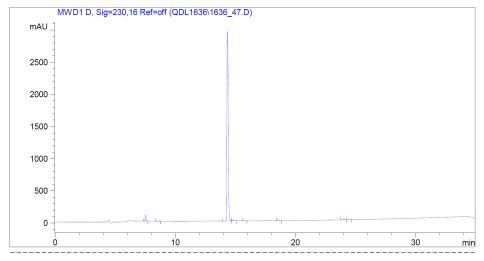
## Compound 13

`ОН



Peak #	RetTime [min]	Туре	Width [min]	Area [mAU*s]	Height [mAU]	Area %
1	14.200	MM	0.3737	31.56440	1.40759	0.5851
2	16.307	MF	0.1412	5245.92725	619.26727	97.2488
3	17.618	FM	0.8307	60.70369	1.21788	1.1253
4	19.965	MM	0.1715	28.37240	2.75685	0.5260
5	24.357	MM	0.3163	27.76843	1.46313	0.5148
Total	ls :			5394.33616	626.11272	



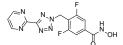


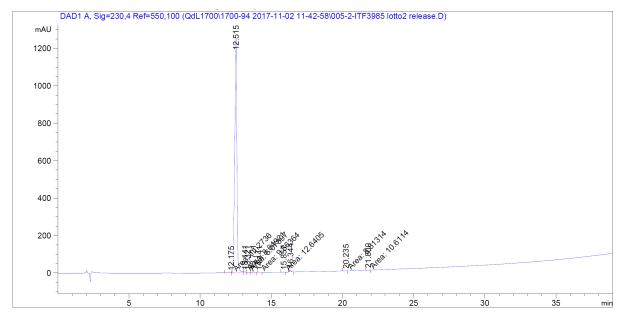
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1	7.513	BV	438.4840	0.074	91.381	1.873
2	8.460	BB	29.0845	0.069	6.349	0.124
3	14.328	BV	2.2477e4	0.121	2950.154	96.020
4	14.786	VV	147.0223	0.123	16.631	0.628
5	15.727	BB	43.1524	0.094	6.988	0.184
6	18.576	BB	100.9549	0.108	14.001	0.431
7	23.995	BB	88.4048	0.134	9.752	0.378
8	24.460	BB	84.4804	0.115	11.134	0.361
Tota	ls :		23408.943	3	106.390	





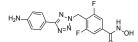
Area Percent Report

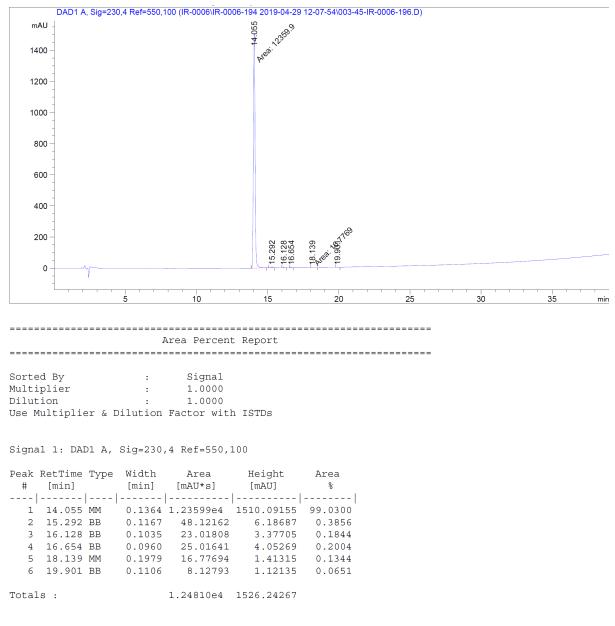
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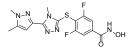
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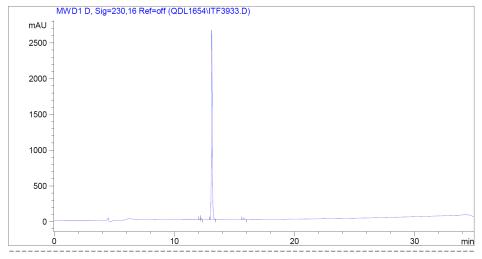
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2	12.515	BB	0.1552	1.32664e4	1256.75830	98.6550
3	13.141	MF	0.1376	8.64921	1.04778	0.0643
4	13.321	FM	0.1469	6.07897	6.89890e-1	0.0452
5	13.721	BB	0.1305	35.58794	4.30420	0.2646
6	14.141	MM	0.2270	9.66364	7.09389e-1	0.0719
7	15.857	MM	0.2234	12.64052	9.43196e-1	0.0940
8	16.344	BB	0.1218	77.54416	9.64533	0.5767
9	20.235	MM	0.2125	8.81314	6.91092e-1	0.0655
10	21.800	MM	0.2404	10.61143	7.35719e-1	0.0789





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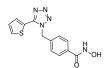


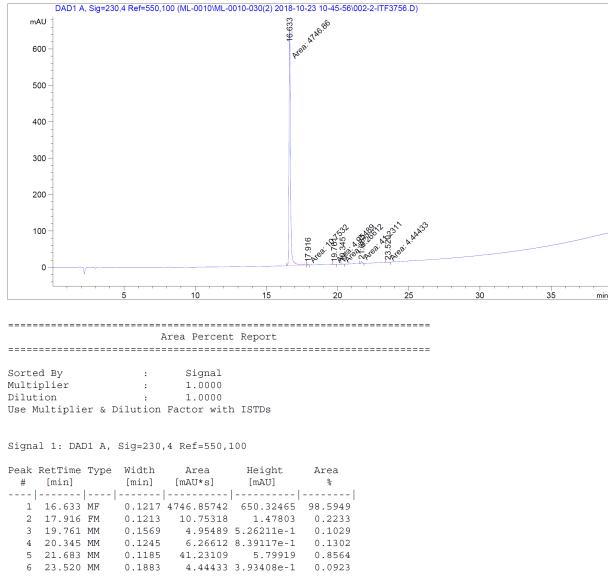
AREA PERCENT REPORT

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Use Multiplier	s &	Dilution Factor with ISTDs

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1	12.157		75.4362	0.058	19.781	0.501
2	12.226	VB	117.5889	0.073	23.137	0.781
3	13.102	BV	1.4711e4	0.085	2660.644	97.740
4	15.761	VB	147.1682	0.096	23.239	0.978
Tota	ls :		15051.009	2	726.801	

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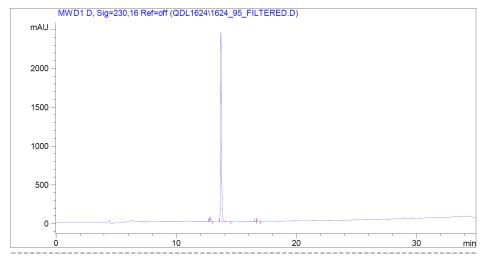




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4814.50704 659.36060

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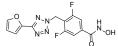


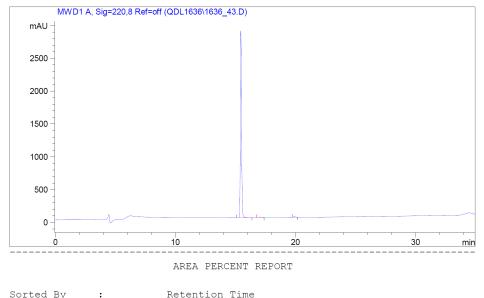
AREA PERCENT REPORT

Sorted By	:	F	Retentio	on Tin	ne
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Dilution	:	1	.000000	)	
Use Multi	plier &	Dilution	Factor	with	ISTDs

Signal 1 : MWD1 D, Sig=230,16 Ref=off									
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1 2 3 4 5	12.765 12.847 13.713 16.632 16.749	VV VB VV BV	142.2237 243.4736 1.3720e4	0.062 0.080 0.086 0.071	34.635 44.129 2442.290 5.910	0.996 1.705 96.064 0.189			
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S21

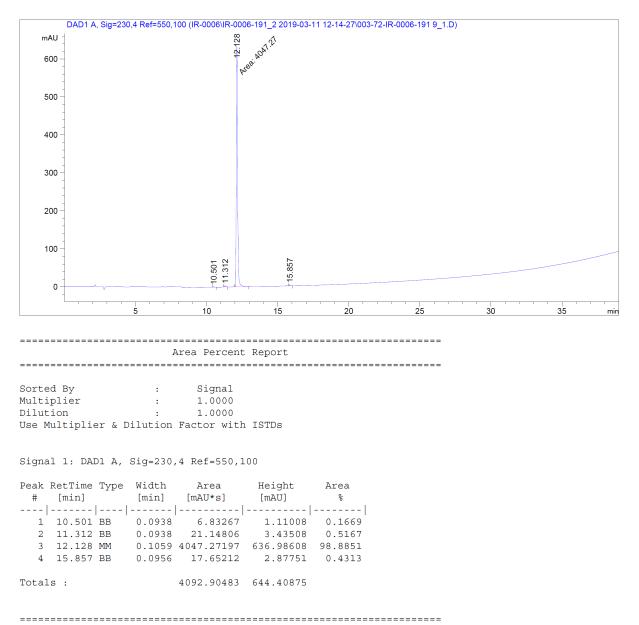


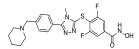


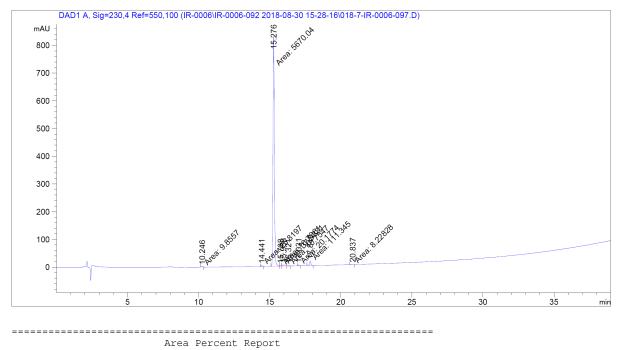
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Multiplier	:	1	L.000000	)	
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Use Multiplier	&	Dilution	Factor	with	ISTDs

Signa	.1 1	:	MWD1 A,	Sig=220,	8 Ref=off	
#	[min]	Туре	Area [mAU*s]	Width [s]	Height [mAU]	
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2	17.019	VB	77.4276	0.119	9.334	0.376
3	19.905	BB	135.7432	0.112	18.491	0.658
Tota	ls :	2	20617.825	2	875.048	

N S H H OF







Area Percent Report

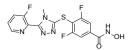
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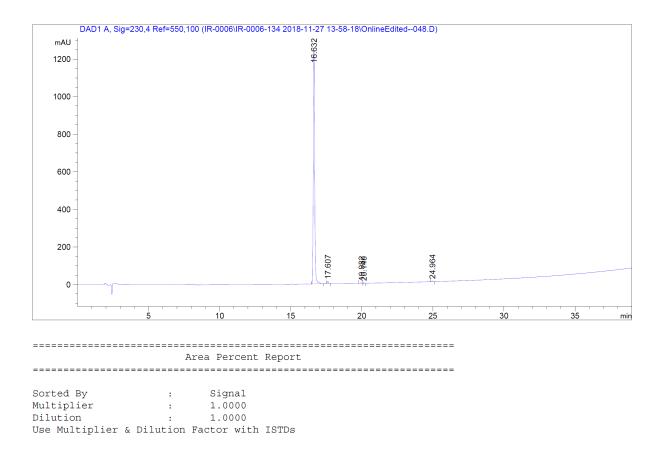
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2	14.441	MM	0.1169	25.81969	3.68123	0.4368
3	15.276	MF	0.1139	5670.03955	829.62567	95.9245
4	15.768	FM	0.1392	16.73606	2.00368	0.2831
5	15.958	FM	0.1398	37.98315	4.52803	0.6426
6	16.321	FM	0.1110	10.75467	1.61549	0.1819
7	17.031	MM	0.1052	20.17744	3.19765	0.3414
8	17.849	MM	0.1235	111.34515	15.02161	1.8837
9	20.837	MM	0.2144	8.22828	4.97986e-1	0.1392

Totals :

5910.93969 861.52480

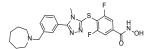


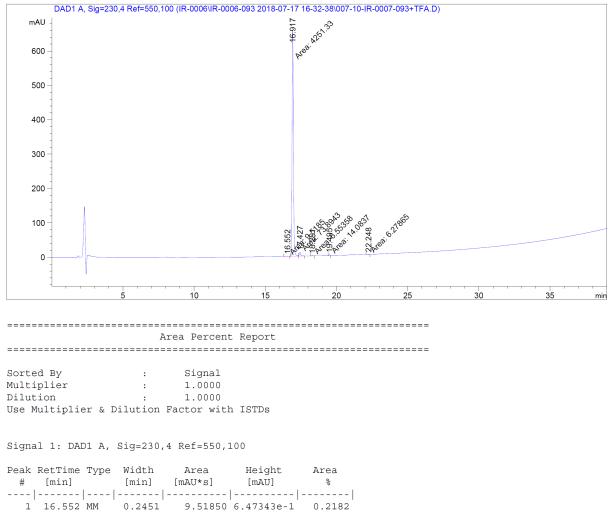


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2	17.607	BB	0.0962	73.10281	11.81493	0.8440
3	19.982	BV	0.1227	19.25979	2.32263	0.2224
4	20.140	VB	0.0995	10.28613	1.54806	0.1188
5	24.964	BB	0.1070	22.88335	3.29540	0.2642

#### Totals : 8661.65123 1265.59016





2	16.917	MF	0.1075	4251.33350	658.83563	97.4705
3	17.427	FM	0.1160	73.89431	10.61377	1.6942
4	18.291	MM	0.1224	6.55358	8.92673e-1	0.1503
5	19.495	MM	0.1005	14.08372	2.33581	0.3229
6	22.248	MM	0.1673	6.27865	6.25553e-1	0.1440

Totals : 4361.66227 673.95077

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N-N N S F N-N F H OH

