THE STRUCTURAL REQUIREMENTS OF HISTONE DEACETYLASE (HDAC) INHIBITORS: SUBEROLYANILIDE HYDROXAMIC ACID (SAHA) ANALOGUES MODIFIED AT C3, C6, AND C7 POSITIONS ENHANCE SELECTIVITY

by

SUN EA CHOI

DISSERTATION

Submitted to the Graduate School

of Wayne State University,

Detroit, Michigan

in partial fulfillment of the requirements

for the degree of

DOCTOR OF PHILOSOPHY

2012

MAJOR: CHEMISTRY (Organic)

Approved by:

Advisor

Date



© COPYRIGHT BY

SUN EA CHOI

2012

All Rights Reserved



DEDICATION

I would like to dedicate this dissertation to some people who have made me who I am today: my advisor Dr. Mary Kay H. Pflum, committee members (Dr. Jin K. Cha, Dr. David Crich, and Dr. Aloke Dutta), Dr. Zhongwu Guo, previous and current group members (Dr. Anton Bieliauskas, Dr. Sujith Weerashinghe, Geetha Padige, Satish Garre etc), room mates (Charlie Johnson, Derek Averill, and John Pompei), friends (Dr. Ivan Lysenka, Dr. Woo, Jun Hee Lee, Sung Jun Park, Yu Chen, Nitin Jabre etc), the oldest sister Moon Ea Choi and her family (Cheul Young Lee and Ha Jin), other sisters (Jung Ea Choi, Young Ea Choi, and Myong Ea Choi), brother Jin Young Choi, mother Hyang Joo Park, and specially, father Chang Soon Choi. I miss you so much, Dad.



TABLE OF CONTENTS

Dedicationii
List of Tablesvii
List of Figures ix
List of Schemes xi
CHAPTER 1 – INTRODUCTION1
1.1 Gene expression by Histone Deacetylase (HDAC) proteins1
1.2 HDAC protein family
1.3 HDAC inhibitors4
1.4 Inhibitor selectivity6
1.5 Rationale for the synthesis of SAHA analogues containing substituents
on the carbon linker7
1.6 Specific aims7
1.7 Development of isoform or class-selective inhibitors
1.8 Preparation of SAHA analogues containing substituents on the linker
near the hydroxamic acid10
1.9 Preparation of SAHA analogues containing substituents on the linker
near the capping group12
1.10 Novel HDAC6-selective inhibitors16
1.11 Evaluation of SAHA analogues containing substituents on the linker
near the hydroxamic acid and capping group17



1.12 Structure activity relationship (SAR) studies from matrix metallo-
proteinases (MMP), another hydroxamic acid binding protein18
1.13 Evaluation of a pyridyl substituent on an HDAC inhibitor,
Largazole21
CHAPTER 2 – SYNTHESIS OF SAHA ANALOGUES MODIFIED AT THE C3
POSITION
2.1 Rationale for design of the SAHA analogues containing substituents
on the C3 position24
2.2 Initial synthesis25
2.3 Optimized synthesis26
2.4 Biological analysis27
2.5 Experimentals
2.5.1 General methods
2.5.2 Experimental Procedures and Compound Characterizations32
2.6 HDAC high-throughput assay45
2.6.1 Fluorescence activity assay for libraries of SAHA analogues45
2.6.2 HDAC assay procedure46
CHAPTER 3 – SYNTHESIS OF SAHA ANALOGUES MODIFIED AT THE C6
POSITION
3.1 Rationale for design of the SAHA analogues modified at the C6
position49
3.2 Initial synthesis50
3.3 Modified synthesis



3.4 Biological analysis5	3
3.5 Experimentals5	59
3.5.1 General methods	59
3.5.2 Experimental Procedures and Compound Characterizations59	9
3.6 HDAC assay procedure7	'2
CHAPTER 4 – SYNTHESIS OF SAHA ANALOGUES MODIFIED AT THE C7	
POSITION	5
4.1 Rationale for design of the SAHA analogues modified at the C7	
position7	5
4.2 Initial synthesis of C7-SAHA analogues7	'6
4.3 Synthesis of the C7-SAHA analogues with pyridyl and bulky	
substituents7	9
4.4 Optimized synthesis for the C7-pyridyl analogue8	1
4.5 Biological analysis8	2
4.6 Future direction8	9
4.7 Experimentals9) 1
4.7.1 General methods9	1
4.7.2 Experimental Procedures and Compound Characterizations97	1
4.8 HDAC assay procedure	8
APPENDICES	
Appendix A – Dose response graphs and data for C3-SAHA library99	9
Appendix B – Supplementary Information for C3-SAHA library 10	5

Appendix C – Dose response graphs and data for C6-SAHA library. 149



Appendix D – Supplementary Information for C6-SAHA library			
Appendix E – Dose response graphs and data for C7-SAHA library	<i>.</i> 201		
Appendix F – Supplementary Information for C7-SAHA library	212		
References	232		
Abstract	244		
Autobiographical Statement	247		



LIST OF TABLES

Table 1.1 – HDAC family
Table 1.2 – HDAC inhibition by SAHA, MS-275, and the C2-SAHA analogues HeLa cell lysates
Table 1.3 – HDAC1 and PRO (He La) inhibition by SAHA, MS-275, and Apicidin, the compound Ea, and derivatives14
Table 1.4 – Collagenase 1 (MMP1), gelatinase-A (MMP2), stromelysin 1 (MMP3), gelatinase-B (MMP9), collagenase 3 (MMP13) inhibition by N-aryl sulfonly homocysteine hydroxamate19
Table 1.5 – Collagenase 1 (MMP1), gelatinase-A (MMP2), stromelysin 1 (MMP3), gelatinase-B (MMP9), collagenase 3 (MMP13) inhibition by N-aryl sulfonlyaziridine hydroxamic acid analogues21
Table 2.1 – HDAC inhibition by SAHA, MS-275, and the C3-SAHA analogues using HeLa cell lysates28
Table 2.2 – IC ₅₀ values of SAHA and the C3-SAHA ethyl variant 1c for HDAC1, HDAC3, and HDAC6
Table 3.1 – HDAC inhibition by SAHA, MS-275, and the C3-SAHA analogues using HeLa cell lysates54
Table 3.2 – IC ₅₀ values of SAHA and the C6-SAHA <i>t</i> -butyl variant 14c for HDAC1, HDAC3, and HDAC658
Table 4.1 – HDAC inhibition by SAHA, C-methyl, benzyl, and 4-naphthyl variants using HeLa cell lysates
Table 4.2 – HDAC inhibition by the C7-SAHA analogues and SAHA using HeLa cell lysates 83





LIST OF FIGURES

Figure 1.1 – Epigenetic mechanisms1
Figure 1.2 – The equilibrium activities of histone acetyltransferase (HAT) and deacetylase (HDAC)2
Figure 1.3 – Structures of metal ion-dependent HDAC inhibitors5
Figure 1.4 – Structure of SAHA bound to an HDAC-like protein6
Figure 1.5 –Structure Activity Relationship (SAR) Studies: HDAC inhibitors modified at the linker10
Figure 1.6 – SAHA analogues containing substituents on the C2, C3, C6, and C7 positions
Figure 1.7 – Known class-selective HDAC inhibitors with bulky group13
Figure 1.8 – Examples of SAHA analogues containing substituents on the linker area near the capping group and on the capping group15
Figure 1.9 – Structures of HDAC6-selective inhibitors17
Figure 1.10 – Structures of largazole and analogues
Figure 2.1 – Structures of SAHA analogues containing substituents on C2 and C3 position
Figure 2.2 – Screen of C3-SAHA analogues against HDAC1, HDAC3, and HDAC6
Figure 2.3 –HDAC Fluorescent activity assay45
Figure 3.1 – Structure of SAHA analogues containing substituents on the C6 position
Figure 3.2 – Initial screen of isoform selectivity of C6-SAHA analogues against HDAC1, HDAC3, and HDAC657
Figure 4.1 – Structure of SAHA analogues containing substituents on the C7 position



Figure 4.2 –	Screen of C7-SAHA analogues against HDAC1, HDAC3, and HDAC6	.85
Figure 4.3 –	HDAC inhibitors modified at the linker regions with two parallel	
	aligned aromatic groups	.87
Figure 4.4 –	Structures of SAHA analogues containing substituents on the C4 and C5 position	.89



LIST OF SCHEMES

Scheme 2.1 – Initial synthesis of C3-SAHA analogues (<i>n</i> -butyl derivative 1a)26
Scheme 2.2 – Optimal synthesis of C3-SAHA analogues 1b - 1e
Scheme 3.1 – Initial synthesis of C6-SAHA analogues (methyl derivative 14a).51
Scheme 3.2 – Modified synthesis of C6-SAHA analogues 14b - 1de 52
Scheme 4.1 – Initial synthesis of C7-SAHA analogues 22a - 22c 77
Scheme 4.2 – Redesigned synthesis of C7-SAHA library for bulky groups80
Scheme 4.3 – Resigned and optimized synthesis of C7-SAHA pyridyl analogue 22d



CHAPTER 1 - INTRODUCTION

1.1 Gene expression by Histone Deacetylase (HDAC) proteins

The nucleosome is a unit of DNA packaged around a histone protein core (Figure 1.1).¹ The four core histone proteins (histone octomers, pink) are wrapped by the DNA double helix (gray), which form chromosomes (violet) through highly condensed nucleosomes. The nucleosomes carry epigenetically inherited information in the covalent modifications of the core histones. Covalent modifications of lysine residues located on histone N-terminal tails alter gene expression.



Figure 1.1 Epigenetic mechanisms.¹ Histone octomers (pink), DNA double stand (gray), and chromosomes (violet). *Reused with permission*



Among the covalent modifications, the acetylation status of histone lysines histone is governed bv deacetylase (HDAC) proteins and histone acetyltransferase (HAT) proteins and is in equilibrium (Figure 1.2). HDAC and HAT proteins are two key enzymes that regulate gene transcription. The neutral, acetylated lysine allows DNA to interact with transcription factors to promote gene expression. Deacetylated positively charged lysine residues interact with the negatively charged phosphate backbone of DNA. The tight electrostatic interaction between the additional lysine residues and the negatively charged DNA backbone prevents activation with gene transcription. The overexpression of HDAC proteins shifts the equilibrium to the unmodified state and results in aberrant transcription in some cancer cells.² More specifically, overexpression of HDAC proteins induces repression of transcription and alteration in the accessibility of genes to transcriptional proteins causes reduced gene expression. Since decreasing gene expression can cause a variety of diseases, including cancers, the family of HDAC proteins has been studied.







2

1.2 HDAC protein family

The HDAC protein family consists of 18 members and is divided into four classes based on size, cellular localization, number of catalytic active site, and homology to yeast HDAC protein (Table 1.1).³ Class I includes HDAC1, HDAC2, HDAC3, and HDAC8. Class II includes HDAC4, HDAC5, HDAC6, HDAC7, HDAC9, and HDAC10. Class IV includes HDAC11 as the sole member because it displays similarities to both class I and II. Class III are NAD⁺-dependent proteins, referred to as sirtuins (SIRT 1-7).⁴ Class I, II, and IV are metal ion-dependant proteins and are sensitive to the inhibitors in this dissertation.

	NAD ⁺ -dependent		
Class I	Class II	Class IV	Class III
HDAC1	HDAC4	HDAC11	SIRT (1-7)
HDAC2	HDAC5		
HDAC3	HDAC6		
HDAC8	HDAC7		
	HDAC9		
	HDAC10		

Γable	1.1.	HDAC	family
-------	------	------	--------

Class I HDAC proteins (HDACs) are found in cancers, including ovarian (HDAC1, 2, and 3),⁵ gastric (HDAC2),⁶ and lung cancers (HDAC1 and HDAC3).⁷ Class I HDACs are produced at higher levels in ovarian cancers compared to normal ovarian tissues, as assessed using small interfering RNA methodology.⁵ Strong expression of HDAC2 was found in 44 out of a total of 71 gastric tumors.⁶ HDAC3 is elevated in 92% of squamous cell lung carcinomas, as assessed using



3

immunoblot analysis.⁷ HDAC8 is involved in acute myeloid leukemia (AML).⁸ A common form of AML results from an abnormal fusion protein, Inv1, that binds HDAC 8. Overexpression of class II HDAC6 is observed in breast and ovarian cancer tissues.⁹ Cell motility was increased by transfecting at HDAC6 expression plasmid into the breast cancer MCF-7 cells. Class II HDAC 10 protein is involved in the formation of tumors of skeletal muscle.¹⁰ HDAC10 was detected at the highest level in the skeletal muscle tumor SJRH30 rhabdomyosarcoma cell line. The different activities that connect each HDAC isoform with cancer formation have been given significant attention on the pharmaceutical and carcinoma studies.^{5, 9}

Even though each individual HDAC protein is involved in the formation of cancers, the role of each isoform in carcinogenesis is not clear yet. Therefore, elucidating the molecular mechanism connecting the HDAC activity of each isoform to cancer formation would facilitate studies that lead to treatment of diseases. To comprehensively understand the role of individual HDAC proteins in the growth and progression of cancer, development of selective HDAC inhibitors is required.

1.3 HDAC inhibitors

New approaches towards studying the causes and treatments of cancer have been rigorously studied since cancers are one of major causes of death in the United States. With a role in cancer, several HDAC inhibitor drugs are in clinical trials for treatment of cancer.¹¹ Specifically, suberoyl anilide hydroxamic acid (SAHA, Vorinostat) was the first HDAC inhibitor approved by the Food and



Drug Administration (FDA) for treatment of cutaneous T-cell lymphoma (CTCL).¹² Another recent FDA-approved HDAC inhibitor is depsipeptide (romidepsin, FK228), also for treatment for CTCL.¹³ Currently, most HDAC inhibitors are paninhibitors, which similarly inhibit all HDAC proteins. Therefore, developing selective inhibitors would aid studies connecting HDAC activity to cancer formation.

Most metal ion-dependent HDAC inhibitors, including SAHA, have a similar structure construction consisting of a capping group that is solvent-exposed, a carbon linker that is surrounded by a hydrophobic tunnel, and a metal binding moiety that is buried in the protein active site (Figure 1.3).





The crystal structure of SAHA bound in the active site of a bacterial homologue support that the SAHA anilide capping group is solvent-exposed near amino acids at the entrance of the active site, the linker positions in the hydrophobic channel, and the hydroxamic acid is located near the zinc atom at bottom of the active site (Figure 1.4). However, slight differences in the active sites of the human HDAC isoforms are not known in detail because limited crystallographic analysis is only available for HDAC2,¹⁴ HDAC3,¹⁵ HDAC4,¹⁶



HDAC7 and HDAC8.¹⁷ Therefore, design of isoform-selective HDAC inhibitors that inhibit only related HDAC proteins is challenging.



Figure 1.4. Structure of SAHA bound to an HDAC-like protein.¹⁸ *Reused with permission*.

1.4 Inhibitor selectivity

Currently, most HDAC inhibitors, including SAHA, nonspecifically inhibit all eleven metal ion-dependent HDAC proteins. As a promising hypothesis, the non-selective HDAC inhibitors might cause cancer patients in the clinic to suffer from the side effects, such as fatigue, anorexia, diarrhea, and cardiac arrhythmia.¹⁹ The clinical toxicity of selective inhibitors is unknown because there is no HDAC isoform selective inhibitor at present. In addition, the similarity in the active sites of the isoforms has challenged inhibitor design.²⁰ Elucidating the relationship between inhibitor selectivity and clinical toxicity might not only help understand



the role of the HDAC isoform function, but also contribute to the development of chemotherapies with fewer side effects for cancer patients.

1.5 Rationale for the synthesis of SAHA analogues containing substituents on the carbon linker

Towards creating isoform selective inhibitors, the structural regions of HDAC inhibitors have been studied. Particularly, the capping region and metal binding moiety have been extensively modified.²¹ The influence of substituents on the linker region is relatively less studied, although the hydrocarbon linker has been investigated, such as varying chain length, producing points of unsaturated chain, and adding an aryl or cyclohexyl ring.²² However, MS-275, which displays selectivity for class I²³, contains an aryl ring in the linker region (Figure 1.3). The intra-chain aryl group structure of MS-275 suggests that selectivity may be influenced by the structure of the linker region. We designed structure activity relationship (SAR) studies of SAHA to investigate the role of the linker on inhibitory activity and selectivity. Moreover, synthesis of a library of SAHA analogs would be simple through only several steps since SAHA can be synthesized in three steps.^{21c} With these advantages, SAHA analogue libraries and SAR studies led us to explore the impact of substituents in the linker region.

1.6 Specific aims

Our goal is syntheses of SAHA analogues with substituents on the linker region. First of all, small molecule libraries of SAHA analogues would elucidate the structural requirements of potent HDAC inhibitors. Second, developing novel isoform or class selective inhibitors would be explored by testing the selectivity of



the SAHA analogues. Third, screening small molecule analogues by using Fluor de Lys[™] activity assay (Enzo) would allow analyzing potency and selectivity, and exploiting veiled interaction between specific cancer formation and selectivity. The evaluation of these analogues will be helpful to improve chemotherapeutic drug design.

SAHA achieved the first FDA approval among HDAC inhibitors for cutaneous T-cell lymphoma (section 1.3). Cancer patients, however, are still suffering from side effects.¹⁹ Because side effects may be caused by the fact that SAHA is a pan inhibitor, the development of isoform or class-selective inhibitors would be critical to understand the relationship between toxicity and individual HDAC activity associated with cancer formation. Therefore, the development of selective inhibitors has been a significant aim for biological and pharmacological studies. Likewise, structure activity relationship (SAR) studies of small molecule HDAC inhibitors are required because only limited numbers of the selective inhibitors are reported. Therefore, our SAHA analogue syntheses and biological activity studies are a fitting starting point to design selective HDAC inhibitor and develop better chemotherapy with fewer side effects compared to current pan inhibitors.

1.7 Development of isoform or class-selective inhibitors

Presently, a minority of examples of SAHA analogues containing modifications on the carbon linker are reported, in spite of the promising area. For example, a few studies of the impact of substituents on the linker have



explored hydrophobic substituents (Figure 1.5).²⁴ No potency improvement was observed in ω -Alkoxy analogues A_a - A_d .^{24a} In contrast to the ω -Alkoxy analogues of SAHA, aminosuberoyl hydroxamic acid analogue Ae is slightly more potent than SAHA.^{24b} Furthermore, studies modifying the chain, such as alternating chain length and creating an unsaturated chain, were performed as HDAC inhibitors.^{22c, 25} None of the sulfonamides B_{a-d} (HDAC1 IC₅₀ 0.1-1 μ M) having different chain length and unsaturated chain displayed potency compared to highly potent HDAC inhibitors, such as trichostatin A (TSA, IC_{50} 0.005 μ M) and SAHA (HDAC1 IC₅₀ 0.096 µM).^{25a} However, when polyaminohydroxamic acid derivatives Ca, Cb were altered in the polyamine chain and terminal group, these analogues promoted increased level of acetylated histones H3, H4 and acetylated α -tubulin.^{25b} In case of **C**_a, the increased level of acetylated α -tubulin was significant while C_b had no effect on the acetylation status of α -tubulin. Despite the modest change in chain length, distinct differences compared to SAHA were observed. As examples of various aryl or cycloalkyl groups in the linker, N-hydroxycarboxamides possessing the 1,4-cylohexylene group D_a and 1.4-phenylene group D_b were synthesized and showed only modest activities (WST-1 IC₅₀ 77.9, 38.8 µM).^{20c} In summary, SAR series of SAHA with substituents have been modestly explored. As a result, in our exploratory studies of the impact of substituents on the linker, several libraries of SAHA analogues were synthesized on the 2, 3, 6, and 7 positions to explore potency and selectivity (Figure 1.6).





Figure 1.5. Structure Activity Relationship (SAR) Studies: HDAC inhibitors modified at the linker. The examples of substituents on the linker (left). The modification of chain length, creation of unsaturated chain, and alternation of aryl and cycloalkyl groups (right).





1.8 Preparation of SAHA analogues containing substituents on the linker near the hydroxamic acid

Since the metal binding site may be partially responsible for the potency of inhibitors, substituents on the SAHA linker area near hydroxamic acid were introduced. Our research group initially reported the synthesis and biological activity of C2-SAHA analogues to explore the impact of substituents near



hydroxamic acid.²⁶ HDAC inhibitory activities of C2-SAHA analogues were measured using in vitro fluorescence activity assay kit (Table 1.2).

Table 1.2. HDAC inhibition by SAHA, MS-275, and the C2-SAHA analogues using HeLa cell lysates

₩ N V V H			
C2-SAHA analogues			
s R	IC ₅₀ , μM ^a		
	0.090 ± 0.004		
	3.2 ± 0.1		
Methyl	134 ± 6		
Ethyl	449 ± 17		
<i>n</i> -Propyl	154 ± 7		
<i>n</i> -Butyl	72 ± 6		
<i>n</i> -Pentyl	40 ± 3		
<i>n</i> -Hexyl	60 ± 5		
Allyl	144 ± 9		
Propargyl	87 ± 5		
Benzyl	226 ± 11		
	C2-SAHA ani C2-SAHA ani R Methyl Ethyl <i>n</i> -Propyl <i>n</i> -Butyl <i>n</i> -Pentyl <i>n</i> -Hexyl Allyl Propargyl Benzyl		

^aValues are the mean of three experiments with standard error given.

The smallest compound, the methyl variant (IC_{50} 134 µM), displayed 1500 and 50-fold decreased inhibition compared to SAHA (IC_{50} 0.09 µM) and MS-275 (IC_{50} 134 µM). Even the most potent pentyl variant showed 439 and 12-fold decreased activity compared to SAHA and MS-275. Regardless of the substituent size, SAHA analogues modified on the C2 position displayed inhibition in the µM range. The high IC_{50} values of the C2-SAHA analogues indicate that only limited steric size is tolerated in the HDAC active site near the



hydroxamic acid. In other words, bulky substituents near the solvent exposed capping group might be more tolerated in the HDAC active site.

The tendency for significantly decreased inhibition due to substituents near the hydroxamic acid proposed designing potent inhibitors. Specifically, the poor inhibition of C2-SAHA analogues suggests that analogues with substituents positioned closer to the capping group on the C3 position might be more tolerated in the HDAC active site. However, we hypothesized that the inhibitory activity could be unpredictable because substituents on each linker position would have different impact in the HDAC active site channel. Besides, the substituents on the C3 position could favorably interact with HDAC active site since the 14 Å internal channel near the hydroxamic acid is nearer to C3 carbon linker than C2 carbon (Figure 1.4). Therefore, a library of C3-SAHA analogues would explore the interaction of the inhibitor with the HDAC active site for potent and selective inhibition. The detailed synthesis and biological activity of the library of C3-SAHA analogues are described in Chapter 2.

1.9 Preparation of SAHA analogues containing substituents on the linker near the capping group

Small molecules with substituents on the capping group or on the linker region near the capping group have shown great potency (nM range) and moderate selectivity (class-selectivity) (Figure 1.7).²⁷ Specifically, FK-228 (depsipeptide), which gained FDA approval for cutaneous T-cell lymphoma in 2009,²⁸ displayed about 300-fold greater potency for HDAC1 and HDAC2 over HDAC6.²⁹ Apicidin also displayed 17-230-fold greater potency for HDAC2, 3, and



8 over HDAC1, 4, 6, 7, and 9.³⁰ Trapoxin B showed HDAC1 selectivity over HDAC6.^{27c} The large capping groups in these HDAC inhibitors suggest that selectivity is influenced by the capping group substituents.



As an example of HDAC selective inhibitor SAR studies with bulky groups on the linker near the capping group, compound E_a (IC₅₀ 730 nM) containing the unusual *L*-Aoda amino acid was selected and modified (Table 1.3).³¹ The compounds contain a ketone motif, pentyl chain, and indole group instead of macrocycle. Although most of compounds lost 2-10 fold activity in the antiproliferation assay, the 3-piperid-1-ylpropanamide variant E_h demonstrated improved enzyme and cellular activities. As a result, this SAR study altering the substituents near the capping group demonstrates the structural requirement between inhibitor structures and HDAC functions and directs the design of specific cancer drugs.



Table 1.3. HDAC1 and PRO (HeLa) inhibition by SAHA, MS-275, Apicidin, the compound \mathbf{E}_{a} , and derivatives



Compounds	R	HDAC1 IC ₅₀ , nM	PRO (HeLa)IC ₅₀ , nM
SAHA		27	460
MS-275		110	1800
Apicidin		44	290
Ea		590	730
E _b	Ме	930	7600
Ec	S N	590	3000
Ed	S-N N	480	3400
E _e	Me	540	2500
E _f	NMe	200	1200
Eg	NMe	220	2000
E _h	N N	190	<390

Since selective inhibition could be influenced by bulky capping groups, SAHA analogues with large substituents on the capping group or on the linker



area near the capping group have been frequently designed, synthesized, and evaluated (Figure 1.8).^{24a, 32 33} Based on a docking analysis in the crystal structures of HDAC7 and HDAC8³⁴ of the ω -alkoxy analogue A_b, a T-shape arrangement between substituents near the SAHA capping group and the lipophilic pockets surrounded by phenylalanine (Phe) residues was found. A π - π interaction between the p-methoxybenzyl moleties and Phe208 and Phe152 residues in the HDAC active site might influence isoform selectivity. Although selective inhibition of the ω -alkoxy analogue was not improved, it had superior N^1 -hvdroxv- N^8 antiproliferative activity. On the other hand. ferrocenlyoctanediamide, JAHA, displayed picomolar inhibition against class IIa HDAC6 (IC₅₀ 8 pM) and anticancer action in intact cells (MCF7 cell line). Cytotoxicity against a breast cancer cell line indicated that SAHA is the most cytotoxic compound (IC₅₀ 730nM in MCF7 breast cancer cell lines) compared to the JAHA series (IC₅₀ 2-5µM in MCF7 breast cancer cell lines). The data suggest that the modification of SAHA with bulky groups improves selectivity with potency, but displays similar cytotoxicity against the cancer cell line to the parent compound in vivo.



Figure 1.8. Examples of SAHA analogues containing substituents on the linker area near the capping group (left) and on the capping group (right)



1.10 Novel HDAC6-selective inhibitors

We have discussed potential isoform or class-selective inhibitors, and common efficacious compounds targeting class I-selectivity.^{23a, 27c, 29-30} Fewer studies have focused on development of class II HDAC selective inhibitors. A recent cardiac study reported that stressed myocardium showed catalytic activity from the class IIb HDAC, HDAC6.³⁵ Also, overexpression of HDAC6 was detected in ovarian and breast cancer tissues.⁹ Since HDAC6 contains two catalytic sites, development and design of HDAC6 selective inhibitor would elucidate the function and mechanism of HDAC6. Tubacin is a well-known HDAC6 selective inhibitor and displayed 4-fold greater potency for HDAC6 over HDAC1 (Figure 1.9).³⁶ Interestingly, the structure of tubacin has similarity with class I selective SAHA analogues with bulky substituents at the capping group. Slightly different modification on the capping group critically effects selectivity. The recent SAR studies of Tubastatin A showed improved selectivity (Figure 1.9).³⁷ Tubastatin A displayed greater than 1000-fold selectivity against HDAC6 (IC₅₀ 15 nM) compared to HDAC1 (16 µM). An extensive library of tubastatin A indicated that tricyclic compounds displayed highly selective inhibition compared to other compounds. The structure of Tubastatin A motivates designing new isoform selective inhibitors. A detailed discussion of tricyclic compounds will be discussed in Chapter 4.



16



Figure 1.9. Structures of HDAC6-selective inhibitors

1.11 Evaluation of SAHA analogues containing substituents on the linker near the hydroxamic acid and capping group

Our initial syntheses of libraries of SAHA analogues on the C2 and C3 position was achieved with substituents containing hydrophobic groups since the carbon linker region of SAHA is surrounded by hydrophobic channel (Figure 1.4). The data showed that only limited tolerance exists in the HDAC active site near the metal binding moiety. In contrast, small molecules with large bulky groups have been synthesized near or on the capping group, leading to potent inhibitors.^{21b, 37-38} The outcome suggests that the area near the capping group of HDAC inhibitors has great tolerance of steric bulky group in the HDAC active sites, confirming our hypothesis. Therefore, our syntheses of libraries of C6 and C7-SAHA analogues have introduced bulky substituents near the capping group (Chapter 3 and 4). Moreover, the substituents of the SAHA analogues on the C7 position, which is located closest to the capping group, might allow monitoring the interactions between hydrophilic substituents and the HDAC active sites



since the substituents would be placed on the entrance of the solvent exposed area.

1.12 Structure activity relationship (SAR) studies from matrix metalloproteinases (MMP), another hydroxamic acid binding protein

Several series of hydrophilic substituents were attached to small molecule inhibitors for improving anti-cancer drugs. Natural or medicinal compounds containing nitrogen have been designed and used in clinical studies or treatments of various diseases because of their outstanding chemical and biological activities. For instance, the matrix metalloproteinases (MMPs), like HDACs, are relevant enzymes involved in physiologically important processes.³⁹ Both MMP and HDAC protein are zinc-including metalloproteinases, which favorably interact with the hydroxamic acid moiety. Structural information on MMPs is related to HDACs because of their relationship as metal-dependent proteases. Since proteolysis of the extracellular matrix is found in numerous arthritis and cancers⁴⁰, several MMP inhibitors as therapeutics were discovered and modified. Even though HDAC and MMP proteins have similar proteases activities, SAR studies of MMP inhibitors with substituents containing nitrogen have been more explored than with HDAC inhibitors.



18

		IC ₅₀ , nM					
	R	MMP1	MMP2	MMP3	MMP9	MMP13	
(i)	F _a	51	0.7	1.6	0.2	0.5	
	N H						
	F _b	20	1.2	2.2	0.2	1.1	
	N N N H						
	Fc	nt	0.30	nt	0.01	nt	
	N H						
	Fd	nt	2.3	3.7	0.5	4.5	
	N H						
	F _e	39	0.4	1.1	0.2	0.4	
	N N H						
	F _f	nt	8.82	nt	1.88	nt	

 Table 1.4.
 Collagenase 1 (MMP1), gelatinase-A (MMP2), stromelysin 1 (MMP3), gelatinase-B (MMP9), collagenase 3 (MMP13) inhibition by *N*-aryl sulfonyl homocysteine hydroxamate analogues



As one fruitful example, the design, synthesis, and evaluation of MMP inhibitors were studied with *N*-aryl sulfonyl homocysteine hydroxamate inhibitors (Table 1.4).⁴¹The data showed that hydrophobic aryl groups significantly influenced potency. The dipyridyl methyl amide analogue F_e displayed similar potency to the monopyridyl analogue F_b while the additional cyclohexyl analogue F_f lost potent activity compared to the single cyclohexyl analogue F_c . On the other hand, both monopyridyl F_b and dipyridyl F_e analogues displayed greater than 20-fold selectivity against MMP2, MMP3, MMP9, and MMP13 compared to MMP1. The polarity of the pyridyl derivatives containing nitrogen might be a significant factor for MMP selectivity.

As another representative example, MMP pyridyl derivatives enhanced biological inhibitory activity (Table 1.5). Compounds H_a , H_b , and J_b displayed poor potency, while inactivity was observed in compounds H_c , I, and J_a . On the other hand, the pyridyl group on compound J_b lead to great potency with the selective inhibitory activity for MMP9 (IC₅₀ 83 nM) against MMP1 (IC₅₀ 15000 nM). The aliphatic substituents on compound H_a and H_b lead to greater inhibitory activity compared to analogues with the hydrophilic substituents (H_c , I, and J_a). Despite the hydrophilicity of pyridyl group, the favorable interaction of the pyridyl derivative with MM9 specified that the nitrogen atom may impart selectivity.



		NHOH NHOH			-O-Ph			
	l: Ar= -Ph-O	-Ph	Ja : Ar= -F Jb : Ar= -	Ja: Ar= -Ph-O-Ph Jb : Ar= -3-pyridyl				
Compounds			IC ₅₀ , nM					
	MMP1	MMP2	MMP3	MMP9	MMP13			
G	104	0.7	0.7	2.5	12			
H _a	>10 000	617	213	184	380			
H _b	26 400	259	595	203	231			
H _c	>100 000	15 000	10 000	4 770	8 775			
I.	56 000	98 000	>100 000	>100 000	>100 000			
Ja	50 000	3 600	2 000	500	>100 000			
J_{b}	15 000	237	164	83	300			

 Table 1.5.
 Collagenase 1 (MMP1), gelatinase-A (MMP2), stromelysin 1 (MMP3), gelatinase-B (MMP9), collagenase 3 (MMP13) inhibition by *N*-arylsulfonylaziridine hydroxamic acid analogues

1.13 Evaluation of a pyridyl substituent on an HDAC inhibitor, Largazole

As the most recent example of the enhanced biological activity of an HDAC inhibitor containing nitrogen, natural product largazole analogues were reported with significant bioactivity (Figure 1.10).⁴² Largazole was isolated from a marine cyanobacterium of the genus *Symploca* and showed selective activity against transformed human mammary epithelial cells (MDA-MB-231, GI₅₀ 7.7 nM) over nontransformed murine mammary epithelial cells (NMuMG, GI₅₀ 122 nM).⁴³ Also, the selectivity was displayed against transformed fibroblastic



osteosarcoma cells (U2OS, GI_{50} 55 nM) over nontransformed fibroblasts (NIH3T3, GI_{50} 480 nM). Analogues K_a and K_b showed significantly increased inhibitory activities for HDAC1 over HDAC6 (80%) while the parent compound (largazole) and analogue K_c displayed modest selective inhibition. Investigation of potential selective inhibitors has been an attractive target for chemists and biologists since specific isoforms might offer opportunities to develop selective anti-cancer drugs. With the biological activity trend, a compound containing a pyridyl group was synthesized, screened, and discussed in our research (Chapter 4).



Figure 1.10. Structures of largazole and analogues



Currently, SAHA and the other candidates inhibit multiple HDAC members. However, isoform-specific HDAC inhibitors are promising targets with respect to clinical efficacy due to the fact that broad-spectrum inhibitors have demonstrated toxicities in the clinic.⁴⁴ The mechanism of relative action between the selectivity and toxicity of HDAC inhibitors in the clinic is not well-defined, but might reveal new mechanism-based therapeutics for cancers. Therefore, several studies have reported a link among different HDAC family members, specific tumor characteristics, and reduced toxicity profiles.⁴⁵ Specifically, HDAC inhibitor cytotoxicities of pediatric acute myeloid leukemia (AML) cell lines were tested by usina MTT (3-[4,5-dimethyl-thiazol-2-yl]-2,5-diphenylterazolium-bromide) assays.^{45e} At clinically practicable concentrations, dual HDAC inhibitors that inhibited both HDAC1 and HDAC6 displayed the best anti-leukemic activities in the four pediatric AML cell lines (THP-1, CMS, Kasumi-1, and MV4-11). As mentioned earlier, pre-clinical evaluation of HDAC6-selective inhibitors was highlighted in cardiovascular disease.³⁵ Furthermore, investigating HDAC inhibitors with hydrophilic substituents including a pyridyl group might enhance selective inhibition compared to common pan inhibitors. Even though the function or regulation of individual HDAC proteins is still not clear, the development of the specific-isoform HDAC protein inhibitors will lead optimal drugs for a variety of specific diseases.



CHAPTER 2 – SYNTHESIS OF SAHA ANALOGUES MODIFIED AT THE C3 POSITION

2.1 Rationale for design of the SAHA analogues containing substituents on the C3 position

Inhibitor binding to a zinc atom at the bottom of the active site plays a critical role in potency. Therefore, introducing substituents near hydroxamic acid would help understand structural requirements of HDAC inhibitors. The SAR study of SAHA on the linker area is relatively unexplored, in spite of it is being a fruitful potential area (Chapter 1.5). Especially, there is the possibility to develop isoform selective inhibitors through designing a library of SAHA analogues on the linker. When SAHA is present in HDAC active site, it has been observed that the linker is tightly surrounded by a hydrophobic tunnel (Figure 1.4). We theorized that hydrophobic substituents attached at the linker would display better interaction with the HDAC active site than hydrophilic substituents.

To explore the impact of substituents in the liker area, we previously studied SAHA analogues with hydrophobic substituents attached on the C2 position (Figure 2.1).²⁶ In this case, inhibitor potency was significantly reduced regardless of substituent size. The lack of potency of the C2-SAHA analogues indicates that limited flexibility exists in the HDAC active site near the hydroxamic



acid group. In contrast, high potency (nM range) HDAC

Figure 2.1. Structures of SAHA analogues containing substituents on the C2 and C3 position


inhibitors have been created with bulky substituent near the solvent-exposed region.^{27c, 31, 46} Therefore, we proposed that HDAC proteins would be more tolerant of SAHA analogues containing substituents positioned closer to the solvent exposed surface.

To systematically probe the impact of substituents present in the linker, SAHA analogues with substituents on the C3 position were synthesized (Figure 2.1).⁴⁷ We theorized that analogues with substituents attached at the C3 position would display more potent inhibition compared to analogues with C2 substituents due to their location closer to the solvent-exposed region.

2.2 Initial synthesis

We initially synthesized the C3-SAHA *n*-butyl analogue **1a**, as shown Scheme 1. The ring of commercially available ε -caprolactone **2** was opened with aniline and trimethyl aluminum to give alcohol **3**, which was subjected to Swern oxidation to give aldehyde **4**. The Horner-Wadsworth-Emmons reaction with trimethyl phosphonoacetate gave the corresponding α , β -unsturated ester **5**. The (E) and (Z)-isomers of ester **5** were separated by column chromatography and then individually treated with a copper (I) bromide dimethylsulfide complex to give the *n*-butyl ester **6a**. Saponification of **6a** gave carboxylic acid **7**, which was coupled with *O*-benzyl-protected hydroxamine. *O*-benzyl-protected hydroxamic acid **8** was deprotected by hydrogenolysis to give the C3-*n*-butyl SAHA **1a**.





Scheme 2.1. Initial synthesis of C3-SAHA analogue (*n*-butyl derivative 1a)

2.3 Optimized synthesis

To create the remaining C3-SAHA analogues, several aspects of the synthesis were improved (Scheme 2.2).



Scheme 2.2. Optimized synthesis of C3-SAHA analogues 1d -1e



First, the 1,4-conjugate addition reaction (5 to 6) was performed using a mixture of (E) and (Z) isomers without the separation. Second, we found that when preparing compound **6e** from methyl lithium, no addition product was observed. However, addition of trimethylsilane chloride (TMSCI) to the reaction gave excellent yield.⁴⁸ With this success, TMSCI was included in the addition reaction with all remaining analogues. Finally, we used a direct, one-step conversion of ester 6 to the final product 1. In the synthesis of C3-n-butyl SAHA 1a, a benzyl-protected hydroxamic acid intermediate 8 was used en route to the hydroxamic acid final product, as previously reported (Scheme 1).²⁶ However, 40% yield after three steps (saponification, coupling O-benzyl hydroxylamine, and benzyl deprotection) was unsatisfying. The direct conversion using neutralized hydroxylamine in methanol was more efficient compared to the threestep conversion and was employed for all remaining analogues (1b-1e). Using theses modified conditions, the phenyl, ethyl, vinyl, and methyl analogues **1b-1e** were synthesized (Scheme 2.2).

2.4 Biological analysis

The inhibitory activities of the C3-SAHA were measured using Fluor de LysTM *in vitro* fluorescence activity assay kit (Biomol) using HeLA cell lysates as the source of HDAC activity by Dr. Sujith Weerasinghe (Table 2.1).²⁶

The methyl variant **1e** was the most potent analogue, displaying an IC_{50} of 350 nM, which is only 4-fold less potent than SAHA (90 nM). Theses results indicate that the active site of HDAC proteins can accommodate a small methyl



substituent at the C3 position. The potency of the remaining analogues decreased with increasing size of the C3 substituent. The *n*-butyl and phenyl analogues (**1a** and **1b**) displayed the weakest inhibitory activity (184 μ M and 73 μ M, respectively). Interestingly, the ethyl-substituted analogue **1c** displayed 91-fold decreased activity compared to the methyl analogue **1e**, despite containing only one additional methylene. Likewise, the vinyl analogue **1d** showed significantly reduce activity compared to the methyl analogue **1e**. In total, the data indicated that a C3-methyl substituted SAHA analogue maintains nM potency, but substituents larger than methyl result in a reduction in potency.

 Table 2.1. HDAC inhibition by SAHA, MS-275, and the C3-SAHA analogues using HeLa cell lysates

Compounds	R	IC ₅₀ , μMª	
SAHA		0.090 ± 0.004	
MS-275		$\textbf{3.2}\pm\textbf{0.1}$	
1a	<i>n</i> -Butyl	184 ± 14	
1b	Phenyl	73 ± 14	
1c	Ethyl	32 ± 4	
1d	Vinyl	15 ± 1	
1e	Methyl	0.350 ± 0.05	

^aValues are the mean of three experiments with standard error given.

The inhibition results are consistent with the hypothesis that linker substituents are accommodated in the HDAC active site when positioned closer to the solvent exposed capping group of SAHA. While the C3-methyl analogue displayed potency comparable to SAHA (4-fold reduced), the previously reported



C2-methyl analogue (IC₅₀ of 134 μ M) displayed 1488-fold reduced activity versus SAHA.²⁶ Interestingly, the C3-*n*-butyl variant **1a** is less potent (184 μ M IC₅₀) than the previously reported C2-*n*-butyl analogue (72 μ M IC₅₀),²⁶ suggesting that the area of the HDAC active site near the C2 and C3 linker position displays structural differences.

We next tested the isoform selectivity of the C3-SAHA analogues. Creating isoform selective HDAC inhibitors has been challenging.²⁰ However, the availability of selective inhibitors would provide powerful chemical tools to dissect the individual functions of the HDAC isoforms, in addition to providing lead antitumor drug candidates. To assess the isoform selectivity of the C3-SAHA analogues, HDAC1 and HDAC3 representing class I and HDAC6 representing class II were tested at a single concentration near to their IC₅₀ values using the Fluor de LysTM kit (Figure 2.2). As expected, SAHA almost equally inhibited HDAC1, HDAC3, and HDAC6.³⁰ In contrast, the ethyl variant **1c** showed greater potency for HDAC6 over HDAC1 and HDAC3 at 32 μ M. The butyl, phenyl, and vinyl variants (**1a**, **1b**, and **1c**) also showed similar, although more modest, preference for HDAC6 over HDAC3.





Figure 2.2. Screen of C3-SAHA analogues against HDAC1, HDAC3, and HDAC6 with 125 nM SAHA, 32 µM 1a-d, and 375 nM 1e.

To more rigorously assess the selectivity observed in the initial screen, we determined the IC_{50} values of the C3-ethyl variant **1c** because it displayed the most promising results in the initial screen. The C3-ethyl analogue **1c** displayed 12-fold selectivity for HDAC6 over HDAC3 and 3-fold selectivity for HDAC6 over HDAC1 (Table 2.2). In addition, it displayed selectivity within class I, with 4-fold preference for HDAC1 over HDAC3. As a control, SAHA displayed similar inhibitor activity against the isoform, as expected (Table 2.2).³⁰ The isoform selectivity analysis shows that a substituent on the C3 position can transform SAHA from non-selective inhibitor to an HDAC6-selective one. As a comparison, the HDAC6-selective inhibitor tubacin displays 7-fold selectivity for HDAC6 over



HDAC1⁴⁹ and has been used widely in cell biology studies.⁵⁰ Therefore, the data indicate that isoform selective SAHA analogues can be generated by attaching a substituent to the linker chain.

Compound	IC ₅₀ /µM ^a			
	HDAC1	HDAC3	HDAC6	
SAHA	0.096 ± 0.016	0.146 ± 0.012	0.074 ± 0.009	
1c	22 ± 2	97 ± 6	8 ± 1	

Table 2.2. IC_{50} values of SAHA and the C3-ethyl SAHA variant 1c for HDAC1, HDAC3, and HDAC6

SAHA analogues with substituents on the C3 position displayed HDAC6selective inhibition, in contrast to the broad-spectrum inhibitor SAHA. These results reveal that small structural changes in the linker region of SAHA can significantly influence selectivity.

2.5 Experimentals

2.5.1 General methods

Starting materials, reagents, and solvents for reactions obtained from Acros, Sigma-Aldrich, and VWR were used as purchased. Moisture-sensitive reactions were performed under argon with dried glassware and dry solvent. Iron-sensitive reactions were performed with acid-washed glassware and were purified with silica gel that was washed with 6M aqueous hydrochloric acid through at least 3 times. Thin-layer chromatography with 60Å, 250µm Partisil® K6F fluorescent indicator plates was used to monitor reactions. Flash



chromatography was performed with 60 Å, 230-400 mesh silica gel (Whatman). Solvents were removed by rotary evaporation (Büchi Rotavapor R-114 and Büchi Waterbath B-480) and a vacuum pump (Welch Vaccum, Thomas Industries, Inc.). NMR spectra were recorded in CDCl₃ or CD₃OD using a Varian Unity 300 MHz or Varian L900 400 MHz. Mass spectrometric analysis was performed at Wayne State University's Central Instrumentation facility using a Waters LCT Premier XE ESI-LC-MS TOF or a Waters GCT EI-TOF. IR spectra were recorded in Jasco FT/IR – 4100. HPLC analysis was performed with a Waters 1525 Binary HPLC pump, Waters 2998 Photodiode Array detector, and a Symmetry® Reverse Phase C₁₈ 5µm column (4.6x150 mm Diameter) using a gradient of 10% Buffer A to 90% Buffer B over 20 min (Buffer A = water with 0.1% TFA; Buffer B = HPLC grade acetonitrile) at 1.0 mL/min at room temperature.

2.5.2 Experimental Procedures and Compound Characterization



5-Hydroxy-N-phenylpentanamide (3). Trimethyl aluminum (1.88 mL, 3.75 mmol) and aniline (0.34 mL, 3.75 mmol) were stepwise added to a solution of ε -caprolactone (0.28 mL, 2.5 mmol) in dry THF (25 mL) at 0°C. The mixture was stirred and warmed to room temperature over 3 h. The reaction mixture was quenched by a dropwise addition of 1.0 M aqueous hydrochloric acid until evolution of gas was not observed. The mixture was subsequently diluted with anhydrous diethyl ether (10 mL) and washed with distilled water (5 mL). The



aqueous layer was extracted with diethyl ether (10 mL) at least 3 times. The organic layer was dried over anhydrous Na₂SO₄, filtered, and concentrated. The residue was purified by column chromatography (20% acetone/CH₂Cl₂) on silica gel to give **3** (469 mg, 91%). ¹H-NMR (\bar{o} , ppm, CHLOROFORM-D): 1.41 (m, 2H), 1.58 (m, 2H), 1.71 (m, 2H), 2.39 (bs, 1H), 2.60 (m, 2H), 3.59 (m, 2H), 7.10 (t, 1H), 7.29 (t, 2H), 7.59 (d, 2H), 7.90 (bs, 1H); ¹³C-NMR (\bar{o} , ppm, CHLOROFORM-D): 25.8, 25.9, 32.1, 39.1, 61.9, 120.2, 124.1, 128.9, 138.8, 173.5; IR: 3298, 3136, 3063, 2936, 2863, 1663, 1599, 1544, 1498, 1442, 1309, 908, 730 cm⁻¹; HRMS (EI-TOF, *m/z*): found [M] 207.1259, calc. for C₁₂H₁₇NO₂, 207.1259.



6-Oxo-6-(phenylamino)hexanal (4). To a solution of DMSO (1.75 mL, 24.62 mmol) in CH₂Cl₂ (75 mL) was added oxalyl chloride (5.60 mL, 11.19 mmol) dropwise and then 5-hydroxy-N-phenylpentanamide 3 (1.55 g, 7.46 mmol) stepwise at -78°C. The reaction mixture was stirred for 45 min before triethylamine (TEA, 7.05 mL, 50.73 mmol) was added dropwise at -78 °C. The mixture was warmed to room temperature and stirred for an additional 1 h. The reaction mixture was guenched by adding distilled water (75 mL). The mixture was diluted with CH₂Cl₂ (25mL) and washed with 1.0 M aqueous hydrochloric acid (25 mL), an aqueous solution of saturated NaHCO₃ (100 mL), and brine (100 mL). The organic layer was dried over anhydrous Na_2SO_4 , filtered, and concentrated. The residue was purified by column chromatography (ether:petroleum ether 4:1) on silica gel to give **4** (1.25 g, 81%). ¹H-NMR (δ , ppm,



CHLOROFORM-D): 1.67-1.72 (m, 4H), 2.36 (t, 2H), 2.47 (t, 2H), 7.07 (t, 1H), 7.28 (t, 2H), 7.52 (d, 2H), 9.74 (bs, 1H); ¹³C-NMR (δ , ppm, CHLOROFORM-D): 21.7, 25.1, 37.4, 43.8, 120.2, 124.5, 129.2, 138.2, 171.3, 202.7; IR: 3305, 3198, 3140, 3059, 2940, 2866, 2826, 2726, 1721, 1664, 1599, 1543, 1498, 1442, 1310, 909, 730 cm⁻¹; HRMS (EI-TOF, *m*/*z*): found [M] 205.1106, calc. for C₁₂H₁₅NO₂, 205.1103.



8-Oxo-8-(phenylamino)-oct-2-enoate (5). To a solution of NaH (435 mg, 10.88 mmol) in THF (64 mL) was added trimethyl phosphonoacetate (1.6 mL, 10.88 mmol) dropwise at 0 °C and the mixture was stirred for 15 min. To the solution was added 6-oxo-6-(phenylamino)hexanal 4 (1.3 g, 6.40 mmol) at -78 °C and the mixture was stirred for 15 min. The mixture was allowed to warm to room temperature and stirred for an additional 1 h. The mixture was guenched by addition of an aqueous solution of saturated NH₄Cl until evolution of gas was not observed. The mixture was washed with distilled H_2O (64 mL) at least 3 times. The organic layer was dried over anhydrous Na₂SO₄, filtered, and concentrated. The residue was purified by column chromatography (ether:petroleum ether 2:3) on silica gel to give 5 (E-isomer; 1,136 mg, 68%, Z-isomer; 289mg, 17%). For preparation of butyl derivative **6a**, the E and Z isomers were used separately, as described below. For the other derivatives 6b-e, the E isomer alone or a mixture of E/Z isomers was used. Synthesis of the mixture of E/Z isomers was similar that of each isomer, except the following reagents were used: trimethyl



phosphonoacetate (391 mL, 2.57 mmol) in THF (15 mL), NaH (102 mg, 4.27 mmol) and 6-oxo-6-(phenylamino)hexanal **4** (310 mg, 1.51 mmol). The residue was purified by column chromatography (ether:petroleum ether 2:3) on silica gel to give **5 (E+Z)** (391 mg, 99%). (*Z*)-isomer ¹H-NMR (δ , ppm, CHLOROFORM-D): 1.54 (m, 2H), 1.76 (m, 2H), 2.38 (t, 2H), 2.68 (q, 2H), 3.71 (s, 3H), 5.79 (d, 1H, J=180 Hz), 6.24 (m, 1H), 7.09 (t, 1H), 7.29 (m, 2H), 7.51 (d, 2H), 7.64 (s, 1H); (E)-isomer ¹H-NMR (δ , ppm, CHLOROFORM-D): 1.54 (m, 2H), 1.76 (m, 2H), 3.71 (s, 3H), 5.82 (d, 1H, J=448 Hz), 6.94 (m, 1H), 7.08 (t, 1H) 7.27 (m, 2H), 7.49 (d, 2H); (E+Z)-isomer ¹³C-NMR (δ , ppm, CHLOROFORM-D): 25.3, 27.8, 32.2, 37.5, 51.7, 120.1, 121.5, 124.3, 129.2, 138.2, 149.2, 150.4, 167.4, 171.3; IR: 3674, 3308, 2950, 1721, 1658, 1600, 1541, 1498, 1441, 1310, 910, 756, 693 cm⁻¹; HRMS (EI-TOF, *m/z*): found [M] 261.1361, calc. for C₁₅H₁₉NO₃, 261.1365.



8-Oxo-8-(phenylamino)-3-*n***-butyloctanoate (6a).** To a solution of Cu(I)Br·SMe₂ (880 mg, 4.28 mmol) in THF (14.3 mL) was added *n*-butyl lithium (5.35 mL, 8.56 mmol) dropwise at -15 °C and the mixture was stirred for 20 min. The reaction mixture was cooled to -78 °C before addition of (Z)-8-oxo-8-(phenylamino)-oct-2enoate **5** (373 mg, 1.43 mmol, Z isomer only) at -78 °C. The reaction was stirred for 3 h at -78 °C to room temperature and then quenched by addition of 1.0 M



aqueous hydrochloric acid until a color of the mixture changed to blue (CuCl_{2(aq)}). The organic layer was dried over anhydrous Na_2SO_4 , filtered, and concentrated. The residue was purified by column chromatography (ether:petroleum ether 2:3) on silica gel to give **6a** (378 mg, 83% from the Z isomer). The synthesis starting from the E isomer of **5** was similar to that above except the following reagents were used: Cu(I)Br SMe₂ (470 mg, 2.28 mmol) in THF (11 mL), *n*-butyl lithium (2.85 mL, 4.56 mmol), and (E)-8-oxo-8-(phenylamino)-oct-2-enoate 5 (200 mg, 0.76 mmol, E isomer only) at -78 °C. Chromatography gave 6a (117 mg, 48% from the E isomer). ¹H-NMR (δ, ppm, CHLOROFORM-D): 0.87 (t, 3H), 1.24-1.32 (m, 10H), 1.70 (m, 2H), 1.84 (m, 1H), 2.21 (m, 2H), 2.33 (t, 2H), 3.65 (s, 3H), 7.07 (t, 1H), 7.29 (t, 2H), 7.51 (d, 2H), 7.62 (bs, 1H); ¹³C-NMR (δ, ppm, CHLOROFORM-D): 14.3, 23.1, 25.9, 26.1, 29.0, 33.5, 33.7, 35.0, 37.7, 39.1, 51.7, 120.0, 124.3, 129.1, 138.3, 171.7, 174.4; IR: 3303, 3197, 3137, 3059, 2928, 2857, 1737, 1662, 1600, 1542, 1499, 1441, 1309, 903, 755, 693 cm⁻¹; HRMS (EI-TOF, *m/z*): found [M] 319.2143, calc. for C₁₉H₂₉NO₃, 319.2147.



8-Oxo-8-(phenylamino)-3-phenyloctanoate (6b). To a solution of Cu(I)Br·SMe₂ (945 mg, 4.59 mmol) in THF (7.7 mL) was added phenyl lithium (4.59 mL, 9.19 mmol) dropwise at -15 °C and the mixture was stirred for 20 min. The reaction mixture was cooled to -78 °C. To the solution was added trimethylsilyl chloride (TMSCI, 1.76 mL, 13.78 mmol) dropwise and then 8-oxo-8-(phenylamino)-oct-2-



enoate 5 (200 mg, 0.77 mmol, only E isomer) stepwise at -78 °C. Only the E isomer of 5 was used because the presence of the Z isomer complicated purification. The mixture was stirred for 3 h at -78 °C and then guenched by addition of an aqueous solution of NH₄CI:NH₄OH (1:1) until a color of the mixture turned to blue $((NH_3)_4CuCl_{2(aq)})$. The mixture was washed with the aqueous solution of NH₄CI:NH₄OH (1:1) (7.7 mL). The organic layer was dried over anhydrous Na₂SO₄, filtered, and concentrated. The residue was purified by column chromatography (ether:petroleum ether 1:1) on silica gel to give 6b (154 mg, 59%). ¹H-NMR (δ, ppm, CHLOROFORM-D): 1.22 (m, 2H), 1.62-1.68 (m, 4H), 2.23 (m, 2H), 2.59 (m, 2H), 3.07 (m, 1H), 3.57 (s, 3H), 7.06 (t, 1H), 7.19 (m, 3H), 7.29 (m, 4H), 7.47 (d, 2H), 7.53 (bs, 1H); ¹³C-NMR (δ. ppm. CHLOROFORM-D): 25.6, 27.0, 35.8, 37.6, 41.8, 42.1, 51.8, 120.1, 124.4, 126.8, 127.6, 128.7, 129.1, 138.3, 144.0, 171.6, 173.2; IR: 3310, 3045, 2924, 2857, 1698, 1603, 1600, 1456, 1378, 1265, 910, 755, 735 cm⁻¹. HRMS (EI-TOF, *m/z*): found [M+Na] 362.1732, calc. for C₂₁H₂₅NO₃Na, 362.1732;



8-Oxo-8-(phenylamino)-3-ethyloctanoate (6c). The synthesis was similar that of **6b** except the following reagents were used: Cu(I)Br·SMe₂ (945 mg, 4.59 mmol) in THF (7.7 mL), ethyl lithium (5.41 mL, 9.19 mmol), TMSCI (1.76 mL, 13.78 mmol), and 8-oxo-8-(phenylamino)-oct-2-enoate **5** (200 mg, 0.77 mmol, E and Z mixture). The product was purified by column chromatography (ether:petroleum ether 1:1) on silica gel to give **6c** (215 mg, 96%). ¹H-NMR (δ ,



ppm, CHLOROFORM-D): 0.85 (t, 3H), 1.23-1.38 (m, 6H), 1.9 (m, 2H), 1.78 (m, 1H), 2.21 (m, 2H), 2.32 (t, 2H), 3.64 (s, 3H), 7.07 (t, 1H), 7.28 (t, 2H), 7.51 (d, 2H), 7.77 (bs, 1H); ¹³C-NMR (δ , ppm, CHLOROFORM-D): 11.0, 25.9, 26.2, 26.5, 33.1, 36.5, 37.7, 38.7, 51.7, 120.1, 124.3, 129.1, 138.4, 171.8, 174.4; IR: 3675, 3308, 3198, 3139, 3061, 2960, 2934, 1734, 1665, 1601, 1543, 1499, 1442, 1309, 911, 756, 733 cm⁻¹; HRMS (EI-TOF, *m/z*): found [M] 291.1830, calc. for $C_{17}H_{25}NO_3$, 291.1834.



8-Oxo-8-(phenylamino)-3-vinyloctanoate (6d). The synthesis was similar to that of **6b** except the following reagents were used: Cul (875 mg, 4.59 mmol) in THF (7.7 mL), vinyl magnesium bromide (6.56 mL, 4.59 mmol), TMSCI (1.76 mL, 13.78 mmol), and 8-oxo-8-(phenylamino)-oct-2-enoate **5** (200 mg, 0.77 mmol, only E isomer). Only the E isomer of **5** was used because the presence of the Z isomer complicated purification. The product was purified by column chromatography (ether:petroleum ether 1:1) on silica gel to give **6d** (191 mg, 86%). ¹H-NMR (δ, ppm, CHLOROFORM-D): 1.33 (m, 2H), 1.39 (m, 2H), 1.70 (m, 2H), 2.30-2.34 (m, 4H), 2.50 (m, 1H), 3.64 (s, 3H), 5.00 (m, 2H), 5.57 (m, 1H), 7.08 (t, 1H), 7.29 (t, 2H), 7.50 (d, 2H), 7.57 (bs, 1H); ¹³C-NMR (δ, ppm, CHLOROFORM-D): 25.6, 26.7, 34.1, 37.7, 40.1, 40.4, 51.7, 115.6, 120.0, 124.4, 129.2, 138.3, 140.9, 171.7, 173.3; IR: 3315, 3199, 3138, 3076, 2939, 2859, 1737, 1601, 1543, 1499, 1442, 1308, 915, 755 cm⁻¹; HRMS (EI-TOF, *m/z*): found [M] 312.1564, calc. for C₁₇H₂₃NO₃Na, 312.1576.





8-oxo-8-(phenylamino)-3-methyloctanoate (6e). The synthesis was similar that of **6b** except the following reagents were used: Cu(I)Br·SMe₂ (945 mg, 4.59 mmol) in THF (7.7 mL), methyl lithium (5.74 mL, 9.19 mmol), TMSCI (1.76 mL, 13.78 mmol) and 8-oxo-8-(phenylamino)-oct-2-enoate **5** (200 mg, 0.77 mmol, E and Z mixture). The residue was purified by column chromatography (ether:petroleum ether 2:3) on silica gel to give **6e** (232 mg, 99%). ¹H-NMR (δ, ppm, CHLOROFORM-D): 0.92 (d, 3H), 1.21-1.40 (m, 4H), 1.72 (m, 2H), 1.95 (m, 1H), 2.11-2.36 (m, 4H), 3.66 (s, 3H), 7.09 (t, 1H), 7.31 (t, 2H), 7.51 (d, 2H), 7.68 (bs, 1H); ¹³C-NMR (δ, ppm, CHLOROFORM-D): 19.9, 25.8, 26.6, 30.3, 36.3, 37.7, 41.7, 51.7, 120.0, 124.3, 129.2, 138.3, 171.7, 174.1; IR: 3305, 3197, 3137, 3060, 2931, 2859, 1738, 1662, 1600, 1539, 1499, 1442, 1309, 1008, 902, 756 cm⁻¹; HRMS (EI-TOF, *m*/z): found [M] 277.1678, calc. for C₁₆H₂₃NO₃, 277.1678.



3-*n***-Butyl-***N***¹-hydroxyl-***N***⁸-phenyloctanoic acid (7). To a solution of 8-oxo-8-(phenylamino)-3-***n***-butyloctanoate 6a** (492mg, 1.54mmol) was added NaOH (6.16 mL, 30.79 mmol) in MeOH (15 mL) and the mixture was refluxed overnight. The reaction was quenched by adding conc. aqueous hydrochloric acid (up to pH 6) and then extracting with H₂O (5 mL) and ethyl acetate (20 mL). The organic layer was dried over anhydrous Na₂SO₄, filtered, and concentrated. The residue



was purified by column chromatography (20% acetone/CH₂Cl₂) on silica gel to give **7** (189 mg, 40%). ¹H-NMR (δ , ppm, CHLOROFORM-D): 0.87 (t, 3H), 1.27-1.37 (m, 10H), 1.63 (m, 2H), 1.86 (m, 1H), 2.17-2.36 (m, 4H), 7.09 (t, 1H), 7.30 (t, 2H), 7.50 (d, 2H), 7.71 (bs, 1H); ¹³C-NMR (δ , ppm, CHLOROFORM-D): 14.3, 23.1, 25.9, 26.1, 29.0, 33.5, 33.7, 35.0, 37.7, 39.1, 120.2, 124.5, 129.1, 138.2, 172.1, 179.5; IR: 3306, 3195, 3137, 3060, 2928, 2858, 1705, 1662, 1599, 1543, 1499, 1442, 1309, 907, 755, 692 cm⁻¹; HRMS (EI-TOF, *m/z*): found [M] 305.1993, calc. for C₁₈H₂₇NO₃, 305.1991.



3-*n***-Butyl-***N***¹-benzyloxy-***N***⁸-phenyloctanediamide (8).** *O***-benzylhydroxylamine hydrochloride salt (144g, 0.9mmol) and Na₂CO₃ (47g, 0.45mmol) were dissolved in distill H₂O (9 mL), extracted with diethyl ether (9 mL) and concentrated. TBTU (289g, 0.9 mmol) and 3-***n***-butyl-***N***¹-hydroxyl-***N***⁸-phenyloctanoic acid 7** (189mg, 0.6mmol) were added to the neutralized O-benzylhydroxylamine residue in CH₃CN (6mL). The reaction mixture was stirred overnight at room temperature and then quenched by adding NaHCO₃ (6 mL). The mixture was extracted with H₂O and DCM (1:1). The organic layer was dried over anhydrous Na₂SO₄, filtered, and concentrated. The residue was purified by column chromatography (10% acetone/DCM) on silica gel to give **8** (121 mg, 49%). ¹H-NMR (δ , ppm, CHLOROFORM-D): 0.86 (t, 3H), 1.22-1.35 (m, 12H), 1.66 (m, 1H), 1.94 (m, 2H), 2.30 (m, 2H), 5.29 (s, 2H), 7.07 (t, 1H), 7.28 (m, 7H), 7.55 (d, 2H), 8.12 (bs, 1H);



¹³C-NMR (δ, ppm, CHLOROFORM-D): 14.3, 23.1, 25.3, 25.7, 29.1, 32.5, 33.7, 35.0, 37.2, 37.9, 78.4, 120.1, 124.3, 128.8, 129.1, 129.4, 138.5, 171.0, 172.3; IR: 3724, 3195, 3140, 3064, 2929, 2858, 1656, 1620, 1600, 1544, 1498, 1442, 1380, 1309, 1253, 1046, 1030, 975, 911, 734, 695 cm⁻¹; HRMS (EI-TOF, *m/z*): found [M] 410.2566, calc. for $C_{25}H_{34}N_2O_3$, 410.2569.



3-*n*-**Butyl**-*N*¹-hydroxyl-*N*⁶-phenyloctandiamide (1a). To a solution of 3-*n*-butyl-*N*¹-benzyloxy-*N*⁶-phenyloctanediamide **8** (121 mg, 0.3 mmol) in methanol (3mL) was added 20% Pd(OH)₂/C (32 mg, 0.03 mmol) in an acid-washed 25mL roundbottom flask and the reaction mixture was purged with H_{2 (g)} for 30 s. The reaction solution was stirred under H_{2 (g)} for 30 min and then filtered through a plug of Celite with MeOH (9 mL). The filtrate was concentrated to give **1a** (89 mg, 92%) as a clear oil. ¹H-NMR (δ , ppm, METHANOL-D4): 0.88 (t, 3H), 1.28-1.39 (m, 10H), 1.68 (m, 2H), 1.86 (m, 1H), 2.02 (d, 2H), 2.37 (t, 2H), 7.07 (t, 1H), 7.28 (t, 2H), 7.52 (d, 2H); ¹³C-NMR (δ , ppm, METHANOL-D4): 13.2, 22.8, 25.9, 28.6, 33.1, 33.2, 35.0, 36.7, 37.6, 120.1, 123.9, 128.6, 138.7, 171.4, 173.5; IR: 3384, 3044, 2929, 2858, 1640, 1600, 1546, 1499, 1468, 1309, 976, 903, 755, 693 cm⁻¹; HRMS (EI-TOF, *m/z*): found [M] 320.2108, calc. for C₁₈H₂₈N₂O₃, 320.2100; HPLC analytical purity analysis: 92%.





3-Phenyl- N^1 -hydroxyl- N^8 -phenyloctandiamide (1b). solution То а of NH₂OH·HCI (315 mg, 4.54 mmol) in methanol (4.5 mL) was added KOH (509 mg, 9.08 mmol) at 0 °C in an acid-washed 25mL round-bottom flask. After stirring for 20 min, 8-oxo-8-(phenylamino)-3-phenyloctanoate (6b) (154 mg, 0.45 mmol) was added and the mixture was stirred for 8 h at 0°C. The reaction mixture was quenched by adding 1mL of distilled water and adjusting to pH 6 by adding concentrated aqueous hydrochloric acid. The mixture was diluted with 30 mL of ethyl acetate, and washed with distilled water. The organic layer was dried over anhydrous Na₂SO₄, filtered and concentrated. The residue was purified by column chromatography (10% methanol/CH₂Cl₂) on acid-washed silica gel to give **1b** (48 mg, 31%). ¹H NMR (δ, ppm, METHANOL-D4): 1.22 (m, 2H), 1.55-1.73 (m, 4H), 2.25-2.43 (m, 4H), 3.09 (m, 1H), 7.06 (t, 1H), 7.12-7.29 (m, 7H), 7.47 (d, 2H); ¹³C-NMR (δ, ppm, METHANOL-D4): 25.6, 26.8, 35.4, 36.6, 40.2, 42.3, 120.1, 124.0, 126.4, 127.5, 128.3, 128.5, 138.6, 143.9, 170.1, 173.4; IR: 3256, 3030, 2932, 2860, 2559, 1646, 1600, 1545, 1499, 1468, 1442, 1420, 1372, 1310, 1253, 906, 758 cm⁻¹; HRMS (EI-TOF, *m/z*): found [M] 340.1789, calc. for C₂₀H₂₄N₂O₃, 340.1787; HPLC analytical purity analysis: 91%.



3-Ethyl-N¹-hydroxyl-N⁸-phenyloctandiamide (1c). A similar procedure to that for **1b** was used, except for the following reagents: NH₂OH·HCl (520 mg, 7.48 mmol) in methanol (7.4 mL), KOH (839 mg, 14.96 mmol), 8-oxo-8-(phenylamino)-3-ethyloctanoate **(6c)** (218 mg, 0.75 mmol) and stirring for 4 h. In this case, the product was purified by column chromatography (8 % methanol/CH₂Cl₂) on acid-washed silica gel to give **1c** (130 mg, 60%). ¹H-NMR (δ , ppm, METHANOL-D4): 0.88 (t, 3H), 1.28-1.41 (m, 6H), 1.68 (m, 2H), 1.81 (m, 1H), 2.01 (m, 2H), 2.36 (t, 2H), 7.07 (t, 1H), 7.28 (t, 2H), 7.52 (d, 2H); ¹³C-NMR (δ , ppm, METHANOL-D4): 9.8, 25.9, 32.6, 36.5, 36.7, 37.1, 120.1, 123.9, 128.6, 138.7, 171.4, 173.5; IR: 3857, 3404, 2935, 2862, 1649, 1600, 1544, 1501, 1469, 1311, 978, 904, 758, 691 cm⁻¹; HRMS (EI-TOF, *m*/*z*): found [M-H] 292.1718, calc. for C₁₆H₂₃N₂O₃, 292.1709; HPLC analytical purity analysis: 99%.



3-Vinyl-N¹-hydroxyl-N⁸-phenyloctandiamide (1d). A similar procedure to that for **1b** was used, except for the following reagents: NH₂OH·HCl (456 mg, 6.57 mmol) in methanol (6.6 mL), KOH (737 mg, 13.13 mmol), 8-oxo-8-(phenylamino)-3-vinyloctanoate **(6d)** (190 mg, 0.66 mmol), and stirring for 6 h. In this case, the product was purified by column chromatography (8 % methanol/CH₂Cl₂) on acid-washed silica gel to give **1d** (83 mg, 43%). ¹H-NMR (δ , ppm, METHANOL-D4): 1.33-1.47 (m, 4H),1.70 (m, 2H), 2.08 (m, 2H), 2.35 (t, 2H), 2.50 (m, 1H), 5.00 (q, 2H), 5.58 (m, 1H), 7.07 (t, 1H), 7.28 (t, 2H), 7.52 (d, 2H); ¹³C-NMR (δ , ppm,



METHANOL-D4): 25.6, 26.5, 33.9, 36.6, 38.3, 40.8, 115.0, 120.1, 124.0, 128.6, 138.7, 140.7, 170.3, 173.4; IR: 3299, 3079, 2931, 1647, 1600, 1542, 1500, 1442, 1312, 920, 758, 692 cm⁻¹; HRMS (EI-TOF, *m/z*): found [M+Na] 313.1533, calc. for $C_{16}H_{22}N_2O_3Na$, 313.1528; HPLC analytical purity analysis: 94%.



3-Methyl-*N*¹**-hydroxyl-***N*⁸**-phenyloctandiamide (1e).** A similar procedure to that for **1b** was used, except for the following reagents: NH₂OH·HCl (533 mg, 7.67 mmol) in methanol (7.7 mL), KOH (860 mg, 15.33 mmol), 8-oxo-8-(phenylamino)-3-methyloctanoate **(6e)** (213 mg, 0.77 mmol), and stirring for 2 h. In this case, the product was purified by column chromatography (10 % methanol/CH₂Cl₂) on acid-washed silica gel to give **1e** (160 mg, 75%). ¹H-NMR (δ , ppm, METHANOL-D4): 0.93 (d, 3H), 1.28 (m, 2H), 1.40 (m, 2H), 1.68 (m, 2H), 1.89 (m, 2H), 2.07 (m, 1H), 2.36 (t, 2H), 7.07 (t, 1H), 7.28 (t, 2H), 7.52 (d, 2H); ¹³C-NMR (δ , ppm, METHANOL-D4): 18.6, 25.8, 26.4, 30.4, 36.2, 36.7, 40.1, 120.1, 123.9, 128.6, 138.7, 171.1, 173.4; IR: 3198, 2927, 2855, 2359, 1657, 1598, 1544, 1499, 1443, 755, 691 cm⁻¹; HRMS (EI-TOF, *m*/*z*): found [M] 278.1635, calc. for C₁₅H₂₂N₂O₃, 278.1630; HPLC analytical purity analysis: 98%.



2.6 HDAC high-throughput assay

2.6.1 Fluorescence activity assay for libraries of SAHA analogues

A number of HDAC inhibitors have been attractive targets as chemotherapeutic drugs due to that the overexpression activity of HDAC, which leads malignant diseases, as discussed (Section 1.2). Our research is also focused on development of novel HDAC inhibitors based on SAHA. Therefore, SAHA analogues were screened compared to SAHA using a Fluorescence high-throughput assay. The deacetylase activity was measured using the Fluor de Lys® activity assay (Enzo) using the manufacturer's protocol(Figure 2.3).⁵¹



Figure 2.3. HDAC Fluorescent activity assay. Deacetylation of the substrate sensitizes to the developer.

To measure global HDAC inhibition, HeLa lysates, which contains a mixture of HDAC1-8 and HDAC10-11, were incubated with or without SAHA



analogues in HDAC assay buffer solution. After the initial incubation, Fluor de Lys® substrate in HDAC assay buffer was added to the reaction. The peptidic substrates consisted of an *ɛ*-acetylated lysine residue and a 4-methylcoumarin-7amide at the carboxy terminal unit. In the reaction catalyzed by HDACs, the acetylated lysine residue of the substrate was deacetylated, while acetylated lysine would remain in the reaction when inhibited by the SAHA analogues. To quench the reaction and allow color development, Fluor de Lys® developer was added to the reaction mixture. In this reaction, the only deacetylated peptidic lysine substrates containing the methylcoumarinamide were cleaved by trypsin to release the fluorescence molecule, methylcoumarin. In other word, the acetylated lysine substrate present when the reaction was inhibited by the SAHA analogues did not result in measurable cleavage by trypsin and did not release the fluorescence molecule (no fluorescence activity). As a result, the high level of deacetylated activity of the substrates indicated low inhibitory activity of the SAHA analogues. The fluorescence intensity was determined using a Geniosplus Fluorimeter (Tecan) with excitation at 360 nm and emission at 465 nm.

2.6.2 HDAC assay procedure

HDAC activity of the C3-SAHA analogues was measured using the Fluor de Lys[™] activity assay (Biomol) using the manufacturer's protocol by Dr. Sujith Weerasinghe. To measure global HDAC inhibition, HeLa lysates (approximately 4µg of total protein) were incubated with small molecule inhibitor or without small molecule inhibitor (2% DMSO) in HDAC assay buffer (50 mM Tris/Cl, pH 8.0, 137



mM NaCl, 2.7 mM KCl, 1 mM MgCl₂) at a final volume of 25 µL for 30 min at 30 °C with shaking. Concentrations of small molecule between 1 nM and 1 mM final concentration were used to determine IC_{50} values. Because the small molecules were stored in DMSO, dilution with HDAC buffer ensured that a maximum of 2% DMSO was present in the final reaction mixture. After the initial incubation, Fluor de LysTM substrate in HDAC assay buffer (100 µM final concentration) was added to make a total reaction volume of 50µL. The reaction mixture was incubated at 30°C for 45 min with shaking. To quench the reaction and allow color development, Fluor de LysTM developer (2.5 µL of 20X diluted up to 50 µL in HDAC assay buffer) was added to give a final 100 µL volume and incubated with shaking for 5 min at room temperature. The fluorescence intensity was determined using a Geniosplus Fluorimeter (Tecan) with excitation at 360 nm and emission at 465 nm.

To perform the isoform selectivity studies, the procedure was similar except that the HeLa cell lysates were replaced with 0.2 μ g HDAC1 (specific activity = 42.5 pmol/min/ μ g), 0.05 μ g HDAC3 (specific activity = 249 pmol/min/ μ g) or 0.25 μ g HDAC6 (specific activity = 257 pmol/min/ μ g), purchased from BPS Biosciences. In addition, the Fluor de LysTM substrate was used at a final concentration of 50 μ M for HDAC1 or 25 μ M for HDAC3 and HDAC6.

For each trial, a no enzyme control sample was used to assess the background. The background-corrected fluorescence units of small molecule-treated samples were then compared to that of untreated samples (set to 100%) to give a percentage deacetylase activity. IC_{50} values were obtained by plotting



the percentage deacetylase activity versus the small molecule concentration and fitting the data to a sigmoidal dose-response curve $(y=100/(1+(x/m3)^{m4}))$ using KaleidaGraph software where m1 is the IC₅₀ value in Molar units. All experiments were performed in triplicate with the mean and standard error reported in the tables and figures.



www.manaraa.com

CHAPTER 3 – SYNTHESIS OF SAHA ANALOGUES MODIFIED AT THE C6 POSITION

3.1 Rationale for design of SAHA analogues modified at the C6 position

A limited number of structure activity relationship (SAR) studies on the linker area of SAHA have been performed, even though the linker region might influence inhibitory activity and selectivity (Section 1.7). In fact, many number of inhibitors that have substituents on the linker have been discovered with great potency and selective inhibition when substituents were attached near or on the capping group (Section 1.9). Specifically, tubacin with a bulky substituent at the capping group has been used in pharmacokinetic and clinical studies (Figure 1.9). Also, based on data from previous C2 and C3-SAHA libraries^{26, 47}, substituents on the C6 position might lead to potent inhibitory activities because C6-SAHA substituents would be located close to the solvent-exposed region of the active site. As discussed in the chapter 2, the C3-SAHA ethyl analogue showed selective inhibition for HDAC6 over HDAC1 and HDAC3.⁴⁷ To expand our understanding of the impact of substituents, synthesis of C6-SAHA analogues with hydrophobic substituents was achieved because the carbon linker is surrounded by a hydrophobic tunnel.

NHOH

Figure 3.1. Structure of SAHA analogues containing substituents on the C6 position

The earlier results from the C2 and C3-SAHA libraries showed that the steric environment on the SAHA carbon linker caused reduced inhibitory activity, in



addition to influencing selective inhibition.^{26, 52} With the potential to improve selectivity, the C6-SAHA library (Figure 3.1) was synthesized. We proposed that the HDAC protein active site would not only be more tolerant of bulkier substituents on the C6 position near the solvent-exposed area but the C6-SAHA analogues would also display more selectivity compared to the C2 and C3-SAHA analogues based on the previous reports about several class-selective inhibitors with bulky substituents in the capping group region (Section 1.9).²⁰

3.2 Initial synthesis

To elucidate the impact of substituents present near the solvent-exposed area, C6-SAHA analogues were synthesized. Like C2 and C3-SAHA analogues (Chapter 1 and 2), we selected hydrophobic substituents since the carbon linker is surrounded by a hydrophobic tunnel (Figure 1.4). Also, we theorized that bulky analogues on the C6 position would display more potent inhibition compared to C2 and C3-SAHA analogues due to their proximity to the solvent-exposed surface.





Scheme 3.1. Initial synthesis of C6-SAHA analogue (methyl derivative 14a)

Initially, we synthesized the C6-SAHA methyl analogue **14a**, as outlined in Scheme 3.1. Due to symmetry compared to the C3-SAHA analogues, synthesis of the C6-SAHA analogues was straightforward and similar to that of the C3-SAHA library. The major differences between two syntheses are the following. Commercially available ε -caprolactone **2** was opened to give methyl 6-hydrohexanoate **9** under Fisher conditions instead of building the anilide derivative. The alcohol compound **9** was subjected to Swern oxidation to give aldehyde **10** similar to the C3-aldehyde formation. For the Horner-Wadsworth-Emmons reaction, using benzyl dimethyl phosphonoacetate instead of using trimethyl phosphonoacetate gave the corresponding α , β -unsturated benzyl ester **11** that allowed incorporation of substituents, which provided the precursor for anilide derivative **13a**. A mixture of (E) and (Z)-isomers of ester **11** were treated with a copper (I) iodide to give the methyl substituted ester **12a**. Similar to the



previous optimized synthesis of the C3-methyl SAHA analogue (Scheme 2) where the 1,4-addition demonstrated quantitative yield, the C6-methyl ester **12a** was synthesized and characterized without impurities according to thin layer chromatography (TLC) and ¹H & ¹³C NMR spectra analysis. Therefore, the methyl ester **12a** without purification was deprotected by hydrogenolysis and coupled with aniline in 53% yield (over the three steps). In contrast to the C3-SAHA library where the anilide derivative was installed at the beginning stage, the anilide **13a** was created from benzyl ester **12a** at a late stage, which attached substituents near the capping group. The methyl ester derivative **13a** was directly converted to the methyl hydroxamic acid **14a**.



3.3 Modified synthesis

Scheme 3.2. Modified synthesis of C6-SAHA analogue 14b - 14d

To create the remaining C6-SAHA analogues, first, purification by column chromatography was required after 1,4-addition since the mixture of (E) and (Z)



isomers **11** were unable to completely react to produce phenyl ester **12b**, as was observed with the methyl derivative **12a** (Scheme 3.2). Using the additional purification step after the 1,4-addition, the *t*-butyl ester **12c**, 2-ethylhexyl ester **12d**, and isopropyl ester **12e** were synthesized. The rest of syntheses for hydrogenolysis, coupling, and conversion to hydroxamic acid were similar to the methyl analogue synthesis. However, despite the purification, there was still remaining unsaturated ester **11** after 1, 4-addition for obtaining phenyl ester **12b** due to the similar polarity. The mixture of unsaturated ester **11** and phenyl ester **12b** were subjected to hydrogenolysis and coupling to give anilide **13b** and unsaturated anilide compound **13b**'. Fortunately, **14b** was completely purified after conversion to hydroxamic acid in 60% yield (over the four steps).

3.4 Biological analysis

The HDAC inhibitory activities of the C6-SAHA library were measured using the Fluor de Lys[®] *in vitro* fluorescence activity assay kit (Enzo). Unlike the C3-SAHA library, the C6-SAHA analogue biological activities were performed by Sun Ea Choi. The activities of the C6-SAHA compounds are summarized in Table 3.1. Interestingly, the planar phenyl variant **14b** was the most potent analogue displaying an IC₅₀ of 344 nM similar to the C3-methyl variant **1e** (IC₅₀ of 350 nM) and comparable to SAHA (4-fold reduced), IC₅₀ of 86 nM. This is in contrast to the C3-phenyl variant **1b** (IC₅₀ of 73000 nM), which displayed 811-fold reduced activity versus SAHA.⁵³ In addition, the smallest C6-methyl variant **14a** (IC₅₀ of 349 nM) displayed similar potency to the phenyl variant. These results indicate that the active site of HDAC proteins can accommodate a bulky



www.manaraa.com

substituent at the C6 position. Moreover, the longest analogues, the 2-ethylhexyl variant **14d**, still displayed potent inhibitory activity in the nM range. Likewise, the bulkiest substituent with three methyl groups at the α -carbon, the *t*-butyl variant **14c**, displayed only 20-fold reduced activity versus SAHA. In summary, the inhibition data show that most C6-SAHA analogues maintain nM potency, but substitution at the α -carbon decreases potent inhibitory activity.

	centysates	
Compounds	R	IC ₅₀ , nMª
SAHA		86 ± 4
MS-275		3200 ± 100
14a	Methyl	349 ± 20
14b	Phenyl	344 ± 40
14c	<i>t</i> -Butyl	1940 ± 300
14d	2-Ethylhexyl	456 ± 30

Table 3.1. HDAC inhibition by SAHA, MS-275, and the C6-SAHA analogues using HeLa

^aValues are the mean of at least three experiments with standard error given.

These results are consistent with the hypothesis that the active site of HDAC proteins accommodates large substituents near the solvent exposed area. As expected, one trend for the C6-SAHA analogues is that the increasing size of substituents has less influence on inhibitory activity compared to the C2 and C3-SAHA analogues.

As mentioned earlier, the presence of methyl groups at the α -carbon decreased inhibitory activity. We speculate that the *t*-butyl variant **14c** might display specific selectivity since the C3-ethyl variant **1c**, which contains an α -



methyl group, displayed selective inhibition for HDAC6 over HDAC1 and HDAC 3 and also showed significantly decreased inhibitory activity compared with the C3methyl variant **1e**. To explore the role of an α -methyl group on selectivity, synthesis of the isopropyl derivative would reveal the effect of α -carbon substituents. Another possibility is that the hybridization at the α -carbon might influence selectivity. For example, the C6-SAHA phenyl **14b** and methyl variant **14a** have sp² and sp³ orbital structures. The data might provide key structural information for binding site recognition. The long chain of the C6-SAHA 2-ethyl hexyl analogue **14d** might also affect isoform selectivity. To verify the influence of sterics on isoform selectivity, testing the isoform selectivity of C6-SAHA analogues is described. The results of the isoform selectivity of the C6-SAHA analogues are outlined in Figure 3.2.

The isoform selectivity of C6-SAHA analogues was tested with HDAC1 and HDAC3 representing class I and HDAC6 representing class II. To assess the isoform selectivity, all compounds were tested at a single concentration near to their IC_{50} values using the Fluor de Lys® kit (Figure 3.2). As observed from previous data, SAHA exhibited roughly equal inhibition against HDAC1, HDAC3, and HDAC6. The phenyl variant **14b**, which displayed the most potent inhibition among the C6-SAHA analogues with HeLa cell lysates, similarly inhibited HDAC1, HDAC3, and HDAC6 as well. In contrast, the methyl variant **14a** showed dual-preference for HDAC1 and HDAC3 over HDAC6 at 500 nM even though the methyl **14a** (IC_{50} of 349 nM) and phenyl variant **14b** (IC_{50} of 344 nM) displayed equal inhibition in the HeLa cell lysates. The difference between sp³ and sp²



orbital structures might affect selectivity but not potency. The 2-ethylhexyl variant 14d with an additional carbon chain displayed selectivity for HDAC3 over HDAC1 and HDAC6 compared to the methyl variant 14a. Similar to the methyl variant **14a** (IC₅₀ of 349 nM), the 2-ethylhexyl variant **14d** (IC₅₀ of 456 nM) imparted selectivity but not potency. However, the bulkiest analogue at the α -carbon position, t-butyl variant **14c**, displayed the opposite selectivity with preference for HDAC1 and HDAC6 over HDAC3. In this case, the α -carbon substituent lead to different interactions with each isoform HDAC active sites. The *t*-butyl substituent encouraged dual-selectivity toward HDAC1 and HDAC6 over HDAC3, while the inhibitory activity of *t*-butyl variant **14c** (IC₅₀ of 1.9 µM) showed 5-fold reduced activity compared to the 2-ethylhexyl variant **14d** (IC₅₀ of 456 nM) and 20-fold less potent than SAHA (IC₅₀ of 86 nM). In summary, the data indicated that the methyl, t-butyl, and 2-ethylhexyl variants (14a, 14c, and 14d) showed dissimilar preference for each isoform HDAC proteins despite parallel potency. The deacetylase activity of individual trial is summarized in Table C.5 in Appendix C.





Figure 3.2. Initial screen of isoform selectivity of C6-SAHA analogues against HDAC1, HDAC3, and HDAC6 with 125 nM SAHA, 500 nM **14a**, **b**, **d**, and 2 µM **14c**.

To more thoroughly assess the selectivity observed in the initial screen, we determined the HDAC1, HDAC3, and HDAC6 IC_{50} values of the C6-*t*-butyl variant **14c** because it showed the most potential to create a dual-selective inhibitor. The C6-*t*-butyl analogue **14c** displayed 6-fold greater potency for HDAC1 over HDAC3 and 2-fold greater potency for HDAC6 over HDAC3 (Table 3.2). In addition, it displayed selectivity within class I for HDAC1 over HDAC3. As a control, SAHA displayed non-selective inhibitor activity against the isoform, as expected (Table 3.2).³⁰ The selectivity analysis shows that a substituent on the C6 position can influence the selectivity of SAHA from non-selective inhibitor to a dual-selective HDAC1 and HDAC6 inhibitor. Furthermore, the C6-SAHA *t*-butyl



analogue displays an IC₅₀ value of 1.9 μ M in the lowmicromolar range, while the C3-SAHA ethyl analogue (HDAC6-selective inhibitor) displayed 16-fold decreasing potency (IC₅₀ of 32 μ M).⁴⁷ Therefore, the data indicate that attaching the *t*-butyl substituent to the linker chain on the C6 position may promote dual-selective inhibition as well as potency on SAHA.

Compound	IC ₅₀ /µM				
	HDAC1	HDAC3	HDAC6		
SAHA	0.096 ± 0.016	0.136 ± 11	0.074 ± 0.009		
14c	0.993 ± 0.061	5.4 ± 0.7	2.4 ± 0.5		

Table 3.2. IC_{50} values of SAHA and the C6-SAHA *t*-butyl variant 14c for HDAC1, HDAC3, and HDAC6

Specific selective HDAC inhibitors support pathological cardiac remodeling studies. For example, a recent cardiac study reported that stressed myocardium increased the catalytic activity of the class IIb HDAC, HDAC6.³⁵ Moreover, the best anti-leukemic activities in the four pediatric AML cell lines were observed by dual HDAC1 and HDAC6 inhibitors that inhibited both.^{45e}. The function or regulation of dual-selective HDAC inhibitors is not well informed in present even though dual-selective HDAC inhibitors might guide development of prospective drugs of anti-diverse diseases.

From the initial isoform selectivity screen (Figure 3.2), SAHA analogues with substituents on the C6 position displayed diverse selective inhibitions, such as class I selectivity (methyl **14a**), dual-class I, II selectivity (*t*-butyl **14c**), and isoform selectivity for HDAC3 (2-ethylhexyl **14d**). Our results reveal that small



structural changes in the C6 position linker region of SAHA can significantly influence selectivity with suitable potency.

3.5 Experimental

3.5.1 General methods

Additional details were shown in Section 2.5.1 of Chapter 2.

3.5.2 Experimental Procedures and Compound Characterization



Methyl 6-hydroxyhexanoate (9). Concentrated aqueous sulfuric acid (adjusted to pH 6 using neutral pH meter paper (pH 1 to pH 14 range) as assessed with) was dropwise added to a solution of *ε*–caprolactone (5.54 mL, 50 mmol) in MeOH (50 mL). The mixture was stirred for 20 min. The mixture was subsequently diluted with anhydrous diethyl ether (25 mL) and washed with distilled water (equal volume to organic layer). The aqueous layer was extracted with diethyl ether (equal volume to organic layer) at least 3 times. The combined organic layers were dried over anhydrous Na₂SO₄, filtered, and concentrated. The residue was purified by column chromatography (12% acetone/CH₂Cl₂) on silica gel to give **9** (7.23 g, 99%). ¹H-NMR (δ, ppm, CHLOROFORM-D): 1.30 (m, 2H), 1.50 (m, 2H), 1.56 (m, 2H), 2.24 (m, 2H), 2.59 (bs, 1H), 3.52 (m, 2H), 3.58 (s, 3H); ¹³C-NMR (δ, ppm, CHLOROFORM-D): 24.8, 25.5, 32.4, 34.1, 51.8, 62.5, 174.5; IR: 3424, 2940, 2866, 1738, 1438, 1205, 857, 744 cm⁻¹; HRMS (EI-TOF, *m/z*): found [M+Na] 169.0840, calc. for C₇H₁₄O₃, 169.0841.





1-Benzyl 8-methyl oct-2-enedioate (11). To a solution of DMSO (1.02 mL, 14.39 mmol) in CH₂Cl₂ (44 mL) was added 2 M oxalyl chloride in dichloromethane (3.27 mL, 6.54 mmol) dropwise and then methyl 6-hydroxyhexanoate **9** (0.638 g, 4.36 mmol) stepwise at -78°C. The reaction mixture was stirred for 45 min before triethylamine (TEA, 4.12 mL, 29.66 mmol)



was added dropwise at -78 °C. The mixture was warmed to room temperature and stirred for an additional 1 h. The reaction mixture was quenched by adding distilled water

(44 mL). The mixture was washed with 1.0 M aqueous hydrochloric acid (44 mL), an aqueous solution of saturated NaHCO₃ (44 mL), and brine (44 mL). The organic layer **10** was dried over anhydrous Na₂SO₄, filtered, and concentrated.

To a solution of NaH (0.513 g, 12.8 mmol) in THF (85 mL) was added benzyl dimethyl phosphonoacetate (3.31 g, 12.8 mmol) dropwise at 0 °C and the mixture was stirred for 15 min. To the solution was added crude methyl 6oxohexanoate **10** (1.23 g, 8.55 mmol) at -78 °C and the mixture was stirred for 15 min. The mixture was allowed to warm to room temperature and stirred for an additional 1 h. The mixture was quenched by addition of an aqueous solution of saturated NH₄Cl until evolution of gas was not observed. The mixture was washed with distilled H₂O (85 mL). The organic layer was collected and the aqueous layer was extracted with diethyl ether (equal volume to aqueous layer) at least 3 times. The combined organic layers were dried over anhydrous


Na₂SO₄, filtered, and concentrated. The residue was purified by column chromatography (diethyl ether: petroleum ether 1:6) on silica gel to give **11** (2.17 g, 92%). (E+Z)-isomer ¹H-NMR (δ, ppm, CHLOROFORM-D): 1.48 (m, 2H), 1.63 (m, 2H), 2.20 (q, 2H), 2.30 (t, 2H), 3.64 (s, 3H), 5.16 (s, 2H), 5.84 (d, 1H, J=180 Hz), 6.98 (m, 1H), 7.35 (m, 5H); ¹³C-NMR (δ, ppm, CHLOROFORM-D): 24.6, 27.6, 32.1, 33.9, 51.7, 66.2, 121.6, 128.3, 128.4, 128.8, 136.3, 149.5, 166.6, 174.0; IR: 3671, 2974, 1735, 1455, 1258, 1066, 907, 748, 698 cm⁻¹; HRMS (EI-TOF, *m/z*): found [M+Na] 299.1269, calc. for C₁₆H₂₀O₄Na, 299.1259.

61



1-Benzyl 8-methyl 3-methyloctanedioate (12a). To a solution of Cu(I)I (1.06 g, 5.57 mmol) in THF (19 mL) was added 1.6M methyllithium in diethyl ether (6.97 mL, 11.15 mmol) dropwise at -15 °C and the mixture was stirred for 20 min. The reaction mixture was cooled to -78 °C before addition of trimethylsilyl chloride (TMSCI, 4.25 mL, 33.48 mmol). To the reaction mixture was dropwise added 1-benzyl 8-methyl oct-2-enedioate **11** (513 mg, 1.86 mmol) at -78 °C. The reaction was stirred for 3 h at -78 °C to room temperature and then quenched by addition of 1.0 M aqueous hydrochloric acid until a color of the mixture changed to blue (CuCl_{2(aq)}). The organic layer was collected and the aqueous layer was extracted with diethyl ether (equal volume to aqueous layer) at least 3 times. The combined organic layers were dried over anhydrous Na₂SO₄, filtered, and concentrated. ¹H-NMR (δ, ppm, CHLOROFORM-D): 0.91 (d, 3H), 1.30 (m, 4H), 1.58 (m, 2H), 1.96



(m, 1H), 2.19 (q, 1H), 2.32 (m, 3H), 3.65 (s, 3H), 5.10 (s, 2H), 7.34 (m, 5H); ¹³C-NMR (δ, ppm, CHLOROFORM-D): 19.9, 25.2, 26.6, 30.4, 34.2, 36.4, 42.0, 51.7, 66.3, 128.4, 128.5, 128.8, 136.3, 173.2, 174.4; HRMS (EI-TOF, *m/z*): found [M+Na] 315.1569, calc. for C₁₇H₂₄O₄Na, 315.1572.



1-Benzyl 8-methyl 3-phenyloctanedioate (12b). To a solution of Cu(I)I (827 mg, 4.34 mmol) in THF (14.5 mL) was added phenyl lithium 2.0M (4.34 mL, 8.69 mmol) dropwise at -15 °C and the mixture was stirred for 20 min. The reaction mixture was cooled to -78 °C. To the solution was added trimethylsilyl chloride (TMSCI, 1.67 mL, 13.03 mmol) dropwise and then 1-benzyl 8-methyl oct-2-enedioate **11** (400 mg, 1.45 mmol) stepwise at -78 °C. The mixture was stirred for 3 h at -78 °C and then quenched by addition of an aqueous solution of saturated NH₄CI: saturated NH₄OH (1:1) until the color of the mixture turned to blue ((NH₃)₄CuCl_{2(aq)}). The mixture was washed with the aqueous solution of saturated NH₄CI: NH₄OH (1:1) (14.5 mL). The organic layer was collected and the aqueous layer was extracted with diethyl ether (equal volume to the aqueous layer). The combined organic layers were dried over anhydrous Na₂SO₄, filtered, and concentrated. The residue was purified by column chromatography (diethyl ether: petroleum ether 1:6) on silica gel to give **12b + 11** (3:1).





1-Benzyl 8-methyl 3-(*tert*-butyl)octanedioate (12c). The synthesis was similar that of 12b except the following reagents were used: Cu(I)I (827 mg, 4.34 mmol) in THF (10.9 mL), *tert*-butyllithium 1.6M (5.43 mL, 8.69 mmol), TMSCI (1.67 mL, 13.03 mmol), and 1-benzyl 8-methyl oct-2-enedioate 11 (300 mg, 1.09 mmol). The product was purified by column chromatography (diethyl ether: petroleum ether 1:6) on silica gel to give 12c (313 mg, 89%). ¹H-NMR (δ, ppm, CHLOROFORM-D): 0.84 (s, 9H), 1.05 (m, 1H), 1.17-1.35 (m, 2H), 1.47-1.62 (m, 3H), 1.68 (m, 1H), 2.10 (q, 1H), 2.23 (t, 2H), 2.41 (q, 1H), 3.64 (s, 3H), 5.09 (s, 2H), 7.34 (m, 5H); ¹³C-NMR (δ, ppm, CHLOROFORM-D): 25.5, 27.6, 28.5, 31.0, 33.8, 34.2, 36.3, 45.2, 51.6, 66.4, 128.4, 128.6, 128.7, 136.3, 174.3, 174.5; IR: 2952, 2869, 1737, 1457, 1367, 1151, 914, 737 cm⁻¹. MS (ESI, *m/z*): found [M⁺+Li] 341.28, calc. for C₂₀H₃₀O₄Li, 341.23.



1-Benzyl 8-methyl 3-(2-ethylhexyl)octanedioate (12d). The synthesis was similar to that of **12b** except the following reagents were used: Cu(I)Br·SMe₂ (1.89 g, 9.19 mmol) in THF (15.3 mL), 2-ethylhexyllithium (10.09 mL, 18.38 mmol), TMSCI (3.52 mL, 27.57 mmol), and 1-benzyl 8-methyl oct-2-enedioate **11**



(400 mg, 1.53 mmol). The product was purified by column chromatography (diethyl ether: petroleum ether 1:8) on silica gel to give **12d** (485 mg, 81%). ¹H-NMR (δ, ppm, CHLOROFORM-D): 0.79 (m, 3H), 0.88 (t, 3H), 1.23-1.31 (m, 15H), 1.58 (m, 2H), 1.91 (m, 1H), 2.25-2.30 (m, 4H), 3.66 (s, 3H), 5.11 (s, 2H), 7.35 (m, 5H); ¹³C-NMR (δ, ppm, CHLOROFORM-D): 10.7, 14.40, 23.4, 25.4, 26.1, 28.9, 32.8, 33.1, 34.2, 36.1, 38.5, 44.4, 66.3, 128.4, 128.6, 128.8, 129.2, 130.4, 173.2, 173.5; IR: 2956, 2858, 1739, 1457, 1167, 912, 741 cm⁻¹. MS (ESI, *m/z*): found [M⁺+K] 429.29, [M⁺+Li] 397.36, [M⁺+Na] 413.31, calc. for C₂₄H₃₈O₄K, 429.65, C₂₄H₃₈O₄Li, 397.50, C₂₄H₃₈O₄Na, 413.55.



1-Benzyl 8-methyl 3-isopropyloctanedioate (12e). The synthesis was similar that of **12b** except the following reagents were used: Cu(I)I (875 mg, 4.59 mmol) in THF (7.7 mL), isopropyl magnesium bromide 1.94M (2.37 mL, 4.59 mmol), TMSCI (1.76 mL, 13.78 mmol) and 1-benzyl 8-methyl oct-2-enedioate **11** (200 mg, 0.77 mmol). The residue was purified by column chromatography (diethyl ether: petroleum ether 1:6) on silica gel to give **12e** (109 mg, 45%). ¹H-NMR (δ, ppm, CHLOROFORM-D): 0.80 (d, 3H), 0.84 (d, 3H), 1.16-1.33 (m, 4H), 1.59 (m, 2H), 1.70 (m, 1H), 1.78 (m, 1H), 2.18 (m, 1H), 2.27 (m, 3H), 3.65 (s, 3H), 5.10 (s, 2H), 7.35 (m, 5H); ¹³C-NMR (δ, ppm, CHLOROFORM-D): 18.4, 19.4, 25.1, 26.8, 29.7, 30.7, 34.0, 36.0, 40.7, 51.5, 66.1, 128.2, 128.3, 128.5, 136.1, 173.9, 174.2; IR: 3033, 2954, 2873, 1737, 1458, 1332, 1261, 1008, 905, 750 cm⁻¹; HRMS (EI-TOF, *m/z*): found [M+Na] 343.1883, calc. for C₁₉H₂₈O₄Na, 343.1885.





Methyl 6-methyl-8-oxo-8-(phenylamino)octanoate (13a). To a solution of crude 1-benzyl 8-methyl 3-methyloctanedioate **12a** (513 mg, 1.86 mmol) in ethyl acetate (19 mL) was added 20% Pd(OH)₂/C (261 mg, 0.372 mmol) and the reaction mixture was purged with H_2 gas for 30 s. The reaction solution was stirred under H₂ gas for 3 h and then filtered through a plug of Celite with ethyl acetate (57 mL). The filtrate was concentrated to give 8-methoxy-3-methyl-8oxooctanoic acid as clear oil. The crude residue, 8-methoxy-3-methyl-8oxooctanoic acid, was transferred to a flask and dissolved in 19 mL of acetonitrile. TBTU (895 mg, 2.79 mmol), diisopropylethylamine (647 mL, 3.72 mmol), and aniline (254 mL, 2.79 mmol) was added to the flask. The reaction mixture was stirred for 3 h. The mixture was then guenched with 19 mL of saturated NaHCO₃ solution, transferred to a separatory funnel and extracted with ethyl acetate (equal volume to aqueous layer) at least 3 times. The combined organic layers were dried over magnesium sulfate, filtered, and evaporated to oil. Flash silica gel chromatography (1:6 diethyl ether: petroleum ether \rightarrow 1:1 diethyl ether: petroleum ether) afforded 274 mg of the anilide 13a as a clear oil (53% ¹H-NMR (δ, ppm, CHLOROFORM-D): 0.91 (d, 3H), 1.13-1.34 over 3 steps). (m, 4H), 1.56 (m, 2H), 2.09 (m, 2H), 2.27 (m, 3H), 3.61 (s, 3H), 7.02 (t, 1H), 7.24 (t, 2H), 7.52 (d, 2H), 8.27 (bs, 1H); ¹³C-NMR (δ, ppm, CHLOROFORM-D): 19.9, 25.1, 26.6, 30.9, 34.2, 36.5, 45.6, 51.8, 120.0, 124.4, 129.2, 138.2, 171.1, 175.3;



IR: 3306, 2952, 2868, 1739, 1601, 1544, 1151, 913, 757 cm⁻¹; HRMS (EI-TOF, *m/z*): found [M+H] 278.1764, calc. for C₁₆H₂₄NO₃, 278.1756, found [M+Na] 300.1584, calc. for C₁₆H₂₄NO₃Na, 300.1576.



Methyl 6-(*tert*-butyl)-8-oxo-8-(phenylamino)octanoate (13c). A similar procedure to that for 13a was used, except for the following reagents: 20% Pd(OH)₂/C (210 mq, 0.299 mmol) and 1-benzyl 8-methyl 3-(*tert*butyl)octanedioate 12c (414 mg, 0.748 mmol) in ethyl acetate (7.5 mL), TBTU (360 mg, 1.121 mmol) in acetonitrile (7.5 mL), diisopropyethylamine (521 mL, 2.99 mmol), aniline (102 mL, 0.748 mmol) and stirring for 4 h. The mixture was then guenched with 7.5 mL of saturated NaHCO₃ solution, transferred to a separatory funnel and extracted with ethyl acetate (equal volume to aqueous layer) at least 3 times. The organic layer was dried over magnesium sulfate. filtered, and evaporated to oil. In this case, flash silica gel chromatography (1:6 diethyl ether: petroleum ether \rightarrow 1:1 diethyl ether: petroleum ether) afforded 185 mg of the anilide **13c** as a clear oil (58% over 2 steps). ¹H-NMR (δ , ppm, CHLOROFORM-D): 0.91 (s, 9H), 1.13 (m, 1H), 1.33 (m, 1H), 1.42 (m, 1H), 1.55 (m, 3H), 1.82 (m, 1H), 2.09 (q, 1H), 2.28 (t, 2H), 2.49 (q, 1H), 3.62 (s, 3H), 7.09 (t, 1H), 7.21 (bs, 1H), 7.31 (t, 2H), 7.50 (d, 2H); ¹³C-NMR (δ, ppm, CHLOROFORM-D): 25.5, 27.8, 28.4, 31.2, 34.0, 34.1, 45.1, 56.1, 62.8, 119.2, 124.3, 129.2, 134.7, 168.5, 171.3; IR: 3055, 2952, 2865, 1732, 1600, 1265, 741,



706 cm⁻¹; HRMS (EI-TOF, *m/z*): found [M+H] 320.2229, calc. for C₁₉H₂₉NO₃, 320.2226, found [M+Na] 342.2048, calc. for C₁₉H₂₉NO₃Na, 342.2045.



Methyl 8-ethyl-6-(2-oxo-2-(phenylamino)ethyl)dodecanoate (13d). A similar procedure to that for 13a was used, except for the following reagents: 20% Pd(OH)₂/C (345 mq. 0.492 mmol) and 1-benzyl 8-methyl 3-(2ethylhexyl)octanedioate **12d** (463 mg, 1.229 mmol) in ethyl acetate (12.3 mL), TBTU (592 mg, 1.844 mmol) in acetonitrile (12.3 mL), diisopropyethylamine (856 mL, 4.916 mmol), aniline (168 mL, 1.844 mmol) and stirring for 3 h. In this case, the mixture was quenched with 12.3 mL of saturated NaHCO₃ solution, transferred to a separatory funnel and extracted with CH₂Cl₂ (equal volume to aqueous layer) at least 3 times. The organic layer was dried over magnesium sulfate, filtered, and evaporated to oil. The product was purified by column chromatography (diethyl ether: petroleum ether 1:8) on silica gel to give 13d (349 mg, 76%). ¹H-NMR (δ, ppm, CHLOROFORM-D): 0.81-0.87 (m, 6H),1.10-1.34 (m, 15H), 1.60 (m, 2H), 2.03 (m, 1H), 2.22-2.32 (m, 4H), 3.65 (s, 3H), 7.08 (t, 1H), 7.32 (t, 2H), 7.51 (d, 2H); ¹³C-NMR (δ, ppm, CHLOROFORM-D): 10.7, 14.4, 23.4, 25.3, 25.8, 26.0, 28.9, 33.1, 33.2, 33.6, 33.8, 36.2, 38.5, 43.2, 51.7, 120.0, 124.3, 129.2, 138.3, 171.4, 174.6; IR: 3322, 3066, 2956, 1740, 1661,



1171, 912, 746, 694 cm⁻¹; MS (ESI, *m/z*): found [M⁺+Li] 382.41, [M⁺+Na] 398.35, [M⁺+K] 414.31, calc. for C₂₃H₃₇NO₃Li, 382.49, C₂₃H₃₇NO₃Na, 398.53, C₂₃H₃₇NO₃K, 414.64.



Methyl 6-isopropyl-8-oxo-8-(phenylamino)octanoate (13e). similar Α procedure to that for 13a was used, except for the following reagents: 20% Pd(OH)₂/C (88 mg, 0.125 mmol) and 1-benzyl 8-methyl 3-isopropyloctanedioate 12e (0.312 mmol) in ethyl acetate (3 mL), TBTU (150 mg, 0.468 mmol) in acetonitrile (3 mL), diisopropyethylamine (218 mL, 1.248 mmol), aniline (43 mL, 0.468 mmol) and stirring for 3 h. In this case, the product was purified by column chromatography (1:6 diethyl ether: petroleum ether \rightarrow 1:1 diethyl ether: petroleum ether) on silica gel to give **13e** (71 mg, 75%). ¹H-NMR (δ , ppm, CHLOROFORM-D): 0.84 (d, 3H), 0.89 (d, 3H), 1.25-1.38 (m, 4H), 1.61 (m, 2H), 1.81 (m, 1H), 1.90 (m, 1H), 2.15 (q, 1H), 2.30 (t, 2H), 2.34 (q, 1H), 3.64 (s, 3H), 7.09 (t, 1H), 7.31 (t, 2H), 7.41 (bs, 1H), 7.51 (d, 2H); ¹³C-NMR (δ, ppm, CHLOROFORM-D): 18.9, 19.5, 25.3, 26.9, 29.7, 30.6, 34.1, 39.6, 41.1, 51.8, 120.0, 124.4, 129.2, 138.3, 171.8, 174.6; IR: 3297, 3140, 2954, 2870, 1739, 1601, 1368, 906, 757, 693 cm⁻¹; HRMS (EI-TOF, *m/z*): found [M+H] 306.2071, calc. for C₁₈H₂₈NO₃, 306.2069, found [M+Na] 328.1884, calc. for C₁₈H₂₈NO₃Na, 328.1889.





N⁸-Hydroxyl-3-methyl-N¹-phenyloctanediamide (14a). To a solution of NH₂OH·HCI (677 mg, 9.735 mmol) in methanol (10 mL) was added KOH (1.092 g, 19.469 mmol) at 0 °C in an acid-washed 25mL round-bottom flask. After stirring for 20 min, methyl 6-methyl-8-oxo-8-(phenylamino)octanoate **13a** (270 mg, 0.974 mmol) was added and the mixture was stirred for 8 h at 0°C. The reaction mixture was adjusting to pH 6 by adding concentrated aqueous hydrochloric acid. The mixture was diluted with 30 mL of ethyl acetate, and washed with 30 mL of distilled water. The organic layer was dried over anhydrous Na₂SO₄, filtered, and concentrated. The residue was purified by column chromatography (9% methanol/ CH_2Cl_2) on acid-washed silica gel to give **14a** (159 mg, 58%) as a clear oil. ¹H-NMR (δ, ppm, METHANOL-D4): 0.98 (d, 3H), 1.24-1.44 (m, 4H), 1.61 (m, 2H), 2.02 (m, 1H), 2.09 (t, 2H), 2.16 (q, 1H), 2.34 (q, 1H), 7.07 (t, 1H), 7.29 (t, 2H), 7.52 (d, 2H); ¹³C-NMR (δ, ppm, METHANOL-D4): 18.7, 25.7, 26.3, 30.8, 32.5, 36.3, 44.4, 120.2, 124.0, 128.6, 138.6, 171.8, 172.9; IR: 3270, 2928, 2868, 1643, 1600, 1500, 1418, 1116, 977, 759, 693 cm⁻¹; HRMS (EI-TOF, *m/z*): found [M+H] 279.1710, calc. for C₁₅H₂₃N₂O₃, 279.1709, found [M+Na] 301.1531, calc. for C₁₅H₂₃N₂O₃Na, 301.1528.





*N*⁸-HydroxyI-*N*⁸, 3-diphenyloctanediamide (14b). The synthesis of methyl 6phenyl-8-oxo-8-(phenylamino)octanoate 13b was similar to that of 14a except the following reagents were used: 20% Pd(OH)₂/C (153 mg, 0.218 mmol) and 1benzyl 8-methyl 3-phenyloctanedioate 12b (0.546 mmol) in ethyl acetate (5.5 mL), TBTU (263 mg, 0.818 mmol) in acetonitrile (5.5 mL), diisopropyethylamine (190 mL, 1.09 mmol), aniline (75 mL, 0.818 mmol) and stirring for 4 h. In this case, the reaction mixture was quenched with 5.5 mL of saturated NaHCO₃ solution, transferred to a separatory funnel and extracted with CH₂Cl₂ (equal volume to aqueous layer) at least 3 times. The organic layer was dried over magnesium sulfate, filtered, and evaporated to oil. Flash silica gel chromatography (diethyl ether: petroleum ether 1:1) afforded the mixture of phenyl substituted anilide 13b and α, β unsaturated anilide 13b' as a clear oil.

To a solution of NH₂OH·HCl (696 mg, 10.721 mmol) in methanol (10.7 mL) was added KOH (1.203 g, 21.442 mmol) at 0 °C in an acid-washed 25mL roundbottom flask. After stirring for 20 min, the mixture of methyl 6-phenyl-8-oxo-8-(phenylamino)octanoate **13b** and α , β unsaturated anilide **13b**' (1.072 mmol) was added and the reaction mixture was stirred for 8 h at 0°C. The rest of the reaction procedure was similar to that for **14a**. The residue was purified by column chromatography (4% methanol/CH₂Cl₂) on acid-washed silica gel to give **14b** (221 mg, 60% over 4 steps). ¹H NMR (δ , ppm, DIMETHYLSULFOXIDE-



D6): 0.85-1.25 (m, 3H), 1.42 (m, 2H), 1.58 (m, 2H), 1.83 (t, bs, 2H), 2.57 (m, 2H), 3.07 (m, 1H), 6.97 (t, 1H), 7.14-7.27 (m, 7H), 7.47 (d, 2H), 8.61 (s, 1H), 9.80 (s, 1H), 10.25 (s, 1H); ¹³C-NMR (δ , ppm, METHANOL-D4): 25.5, 26.9, 32.5, 35.5, 42.8, 44.5, 120.4, 124.1, 126.4, 127.5, 128.4, 128.5, 138.4, 144.1, 171.7, 171.9; IR: 3235, 3027, 2928, 2859, 1874, 1641, 1599, 1544, 1498, 1467, 1116, 977, 757,699 cm⁻¹; HRMS (EI-TOF, *m*/*z*): found [M+H] 341.1877, calc. for C₂₀H₂₅N₂O₃, 341.1865, found [M+Na] 363.1697, calc. for C₂₀H₂₅N₂O₃Na, 363.1685.



3-(*tert*-Butyl)-*N*⁸-hydroxyl-*N*¹-phenyloctanediamide (14c). A similar procedure to that for 14a was used, except for the following reagents: NH₂OH·HCl (348 mg, 5.008 mmol) in methanol (7.4 mL), KOH (562 mg, 10.018 mmol), methyl 6-(*tert*-butyl)-8-oxo-8-(phenylamino)octanoate 13c (160 mg, 0.501 mmol) and stirring for 4 h. In this case, the product was purified by column chromatography (4 % methanol/CH₂Cl₂) on acid-washed silica gel to give 14c (158 mg, 99%). ¹H-NMR (δ , ppm, METHANOL-D4): 0.92 (s, 9H), 1.15 (m, 1H), 1.28 (m, 1H), 1.40 (m, 1H), 1.58 (m, 3H), 1.77 (m, 1H), 2.04 (t, 2H), 2.16 (q, 1H), 2.53 (q, 1H), 7.07 (t, 1H), 7.29 (t, 2H), 7.50 (d, 2H); ¹³C-NMR (δ , ppm, METHANOL-D4): 26.1, 26.7, 28.6, 30.8, 32.6, 33.3, 38.5, 45.0, 120.2, 123.9, 128.6, 138.8, 171.8, 173.9; IR: 3350, 2956, 2870, 1938, 1648, 1547, 1500, 1119, 976, 757, 693 cm⁻¹; HRMS (EI-TOF, *m/z*): found [M+H] 321.2180, calc. for C₁₈H₂₉N₂O₃, 321.2178, found [M+Na] 343.1998, calc. for C₁₈H₂₉N₂O₃Na, 343.1988.





 $3-(2-Ethylhexyl)-N^{8}-hydroxyl-N^{1}-phenyloctanediamide$ (14d). similar Α procedure to that for 14a was used, except for the following reagents: NH₂OH·HCI (629 mg, 9.054 mmol) in methanol (9 mL), KOH (1.016 g, 18.108 mmol), methyl 8-ethyl-6-(2-oxo-2-(phenylamino)ethyl)dodecanoate 13d (340 mg, 0.905 mmol), and stirring for 6 h. In this case, the product was purified by column chromatography (4 % methanol/CH₂Cl₂) on acid-washed silica gel to give 14d (199 mg, 58%). ¹H-NMR (δ, ppm, METHANOL-D4): 0.85 (m, 6H), 1.19-1.37 (m, 16H),1.61 (m, 2H), 2.02 (bs, 1H), 2.09 (t, 2H), 2.24 (m, 2H), 7.07 (t, 1H), 7.29 (t, 2H), 7.53 (d, 2H); ¹³C-NMR (δ, ppm, METHANOL-D4): 9.7, 9.9, 13.4, 23.0, 26.0, 28.5, 28.8, 32.6, 32.8, 33.0, 34.0, 36.1, 38.4, 42.3, 120.1, 124.0, 128.6, 138.7, 171.8, 173.1; IR: 3391, 3256, 3065, 2956, 1643, 1600, 1539, 1500, 1308, 903, 756, 692 cm⁻¹; HRMS (EI-TOF, *m/z*): found [M+H] 377.2798, calc. for C₂₂H₃₇N₂O₃, 377.2804.

3.5 HDAC assay procedure

HDAC activity was measured using the Fluor de Lys® activity assay (Enzo) using the manufacturer's protocol. To measure global HDAC inhibition, HeLa lysates (approximately 4µg of total protein) were incubated with small



molecule inhibitor or without small molecule inhibitor (2% DMSO) in HDAC assay buffer (50 mM Tris/Cl, pH 8.0, 137 mM NaCl, 2.7 mM KCl, 1 mM MgCl₂) in a final volume of 25 µL for 20 min at 23 °C with 600 rmp shaking. Concentrations of small molecule between 1 nM and 1 mM were used to determine IC₅₀ values (Appendix C. Table C.1-C.6). Because the small molecules were stored in DMSO, dilution with HDAC buffer ensured that a maximum of 2% DMSO was present in the final reaction mixture. After the initial incubation, Fluor de Lys® substrate in HDAC assay buffer (100 μ M final concentration) was added to make a total reaction volume of 50µL. The reaction mixture was incubated at 30°C for 30 min with 600 rmp shaking. To quench the reaction and allow color development, Fluor de Lys® developer (2.5 µL of 20X diluted up to 50 µL in HDAC assay buffer) was added to give a final 100 µL volume and incubated with shaking for 5 min at room temperature. The fluorescence intensity was determined using a Geniosplus Fluorimeter (Tecan) with excitation at 360 nm and emission at 465 nm.

To perform the isoform selectivity studies, the procedure was similar except that the HeLa cell lysates were replaced with 0.2 μ g HDAC1 (specific activity = 42.5 pmol/min/ μ g), 0.05 μ g HDAC3 (specific activity = 249 pmol/min/ μ g) or 0.25 μ g HDAC6 (specific activity = 257 pmol/min/ μ g), purchased from Enzo Life Sciences. In addition, the Fluor de Lys® substrate was used at a final concentration of 50 μ M for HDAC1 and HDAC6 or 25 μ M for HDAC3.

For each trial, a no enzyme control sample was used to assess the background. The background-corrected fluorescence units of small molecule-



treated samples were then compared to that of untreated samples (set to 100%) to give a percentage deacetylase activity. IC_{50} values were obtained by plotting the percentage deacetylase activity versus the small molecule concentration and fitting the data to a sigmoidal dose-response curve (y=100/(1+(x/m3)^{m4}) using KaleidaGraph software where m1 is the IC_{50} value in Molar units. All experiments were performed in triplicate with the mean and standard error reported in the tables and figures.

CHAPTER 4 – SYNTHESIS OF SAHA ANALOGUES MODIFIED AT THE C7 POSITION

4.1 Rationale for design of the SAHA analogues modified at the C7 position

SAHA analogues with substituents on C2 and C3 position displayed decreasing inhibitory activity while C6-SAHA analogues displayed similar potency to the parent compound, SAHA. These results indicate that only limited steric environment exists near hydroxamic acid. For example, the C6-SAHA analogue with the phenyl substituent displayed only 4-fold decreased inhibition while the C3-SAHA analogue with the phenyl substituent displayed more 800-fold decreased inhibitory activity compared to SAHA. Based on an analysis of the HDAC crystal structure (Figure 1.4)⁵⁴, more space near the capping group area is available to accommodate bulky groups compared to the area near the hydroxamic acid. Moreover, large capping groups have been synthesized and displayed nM range inhibition.^{21b, 38} Several class-selective HDAC inhibitors have been synthesized that contain large groups in capping group region.²⁰ Therefore. design, synthesis, and evaluation of a C7-SAHA library (Figure 4.1) are necessary to elucidate the structural requirement of HDAC inhibitors, since C7-SAHA analogues are located closest to the solvent-exposed region through the

linker area.

NHOH

Figure 4.1. Structure of SAHA analogues containing substituents on the C7 position

C7-SAHA analogues with hydrophobic substituents were generated. Synthesizing C7-SAHA analogues with



only hydrophobic substituents might be sub-optimal since the C7 position is between the hydrophobic tunnel and the solvent exposed area. Therefore, we synthesized the methyl pyridyl variant to study the influence of polar groups. In addition, since medicinal and natural compounds containing nitrogen were involved in diverse therapeutic areas (Chapter 1), we chose the pyridyl derivative.^{41-42, 55} Since hydrophobic substituents attached at the C6 position, a position that is close to the solvent-exposed location, displayed more potent inhibition compared to the C2 and C3-SAHA libraries, C7-SAHA analogues might also display potent inhibition compared to the C2, C3, and C6-SAHA analogues. Therefore, large aromatic groups should be incorporated on the C7 position. We designed a variety of substituents from the small methyl substituent to the large 4-methylnaphthyl, methylbiphenyl, methylanthracene, and methyltetrahydroanthracene substituents to address what effect large groups impart on potency. Due to the structural similarity to the previously reported C2-SAHA analogues, a straightforward synthetic approach was envisioned.

4.2 Initial synthesis of C7-SAHA analogues

Initially, C7-SAHA analogues with methyl **22a**, benzyl **22b**, and 4methylnaphthyl **22c** substituents were synthesized by Dr. A. Bieliauskas. The early synthetic route for C7-SAHA analogues is outlined in Scheme 4.1.





Scheme 4.1. Initial synthesis of C7-SAHA analogues 22a-22c

Benzyl ester **16** was obtained by coupling conditions with benzyl alcohol and 6-bromohexanoic acid **15**. *t*-Butyl malonate derivatives **17** after nucleophilic substitution reaction provided the scaffold to create alkylated malonate derivatives **18a-c**. In acidic conditions, the *t*-butyl groups in **18a-c** were deprotected and decarboxylation was accomplished under reflux to give monocarboxylic acid **19a-c**, which was coupled with aniline. The benzyl group in **20a-c** was removed by Pd/C, and was coupled with *O*-benzyl-protected hydroxamine. *O*-benzyl-protected hydroxamic acid **21a-c** was deprotected by hydrogenolysis to give the C7- SAHA methyl, benzyl, and methylnaphthyl **22a-c**.



77

HDAC inhibitory activities of the C7-methyl, benzyl, and 4-methylnaphthyl SAHA analogues **22a-c** were measured using the Fluor de Lys[™] *in vitro* fluorescence activity assay kit (Biomol) by Dr. S. V. W. Weerasinghe (Table 4.1).

~~									
	Compounds	R	IC ₅₀ , nMª						
	SAHA		86 ± 4						
	22a	Methyl	105 ± 6						
	22b	Benzyl	109 ± 5						
	22c	1-Naphthylmethyl	16 ± 1						

Table 4.1. HDAC inhibition by SAHA, C7-methyl, benzyl, and 4-naphthyl variants using HeLa cell lysates

^aValues are the mean of at least three experiments with standard error given.

The C7-methyl and benzyl analogues **22a-b** were equipotent in 100 nM range similar to SAHA (86 nM). The inhibition results are consistent with the hypothesis that greater steric tolerance exists in HDAC active site at the entrance area of capping group than the metal binding moiety region. Moreover, the largest compound, C7-SAHA naphthylmethyl analogue **22c** among three analogues, displayed greater than 5-fold increasing inhibitory activity compared to SAHA. The addition of certain groups at the C7 position showed favourable interaction between the entrance area of HDAC active site and large bulky groups at the C7 position.



4.3 Synthesis of the C7-SAHA analogues with pyridyl and bulky substituents

To thoroughly explore the impact of the large bulky groups at the C7 position, additional large groups should be investigated. For example, the 4methylbiphenyl and 9-methylanthracene variants **22e-f** should be synthesized to verify how large groups at the C7 position could interact with the HDAC active site. In addition, the inclusion of polar groups should be included to validate interaction between HDAC active site and hydrophilic substituents at the C7 position, the end edge of the hydrophobic channel. However, the synthesis of C7-SAHA analogues containing bulkier and larger substituents than the methyl, benzyl, and 4-methylnaphthyl variants 22a-c faced issue in the nucleophilic substitution reaction (17->18) (Scheme 4.1). Therefore, the synthesis methodology was redesigned (Scheme 4.2). First of all, we used commercially available methyl 6-bromohexanoate 23 as the starting material instead of using coupling reaction to obtain benzylester 16 (two-step) (Scheme 4.1). Second, the nucleophilic substitution reaction was accomplished with dibenzylmalonate, which has a planar structure compared to the bulky *t*-butylmalonate (Scheme 4.1) to give the dibenzylmalonate derivatives **24** (Scheme 4.2). Finally, direct conversion to hydroxamic acid 22 was accomplished in one step without saponification, coupling O-benzyl hydroxylamine, and benzyl deprotection.⁴⁷ The 4-(1,1'-Biphenyl)methyl variant 22e was synthesized by Geetha Padige, the 9anthracenylmethyl 22f and 9-(1,2,3,4-tetrahydroanthracenyl)methyl 22q



derivatives were synthesized by Satish Garre, and the 4-pyridylmethyl variant **22d** was synthesized under my responsibility.

The alternative synthetic route of the C7-SAHA library had been designed by the main concern for bulky subsitutuent attachment when the nucleophilic substitution (**24**->**25**) reaction was performed with large groups. Additionally, several steps were improved in Scheme 4.2.



Scheme 4.2. Redesigned synthesis of C7-SAHA library for bulky groups

After successful nucleophilic substitution reaction with the dibenzylmalonate derivatives **24** and remaining substituents (pyridylmethyl, biphenylmethyl, and anthracenylmethyl groups), alkylated malonate derivatives **25d-f** were deprotected by Pd/C under hydrogen gas. Interestingly, the pyridyl and anthracenylmethyl groups were reduced when the dibenzyl groups of compounds **25d-f** were deprotected. Zacharie and co-workers have proven the reduction from pyridine derivatives to piperidine derivatives in the mild condition.⁵⁶ After deprotection by Pd/C, decarboxylation under the reflux condition, and coupling with aniline (three-step), there were additional anilide



products, the anthracenylmethyl anilide derivative **26f** and the tetrahydroanthracenylmethyl anilide derivative **26g**. In contrast, pyridyl and piperidylmethyl anilide derivatives **26d**, **26d**⁷ were unable to be isolated. The anthracenylmethyl and tetrahydroanthracenylmethyl anilide derivatives **26f**, **26g** were directly convert to hydroxamic acid **22f**, **22g**.

4.4 Optimized synthesis for the C7-pyridyl analogue

To synthesize the C7-pyridyl hydroxamic acid **22d**, the synthetic method was redesigned since the pyridyl and piperidylmethyl anilide derivatives were not isolated (Scheme 4.3). The initial synthesis performed by Dr. Bieliauskas was modified since the pyridylmethyl group is smaller than naphthylmethyl group. However, several reaction conditions were improved.

First of all, benzyl ester **16** was obtained under Fisher condition (95% yield) with benzyl alcohol and 6-bromohexanoic acid **15** instead of the coupling reaction (80% yield). The nucleophilic substitution reaction with *t*-butyl malonate generated derivative **17**, which was alkylated with bromomethyl pyridine to produce alkylated malonate derivatives **18d**. Compared to Dr. Bieliaskas' synthesis, the alkylation was performed under the kinetic condition in DMF at 0 °C (**16** in 99% yield and **18d** in 55% yield) for shorter time (2-3h). Under acidic condition, the *t*-butyl groups on compound **18d** were deprotected and decarboxylation was observed under reflux to give the monocarboxylated derivative. Without purification, the coupling reaction was performed to give anilide **20d** (yield 99% over three steps). To obtain the final C7-SAHA



pyridylmethyl hydroxamic acid **22d**, direct conversion was achieved in one step (43%).



Scheme 4.3. Redesigned and optimized synthesis for C7-SAHA pyridylmethyl analogue 22d

4.5 Biological analysis

HDAC inhibitory activities of the remaining C7-SAHA analogues were measured using the Fluor de Lys® *in vitro* fluorescence activity assay kit using Hela cell lysates (Table 4.2). HDAC inhibition of biphenylmethyl variant **22e** was tested by Geetha Padige.



Iyou		
Compounds	R	IC ₅₀ , nMª
SAHA		86 ± 4
22d	4-Pyridylmethyl	450 + 35
	5 5 5	
220	4-(1 1'-Binhenyl)methyl	4 + 0 3
220		4 ± 0.5
0.04	0. A athree e an ilm athrid	00 1 1
221	9-Antinacenyimethyi	20 ± 1
22g	9-(1,2,3,4-Tetrahydroanthracenyl)methyl	102 ± 30

 Table 4.2. HDAC inhibition by C7-SAHA analogues and SAHA using HeLa cell lysates

^aValues are means of more than three experiments with standard error given.

One of the large compounds, C7-SAHA 4-(1,1'-biphenyl)methyl analogue **22e** displayed greater than 22-fold increase in inhibitory activity compared to SAHA (86 nM) or the smallest compound C7-SAHA methyl analogue **22a** (105 nM). Variants **22b**, **22e** with the large groups, such as naphthylmethyl and biphenylmethyl, were more potent than the smallest variant **22a** with methyl group for C7-SAHA inhibitory activities (Table 4.2). However, the bulky tetrahydroanthracenylmethyl subtituents displayed potency similar to SAHA. The data suggest that C7-SAHA analogues with planar aromatic groups interacted favourably in the binding area of HDAC active site. Moreover, the addition of certain groups at the C7 position likely promotes interaction between the entrance area of HDAC active site and the inhibitor.

Even though we found that greater steric tolerance exists in the HDAC active site in the entrance area of the capping group than the metal binding moiety region, the pyridylmethyl analogue displayed the weakest inhibitory activity (IC_{50} 450 nM). The polarity of the nitrogen atom might interact



unfavorably the binding area of the HDAC active site. As a result, the potency was influenced not only by the size of subsitutuents, but also the polarity, as shown by the fact that the pyridylmethyl group of equal size to the benzyl group (IC_{50} 109 nM).

To more thoroughly verify the structural requirements of SAHA analogues, the isoform selectivity of the C7-SAHA analogues was tested by using HDAC1 and HDAC3 representing class I and HDAC6 representing class II (Figure 4.2). To assess the isoform selectivity of the C7-SAHA analogues, all compounds were initially tested at a single concentration near to their IC_{50} values using the Fluor de Lys® kit (Enzo).





C7-SAHA Isoform Selectivity Screen

Figure 4.2. Screen of C7-SAHA analogues against HDAC1, HDAC3, and HDAC6 with 100 nM methyl, benzyl, tetrahydroanthracenylmethyl, and biphenylmethyl (22a, 22b, 22g, and 22e) variants, 500 nM pyridylmethyl and anthracenylmethyl variants (22d and 22f), and 10 nM naphthylmethyl variant (22c).

The methyl **22a**, and benzyl **22b** variants showed similar inhibition for HDAC1, HDAC3, and HDAC6 at 100 nM, despite slight selectivity for HDAC6 over HDAC1 and HDAC3. The biphenyl variant **22e**, which displayed the most potent inhibition from using Hela cell lysates, showed a slightly preference for



HDAC6 over HDAC1 and HDAC3 as well. In this case, however, two flexible perpendicular aromatic groups might enhance interaction with all of HDAC protein active sites to increase potency, not selectively. In addition, the biphenylmethyl variant **22e** did not show inhibition at 10 nM concentration near to the Hela cell lysate IC₅₀ value (4 nM) for HDAC1, HDAC3, and HDAC6. In contrast, the naphthylmethyl 22c and tetrahydroanthracenylmethyl 22g variants showed greater potency for HDAC3 over HDAC1 and HDAC6 at 10 nM and 100 nM. Interestingly, both compounds contain two planar aromatic groups. Moreover, the pyridylmethyl 22d and anthracenylmethyl 22f variants showed unique dual-selective inhibition at 500 nM for HDAC1 and HDAC6 over HDAC3. Surprisingly, the C7-SAHA anthracenylmethyl compound **22f** was unable to inhibit when tested at 10 nM concentration near to the Hela cell lysate IC_{50} value (20 nM). After several screening, we found that the anthracenylmethyl variant 22f inhibited 50% at 500 nM against HDAC1 and HDAC6. The biphenylmethyl 22e and anthracenylmethyl **22f** variants might display more selective inhibition for other HDAC proteins, such as HDAC2, HDAC4, HDAC5, HDAC7, HDAC8, and HDAC10 due to the fact that showed inhibition at 25-time higher concentration (100 nM and 500 nM) against HDAC1, HDAC3, and HDAC6 than their Hela cell lysate IC_{50} values (4 nM and 20 nM).



With the potential of chemotherapeutic use of selective HDAC inhibitors, several class-selective and isoform-selective HDAC inhibitors have been studied. Most of selective HDAC inhibitors displayed preference for HDAC1 or HDAC8

against HDAC3.17b, 20, 38b, 57-58

which have two-



aromatic group, showed with two parallel aligned aromatic groups 4.3).^{38b} (Figure preference for HDAC8 Nevertheless. the C7-SAHA naphthylmethyl analogue 22c and tetrahydroanthracenylmethyl analogue 22g containing similar structures to the compounds 27a and 27b display unique HDAC3 selectivity. Two parallel aligned aromatic group subsitutuents on the linker region may influence selectivity due to the presence of favorable π - π interactions with particular HDAC active site. Additionally, a dual-selective HDAC1 and HDAC6 inhibitor (pyridyl 22d and anthracene 22f) might promote design of drugs. Therefore, studying the C7-SAHA analogues, which displayed HDAC3 selective inhibition (the naphthylmethyl 22c and tetrahydroanthracenylmethyl 22g) and dual-HDAC1 and HDAC6 selective inhibition (the pyridylmethyl **22d** and anthracenylmethyl **22f** variants), might be a great starting

point to develop a variety of dual or isoform-selective HDAC inhibitors.

To more thoroughly assess the selectivity observed in the initial screen, we determined individual HDAC1, HDAC3, and HDAC6 IC₅₀ values of the anthracene variant **22f**, and SAHA as a comparison. Pathological cardiac remodeling studies have been reported using selective HDAC inhibitors (Section



1.9). Specifically, development of dual-selective inhibitors has been an attractive target in pharmacokinetic study due to the hypothesis by that cancer formation is more complex than related to only single isoform HDAC protein. However, a lack of information on dual-selective HDAC inhibitors is a current challenge. For promising chemotherapeutic use, the anthracenylmethyl analogue 22f among C7-SAHA analogues, which displayed dual-selective inhibition for HDAC1 and HDAC6, was analyzed by using the Fluor de Lys® kit (Enzo). The C7anthracenylmethyl analogue 22f displayed 4-fold selectivity for HDAC1 over HDAC3 and 3-fold class selectivity for HDAC6 over HDAC3 (Table 4.3). In addition, it displayed selectivity within class I, with 4-fold preference for HDAC1 over HDAC3. As a control, SAHA displayed non-selective inhibitor activity against the isoform, as expected (Table 4.3).³⁰ The selectivity analysis shows that substituents on the C7 position can influence selectivity. As a comparison, the C6-SAHA *t*-butyl analogue (dual-HDAC1 and HDAC6 selective inhibitor, IC_{50} value of 1.9 µM) displayed 22-fold less potency compared to SAHA (86 nM) while the C7-SAHA anthracene analogue **22f** (20 nM) showed 4-fold better potency compared to SAHA. Therefore, the data indicate that attaching the anthracene substituent on the linker chain on the C7 position promotes selectivity with potency.

DACS, and TIDACO					
Compound	IC ₅₀ /nM				
	HDAC1	HDAC3	HDAC6		
SAHA	96 ± 16	136 ± 11	74 ± 9		
22f	300 ± 66	1200 ± 50	443 ± 73		

 Table 4.3.
 IC₅₀ values of SAHA and the C7-SAHA anthracene 22f for HDAC1,

 HDAC3, and HDAC6



SAHA analogues with substituents on the C7 position displayed selective inhibition, including dual-class I, II selectivity (pyridyl 22d and anthracene 22f selectivity HDAC3 variants) and isoform for (naphthyl 22c and tetrahydroanthracne **22g** variants) and HDAC6 (biphenyl variant **22e**). The results reveal that small structural changes in the C7 position linker region of SAHA will lead in designing drugs by improving selectivity and potency compared to the broad-spectrum inhibitor SAHA. Furthermore, studying selective inhibitor structures in detail will be able to be explored through our selective compound analysis in a variety of scope.

4.6 Future direction

We have synthesized and analyzed SAHA analogues that placed a variety of substituents in the carbon linker. The results from the C3, C6, and C7 library suggest that SAHA analogues with substituents on the carbon linker are promising to develop new anti-cancer drugs. To more systematically assess the structural effect in HDAC active site, more analogues positioning subsituetns at

the C4, and C5

HOHN HOHN

Figure 4.4. Structures of SAHA analogues containing substituents on the

be synthesized

C4 and C5 (Figure 4.4). In addition, analysis of isoform selectivity of the C3-SAHA analogues suggests that substituents on the SAHA linker influence selectivity. We have shown that the



steric environment of the C6 position displays less influences on potency compared to SAHA analogues with substituents near the hydroxamic acid. However, substituents at α -carbon on C6 position still decreased inhibitory activity. Interestingly, despite the poor potency of the C6-SAHA *t*-butyl analogue, it displayed selectivity. Likewise, the C3-SAHA ethyl analogue with an additional methylene group at the α -carbon compared to the C3-SAHA methyl analogue displayed selective inhibition (HDAC6 selectivity). The effect of the α -carbon on C6 substituents could be thoroughly investigated with the synthesis of isopropyl and adamantyl group analogues. Besides, the long chain of the 2-ethyl hexyl SAHA analogues on the C6 position also affected isoform selectivity (HDAC3selectivity) with potency. Favourable interactions of the long aliphatic chain in HDAC active site could be verified through synthesis of C6-SAHA octyl to undecyl analogues. Furthermore, C7-SAHA analogues show potent inhibition with large and polar group substituents. The influence of the enantiomers with bulky or polar groups near the capping group would allow assessing the structural requirements of the compounds in detail. Therefore, screening the enantiomers of all SAHA analogues might show promising properties. Moreover, testing the inhibitory activities against all HDAC proteins, from HDAC1 to HDAC11, will provide the structures of selective inhibitors. Developing new costeffective, high through-put screening methods are needed to test selectivity against all HDAC1-11. Therefore, the biological evaluation of the current compound enantiomers, the additional synthesis of different structural



compounds, and the development of easy-access high through-put assay will contribute to develop promising cancer drugs.

4.7 Experimental

4.7.1 General methods

Additional details were shown in Section 2.5.1 of Chapter 2.

4.7.2 Experimental Procedures and Compound Characterizations



1, **1**-Dibenzyl 6-methyl hexane-1, 1, 6-tricarboxylate (24). To a solution of NaH (144 mg, 6 mmol) in DMF (20 mL) was added dibenzylmalonate (1.14 mL, 6 mmol) dropwise at 0 °C and the mixture was stirred for 15 min. To the solution was added methyl 6-bromohexanoate **23** (0.57 g, 2 mmol) and the mixture was stirred for 3 h. The mixture was filtered through celite with ethyl acetate and concentrated. The residue was purified by column chromatography (diethyl ether:petroleum ether 1:19) on silica gel to give **24** (682 mg, 81%). ¹H-NMR (δ , ppm, CHLOROFORM-D): 1.31 (m, 4H), 1.58 (m, 2H), 1.94 (q, 2H), 2.26 (t, 2H), 3.43 (t, 1H), 3.65 (s, 3H), 5.14 (s, 4H), 7.31 (m, 10H); ¹³C-NMR (δ , ppm, CHLOROFORM-D): 24.8, 27.1, 28.8, 28.9, 34.1, 51.7, 52.1, 67.3, 128.4, 128.6, 128.8, 135.6, 169.4, 174.3; IR: 3033, 2949, 2862, 1734, 1498, 1456, 1333, 1214,



1156, 907, 741, 698 cm⁻¹; HRMS (EI-TOF, *m*/*z*): found [M+Na] 435.1767, calc. for C₂₄H₂₈O₆, 435.1784.



6, 6-Dibenzyl 1-methyl 7-(pyridine-4-yl)heptane-1, 6, 6-tricarboxylate (25). To a solution of NaH (256 mg, 6.4 mmol) in DMF (53 mL) was added 1, 1-dibenzyl 6-methyl hexane-1, 1, 6-tricarboxylate 24 (2.20 g, 5.33 mmol) dropwise at 0 °C and the mixture was stirred for 15 min. Separately, 1.5 equivalents of 4-bromomethylpyridine hydrobromide salt (2.02 g, 8.00 mmol) was dissolved in distilled water (8 mL) and added to a separatory funnel, followed by 0.7 equivalent of Na_2CO_3 (396 mg, 3.74 mmol). After the separatory funnel was shaken until gas evolution was not observed, the mixture was extracted with ethyl acetate (8 mL) at least 4 times. The organic layers were dried over magnesium sulfate, filtered, and concentrated by rotary evaporation. To the flask containing the activated dibenzyl malonate derivatives solution 24 was added the solution of the neutralized and concentrated 4-bromo-methylpyridine and the mixture was stirred for 4h at 0 °C. The reaction was guenched with distilled water (26.5 mL) and extracted with ethyl acetate (equal volume to aqueous layer). The organic layer was pooled and extracted with distilled water (equal volume to organic layer) at least 4 times. The organic layer was dried over magnesium sulfate, filtered, and concentrated to oil. The residue was purified by column chromatography (ethyl



acetate:hexanes 1:3) on silica gel to give **25** (1.61 g, 60%). ¹H-NMR (δ , ppm, CHLOROFORM-D): 1.21 (m, 4H), 1.50 (m, 2H), 1.75 (t, 2H), 2.20 (t, 2H), 3.19 (s, 2H), 3.64 (s, 3H), 5.08 (s, 4H), 6.82 (d, 1H), 6.91 (d, 1H), 7.24-7.31 (m, 7H), 8.35 (d, 1H), 8.36 (d, 1H); ¹³C-NMR (δ , ppm, CHLOROFORM-D): 24.1, 24.8, 29.3, 32.3, 34.0, 37.8, 51.7, 58.7, 67.5, 125.3, 128.765, 128.787, 128.816, 135.3, 145.3, 149.9, 170.6, 174.1; IR: 3032, 2951, 1731, 1601, 1455, 1218, 1170, 912, 733, 698 cm⁻¹; HRMS (EI-TOF, *m*/*z*): found [M+H] 504.2387, calc. for C₃₀H₃₄NO₆, 504.2386.



Benzyl 6-bromohexanoate (16). Benzyl alcohol (0.07 mL, 0.68 mmol) and concentrated aqueous sulfuric acid (3 μL, 0.056 mmol) were stepwise added to a solution of 6-bromohexanoic acid **15** (0.11 g, 0.56 mmol) in diethyl ether (5 mL) at 0°C. The mixture was stirred for 30min and warmed to room temperature. The reaction mixture was quenched with distilled water (5 mL). The mixture was extracted with diethyl ether (5 mL) at least 4 times. The organic layer was evaporated. The concentrated organic layer was extracted with distilled water (equal volume to the concentrated organic layer) at least 3 times. The organic layer was purified by column chromatography (diethyl ether:petroleum ether 1:19) on silica gel to give **16** (153 mg, 95%). ¹H-NMR (δ, ppm, CHLOROFORM-D): 1.47



(m, 2H), 1.68 (m, 2H), 1.86 (m, 2H), 2.38 (t, 2H), 3.38 (t, 2H), 5.12 (s, 2H), 7.36 (m, 5H); ¹³C-NMR (δ, ppm, CHLOROFORM-D): 24.3, 27.9, 32.6, 33.7, 34.3, 66.4, 128.5, 128.8, 136.3, 173.5; IR: 3033, 2939, 1733, 1455, 1254, 1165, 736, 697 cm⁻¹; HRMS (EI-TOF, *m/z*): found [M+Na] 307.0314, calc. for C₁₃H₁₇O₂NaBr, 307.0310.



6-Benzyl 1,1-di-*tert***-butyl hexane-1,1,6-tricarboxylate (17).** To a solution of NaH (589 mg, 14.7 mmol) in DMF (49 mL) was added di-*t*-butylmalonate (3.30 mL, 14.7 mmol) dropwise at 0 °C and the mixture was stirred for 15 min. To the solution was added benzyl 6-bromohexanoate **16** (1.4 g, 4.91 mmol) at 0 °C and the mixture was stirred for 3 h at room temperature. The mixture was filtered through celite with ethyl acetate and concentrated. The residue was purified by column chromatography (diethyl ether:petroleum ether 1:19) on silica gel to give **17** (2.04 g, 99%).¹H-NMR (δ , ppm, CHLOROFORM-D): 1.34 (m, 4H), 1.45 (s, 18H), 1.65 (m, 2H), 1.79 (q, 2H), 2.34 (t, 2H), 3.10 (t, 1H), 5.11 (s, 2H), 7.35 (m, 5H); ¹³C-NMR (δ , ppm, CHLOROFORM-D): 24.9, 27.1, 28.2, 28.6, 29.0, 34.4, 54.1, 66.3, 81.5, 128.4, 128.8, 135.6, 169.1, 173.7; IR: 3033, 2979, 2935, 2861, 1729, 1498, 1369, 1256, 1169, 1139, 748 cm⁻¹; found MS(ESI): m/z = 427.30 (M⁺+Li), 443.30 (M⁺+Na), 459.27 (M⁺+K), calc. for C₂₄H₃₆LiO₆, 427.48, C₂₄H₃₆NaO₆, 443.53, C₂₄H₃₆KO₆, 459.64.





1-Benzyl 6,6-di-tert-butyl 7-(pyridine-4-yl)heptane-1,6,6-tricaboxylate (18d). To NaH (171 mg, 4.28 mmol) and 4-bromo-methylpyridine hydrobromide salt (1.0 g, 4.28 mmol) was added DMF (16 mL) dropwise at 0 °C and the mixture was stirred for 20min. Separately, to NaH (171 mg, 4.28 mmol) in DMF (20 mL) was added 6-benzyl 1,1-di-tert-butyl hexane-1,1,6-tricarboxylate 17 (1.5 g, 3.57 mmol) dropwise at 0 °C and the mixture was stirred for 20 min. To the solution of the activated 6-benzyl 1,1-di-tert-butyl hexane-1,1,6-tricarboxylate 17 was added the solution of the neutralized 4-bromo-methylpyridine dropwise at 0 °C and the mixture was stirred for 3h at room temperature. The reaction mixture was filtered through celite with ethyl acetate and concentrated. The residue was purified by column chromatography (diethyl ether:petroleum ether 1:5) on silica gel to give **18d** (513 mg, 55%). ¹H-NMR (δ, ppm, CHLOROFORM-D): 1.29 (m, 4H), 1.43 (s, 18H), 1.65 (m, 4H), 2.34 (t, 2H), 3.12 (s, 2H), 5.10 (s, 2H), 7.07 (d, 2H), 7.34 (m, 5H), 8.47 (d, 2H); ¹³C-NMR (δ, ppm, CHLOROFORM-D): 24.0, 24.9, 28.1, 29.5, 32.2, 34.4, 37.4, 59.1, 66.4, 82.0, 125.6, 128.4, 128.8, 136.2, 146.3, 149.7, 170.3, 173.6; IR: 3036, 2976, 2935, 2867, 1727, 1605, 1248, 1159, 846, 737, 696 cm⁻¹; HRMS (EI-TOF, m/z): found [M+H] 512.3016, calc. for C₃₀H₄₂NO₆, 512.3012.





Benzyl 8-oxo-8-(phenylamino)-7-(pyridine-4-ylmethyl)octanoate (20d). To a flask equipped with a reflux condenser and containing 1-benzyl 6,6-di-tert-butyl 7-(pyridine-4-yl)heptane-1,6,6-tricaboxylate **18d** (510 mg, 997 mmol) was added 10 mL of 10% TFA in acetic acid. The reaction mixture was refluxed overnight and evaporated to oil. The residue was dissolved in ethyl acetate (10 mL) and transferred to a separatory funnel. The solution was extracted with saturated NaHCO_{3(ao)} (equal volume to organic layer) at least 4 times. The organic layer was dried over magnesium sulfate, filtered, and evaporated. The crude residue was dissolved in acetonitrile (10 mL). To the solution of crude carboxylic acid derivative was added individually in order listed in a stepwise: TBTU (480 mg), diisopropylethylamine (695 mL), and aniline (136 mL). The reaction mixture was stirred overnight at room temperature. The reaction was quenched by addition of an aqueous solution of saturated NaHCO₃ (10 mL). The mixture was extracted with CH_2CI_2 (equal volume to aqueous layer) at least 4 times. The organic layer was dried over magnesium sulfate, filtered, and concentrated to an oil. The residue was purified by column chromatography (ether:petroleum ether 1:1) on silica gel to give **20d** (572 mg, 99%). ¹H-NMR (δ , ppm, CHLOROFORM-D): 1.34 (m, 4H), 1.49 (m, 1H), 1.61 (m, 2H), 1.79 (m, 1H), 2.33 (t, 2H), 2.47 (m, 1H), 2.69 (q, 1H), 3.02 (q, 1H), 5.09 (s, 2H), 7.09 (m, 3H), 7.25 (m, 2H), 7.32 (m, 4H), 7.38 (d, 2H), 7.89 (m, 1H), 8.40 (d, 2H); ¹³C-NMR (δ, ppm, CHLOROFORM-


D): 24.8, 27.1, 29.0, 33.1, 34.3, 38.6, 49.9, 66.4, 120.4, 124.7, 128.3, 128.4, 128.5, 128.8, 129.2, 136.2, 137.9, 149.4, 149.8, 173.0, 173.9; IR: 3304, 3221, 3035, 2931, 2858, 1734, 1602, 1443, 1173, 912, 752, 696 cm⁻¹. HRMS (EI-TOF, *m/z*): found [M+H] 431.2331, calc. for C₂₇H₃₁N₂O₃, 431.2335.



 N^{8} -hydroxy- N^{1} -phenyl-2-(pyridin-4-ylmethyl)octanediamide (22d). To a solution of NH₂OH·HCI (536 mg, 7.67 mmol) in methanol (8 mL) was added KOH (860 mg, 15.3 mmol) at 0 °C in an acid-washed 25mL round-bottom flask. After stirring for 20 8-oxo-8-(phenylamino)-7-(pyridine-4min, benzvl ylmethyl)octanoate **20d** (330 mg, 0.767 mmol) was added and the mixture was stirred for 8h at 0°C. The reaction mixture was guenched by adding 1mL of distilled water and adjusting to pH 6 by adding concentrated aqueous hydrochloric acid. The mixture was diluted with 8 mL of ethyl acetate, and extracted with distilled water (equal volume to organic layer) at least 4 times. The organic layer was dried over magnesium sulfate, filtered and concentrated. The residue was purified by column chromatography (8% methanol/CH₂Cl₂ with 0.1% Et₃N) on acid-washed silica gel to give **22d** (116 mg, 43%). ¹H-NMR (δ , ppm, METHANOL-D): 1.39 (m, 4H), 1.60 (m, 3H), 1.77 (m, 1H), 2.08 (t, 2H), 2.86 (m, 2H), 2.93-3.00 (m, 2H), 7.06 (t, 1H), 7.25 (t, 2H), 7.43 (d, 2H), 7.50 (d, 2H), 8.48 (d, 2H); ¹³C-NMR (δ, ppm, CHLOROFORM-D): 25.4, 26.9, 28.8, 32.4, 32.8, 38.4, 120.3, 124.3, 125.8, 128.6, 138.1, 146.7, 153.8, 171.7, 174.1; IR: 3440, 3335,



2866, 1720, 1641, 1528, 1442, 1133, 759, 660 cm⁻¹; HRMS (EI-TOF, *m/z*): found [M+H] 356.1966, calc. for C₂₀H₂₆N₃O₃, 356.1974. HPLC analytical purity analysis: 90%.

4.8 HDAC assay procedure

HDAC activity was measured using the Fluor de Lys® activity assay (Biomol & Enzo) using the manufacturer's protocol. Additional details were shown in Section 3.6 of Chapter 3.





APPENDIX A. DOSE RESPONSE GRAPHS AND DATA FOR C3-SAHA LIBRARY

Figure A.1. Dose response curve of C3-SAHA analogue **1a-e** tested using the HDAC activity from HeLa cells lysates from three independent trials with error bars indicating standard error. In some case, the error bars are smaller than the marker size. Data were fit to the sigmoidal curve using Kaleidograph 4.0 (Synergy Software) to determine the IC₅₀. The insets were the results of the data analysis. The data are reported in Table 2.1.

Concentration (M)	Trial 1	Trial 2	Trial 3	Mean	S.E
3.125 x 10⁻⁵	83	85	81	83	1
6.25 x 10⁻⁵	72	69	73	71	1
1.25 x 10 ⁻⁴	54	54	51	53	1
2.50 x 10 ⁻⁴	47	46	46	46	1
5.00 x 10 ⁻⁴	31	35	34	33	1
1.00 x 10 ⁻⁴	19	22	20	20	1

Table A.1 Inhibition	of HDAC Activit	v of SAHA C3-But	vl with Hela Lvsat	e
		.y ol o/	yi mulii ilola Eyoac	-



Concentration (M)	Trial 1	Trial 2	Trial 3	Mean	S.E
1.00 x 10 ⁻⁶	98	80	86	88	5
1.5625 x 10 ⁻⁵	88	79	74	80	4
3.125 x 10⁻⁵	74	65	66	68	3
6.25 x 10⁻⁵	59	54	50	54	3
1.25 x 10 ⁻⁴	40	38	38	37	1
2.50 x 10 ⁻⁴	25	26	24	25	1
5.00 x 10 ⁻⁴	15	14	14	14	1

Table A.2 Inhibition of HDAC Activity of SAHA C3-Phenyl with Hela Lysate

Table A.3 Inhibition of HDAC Activity of C3-SAHA Ethyl with Hela Lysate

Concentration (M)	Trial 1	Trial 2	Trial 3	Mean	S.E
1.00 x 10 ⁻⁶	88	85	82	85	2
7.8125 x 10⁻⁵	75	69	67	70	2
1.5625 x 10 ⁻⁵	67	62	61	63	1
3.125 x 10 ⁻⁵	52	57	57	55	2
6.25 x 10⁻⁵	42	46	34	41	4
1.25 x 10 ⁻⁴	27	28	28	28	1
2.50 x 10 ⁻⁴	18	15	14	16	1

Table A.4 Inhibition of HDAC Activity of SAHA C3-Vinyl with Hela Lysate

Concentration (M)	Trial 1	Trial 2	Trial 3	Mean	S.E
1.00 x 10 ⁻⁶	84	75	99	86	7
3.906 x 10 ⁻⁶	83	60	69	71	7
7.8125 x 10 ⁻⁶	72	55	57	61	5
1.5625 x 10⁻⁵	60	43	47	50	5
3.125 x 10 ⁻⁵	48	34	37	40	4
6.25 x 10 ⁻⁵	32	23	27	27	3

Table A.5 Inhibition of HDAC Activity of C3-SAHA Methyl with Hela Lysate

Concentration (M)	Trial 1	Trial 2	Trial 3	Mean	S.E
1.00 x 10 ⁻⁹	95	93	77	88	4
6.25 x 10 ⁻⁸	85	75	72	77	4
1.25 x 10 ⁻⁷	77	72	62	72	3
2.50 x 10 ⁻⁷	62	58	54	58	2
5.00 x 10 ⁻⁷	45	46	43	44	1
1.00 x 10 ⁻⁶	31	28	29	29	1



Compound	HDAC Isoform	Trial 1	Trial 2	Mean	S.E
0.111	HDAC1	27	35	31	4
SAHA (125 pM)	HDAC3	44	45	45	1
(1231111)	HDAC6	32	37	35	3
	HDAC1	44	47	46	2
C3-Methyl	HDAC3	53	62	57	5
	HDAC6	73	75	74	1
	HDAC1	38	39	39	1
C3-Ethyl	HDAC3	71	95	83	12
(52 µW)	HDAC6	17	18	18	1
	HDAC1	23	26	25	2
C3-Vinyl	HDAC3	47	51	49	2
(32 µM)	HDAC6	26	28	27	1
	HDAC1	33	33	33	0
C3-Butyll	HDAC3	52	52	52	0
(32 µivi)	HDAC6	22	25	24	2
	HDAC1	42	48	45	3
C3-Phenyl	HDAC3	50	51	51	1
(32 μινι)	HDAC6	24	27	26	2

Table A.6 Isoform Selective HDAC Inhibition of SAHA C3 Analogues

Deacetylase activity of HDAC1, HDAC3 and HDAC6 was determined with SAHA and with SAHA C3 analogs at given concentration using an in vitro fluorescence assay as described. The background fluorescence activity (No enzyme added) was subtracted and the percentage deacetylase activity was calculated with compared to the No small molecule treated (100%). Percentage deacetylase activity of each independent trial, mean percentage deacetylase activity and standard error (S.E) are shown.





Figure A.2. Dose response curves of SAHA tested against HDAC1, HDAC3, and HDAC6 from three independent trials with error bars indicating standard error. In some cases, the error bars are smaller than the marker size. The data is reported in the manuscript in Table 2.2.





Figure A.3. Dose response curves of the C3- SAHA ethyl analogue **1c** tested against HDAC1, HDAC3, and HDAC6 from three independent trials with error bars indicating standard error. In some cases, the error bars are smaller than the marker size. The data is reported in the manuscript in Table 2.2.

Table A.7 Inhibition of HDAC1 Activity by SAHA

Concentration (M)	Trial 1	Trial 2	Trial 3	Mean	S.E
3.125 x 10 ⁻⁸	68	91	82	80	7
6.25 x 10 ⁻⁸	55	62	57	58	2
1.25 x 10⁻′	48	27	37	37	6
2.50 x 10 ⁻⁷	37	40	25	34	5

Table A.8 Inhibition of HDAC3 Activity by SAHA

Concentration (M)	Trial 1	Trial 2	Trial 3	Mean	S.E
3.125 x 10 ⁻⁸	88	78	74	80	4
6.25 x 10 ⁻⁸	76	74	70	73	2
1.25 x 10 ⁻⁷	63	45	44	56	5
2.50 x 10 ⁻⁷	27	39	37	34	4



Concentration (M)	Trial 1	Trial 2	Trial 3	Mean	S.E
3.125 x 10 ⁻⁸	66	76	73	72	3
6.25 x 10 ⁻⁸	64	62	60	62	1
1.25 x 10 ⁻⁷	37	28	32	32	2
2.50 x 10 ⁻⁷	13	12	9	11	1

Table A.9 Inhibition of HDAC6 Activity by SAHA

Table A.10 Inhibition of HDAC1 Activity by SAHA C3-Ethyl

Concentration (M)	Trial 1	Trial 2	Trial 3	Mean	S.E
1.00 x 10 ⁻⁶	102	89	ND	96	9
7.8125 x 10 ⁻⁶	83	94	86	88	6
1.5625 x 10⁻⁵	58	65	51	58	7
3.125 x 10 ⁻⁵	39	38	ND	39	1

Table A.11 Inhibition of HDAC3 Activity by SAHA C3-Ethyl

Concentration (M)	Trial 1	Trial 2	Trial 3	Mean	S.E
3.125 x 10⁻⁵	95	71	ND	83	12
62.50 x 10 ⁻⁵	58	57	66	60	3
1.25 x 10 ⁻⁴	46	35	53	45	5
2.50x 10 ⁻⁵	20	21	25	22	2

Table A.12 Inhibition of HDAC6 Activity by SAHA C3-Ethyl

Concentration (M)	Trial 1	Trial 2	Trial 3	Mean	S.E
1.000 x 10 ⁻⁶	81	76	78	78	1
3.906 x 10 ⁻⁶	69	65	64	66	2
7.812 x 10 ⁻⁶	52	58	51	54	2
1.562 x 10 ⁻⁵	38	40	38	39	1
3.125 x 10 ⁻⁵	17	18	ND	18	1



APPENDIX B. SUPPLEMENTARY INFORMATION FOR C3-SAHA LIBRARY



B.1 5-Hydroxy-*N*-phenylpentanamide (**3**) **B.1.1** ¹H NMR



B.1.3 IR



No.	Position	Intensity	No.	Position	Intensity
1	647.001	91.0387	2	692.32	80.474
3	729.925	55.4341	4	754.995	79.59
5	908.308	71.8178	6	961.341	95.907
7	1051.01	88.7738	8	1074.16	89.0851
9	1177.33	95.3979	10	1251.58	89.3905
11	1309.43	85.4377	12	1442.49	65.4784
13	1498.42	71.2467	14	1543.74	62.6047
15	1598.7	64.7477	16	1663.3	66.9215
17	2862.81	93.2437	18	2936.09	82.5852
19	3063.37	101.173	20	3136.65	99.3077
21	3297.68	83.2347			10.00170.0.11

[Comment]	
Sample Name	
Licor	
Division	
Company	Wayne State
(Measurement Inf	ormation]
Model Name	FT/IR-4100typeA
Serial Number	B071461016
Light Source	Standard
Detector	TGS
Accumulation	Auto (66)
Resolution	4 cm-1
Zero Filling	On
Apodization	Cosine
Gain	Auto (4)
Aperture	Auto (7.1 mm)
Scanning Speed	Auto (2 mm/sec)
Filter	Auto (30000 Hz)



B.1.4 HRMS

Elemental Composition Report

Page 1

Single Mass Analysis (displaying only valid results) Tolerance = 4.0 mDa / DBE: min = -1.5, max = 50.0 Isotope cluster parameters: Separation = 1.0 Abundance = 1.0%

Monoisotopic Mass, Odd and Even Electron lons 72 formula(e) evaluated with 3 results within limits (all results (up to 1000) for each mass)

Sun Ea Choi	091807 PG 23 A	cohol							05-Oct-2007	10:36:24
SPEI 70eV L071005_904 1	20 (2.000) Cm (94:	122-260:298x2	.000)	GC-TOF			207.1259		TO	F MS EI+ 4.64e5
100										
0 19	9.0664	201.0805	203.0939 02.0 203.0	204.0994	205.1122 205.0	206.1189 206.0	207.0	208.1331	209.1340 209.0	210.1299 m/z 210.0
Minimum: Maximum:		4.0	5.0	-1.5 50.0						
Mass	Calc. Mass	mDa	PPM 1	DBE	Score	Form	ula			
207.1259	207.1259 207.1246 207.1219	-0.1 1.3 4.0	-0.3 6.2 19.1	5.0 5.5 1.0	2 1 3	C12 C10 C7	H17 N H15 N4 H17 N3	02 4 0 04		

B.2 6-Oxo-6-(phenylamino)hexanal (4) **B.2.1** ¹H NMR









B.2.3 IR



Filter

B.2.4 HRMS

Elemental Composition Report	Aug 16 /or	Page 1
Single Mass Analysis Tolerance = 5.0 mDa / DBE: min = -1.5, max = 50.0 Isotope cluster parameters: Separation = 1.0 Abundance	B•• k *1 ce = 1.0%	P.g. 12
Monoisotopic Mass, Odd and Even Electron lons 190 formula(e) evaluated with 4 results within limits (all results (up to	o 1000) for each mass)	

Anton Bielis SPEI 70eV 081707 PG12 17-Aug-2007 13:43:43 GC-TOF TOF MS EI+ 560 L070817_866 89 (1.908) Cm ((84+86:90)-13:29x2.000) 205.1106 100-% 206.1194 199.0617 211.2611^{211.9625} 215.1022 216.0933 m/z 203.0949 201.0829 207.2220 209.0717 0 198.0 200.0 202.0 204.0 206.0 208.0 210.0 212.0 214.0 216.0 Minimum: Maximum: -1.5 10.0 50.0 5.0 PPM DBE Formula Mass Calc. Mass πDa Score 205.1106 205.1103 6.0 C12 H15 N 02 0.3 1.6 1 C10 H13 N4 O C9 H17 O5 C7 H15 N3 O4 205.1089 1.7 8.2 6.5 2 1.5 205.1076 205.1063 3.0 14.7 3 21.2 4.4 4

B.3 8-Oxo-8-(phenylamino)-oct-2-enoate (5)

B.3.1 ¹H NMR (E)





B.3.2 ¹H NMR (**Z**)











B.3.5 HRMS



B.4 8-Oxo-8-(phenylamino)-3-*n*-butyloctanoate (6a)

B.4.1 ¹H NMR













Zero Filling

Apodization

Gain Aperture Scanning Speed

Filter

On

Cosine Auto (4) Auto (7.1 mm)

Auto (2 mm/sec) Auto (30000 Hz)



B.4.4 HRMS

Elemental Composition Report

Single Mass Analysis

Tolerance = 5.0 mDa / DBE: min = -1.5, max = 50.0 Isotope cluster parameters: Separation = 1.0 Abundance = 1.0%

Monoisotopic Mass, Odd and Even Electron Ions 228 formula(e) evaluated with 5 results within limits (all results (up to 1000) for each mass)

Sun Ea Choi SPEI 70eV L0708223_877	082707 PG 16 90 (1.944) Cm ((71+76+80+88+90	+100)-16:29 319	GC-TC (2.000) 9.2143	F		28-Aug-	2007 11:42:48 TOF MS EI+ 399
% 0 305.1190 305.0) <u>308.0508</u> 31 310.0	10.3984 313.1193	³ 317.2019	320.2194 321.2 320.0	247 324.1273 325.0	329.8572 330.0	335.2289.336.3106 335.0	339.7419 m/z 340.0
Minimum: Maximum:		5.0	10.0	-1.5 50.0				
Mass	Calc. Mass	mDa	PPM	DBE	Score	Formula		
319.2143	319.2147 319.2134 319.2121 319.2174 319.2107	-0.5 0.9 2.2 -3.2 3.5	-1.5 2.7 6.9 -9.9 11.1	6.0 6.5 1.5 10.5 2.0	1 2 3 4 5	C19 H29 C17 H27 C16 H31 C22 H27 C14 H29	N 03 N4 02 06 N2 N3 05	

B.5 8-Oxo-8-(phenylamino)-3-phenyloctanoate (**6b**) **B.5.1** ¹H NMR



Page 1





B.5.3 IR

QC_Compare-6889.jws





B.5.4 HRMS











Page 1

phe

1: TOF MS ES+ 2.95e+003

B.6.2 ¹³C NMR





QC_Compare-926.jws





B.6.4 HRMS

للاستشارات

Elemental Composition Report

Single Mass Analysis

Tolerance = 5.0 mDa / DBE: min = -1.5, max = 50.0 Isotope cluster parameters: Separation = 1.0 Abundance = 1.0%

Monoisotopic Mass, Odd and Even Electron Ions 238 formula(e) evaluated with 6 results within limits (all results (up to 1000) for each mass)







Page 1

B.7.2 ¹³C NMR





B.7.3 IR







B.7.4 HRMS

Elemental Composition Report

Single Mass Analysis

Tolerance = 5.0 PPM / DBE: min = -1.5, max = 50.0 Element prediction: Off Number of isotope peaks used for i-FIT = 3 J. J. Mone

1				31	13.1608							
	172.0951	223.0956	251.1263 ²	90.1779	389	2791_407.1991	505.25	515 535.	2779 6	01.3251	617.4836	m/z
100	150	200	250	300	350	400 450	500	55	0	600	650	111/2
Minimum: Maximum:			5.0	5.0	-1.5 50.0							
Mass	Calc.	Mass	mDa	PPM	DBE	i-FIT	i-FIT	(Norm)	Formu	la		
312,1564	312.13 312.13	559 576	0.5 -1.2	1.6 -3.8	5.5 6.5	51.4 51.9	0.5		C14 C17	H22 H23	N3 05 N 03	23Na

B.8 8-Oxo-8-(phenylamino)-3-methyloctanoate (**6e**) **B.8.1** ¹H NMR





B.8.2 ¹³C NMR



المتسارات

B.8.1 HRMS

للاستشارات

Elemental Composition Report

Single Mass Analysis

Tolerance = 5.0 mDa / DBE: min = -1.5, max = 50.0 Isotope cluster parameters: Separation = 1.0 Abundance = 1.0%

Monoisotopic Mass, Odd and Even Electron lons 225 formula(e) evaluated with 5 results within limits (all results (up to 1000) for each mass)

Sun Choi Feb GCEI 70eV L080214_1002	18 08-Methyl-C3-este 79 (1.317) Cm ((63:64	r !+67+77+79+	88+122:123 277.10	GC-TOF 3)-258:292x2.000 684))				19-Feb	2008 13:18:19 TOF MS EI+ 1.07e5
275.1558	276 162	276.7187	276 0022	277.3405	278.17	29 278.3375	2	79.1699	270 2276	280 1705
0 K	.50 276.00	276.50	277.00	277.50	278.00	278.50	279.0	00	279.50	280.00 m/z
Minimum: Maximum:		5.0	10.0	-1.5 50.0						
Mass	Calc. Mass	mDa	PPM	DBE	Score	Form	ula			
277.1684	277.1678 277.1665 277.1705 277.1651 277.1638	0.6 1.9 -2.1 3.3 4.6	2.2 7.0 -7.5 11.8 16.7	6.0 6.5 10.5 1.5 2.0	3 1 5 2 4	C16 C14 C19 C13 C11	H23 H21 H21 H25 H23	N 03 N4 02 N2 06 N3 05	Y	

B.9 3-*n*-Butyl-*N*¹-hydroxyl-*N*⁸-phenyloctanoic acid (**7**) **B.9.1** ¹H NMR



Page 1

B.9.2 ¹³C NMR P.8 19 ## 105 / 01 Silan CD (23 10 - 5 LIZ 10 LIZ 10 300 mp N MA)180 40 160 140 120 1-7 80 60 20 ppm . 3



B.9.3 IR



B.9.4 HRMS

Elemental Composition Report

Single Mass Analysis (displaying only valid results)

Tolerance = 4.0 mDa / DBE: min = -1.5, max = 50.0 Isotope cluster parameters: Separation = 1.0 Abundance = 1.0%

Monoisotopic Mass, Odd and Even Electron Ions 52 formula(e) evaluated with 2 results within limits (all results (up to 1000) for each mass)

Sun Ea Choi	09050	7-63 bulyic	arboxilic acid		00.7	05			05-Oct-2007 11:10:57
100-	6 125 (2.08	4) Cm (107:	126-7:32x2.0	00)	GC-1	305.19	993		TOF MS EI+ 7.71e4
%294.	1102 299	6.1175 297	.1192 299.	1245 _ 301	.1466303.;	1726	306.2058 307.2051	310.1192	313.1515
-	294.0	296.0	298.0	300.0	302.0	304.0	306.0 308.0	310.0	312.0 314.0
Minimum:					-1.5				
Maximum:			4.0	5.0	50.0				
Mass	Calc.	Mass	mDa	PPM	DBE	Score	Formula		
305.1993	305.1 305.1	991 978	0.2 1.6	0.8 5.2	6.0 6.5	1 2	C18 H27 C16 H25	N 03 N4 02	



Page 1



B.10 3-*n*-Butyl-*N*¹-benzyloxy-*N*⁸-phenyloctanediamide (8) **B.10.1** ¹H NMR



B.10.2 ¹³C NMR





B.10.3 IR




B.10.4 HRMS

Elemental Composition Report

Single Mass Analysis

Tolerance = 5.0 mDa / DBE: min = -1.5, max = 50.0 Isotope cluster parameters: Separation = 1.0 Abundance = 1.0%

Monoisotopic Mass, Odd and Even Electron Ions

329 formula(e) evaluated with 7 results within limits (all results (up to 1000) for each mass)

Sun Ea Choi	091007-C3 buty	d-benzylhydroxylar	nine	00 T	OF						08-Oct	-2007 11:03:42
L071008_915 1	142 (2.367) Cm ((122:126+133+142·	+146+202)-1	GC-1 5:45x2.000)	0F	410.256	6					TOF MS EI+ 1.86e3
%- 391.21 0	07	399.3897 40	1.4128	406.2	407.236	34	411.2	610	415.	4591	417.3020) 421.4738 m/z
392 Minimum: Maximum:	.5 395.0	5.0	402.5	405.0 -1.5 50.0	407.5	410.0	412	2.5	415.	0	417.5	420.0
Mass	Calc. Mass	mDa	PPM	DBE	Score		Form	ula				
410.2566	410.2569 410.2556 410.2543 410.2596 410.2529 410.2610 410.2615	-0.4 1.0 2.3 -3.0 3.7 -4.4 -4.9	-0.9 2.4 5.7 -7.4 8.9 -10.7 -11.9	10.0 10.5 5.5 14.5 6.0 14.0 1.5	3 4 5 1 6 2 7		C25 C23 C22 C28 C20 C30 C30 C16	H34 H32 H36 H32 H34 H34 H36	N2 N5 N3 N4 O N5	03 02 06 05 07		

B.11 3-*n*-Butyl-*N*¹-hydroxyl-*N*⁸-phenyloctandiamide (**1a**) **B.11.1** ¹H NMR



133

Page 1

B.11.2 ¹³C NMR





www.manaraa.com

B.11.3 IR



B.11.4 HRMS

Single Mass Analysis (displaying only valid results) Tolerance = 4.0 mDa / DBE: min = -1.5, max = 50.0 Isotope cluster parameters: Separation = 1.0 Abundance = 1.0%

Monoisotopic Mass, Odd and Even Electron lons 41 formula(e) evaluated with 1 results within limits (all results (up to 1000) for each mass)



Sun Ea Choi 091407-PG 21 SPEI 70eV GC-TOF L071005_907a 161 (2.683) Cm ((120+126:127+130+161+164)-317:356x2.000) 100





%-							321.2240			
-1314.162 0-1-+	315.0	316.307 	7 317.343 317.0	2 318.338 318.0	319.2182 9 319.0	320.0	320.3456 321.0	322.2647 322.0	323.3225 323.0	324.2744 324.0
Minimum: Maximum:			4.0	5.0	-1.5 50.0					
Mass	Calc.	Mass	mDa	PPM	DBE	Score	Formula			
320.2108	320.21	00	0.8	2.6	6.0	1	C18 H2	8 N2 03	5	



B.11.5 HPLC





B.12 3-Phenyl- N^1 -hydroxyl- N^8 -phenyloctandiamide (**1b**)

B.12.1 ¹H NMR











www.manaraa.com

B.12.3 IR





B.12.4 HRMS

Elemental Composition Report

Single Mass Analysis

Tolerance = 5.0 mDa / DBE: min = -1.5, max = 50.0 Isotope cluster parameters: Separation = 1.0 Abundance = 1.0%

Monoisotopic Mass, Odd and Even Electron Ions

330 formula(e) evaluated with 7 results within limits (all results (up to 1000) for each mass)

Sun Choi GCEI 70eV	March 05 08-Phenyl-C3	3-hydroxylamir	ne	GC-TOF			17-Mar-2008 15:16	08
L080317_102	29 154 (2.568) Cm ((129:	130+154)-16:	33x2.000)				TOF MS E	1+
100				340.17	89		1	84
0	332.1134 333.1385 332.0 334.0	336.188	2 ^{338.1549} 33	8.9135 340.0	341.1850 342.1830 342.0	343.1959 	346.1505 347.1494 349.1252	? 1/z
Minimum: Maximum:		5.0	10.0	-1.5 50.0				
Mass	Calc. Mass	mDa	PPM	DBE	Score	Formula		
340.1789	340.1787 340.1774 340.1814 340.180 340.1827 340.1827 340.1747 340.1832	0.2 1.6 -2.4 2.9 -3.8 4.3 -4.3	0.7 4.6 -7.2 8.6 -11.1 12.5 -12.6	10.0 10.5 14.5 5.5 14.0 6.0 1.5	3 4 2 5 1 6 7	C20 H24 C18 H22 C23 H22 C17 H26 C25 H24 C15 H24 C11 H26	N2 03 N5 02 N3 N 06 0 N4 05 N5 07	

B.12.5 HPLC





Page 1

B.13 3-Ethyl- N^1 -hydroxyl- N^8 -phenyloctandiamide (**1c**)













B.13.3 IR





B.13.4 HRMS

Single Mass Analysis

Tolerance = 6.0 PPM / DBE: min = -1.5, max = 50.0 Element prediction: Off Number of isotope peaks used for i-FIT = 3

Monoisotopic Mass, Even Electron Ions 348 formula(e) evaluated with 2 results within limits (up to 50 closest results for each mass) Elements Used: C: 0-500 H: 0-1000 N: 0-4 O: 0-10 Na: 0-1 pflum; sun choi Apr1808C3ethylhydroxylamine mw292 LCT0001 10pg/ul meoh 10ul full 150ul/min meoh LeuEnk 100pg/ul 2008-0507-0001-31 21 (0.477) Cm (19:25-1:13x2.000)



B.13.5 HPLC





2::0::5 07-May-2008

1: TOF MS ES-







www.manaraa.com

B.14.4 HRMS

Single Mass Analysis Tolerance = 5.0 PPM / DBE: min = -1.5, max = 50.0 Element prediction: Off Number of isotope peaks used for i-FIT = 3



 Monoisotopic Mass, Even Electron Ions

 352 formula(e) evaluated with 1 results within limits (up to 50 best isotopic matches for each mass)

 Elements Used:

 C: 0-50
 H: 0-50

 Uan 30 09-C3-vinylhydroxamic PG37

 Lew 2008-07b.pro

 2009_0202_0297 15 (0.318) Cm (12:17-(1:9+29:36)x2.000)

 1: TOF MS ES+









145

B.15 3-Methyl- N^1 -hydroxyl- N^8 -phenyloctandiamide (**1e**)

B.15.1 ¹H NMR





www.manaraa.com

B.15.3 IR



المتسارات

www.manaraa.com

B.15.4 HRMS

Elemental Composition Report Page 1 Single Mass Analysis Tolerance = 5.0 mDa / DBE: min = -1.5, max = 50.0 Isotope cluster parameters: Separation = 1.0 Abundance = 1.0% Monoisotopic Mass, Odd and Even Electron Ions 222 formula(e) evaluated with 6 results within limits (all results (up to 1000) for each mass) Sun Choi Feb21 08-methyl-C3-hydroxylamine 22-Feb-2008 11:09:55 GCEI 70eV GC-TOF L080221_1006b 92 (1.533) Cm ((92+100+103:104)-440:480x2.000) TOF MS EI+ 278.1635 5.91e3 100-% 279.1694 271.1606 272.1817 274.1767 275.1748 277.1665 280.1746 283.1255 282.1344 286.1835 0 — m/z 270.0 272.0 274.0 276.0 278.0 280.0 282.0 284.0 286.0 Minimum: -1.5 Maximum: 5.0 10.0 50.0 Mass Calc. Mass mDa РРМ DBE Score Formula 278.1635 278.1630 0.4 1.6 6.0 1 C15 H22 N2 03 278.1617 1.8 6.4 6.5 4 C13 H20 N5 02 278.1657 -2.2 -8.1 10.5 2 C18 H20 NЗ 278.1604 3.1 11.2 1.5 5 C12 H24 Ν 06

B.15.5 HPLC





APPENDIX C. DOSE RESPONSE GRAPHS AND DATA FOR C6-SAHA LIBRARY

Table C.I. Feld	Table C. I. Percentage TDAC activity after incubation of SATIA with Held Lysate									
Concentration	Trial 1	Trial 2	Trial 3	Mean	Standard					
(M)					Error (S.E.)					
3.125 x 10 ⁻⁸	75	75	ND	75	0					
6.25 x 10 ⁻⁸	63	56	51	57	3					
1.25 x 10 ⁻⁷	44	35	40	40	3					
2.5 x 10 ⁻⁷	31	21	26	26	3					
5.0 x 10 ⁻⁷	20	16	15	17	2					

Table C.1. Percentage HDAC activity after incubation of SAHA with Hela Lysate





Figure C.1. Dose response curve of SAHA tested using the HDAC activity from HeLa cells lysates from three independent trials In some case, the error bar is smaller than the marker size. Data were fit to the sigmoidal curve using Kaleidograph 4.0 (Synergy Software) to determine the IC_{50} . The insets were the results of the data analysis. The data are reported in Table 3.1.



Lysale					
Concentration	Trial 1	Trial 2	Trial 3	Mean	Standard Error
(M)					(S.E.)
1.95 x 10 ⁻⁶	58	59	58	58	0.3
3.91 x 10 ⁻⁶	44	47	49	47	1
7.81 x 10 ⁻⁶	32	35	33	33	1
1.56 x 10 ⁻⁵	27	27	26	27	0.3
6.25 x 10 ⁻⁵	9	12	11	11	1

 Table C.2.
 Percentage HDAC activity after incubation of MS-275 with Hela

 Lysate





Figure C.2. Dose response curve of MS-275 tested using the HDAC activity from HeLa cells lysates from three independent trials. In some cases, the error bars are smaller than the marker size. Data were fit to the sigmoidal curve using Kaleidograph 4.0 (Synergy Software) to determine the IC_{50} . The insets were the results of the data analysis. The data are reported in Table 3.1.



Table	C.3.	Percentage	HDAC	activity	after	incubation	of	C6-SAHA	methyl
analog	ue 14	la with Hela L	ysate						

Concentration	Trial 1	Trial 2	Trial 3	Mean	Standard Error
(M)					(S.E.)
6.25 x 10 ⁻⁸	104	72	102	92	10
1.25 x 10⁻′	94	50	85	76	13
2.5 x 10⁻′	66	51	79	65	8
5.0 x 10⁻′	30	32	40	34	3
1.0 x 10 ⁻⁶	24	20	22	22	1

IC50 Curve of C6-Methyl Analogue



Figure C.3. Dose response curve of C6-SAHA methyl analogue **14a** tested using the HDAC activity from HeLa cells lysates from three independent trials. In some case, the error bar is smaller than the marker size. Data were fit to the sigmoidal curve using Kaleidograph 4.0 (Synergy Software) to determine the IC₅₀. The insets were the results of the data analysis. The data are reported in Table 3.1.



Table	C.4.	Percentage	HDAC	activity	after	incubation	of	C6-SAHA	phenyl
analog	ue 14	b with Hela L	ysate						

Concentration	Trial 1	Trial 2	Trial 3	Mean	Standard Error
(M)					(S.E.)
6.25 x 10 ⁻⁸	87	87	82	85	1
1.25 x 10⁻′	75	73	75	74	0.7
2.5 x 10⁻′	59	41	54	51	5
5.0 x 10⁻′	45	47	51	47	1
1.0 x 10 ⁻⁶	27	23	20	23	2



IC50 Curve of C6-Phenyl Analogue





Table	C.5.	Percentage	HDAC	activity	after	incubation	of	C6-SAHA	<i>t</i> -butyl
analog	ue 14	c with Hela L	ysate						

Concentration	Trial 1	Trial 2	Trial 3	Mean	Standard	Error
(M)					(S.E.)	
1.11 x 10 ⁻⁷	94	99	114	102	6	
3.33 x 10⁻′	65	87	103	85	11	
1.0 x 10 ⁻⁶	55	58	71	61	4	
3.0 x 10⁻ ⁶	40	37	41	39	1	
9.0 x 10 ⁻⁶	28	20	18	22	3	

ICso Curve of C6-t-Butyl Analogue



Figure C.5. Dose response curve of C6-SAHA *t*-butyl analogue **14c** tested using the HDAC activity from HeLa cells lysates from three independent trials. In some case, the error bar is smaller than the marker size. Data were fit to the sigmoidal curve using Kaleidograph 4.0 (Synergy Software) to determine the IC₅₀. The insets were the results of the data analysis. The data are reported in Table 3.1.



Table C.6. Percentage HDAC	; activity after	incubation of	C6-SAHA	2-ethylhexyl
analogue 14d with Hela Lysate	Э			

Concentration	Trial 1	Trial 2	Trial 3	Mean	Standard Error
(M)					(S.E.)
1.11 x 10⁻′	93	69	78	80	7
3.33 x 10 ⁻⁷	62	54	55	57	2
1.0 x 10 ⁻⁶	42	22	38	34	6
3.0 x 10 ⁻⁶	12	8	13	11	1
9.0 x 10 ⁻⁶	4	2	2	2.7	0.7



Figure C.6. Dose response curve of C6-SAHA 2-ethylhexyl analogue **14d** tested using the HDAC activity from HeLa cells lysates from three independent trials with error bars indicating standard error. In some case, the error bar is smaller than the marker size. Data were fit to the sigmoidal curve using Kaleidograph 4.0 (Synergy Software) to determine the IC_{50} . The insets were the results of the data analysis. The data are reported in Table 3.1.



Compound	HDAC Isoform	Trial 1	Trial 2	Mean	S.E.
	HDAC1	30	35	32	2
SAHA	HDAC3	44	45	44	1
(1251111)	HDAC6	32	36	34	2
	HDAC1	35	42	38	3
C6-Methyl	HDAC3	32	33	32	0.5
	HDAC6	61	58	59	1
	HDAC1	57	56	56	0.5
C6-Phenyl (500 nM)	HDAC3	68	67	67	0.5
	HDAC6	61	58	59	1
	HDAC1	44	46	45	1
C6- <i>t</i> -Butyl	HDAC3	79	82	80	1
(2 µm)	HDAC1 30 HDAC3 44 HDAC6 32 HDAC1 35 HDAC3 32 HDAC3 32 HDAC6 61 HDAC6 61 HDAC3 68 HDAC6 61 HDAC3 68 HDAC6 61 HDAC6 56 HDAC6 56 HDAC6 91 HDAC6 91 HDAC1 42 HDAC3 50 HDAC6 24	55	55	0.5	
	HDAC1	77	73	75	2
C6-2-Ethylhexyl	HDAC3	51	54	52	1
(500 NNI)	HDAC6	91	95	93	2
	HDAC1	42	48	45	3
C6-Isopropyl	HDAC3	50	51	51	1
(µivi)	A HDAC1 HDAC3 HDAC6 HDAC1 HDAC3 HDAC6 HDAC1 HDAC6 HDAC1 HDAC3 HDAC6 HDAC1 HDAC3 HDAC6 HDAC1 HDAC3 HDAC6 HDAC1 HDAC3 HDAC6 HDAC1 HDAC3 HDAC6 HDAC1 HDAC3 HDAC6 HDAC1 HDAC3 HDAC6 HDAC1 HDAC3 HDAC6 HDAC1 HDAC6 HDAC3 HDAC6 HDAC6 HDAC1 HDAC6	24	27	26	2

Table C.7. Deacetylase activity percentage remaining after incubation of HDAC1, HDAC3, or HDAC6 with SAHA or the C6-SAHA analogues **14a-e**.

Deacetylase activity of HDAC1, HDAC3 and HDAC6 was determined with SAHA and with C6-SAHA analogues at given concentration using an in vitro fluorescence assay as described (Section 3.6). The fluorescence activity of background (No enzyme added) was subtracted from the no small molecule treated (positive control) and the percentage of the deacetylase activity was set to 100%. Deacetylase activity percentage of each independent trial, mean percentage of deacetylase activity, and standard error (S.E.) are illustrated. The data are reported in the manuscript in Figure 3.2.



Concentration	Trial 1	Trial 2	Trial 3	Mean	Standard Error
(M)					(S.E.)
3.125 x 10 ⁻⁸	68	91	82	80	7
6.25 x 10 ⁻⁸	55	62	57	58	2
1.25 x 10 ⁻⁷	48	27	37	37	6
2.50 x 10 ⁻⁷	37	40	25	34	5

Table C.8. HDAC1 activity percentage after incubation of SAHA.



HDAC1 IC 50 Curve of SAHA

Figure C.7. Dose response curve of SAHA tested using the HDAC1 activity from three independent trials with error bars indicating standard error. Data were fit to the sigmoidal curve using Kaleidograph 4.0 (Synergy Software) to determine the IC_{50} . The insets were the results of the data analysis. The data are reported in Table 3.2.



	Tuble eler i bi too doarney poroontage anor modbadon or or an a									
Concentration	Trial 1	Trial 2	Trial 3	Mean	Standard	Error				
(M)					(S.E.)					
3.125 x 10 ⁻⁸	88	78	74	80	4					
6.25 x 10 ⁻⁸	76	74	70	73	2					
1.25 x 10 ⁻⁷	63	45	44	56	5					
2.50 x 10 ⁻⁷	27	39	37	34	4					

Table C.9. HDAC3 activity percentage after incubation of SAHA.



HDAC3 IC 50 Curve of SAHA

Figure C.8. Dose response curve of SAHA tested using the HDAC3 activity from three independent trials with error bars indicating standard error. Data were fit to the sigmoidal curve using Kaleidograph 4.0 (Synergy Software) to determine the IC_{50} . The insets were the results of the data analysis. The data are reported in Table 3.2.



Table errer net to a damy percentage and medballen of er and									
Concentration	Trial 1	Trial 2	Trial 3	Mean	Standard	Error			
(M)					(S.E.)				
3.125 x 10 ⁻⁸	66	76	73	72	3				
6.25 x 10 ⁻⁸	64	62	60	62	1				
1.25 x 10⁻′	37	28	32	32	2				
2.50 x 10 ⁻⁷	13	12	9	11	1				

Table C.10. HDAC6 activity percentage after incubation of SAHA.



HDAC6 IC 50 Curve of SAHA

Figure C.9. Dose response curve of SAHA tested using the HDAC6 activity from three independent trials with error bars indicating standard error. In some case, the error bars are smaller than the marker size. Data were fit to the sigmoidal curve using Kaleidograph 4.0 (Synergy Software) to determine the IC_{50} . The insets were the results of the data analysis. The data are reported in Table 3.2.



analogue i iei					
Concentration	Trial 1	Trial 2	Trial 3	Mean	Standard Error
(M)					(S.E.)
2.50 x 10⁻′	102	92	82	92	5
5.00 x 10⁻′	86	85	80	84	1
1.00 x 10 ⁻⁶	68	44	35	49	9
3.125 x 10⁻⁵	7	1	1	3	2

Table C.11. HDAC1 activity percentage after incubation of C6-SAHA *t*-butyl analogue **14c**.



HDAC1 IC 50 Curve of C6+Butyl Analogue

Figure C.10. Dose response curve of C6-SAHA *t*-butyl analogue **14c** tested using the HDAC1 activity from three independent trials with error bars indicating standard error. Data were fit to the sigmoidal curve using Kaleidograph 4.0 (Synergy Software) to determine the IC_{50} . The insets were the results of the data analysis. The data are reported in Table 3.2.



Concentration	Trial 1	Trial 2	Trial 3	Mean	Standard Error
(M)					(S.E.)
1.00 x 10 ⁻⁶	87	85	81	84	1
4.00 x 10 ⁻⁶	76	63	52	64	6
1.5625 x 10 ⁻⁵	21	20	13	18	2
3.125 x 10 ⁻⁵	7	6	6	6	-

Table C.12. HDAC3 activity percentage after incubation of C6-SAHA *t*-butyl analogue **14c**.



HDAC3 IC50 Curve of C6-t-Butyl Analogue

Figure C.11. Dose response curve of C6-SAHA *t*-butyl analogue **14c** tested using the HDAC3 activity from three independent trials. In some case, the error bar is smaller than the marker size. Data were fit to the sigmoidal curve using Kaleidograph 4.0 (Synergy Software) to determine the IC_{50} . The insets were the results of the data analysis. The data are reported in Table 3.2.



analoguo 110.					
Concentration	Trial 1	Trial 2	Trial 3	Mean	Standard Error
(M)					(S.E.)
5.00 x 10 ⁻⁷	98	90	88	92	3
1.00 x 10 ⁻⁶	89	82	86	85	2
2.00 x 10 ⁻⁶	48	35	48	44	4
4.00 x 10 ⁻⁶	45	29	45	40	5

Table C.13. HDAC6 activity percentage after incubation of C6-SAHA *t*-butyl analogue **14c**.



HDAC6 IC50 Curve of C6-t-BUtyl Analogue

Figure C.12. Dose response curve of C6-SAHA *t*-butyl analogue **14c** tested using the HDAC6 activity from three independent trials with error bars indicating standard error. Data were fit to the sigmoidal curve using Kaleidograph 4.0 (Synergy Software) to determine the IC_{50} . The insets were the results of the data analysis. The data are reported in Table 3.2.



APPENDIX D. SUPPLEMENTARY INFORMATION FOR C6-SAHA LIBRARY

D.1 Methyl 6-hydroxyhexanoate (9)

D.1.1¹H NMR







D.1.3 IR



QC_Compare-4860.jws



D.1.4 HRMS

Elementa	l Compositio	on Report							Page 1
Single Ma Tolerance = Element pro Number of	ss Analysis 5.0 PPM / ediction: Off isotope peaks	DBE: min = - used for i-FI	1.5, max = { T = 3	50.0	~	, in	ન		
Monoisotopii 31 formula(e Elements Use C: 0-500 ofilum- Sun Cl Snay 2008-07 2008_0818_0	c Mass, Even El evaluated with ed: H: 0-1000 O: objuly2708-C6-ald b.pro 082_10 13 (0.300)	ectron lons 1 results with 0-6 23Na: cohol-PG127 m Cm (10:18-28:	in limits (up te 0-1 w146 LCT0082 45x2.000)	o 50 best isof 10pg/ul mech	topic matches fi 2ul 4cm stk RF1	or each mass) 50	LCT Pre	mier 18-Au	g-2008 15:04:26 1: TOF MS ES+ 7.98e+003
100-						169	.0840		1.0001000
%- 0	94106.9278	123.8915	133.2541	140.9966	153.1449	164.9216	170.0888	183.0798	187.0969 m/z
	110.0	120.0	130.0	140.0	150.0	160.0	170.0	180.0	190.0
Minimum: Maximum:		5.0	5.0	-1.5 50.0					
Mass	Calc. Mass	mDa	PPM	DBE	i-FIT	i-FIT (Nor	m) Formu	la	
169.0840	169.0841	-0.1	-0.6	0.5	52.3	0.0	C7 H	14 03	23Na



D.2 1-Benzyl 8-methyl oct-2-enedioate (11)

D.2.1 ¹H NMR









www.manaraa.com

D.2.3 IR

QC_Compare-13597.jws





D.2.4 HRMS



D.3 1-Benzyl 8-methyl 3-methyloctanedioate (12a)

D.3.1 ¹H NMR








D.4 1-Benzyl 8-methyl 3-(*tert*-butyl)octanedioate (12c)

D.4.1 ¹H NMR









D.4.3 IR







D.5 1-Benzyl 8-methyl 3-(2-ethylhexyl)octanedioate (12d) D.5.1 1 H NMR









QC_Compare-7568.jws













D.6.2 ¹³C NMR















D.6.4 HRMS

Single Mass Analysis Tolerance = 5.0 PPM / DBE: min = -1.5, max = 150.0 Element prediction: Off Number of isotope peaks used for i-FIT = 6

Monoisotopic Mass, Even Electron Ions 845 formula(e) evaluated with 4 results within limits (up to 50 closest results for each mass) Elements Used: C: 0-100 H: 0-1000 N: 0-10 O: 0-10 23Na: 0-1

SUN CHOI Aug 20 11-C6-Isopropylester LCT2008-07b.pro 2010-clf.spl

2011_0822_2184 14 (0.283) Cm (11:19-1:8x2.000)

22-Aug-2011LCT Premier10:11:10 1: TOF MS ES+ 2.58e+004

											343,1883					2.58e+004
100 285.07	98				317.1054321.20	069 327.3	2146				_344.	1925	355.2256	361.111	10	371.2201
285.0	290.0 295.0	300.0	305.0	310.0 3	315.0 320.0	325.0	330.0	33	5.0	340	.0 345.0	350.0	355.0	360.0	365.0	370.0
Minimum: Maximum:		50.0	5.0	-1.5 150.0												
Mass	Calc. Mass	mDa	PPM	DBE	i-FIT	i-FIT	(Norm)	Form	ula							
343.1883	343.1882 343.1885 343.1869 343.1899	0.1 -0.2 1.4 -1.6	0.3 -0.6 4.1 -4.7	9.5 5.5 4.5	60.4 60.4 63.1 58.5	2.1 2.2 4.8		C17 C19 C16 C20	H23 H28 H27 H24	N6 04 N2 N4	02 23Na 06 23Na					











D.7.3 IR

QC_Compare-4409.jws













D.8.2 ¹³C NMR







D.9 Methyl 8-ethyl-6-(2-oxo-2-(phenylamino)ethyl)dodecanoate (**13d**) **D.9.1** ¹H NMR









185

D.9.3 IR

QC_Compare-7572.jws

















QC_Compare-13464.jws





D.10.4 HRMS

Single Mass Analysis Tolerance = 5.0 PPM / DBE: min = -1.5, max = 150.0 Element prediction: Off Number of isotope peaks used for i-FIT = 6

Monoisotopic Mass, Even Electron Ions 845 formula(e) evaluated with 1 results within limits (up to 50 closest results for each mass) Elements Used: C: 0-100 H: 0-1000 N: 0-10 O: 0-15 23Na: 0-1 SUN, CHOI Sept 27 11-05-Isopropytanlide LCT2008-07b.pro 2010-dt.spl

LC12008-076.	pro 2010-cit.spi																	
2011_0927_22	246 260 (5.695) Cn	n (257:269-130:19	95x2.000)											2	7-Sep-20	1:	TOF MS 8.79	ES+ 2+003
100 300.253	33 306.2	071 _307.2094	312.2153	314.2699		322.2363	,323.2385	328	.1884	29.191	9	336	.2508,337	.2497	344.16	524345.3	113 _346	3151
300.0 3	302.5 305.0	307.5 310.	0 312.5	315.0	317.5 320.0	322.5	325.0	327.5	5 33	0.0	332.5	335.0	337.5	340.0	342.5	345.0	34	7.5
Minimum: Maximum:		50.0	5.0	-1.5 150.0														
Mass	Calc. Mass	mDa	PPM	DBE	i-FIT	i-FIT	(Norm)	Formul	a									
306.2071	306,2069	0.2	0.7	5.5	49.8	0.0		C18 H	28 N	1 03								

roury 400 spectrometer

D.11 *N*⁸-Hydroxyl-3-methyl-*N*¹-phenyloctanediamide (**14a**) **D.11.1** ¹H NMR







Mercury 400 spectrometer



D.11.3 IR









Mercury 400 spectrometer





192

Mercury 400 spectrometer











D.12.4 HRMS







Mercury 400 spectrometer



www.manaraa.com

JAN 23, 2010















Mercury 400 spectrometer

للاستشارات



Mercury 400 spectrometer







-1.6

4.8

-0.6

1.8

377.2804 377.2780

377.2798

5.5 2.5

15.6

21.9

0.0

6.3



APPENDIX E. DOSE RESPONSE GRAPHS AND DATA FOR C7-SAHA LIBRARY

Table L.T. Fercentage TDAC activity after incubation of SAHA with held Lysa									
Concentration	Trial 1	Trial 2	Trial 3	Mean	Standard	Error			
(M)					(S.E.)				
3.125 x 10 ⁻⁸	75	75	76	75	0				
6.25 x 10 ⁻⁸	63	56	51	57	3				
1.25 x 10 ⁻⁷	44	35	40	40	3				
2.5 x 10 ⁻⁷	31	21	26	26	3				
5.0 x 10⁻′	20	16	15	17	2				

 Table E.1. Percentage HDAC activity after incubation of SAHA with Hela Lysate





Figure E.1. Dose response curve of SAHA tested using the HDAC activity from HeLa cells lysates from three independent trials. In some case, the error bar is smaller than the marker size. Data were fit to the sigmoidal curve using Kaleidograph 4.0 (Synergy Software) to determine the IC_{50} . The insets were the results of the data analysis. The data are reported in Table 4.1.



analogue zzu w												
Concentration	Trial 1	Trial 2	Trial 3	Mean	Standard	Error						
(M)					(S.E.)							
1.11 x 10 ⁻⁷	70	70	86	75	5							
3.33 x 10 ⁻⁷	63	66	49	59	5							
1.00 x 10 ⁻⁶	45	24	31	33	6							
3.00 x 10 ⁻⁶	18	5	18	14	4							
9.00 x 10 ⁻⁶	8	-2	24	3	3							

 Table E.2.
 Percentage HDAC activity after incubation of C7-SAHA pyridyl analogue 22d with Hela Lysate

IC50 Curve of C7-Pyridyl Analogue



Figure E.2. Dose response curve of C7-SAHA pyridyl analogue **22d** tested using the HDAC activity from HeLa cells lysates from three independent trials. Data were fit to the sigmoidal curve using Kaleidograph 4.0 (Synergy Software) to determine the IC_{50} . The insets are the results of the data analysis. The data were reported in Table 4.2.



Table	E.3.	Percentage	HDAC	activity	after	incubation	of	C7-SAHA
methyla	anthrac	ene analogue	e 22f with	Hela Lys	ate.			

Concentration (M)	Trial 1	Trial 2	Trial 3	Mean	S.E.
4.10 x 10 ⁻⁹	81	76	75	77	2
1.23 x 10⁻ ⁸	47	60	61	56	4
3.70 x 10 ⁻⁸	33	38	49	40	4
1.11 x 10 ⁻⁷	27	15	23	22	3
3.33 x 10 ⁻⁷	10	12	13	12	1
1.00 x 10 ⁻⁶	7	5	8	7	1



Figure E.3. Dose response curve of C7-SAHA anthracenylmethyl analogue **22f** tested using the HDAC activity from HeLa cells lysates from three independent trials. In some case, the error bars are smaller than the marker size. The insets were the results of the data analysis. The data are reported in Table 4.2.



Table	E.4.	Percentage	HDAC	activity	after	incubation	of	C7-SAHA
methylt	etrahy	dro-anthracen	e analog	jue 22g w	ith Hela	Lysate.		

		<u> </u>			
Concentration (M)	Trial 1	Trial 2	Trial 3	Mean	S.E.
1.00 x 10 ⁻⁸	92	124	92	102	10
5.00 x 10 ⁻⁸	38	68	76	60	11
2.50 x 10 ⁻⁷	27	27	30	28	1
1.25 x 10 ⁻⁶	11	25	15	17	4
6.25 x 10 ⁻⁶	-2	2	0.5	0	1

IC50 Curve of C7-Tetrahydroanthracene



Figure E.4. Dose response curve of C7-SAHA tetrahydroanthracenylmethyl analogue **22g** tested using the HDAC activity from HeLa cells lysates from three independent trials with error bars indicating standard error. In some case, the error bars are smaller than the marker size. Data were fit to the sigmoidal curve using Kaleidograph 4.0 (Synergy Software) to determine the IC₅₀. The insets were the results of the data analysis. The data are reported in Table 4.2.


Compound	HDAC Isoform	Trial 1	Trial 2	Mean	S.E.
	HDAC1	30	35	32	2
SAHA	HDAC3	44	45	44	1
(125 1111)	HDAC6	32	36	34	2
_	HDAC1	38	52	45	7
C7-Methyl	HDAC3	27	57	42	10
(100 110)	HDAC6	21	35	28	7
	HDAC1	66	87	76	10
C7-Benzyl	HDAC3	54	88	71	11
(100 mm)	HDAC6	55	66	60	5
	HDAC1	44	68	56	10
C7-Pyridyl	HDAC3	101	92	97	4
(500 nM)	HDAC6	62	55	59	3
	HDAC1	64	66	65	1
C7-Tetrahydro-	HDAC3	47	60	53	6
(100 nM)	HDAC6	76	84	80	4
	HDAC1	91	114	102	10
C7-Biphenyl	HDAC3	91	96	93	2
(100 mm)	HDAC6	71	82	76	5
	HDAC1	103	121	112	9
(10 nM)	HDAC3	55	60	57	2
	HDAC6	82	104	93	10
	HDAC1	42	47	44	2
(500 nM)	HDAC3	89	90	89	0
	HDAC6	50	56	53	3

Table E.5. Deacetylase activity percentage remaining after incubation of HDAC1, HDAC3, or HDAC6 with SAHA and the C7-SAHA analogues **22a-g**.

Deacetylase activity of HDAC1, HDAC3 and HDAC6 was determined with SAHA and with C7-SAHA analogues at given concentration using an in vitro fluorescence assay as described (Section 3.6). The fluorescence activity of background (No enzyme added) was subtracted from the no small molecule treated (positive control) and the percentage of the deacetylase activity was set



to 100%. Deacetylase activity percentage of each independent trial, mean percentage of deacetylase activity, and standard error (S.E.) are illustrated. The data are reported in the manuscript in Figure 4.2.

Concentration (M)	Trial 1	Trial 2	Trial 3	Mean	Standard Error (S.E.)
3.125 x 10 ⁻⁸	68	91	82	80	7
6.25 x 10 ⁻⁸	55	62	57	58	2
1.25 x 10⁻′	48	27	37	37	6
2.50 x 10⁻′	37	40	25	34	5

Table E.6. HDAC1 activity percentage after incubation of SAHA.

HDAC1	IC 50 Curve	of SAHA
-------	-------------	---------



Figure E.5. Dose response curve of SAHA tested using the HDAC1 activity from three independent trials with error bars indicating standard error. In some case, the error bar is smaller than the marker size. Data were fit to the sigmoidal curve using Kaleidograph 4.0 (Synergy Software) to determine the IC₅₀. The insets were the results of the data analysis. The data are reported in Table 4.3.



TADIE E.7. HDAC	3 activity pe	ercentage a	inter incubai	ION OF SAH	А.	
Concentration	Trial 1	Trial 2	Trial 3	Mean	Standard Er	ror
(M)					(S.E.)	
3.125 x 10 ⁻⁸	88	78	74	80	4	
6.25 x 10 ⁻⁸	76	74	70	73	2	
1.25 x 10⁻′	63	45	44	56	5	
2.50 x 10 ⁻⁷	27	39	37	34	4	





Figure E.6. Dose response curve of SAHA tested using the HDAC3 activity from three independent trials with error bars indicating standard error. In some case, the error bar is smaller than the marker size. Data were fit to the sigmoidal curve using Kaleidograph 4.0 (Synergy Software) to determine the IC₅₀. The insets were the results of the data analysis. The data are reported in Table 4.3.



	o activity p	creenaye e			Α.
Concentration	Trial 1	Trial 2	Trial 3	Mean	Standard Error
(M)					(S.E.)
3.125 x 10 ⁻⁸	66	76	73	72	3
6.25 x 10 ⁻⁸	64	62	60	62	1
1.25 x 10 ⁻⁷	37	28	32	32	2
2.50 x 10 ⁻⁷	13	12	9	11	1

Table E.8. HDAC6 activity percentage after incubation of SAHA.



HDAC6 IC 50 Curve of SAHA

Figure E.7. Dose response curve of SAHA tested using the HDAC6 activity from three independent trials with error bars indicating standard error. In some case, the error bars are smaller than the marker size. Data were fit to the sigmoidal curve using Kaleidograph 4.0 (Synergy Software) to determine the IC_{50} . The insets were the results of the data analysis. The data are reported in Table 4.3.



Table	E.9.	HDAC1	activity	percentage	after	incubation	of	C7-SAHA
anthrac	cenylm	ethyl 22f.						

Concentration	Trial 1	Trial 2	Trial 3	Mean	Standard Error
(M)					(S.E.)
1.11 x 10 ⁻⁷	103	96	86	96	4
3.33 x 10 ⁻⁷	33	42	43	39	3
1.00 x 10 ⁻⁶	17	16	17	17	0



HDAC1 IC 50 Curve of C7-Anthracene Analogue

Figure E.8. Dose response curve of C7-SAHA anthracenylmethyl analogue **22f** tested using the HDAC1 activity from three independent trials with error bars indicating standard error. Data were fit to the sigmoidal curve using Kaleidograph 4.0 (Synergy Software) to determine the IC_{50} . The insets were the results of the data analysis. The data are reported in Table 4.3.



	10/100 40	and poio	ontago an			0/ 11 // 1
anthracenylmeth	yl 22f .					
Concentration	Trial 1	Trial 2	Trial 3	Mean	Standard	Error
(M)					(S.E.)	
3.33 x 10 ⁻⁷	84	87	86	86	1	
1.00 x 10 ⁻⁶	51	57	70	59	5	

27

21

4

Table F 10 HDAC3 activity percentage after incubation of C7-SAHA



HDAC3 IC 50 Curve of C7-Anthracene Analogue

23

13

3.00 x 10⁻⁶

Figure E.9. Dose response curve of C7-SAHA anthracenylmethyl analogue 22f tested using the HDAC3 activity from three independent trials with error bars indicating standard error. In some case, the error bar is smaller than the marker size. Data were fit to the sigmoidal curve using Kaleidograph 4.0 (Synergy Software) to determine the IC_{50} . The insets are the results of the data analysis. The data were reported in Table 4.3.



Table	E.11.	HDAC6	activity	per	centage	after	incuba	ation	of	C7-SAHA
anthrace	enylmet	hyl 22f .								
Concen	tration	Trial 1	Trial	2	Trial 3	Ν	<i>l</i> lean	Star	ndard	Error

Concentration	Trial 1	Trial 2	Trial 3	Mean	Standard	Error
(M)					(S.E.)	
1.00 x 10 ⁻⁷	85	84	63	77	7	
3.00 x 10 ⁻⁷	52	53	56	54	1	
9.00 x 10 ⁻⁷	37	36	44	39	2	

100 $y = 100/(1+(x/m3)^m4)$ Value Error m3 4.4284e-7 7.3436e-8 0.74014 0.14047 m4 80 20.73 Chisq NA 0.98605 R NA Deacetylase Activity Percentage (%) 60 40 20 0 10-8 10-6 10-7 105 Anthracene Analogue Concentration (M)

HDAC6 IC₅₀ Curve of C7-Anthracene Analogue

Figure E.10. Dose response curve of C7-SAHA anthracenylmethyl analogue **22f** tested using the HDAC6 activity from three independent trials with error bars indicating standard error. In some case, the error bar is smaller than the marker size. Data were fit to the sigmoidal curve using Kaleidograph 4.0 (Synergy Software) to determine the IC_{50} . The insets were the results of the data analysis. The data were reported in Table 4.3.



APPENDIX F. SUPPLEMENTARY INFORMATION FOR C7-SAHA LIBRARY

F.1. 1,1-Dibenzyl 6-methyl hexane-1, 1, 6-tricarboxylate (**24**). **F.1.1**. ¹H NMR

















F.2.2. ¹³C NMR











F.2.4. HRMS

Elemental Composition Report Page 1 Single Mass Analysis Tolerance = 5.0 PPM / DBE: min = -1.5, max = 50.0 :lement prediction: Off Number of isotope peaks used for i-FIT = 3 Monoisotopic Mass, Even Electron Ions Morroisoupic mass, Even Electron Ions 426 formula(e) evaluated with 2 results within limits (up to 50 best isotopic matches for each mass) Elements Used: C: 0-500 H: 0-1000 N: 0-4 O: 0-6 23Na: 0-1 Pfum: Sun Choi oct1808-C7-pyridinePg18 mw503 LCT0172 0.2uL meoh Shay 2008_070.pro 2008_1020_0172_03 13 (0.283) Cm (12:16-25:36x4.000) LCT Premier 20-Oct-2008 3::0::8 1: TOF MS ES+ 1.45e+004 504.2387 100 % 505.2423 526.2208 542.1961 329.0807 442.2268 580.2759 0 m/z 440 560 580 320 340 360 380 400 420 460 480 500 520 540 -1.5 Minimum: 5.0 5.0 Maximum: mDa PPM DBE i-FIT i-FIT (Norm) Formula Mass Calc. Mass 28.1 C30 H34 N 06 C28 H35 N 06 23Na 504.2387 504.2386 0.1 14.5 0.0 0.2

F.3. Benzyl 6-bromohexanoate (16). **F.3.1**. ¹H NMR





F.3.2. ¹³C NMR











F.3.4. HRMS

Elemental	Composition	Report								Page 1
Single Ma Tolerance = Tement pre	ss Analysis 5.0 PPM / DB ediction: Off sotope peaks us	E: min = -1	.5, max = = 3	50.0						
Monoisotopio 72 formula(e Elements Us C: 0-500 H	Mass, Even Elect) evaluated with 1 ed: : 0-1000 O: 0-4	ron lons results within 23Na: 0-1	limits (all Br: 0-1	results (up to	1000) for each	mass)				
LCT2008-075 2010_0702_1	pro 2010-cif.spl 067_14 13 (0.284) Cr	obenzylester L m (10:19-(1:8+	CT1067 mv 33:45)x2.00	v 284 meoh 00)			LCT	Premier 02-	-Jul-20 1: TC	10 16:07:3 DF MS ES+ 3.71e+00
100	307	.0314 309.02	298							
%	763 304.0739	31	0.0333		323	327	.1362	395	33	5.1624
300.0	305.0	310.0		315.0	320.0	325.0	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	30.0	3	-,⁺` m/ 35.0
Minimum: Maximum:		5.0	5.0	-1.5 50.0						
Mass	Calc. Mass	mDa	PPM	DBE	i-FIT	i-FIT (Norm) F	ormula		
307.0314	307.0310	0.4	1.3	4.5	53.4	0.0	C	13 H17	02	23Na













QC_Compare-7570.jws











F.5.2. ¹³C NMR





F.5.3. IR





المنسارات









F.6.2. ¹³C NMR





F.6.4. HRMS

للاستشارات

	Composition	Report					Page	1
Single Ma Folerance = Element pro Number of	ass Analysis = 5.0 PPM / DB ediction: Off isotope peaks use	E: min = -1 ed for i-FIT	.5, max = 5 = 3	50.0				,
Monoisotopi 283 formula	c Mass, Even Elect a(e) evaluated with	ron lons 7 results wit	hin limits (up	to 700 bes	t isotopic matche	es for each mass)		
Elements Us C: 0-120 SUN CHOI	sed: H: 0-1000 N: 0- May 26 10-C7-Pyrid	16 O: 0-3 vlaniline	0 23Na: (D-1				
_CT2008-07b 2010_0526_9	p.pro 2010-cif.spl 990 13 (0.284) Cm (11	:16-1:6x2.000)			LC	T Premier 26-May-2010 14:05: 1: TOF MS ES 1.78e+0	49 + 03
100-				431.233	1			7.58
-								
70-				43	0 0075			
				17	52.2375			
399.2	2524 405.8386 411.	2564 42	2.9483 425.2	821	433.2421 444.8	506 452.0164 455	.0260,457.0851 468.884	۹_
0 399.2 40	2524 405.8386 411. 00.0 410.0	2564 42	2.9483_425.2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	821 430.0	433.2421 444.8 440.0	506 452.0164 455 450.0	0260,457.0851 468.884 460.0	9 _z
399.2 40 1111mum: 1421mum:	2524 405 8386 411. 50.0 410.0	2564 42) 5.0	2.9483 425.2 420.0 5.0	430.0 -1.5 50.0	433.2421 444.8 440.0	506 452.0164 455 450.0	.0260.457.0851 468.884 460.0	∮z
0 399.2 40 Jinimum: Jaximum: Jass	2524 405.8386 411. 20.0 410.0 Calc. Mass	2564 42 5.0 mDa	2.9483 425.2 420.0 5.0 PPM	430.0 -1.5 50.0 DBE	433.2421 444.8 440.0 i-FIT	506 452.0164 455 450.0 i-FIT (Norm)	02604570851 468.884 460.0 m	}z
dinimum: Maximum: Mass	2524 405.8386 411. 00.0 410.0 Calc. Mass 431.2335	2564 42 5.0 mDa -0.4	2.9483.425.2 420.0 5.0 PPM -0.9	821 430.0 -1.5 50.0 DBE 13.5	433.2421 444.8 440.0 i-FIT 63.2	506 452.0164 455 450.0 i-FIT (Norm) 0.2	0260 457.0851 468.884 460.0 Formula C27 H31 N2 03	lz Ym
ass 31.2331	2524 405.8386 411. 00.0 410.0 Calc. Mass 431.2335 431.2311	2564 42 5.0 mDa -0.4 2.0	2.9483 425.2 420.0 5.0 PPM -0.9 4.6	821 430.0 -1.5 50.0 DBE 13.5 10.5	433.2421 444.8 440.0 i-FIT 63.2 65.3	506 452.0164 455 450.0 i-FIT (Norm) 0.2 2.2	0250 457 0851 468.884 460.0 Formula C27 H31 N2 03 C25 H32 N2 03	y fink
ass 399.2 40 dinimum: laximum: lass 31.2331	2524 405.8386 411. 000 410.0 Calc. Mass 431.2335 431.2311 431.2351	2564 422 5.0 mDa -0.4 2.0 -2.0	2.9483 425.2 420.0 5.0 PPM -0.9 4.6 -4.6	821 430.0 -1.5 50.0 DBE 13.5 10.5 14.5	433.2421 444.8 440.0 1-FIT 63.2 65.3 66.2	506 452.0164 455 450.0 i-FIT (Norm) 0.2 2.2 3.1	0260 457.0851 468.884 460.0 Formula C27 H31 N2 03 C25 H32 N2 03 23Na C30 H32 0 23Na	Jz Ann
ass all.2331	Calc. Mass 431.2335 431.2351 431.2351 431.2343	2564 42 5.0 mDa -0.4 2.0 -2.0 -1.2	2 9483 425.2 420.0 5.0 PPM -0.9 4.6 -4.6 -2.8	821 430.0 -1.5 50.0 DBE 13.5 10.5 14.5 2.5	433.2421 444.8 440.0 i-FIT 63.2 65.3 66.2 70.5	506 452.0164 455 450.0 i-FIT (Norm) 0.2 2.2 3.1 7.4	0260 457.0851 468.884 460.0 Formula C27 H31 N2 03 C25 H32 N2 03 C30 H32 0 23Na C30 H32 0 23Na C14 H32 N8 06 23Na	Az Ann
agge 2 40 tinimum: taximum: tass 131.2331	Calc. Mass 431.2335 431.2351 431.2351 431.2343 431.2340	2564 42 5.0 mDa -0.4 2.0 -2.0 -1.2 -0.9	2.9483.425.2 420.0 5.0 PPM -0.9 4.6 -4.6 -2.8 -2.1	821 430.0 -1.5 50.0 DBE 13.5 10.5 14.5 2.5 6.5	433.2421 444.8 440.0 i-FIT 63.2 65.3 66.2 70.5 71.7	506 452.0164 455 450.0 i-FIT (Norm) 0.2 2.2 3.1 7.4 8.7	0260 457.0851 468.8844 460.0 Formula C27 H31 N2 03 C25 H32 N2 03 C30 H32 0 23Na C14 H32 N8 06 23Na C12 H37 N14 04	y fine
1399.2 40 11nimum: 14ximum: 1435 131.2331	Calc. Mass 431.2335 431.2311 431.2351 431.2351 431.2343 431.2340 431.2326	2564 42 5.0 mDa -0.4 2.0 -2.0 -1.2 -0.9 0.5	2.9483 425.2 420.0 5.0 PPM -0.9 4.6 -4.6 -2.8 -2.1 1.2	821 430.0 -1.5 50.0 DBE 13.5 10.5 14.5 2.5 6.5 1.5	4332421 444.8 440.0 i-FIT 63.2 65.3 66.2 70.5 71.7 72.3	506 452.0164 455 450.0 i-FIT (Norm) 0.2 2.2 3.1 7.4 8.7 9.2	0250 457 0851 468 884 460.0 Formula C27 H31 N2 03 C25 H32 N2 03 C30 H32 02 23Na C14 H32 N8 06 C14 H32 N8 06 C14 H31 N10 08	Az Yank

F.7. N⁸-hydroxy-N¹-phenyl-2-(pyridin-4-ylmethyl)octanediamide (22d) F.7.1. ¹H NMR



F.7.2. ¹³C NMR





F.7.3. IR



F.7.4. HRMS

Elemental Composition Report							Page 1				
Single Ma	ss Analysis										
olerance =	5.0 PPM / DB	E: min = -1	.5, max = 50.	0							
fumber of i	isotope peaks use	ed for i-FIT	= 3								
Ionoisotopia	c Mass, Even Electi	ron lons									
30 formula(e) evaluated with 2	results within	n limits (up to	50 best iso	topic matche	s for each r	nass)				
: 0-100	H: 0-1000 N: 0-4	B O: 0-15	23Na: 0-1								
UN CHOI	Sep1501-07-Pyridy	l hydrooxami	acid PG 152								
LCT2008-07b.pro 2010-cif.spl 2010_0916_1296 14 (0.301) Cm (12:16-1:7x2.000)							LC.	LCT Premier 16-Sep-2010 15:06:40 1: TOF MS ES+			
						356.1	966			1.510+004	
%							257 1000				
343.1	460 346 0521	348	9265 350 2449	352 182	3 354.1758	355.2005	357.1999	8.2025	359.1007	361 2216	
0- 1-1-1-1-1 -34	4.0 346.0	348.0	350.0	352.0	354.0	356.0	35	8.0	360.0	m/z	
inimum:				-1.5							
laximum:		5.0	5.0	50.0							
lass	Calc. Mass	mDa	PPM	DBE	i-FIT	i-FIT	(Norm)	Formul	la		
56.1966	356.1974	-0.8	-2.2	9.5	120.1	0.0		C20 H	H26 N3	03 - Y	
	356.1950	1.6	4.5	6.5	124.4	4.3		C18 1 23Na	H27 N3	03	



3 4.755

2029952

5.67

82024





REFERENCES

1. Moving AHEAD with an international human epigenome project. *Nature* **2008**, *454* (7205), 711-5.

2. Yoo, C. B.; Jones, P. A., Epigenetic therapy of cancer: past, present and future. *Nat Rev Drug Discov* **2006**, *5* (1), 37-50.

3. Gregoretti, I. V.; Lee, Y. M.; Goodson, H. V., Molecular evolution of the histone deacetylase family: functional implications of phylogenetic analysis. *J Mol Biol* **2004**, 338 (1), 17-31.

4. Grozinger, C. M.; Schreiber, S. L., Deacetylase enzymes: biological functions and the use of small-molecule inhibitors. *Chem Biol* **2002**, *9* (1), 3-16.

5. Khabele, D.; Son, D. S.; Parl, A. K.; Goldberg, G. L.; Augenlicht, L. H.; Mariadason, J. M.; Rice, V. M., Drug-induced inactivation or gene silencing of class I histone deacetylases suppresses ovarian cancer cell growth: implications for therapy. *Cancer Biol Ther* **2007**, *6* (5), 795-801.

6. Song, J.; Noh, J. H.; Lee, J. H.; Eun, J. W.; Ahn, Y. M.; Kim, S. Y.; Lee, S. H.; Park, W. S.; Yoo, N. J.; Lee, J. Y.; Nam, S. W., Increased expression of histone deacetylase 2 is found in human gastric cancer. *APMIS* **2005**, *113* (4), 264-8.

7. Bartling, B.; Hofmann, H. S.; Boettger, T.; Hansen, G.; Burdach, S.; Silber, R. E.; Simm, A., Comparative application of antibody and gene array for expression profiling in human squamous cell lung carcinoma. *Lung Cancer* **2005**, *49* (2), 145-54.

8. Krennhrubec, K.; Marshall, B. L.; Hedglin, M.; Verdin, E.; Ulrich, S. M., Design and evaluation of 'Linkerless' hydroxamic acids as selective HDAC8 inhibitors. *Bioorg Med Chem Lett* **2007**, *17* (10), 2874-8.



9. Saji, S.; Kawakami, M.; Hayashi, S.; Yoshida, N.; Hirose, M.; Horiguchi, S. I.; Itoh, A.; Funata, N.; Schreiber, S. L.; Yoshida, M.; Toi, M., Significance of HDAC6 regulation via estrogen signaling for cell motility and prognosis in estrogen receptor-positive breast cancer. *Oncogene* **2005**, *24* (28), 4531-4539.

(a) de Ruijter, A. J.; van Gennip, A. H.; Caron, H. N.; Kemp, S.; van Kuilenburg,
 A. B., Histone deacetylases (HDACs): characterization of the classical HDAC family.
 Biochem J 2003, *370* (Pt 3), 737-49; (b) Fischer, D. D.; Cai, R.; Bhatia, U.; Asselbergs,
 F. A.; Song, C.; Terry, R.; Trogani, N.; Widmer, R.; Atadja, P.; Cohen, D., Isolation and
 characterization of a novel class II histone deacetylase, HDAC10. *J Biol Chem* 2002, *277* (8), 6656-66.

11. (a) Kramer, O. H.; Gottlicher, M.; Heinzel, T., Histone deacetylase as a therapeutic target. *Trends in endocrinology and metabolism: TEM* **2001,** *12* (7), 294-300; (b) Garber, K., HDAC inhibitors overcome first hurdle. *Nat Biotechnol* **2007,** *25* (1), 17-9.

12. Grant, S.; Easley, C.; Kirkpatrick, P., Vorinostat. *Nat Rev Drug Discov* **2007**, 6 (1), 21-2.

Robey, R. W.; Chakraborty, A. R.; Basseville, A.; Luchenko, V.; Bahr, J.; Zhan,
 Z.; Bates, S. E., Histone deacetylase inhibitors: emerging mechanisms of resistance.
 Mol Pharm **2011**, *8* (6), 2021-31.

14. Bressi, J. C.; Jennings, A. J.; Skene, R.; Wu, Y.; Melkus, R.; De Jong, R.; O'Connell, S.; Grimshaw, C. E.; Navre, M.; Gangloff, A. R., Exploration of the HDAC2 foot pocket: Synthesis and SAR of substituted N-(2-aminophenyl)benzamides. *Bioorg Med Chem Lett* **2010**, *20* (10), 3142-5.



15. Watson, P. J.; Fairall, L.; Santos, G. M.; Schwabe, J. W., Structure of HDAC3 bound to co-repressor and inositol tetraphosphate. *Nature* **2012**, *481* (7381), 335-40.

16. Bottomley, M. J.; Lo Surdo, P.; Di Giovine, P.; Cirillo, A.; Scarpelli, R.; Ferrigno, F.; Jones, P.; Neddermann, P.; De Francesco, R.; Steinkuhler, C.; Gallinari, P.; Carfi, A., Structural and functional analysis of the human HDAC4 catalytic domain reveals a regulatory structural zinc-binding domain. *J Biol Chem* **2008**, *283* (39), 26694-704.

17. (a) Somoza, J. R.; Skene, R. J.; Katz, B. A.; Mol, C.; Ho, J. D.; Jennings, A. J.; Luong, C.; Arvai, A.; Buggy, J. J.; Chi, E.; Tang, J.; Sang, B. C.; Verner, E.; Wynands, R.; Leahy, E. M.; Dougan, D. R.; Snell, G.; Navre, M.; Knuth, M. W.; Swanson, R. V.; McRee, D. E.; Tari, L. W., Structural snapshots of human HDAC8 provide insights into the class I histone deacetylases. *Structure* **2004**, *12* (7), 1325-34; (b) Vannini, A.; Volpari, C.; Filocamo, G.; Casavola, E. C.; Brunetti, M.; Renzoni, D.; Chakravarty, P.; Paolini, C.; De Francesco, R.; Gallinari, P.; Steinkuhler, C.; Di Marco, S., Crystal structure of a eukaryotic zinc-dependent histone deacetylase, human HDAC8, complexed with a hydroxamic acid inhibitor. *Proceedings of the National Academy of Sciences of the United States of America* **2004**, *101* (42), 15064-9.

18. Marks, P.; Rifkind, R. A.; Richon, V. M.; Breslow, R.; Miller, T.; Kelly, W. K., Histone deacetylases and cancer: causes and therapies. *Nat Rev Cancer* **2001**, *1* (3), 194-202.

19. O'Connor, O. A.; Heaney, M. L.; Schwartz, L.; Richardson, S.; Willim, R.; MacGregor-Cortelli, B.; Curly, T.; Moskowitz, C.; Portlock, C.; Horwitz, S.; Zelenetz, A. D.; Frankel, S.; Richon, V.; Marks, P.; Kelly, W. K., Clinical experience with intravenous and oral formulations of the novel histone deacetylase inhibitor suberoylanilide



hydroxamic acid in patients with advanced hematologic malignancies. *J Clin Oncol* **2006**, *24* (1), 166-73.

20. Bieliauskas, A. V.; Pflum, M. K. H., Isoform-selective histone deacetylase inhibitors. *Chemical Society Reviews* **2008**, *37* (7), 1402-1413.

21. (a) Suzuki, T.; Ando, T.; Tsuchiya, K.; Fukazawa, N.; Saito, A.; Mariko, Y.; Yamashita, T.; Nakanishi, O., Synthesis and histone deacetylase inhibitory activity of new benzamide derivatives. *J Med Chem* **1999**, *42* (15), 3001-3; (b) Dai, Y.; Guo, Y.; Guo, J.; Pease, L. J.; Li, J.; Marcotte, P. A.; Glaser, K. B.; Tapang, P.; Albert, D. H.; Richardson, P. L.; Davidsen, S. K.; Michaelides, M. R., Indole amide hydroxamic acids as potent inhibitors of histone deacetylases. *Bioorg Med Chem Lett* **2003**, *13* (11), 1897-901; (c) Mai, A.; Massa, S.; Pezzi, R.; Rotili, D.; Loidl, P.; Brosch, G., Discovery of (aryloxopropenyl)pyrrolyl hydroxyamides as selective inhibitors of class IIa histone deacetylase homologue HD1-A. *J Med Chem* **2003**, *46* (23), 4826-9.

22. (a) Bouchain, G.; Delorme, D., Novel hydroxamate and anilide derivatives as potent histone deacetylase inhibitors: synthesis and antiproliferative evaluation. *Curr Med Chem* **2003**, *10* (22), 2359-72; (b) Nagaoka, Y.; Maeda, T.; Kawai, Y.; Nakashima, D.; Oikawa, T.; Shimoke, K.; Ikeuchi, T.; Kuwajima, H.; Uesato, S., Synthesis and cancer antiproliferative activity of new histone deacetylase inhibitors: hydrophilic hydroxamates and 2-aminobenzamide-containing derivatives. *Eur J Med Chem* **2006**, *41* (6), 697-708; (c) Uesato, S.; Kitagawa, M.; Nagaoka, Y.; Maeda, T.; Kuwajima, H.; Yamori, T., Novel histone deacetylase inhibitors: N-hydroxycarboxamides possessing a terminal bicyclic aryl group. *Bioorg Med Chem Lett* **2002**, *12* (10), 1347-9; (d) Jung, M.; Brosch, G.; Kolle, D.; Scherf, H.; Gerhauser, C.; Loidl, P., Amide analogues of



trichostatin A as inhibitors of histone deacetylase and inducers of terminal cell differentiation. *J Med Chem* **1999**, *42* (22), 4669-79.

23. (a) Hu, E.; Dul, E.; Sung, C. M.; Chen, Z.; Kirkpatrick, R.; Zhang, G. F.; Johanson, K.; Liu, R.; Lago, A.; Hofmann, G.; Macarron, R.; de los Frailes, M.; Perez, P.; Krawiec, J.; Winkler, J.; Jaye, M., Identification of novel isoform-selective inhibitors within class I histone deacetylases. *J Pharmacol Exp Ther* **2003**, *307* (2), 720-8; (b) Beckers, T.; Burkhardt, C.; Wieland, H.; Gimmnich, P.; Ciossek, T.; Maier, T.; Sanders, K., Distinct pharmacological properties of second generation HDAC inhibitors with the benzamide or hydroxamate head group. *Int J Cancer* **2007**, *121* (5), 1138-48.

24. (a) Hanessian, S.; Auzzas, L.; Giannini, G.; Marzi, M.; Cabri, W.; Barbarino, M.; Vesci, L.; Pisano, C., Omega-alkoxy analogues of SAHA (vorinostat) as inhibitors of HDAC: a study of chain-length and stereochemical dependence. *Bioorg Med Chem Lett* **2007,** *17* (22), 6261-5; (b) Belvedere, S.; Witter, D. J.; Yan, J.; Secrist, J. P.; Richon, V.; Miller, T. A., Aminosuberoyl hydroxamic acids (ASHAs): a potent new class of HDAC inhibitors. *Bioorg Med Chem Lett* **2007,** *17* (14), 3969-71.

25. (a) Lavoie, R.; Bouchain, G.; Frechette, S.; Woo, S. H.; Abou-Khalil, E.; Leit, S.; Fournel, M.; Yan, P. T.; Trachy-Bourget, M. C.; Beaulieu, C.; Li, Z.; Besterman, J.; Delorme, D., Design and synthesis of a novel class of histone deacetylase inhibitors. *Bioorg Med Chem Lett* **2001**, *11* (21), 2847-50; (b) Varghese, S.; Senanayake, T.; Murray-Stewart, T.; Doering, K.; Fraser, A.; Casero, R. A., Jr.; Woster, P. M., Polyaminohydroxamic acids and polyaminobenzamides as isoform selective histone deacetylase inhibitors. *J Med Chem* **2008**, *51* (8), 2447-56.



26. Bieliauskas, A. V.; Weerasinghe, S. V.; Pflum, M. K., Structural requirements of HDAC inhibitors: SAHA analogs functionalized adjacent to the hydroxamic acid. *Bioorg Med Chem Lett* **2007**, *17* (8), 2216-9.

27. (a) Vinodhkumar, R.; Song, Y. S.; Ravikumar, V.; Ramakrishnan, G.; Devaki, T., Depsipeptide a histone deacetlyase inhibitor down regulates levels of matrix metalloproteinases 2 and 9 mRNA and protein expressions in lung cancer cells (A549). Chem Biol Interact 2007, 165 (3), 220-9; (b) You, J. S.; Kang, J. K.; Lee, E. K.; Lee, J. C.; Lee, S. H.; Jeon, Y. J.; Koh, D. H.; Ahn, S. H.; Seo, D. W.; Lee, H. Y.; Cho, E. J.; Han. J. W.. Histone deacetylase inhibitor apicidin downregulates DNA methyltransferase 1 expression and induces repressive histone modifications via recruitment of corepressor complex to promoter region in human cervix cancer cells. Oncogene 2008, 27 (10), 1376-86; (c) Furumai, R.; Komatsu, Y.; Nishino, N.; Khochbin, S.; Yoshida, M.; Horinouchi, S., Potent histone deacetylase inhibitors built from trichostatin A and cyclic tetrapeptide antibiotics including trapoxin. Proceedings of the National Academy of Sciences of the United States of America **2001**, 98 (1), 87-92.

28. Woo, S.; Gardner, E. R.; Chen, X.; Ockers, S. B.; Baum, C. E.; Sissung, T. M.; Price, D. K.; Frye, R.; Piekarz, R. L.; Bates, S. E.; Figg, W. D., Population pharmacokinetics of romidepsin in patients with cutaneous T-cell lymphoma and relapsed peripheral T-cell lymphoma. *Clin Cancer Res* **2009**, *15* (4), 1496-503.

29. Furumai, R.; Matsuyama, A.; Kobashi, N.; Lee, K. H.; Nishiyama, M.; Nakajima, H.; Tanaka, A.; Komatsu, Y.; Nishino, N.; Yoshida, M.; Horinouchi, S., FK228 (depsipeptide) as a natural prodrug that inhibits class I histone deacetylases. *Cancer Res* **2002**, *62* (17), 4916-21.



30. Khan, N.; Jeffers, M.; Kumar, S.; Hackett, C.; Boldog, F.; Khramtsov, N.; Qian, X.; Mills, E.; Berghs, S. C.; Carey, N.; Finn, P. W.; Collins, L. S.; Tumber, A.; Ritchie, J. W.; Jensen, P. B.; Lichenstein, H. S.; Sehested, M., Determination of the class and isoform selectivity of small-molecule histone deacetylase inhibitors. *Biochem J* **2008**, *409* (2), 581-9.

31. Jones, P.; Altamura, S.; Chakravarty, P. K.; Cecchetti, O.; De Francesco, R.; Gallinari, P.; Ingenito, R.; Meinke, P. T.; Petrocchi, A.; Rowley, M.; Scarpelli, R.; Serafini, S.; Steinkuhler, C., A series of novel, potent, and selective histone deacetylase inhibitors. *Bioorg Med Chem Lett* **2006**, *16* (23), 5948-52.

32. Hanessian, S., Vorinostat-Like Molecules as Structural, Stereochemical, and Pharmacological Tools. *ACS Medicinal Chemistry Letters* **2010**, *1*, 70-74.

33. Spencer, J., Synthesis and Biological Evaluation of JAHAs: Ferrocene-Based Histone Deacetylase Inhibitors. *ACS Medicinal Chemistry Letters* **2011**, *2*, 358-362.

34. (a) Schuetz, A.; Min, J.; Allali-Hassani, A.; Schapira, M.; Shuen, M.; Loppnau, P.; Mazitschek, R.; Kwiatkowski, N. P.; Lewis, T. A.; Maglathin, R. L.; McLean, T. H.; Bochkarev, A.; Plotnikov, A. N.; Vedadi, M.; Arrowsmith, C. H., Human HDAC7 harbors a class IIa histone deacetylase-specific zinc binding motif and cryptic deacetylase activity. *J Biol Chem* **2008**, *283* (17), 11355-63; (b) Vannini, A.; Volpari, C.; Gallinari, P.; Jones, P.; Mattu, M.; Carfi, A.; De Francesco, R.; Steinkuhler, C.; Di Marco, S., Substrate binding to histone deacetylases as shown by the crystal structure of the HDAC8-substrate complex. *EMBO Rep* **2007**, *8* (9), 879-84.

35. Lemon, D. D.; Horn, T. R.; Cavasin, M. A.; Jeong, M. Y.; Haubold, K. W.; Long,C. S.; Irwin, D. C.; McCune, S. A.; Chung, E.; Leinwand, L. A.; McKinsey, T. A., Cardiac



HDAC6 catalytic activity is induced in response to chronic hypertension. *J Mol Cell Cardiol* **2011**, *51* (1), 41-50.

36. Mai, A.; Massa, S.; Pezzi, R.; Simeoni, S.; Rotili, D.; Nebbioso, A.; Scognamiglio, A.; Altucci, L.; Loidl, P.; Brosch, G., Class II (IIa)-selective histone deacetylase inhibitors. 1. Synthesis and biological evaluation of novel (aryloxopropenyl)pyrrolyl hydroxyamides. *J Med Chem* **2005**, *48* (9), 3344-53.

37. Butler, K. V.; Kalin, J.; Brochier, C.; Vistoli, G.; Langley, B.; Kozikowski, A. P., Rational design and simple chemistry yield a superior, neuroprotective HDAC6 inhibitor, tubastatin A. *J Am Chem Soc* **2010**, *132* (31), 10842-6.

(a) Dai, Y.; Guo, Y.; Curtin, M. L.; Li, J.; Pease, L. J.; Guo, J.; Marcotte, P. A.;
Glaser, K. B.; Davidsen, S. K.; Michaelides, M. R., A novel series of histone deacetylase inhibitors incorporating hetero aromatic ring systems as connection units. *Bioorg Med Chem Lett* 2003, *13* (21), 3817-20; (b) Remiszewski, S. W.; Sambucetti, L. C.; Bair, K. W.; Bontempo, J.; Cesarz, D.; Chandramouli, N.; Chen, R.; Cheung, M.; Cornell-Kennon, S.; Dean, K.; Diamantidis, G.; France, D.; Green, M. A.; Howell, K. L.; Kashi, R.; Kwon, P.; Lassota, P.; Martin, M. S.; Mou, Y.; Perez, L. B.; Sharma, S.; Smith, T.; Sorensen, E.; Taplin, F.; Trogani, N.; Versace, R.; Walker, H.; Weltchek-Engler, S.; Wood, A.; Wu, A.; Atadja, P., N-hydroxy-3-phenyl-2-propenamides as novel inhibitors of human histone deacetylase with in vivo antitumor activity: discovery of (2E)-N-hydroxy-3-[4-[[(2-hydroxyethyl)[2-(1H-indol-3-yl)ethyl]amino]methyl]phenyl]-2-propenamide (NVP-LAQ824). *J Med Chem* 2003, *46* (21), 4609-24.

39. Gupta, S. P., Quantitative structure-activity relationship studies on zinccontaining metalloproteinase inhibitors. *Chem Rev* **2007**, *107* (7), 3042-87.



40. Leung, D.; Abbenante, G.; Fairlie, D. P., Protease inhibitors: current status and future prospects. *J Med Chem* **2000**, *43* (3), 305-41.

41. Hanessian, S.; Moitessier, N.; Gauchet, C.; Viau, M., N-Aryl sulfonyl homocysteine hydroxamate inhibitors of matrix metalloproteinases: further probing of the S(1), S(1)', and S(2)' pockets. *J Med Chem* **2001**, *44* (19), 3066-73.

42. Bhansali, P.; Hanigan, C. L.; Casero, R. A.; Tillekeratne, L. M., Largazole and analogues with modified metal-binding motifs targeting histone deacetylases: synthesis and biological evaluation. *J Med Chem* **2011**, *54* (21), 7453-63.

43. Taori, K.; Paul, V. J.; Luesch, H., Structure and activity of largazole, a potent antiproliferative agent from the Floridian marine cyanobacterium Symploca sp. *J Am Chem Soc* **2008**, *130* (6), 1806-7.

44. Karagiannis, T. C.; El-Osta, A., Will broad-spectrum histone deacetylase inhibitors be superseded by more specific compounds? *Leukemia* **2007**, *21* (1), 61-5.

45. (a) Krusche, C. A.; Wulfing, P.; Kersting, C.; Vloet, A.; Bocker, W.; Kiesel, L.; Beier, H. M.; Alfer, J., Histone deacetylase-1 and -3 protein expression in human breast cancer: a tissue microarray analysis. *Breast Cancer Res Treat* **2005**, *90* (1), 15-23; (b) Hirokawa, Y.; Arnold, M.; Nakajima, H.; Zalcberg, J.; Maruta, H., Signal therapy of breast cancers by the HDAC inhibitor FK228 that blocks the activation of PAK1 and abrogates the tamoxifen-resistance. *Cancer Biol Ther* **2005**, *4* (9), 956-60; (c) Fritsche, P.; Seidler, B.; Schuler, S.; Schnieke, A.; Gottlicher, M.; Schmid, R. M.; Saur, D.; Schneider, G., HDAC2 mediates therapeutic resistance of pancreatic cancer cells via the BH3-only protein NOXA. *Gut* **2009**, *58* (10), 1399-409; (d) Marshall, G. M.; Gherardi, S.; Xu, N.; Neiron, Z.; Trahair, T.; Scarlett, C. J.; Chang, D. K.; Liu, P. Y.; Jankowski, K.;


Iraci, N.; Haber, M.; Norris, M. D.; Keating, J.; Sekyere, E.; Jonquieres, G.; Stossi, F.; Katzenellenbogen, B. S.; Biankin, A. V.; Perini, G.; Liu, T., Transcriptional upregulation of histone deacetylase 2 promotes Myc-induced oncogenic effects. *Oncogene* **2010**, *29* (44), 5957-68; (e) Xu, X.; Xie, C.; Edwards, H.; Zhou, H.; Buck, S. A.; Ge, Y., Inhibition of histone deacetylases 1 and 6 enhances cytarabine-induced apoptosis in pediatric acute myeloid leukemia cells. *PLoS One* **2011**, *6* (2), e17138.

46. Liu, T.; Kapustin, G.; Etzkorn, F. A., Design and synthesis of a potent histone deacetylase inhibitor. *J Med Chem* **2007**, *50* (9), 2003-6.

47. Choi, S. E.; Weerasinghe, S. V.; Pflum, M. K., The structural requirements of histone deacetylase inhibitors: Suberoylanilide hydroxamic acid analogs modified at the C3 position display isoform selectivity. *Bioorg Med Chem Lett* **2011**, *21* (12), 6139-42.

48. Hanessian, S.; Chahal, N.; Giroux, S., Iterative synthesis of deoxypropionate units: the inductor effect in acyclic conformation design. *J Org Chem* **2006**, *71* (19), 7403-11.

49. Estiu, G.; Greenberg, E.; Harrison, C. B.; Kwiatkowski, N. P.; Mazitschek, R.; Bradner, J. E.; Wiest, O., Structural origin of selectivity in class II-selective histone deacetylase inhibitors. *J Med Chem* **2008**, *51* (10), 2898-906.

50. (a) Hideshima, T.; Bradner, J. E.; Wong, J.; Chauhan, D.; Richardson, P.; Schreiber, S. L.; Anderson, K. C., Small-molecule inhibition of proteasome and aggresome function induces synergistic antitumor activity in multiple myeloma. *Proceedings of the National Academy of Sciences of the United States of America* **2005**, *102* (24), 8567-72; (b) Namdar, M.; Perez, G.; Ngo, L.; Marks, P. A., Selective inhibition of histone deacetylase 6 (HDAC6) induces DNA damage and sensitizes



transformed cells to anticancer agents. *Proceedings of the National Academy of Sciences of the United States of America* **2010**, *107* (46), 20003-8.

51. <u>http://www.enzolifesciences.com/BML-AK500/fluor-de-lys-hdac-fluorometric-</u> activity-assay-kit/.

52. Choi, S. E.; Weerasinghe, S. V.; Pflum, M. K., The structural requirements of histone deacetylase inhibitors: Suberoylanilide hydroxamic acid analogs modified at the C3 position display isoform selectivity. *Bioorg Med Chem Lett* **2011**.

53. Sun Ea Choi, S. V. W. W., and Mary Kay Pflum, The Structural Requirements of Histone Deacetylase Inhibitors: Suberoylanilide Hydroxamic Acid Analogues Modified at the C3 Position Display Isoform Selectivity. **2011**.

54. Finnin, M. S.; Donigian, J. R.; Cohen, A.; Richon, V. M.; Rifkind, R. A.; Marks, P. A.; Breslow, R.; Pavletich, N. P., Structures of a histone deacetylase homologue bound to the TSA and SAHA inhibitors. *Nature* **1999**, *401* (6749), 188-93.

55. Hanessian, S., Design and synthesis of MMP inhibitors using N-arylsulfonylaziridine hydroxamic acids as constrained scaffolds. *Tetrahedron* **2001**, *57*, 6885-6900.

56. Zacharie, B.; Moreau, N.; Dockendorff, C., A mild procedure for the reduction of pyridine N-oxides to piperidines using ammonium formate. *J Org Chem* **2001**, *66* (15), 5264-5.

57. Moradei, O. M.; Mallais, T. C.; Frechette, S.; Paquin, I.; Tessier, P. E.; Leit, S. M.; Fournel, M.; Bonfils, C.; Trachy-Bourget, M. C.; Liu, J.; Yan, T. P.; Lu, A. H.; Rahil, J.; Wang, J.; Lefebvre, S.; Li, Z.; Vaisburg, A. F.; Besterman, J. M., Novel aminophenyl



benzamide-type histone deacetylase inhibitors with enhanced potency and selectivity. *J Med Chem* **2007**, *50* (23), 5543-6.

58. Nielsen, T. K.; Hildmann, C.; Dickmanns, A.; Schwienhorst, A.; Ficner, R., Crystal structure of a bacterial class 2 histone deacetylase homologue. *J Mol Biol* **2005**, *354* (1), 107-20.



ABSTRACT

THE STRUCTURAL REQUIREMENTS OF HISTONE DEACETYLASE INHIBITORS: SUBEROYLANILIDE HYDROXAMIC ACID (SAHA) ANALOGUES MODIFIED AT C3, C6, AND C7 POSITIONS ENHANCE SELECTIVITY

by

SUN EA CHOI

May 2012

Advisor: Dr. Mary Kay H. Pflum

Major: Chemistry (Organic)

Degree: Doctor of Philosophy

Histone deacetylase (HDAC) proteins are targets for drug design towards the treatment of cancers since overexpression of HDAC proteins is linked to cancer. Several HDAC inhibitors, including the FDA approved drug suberoylanilide hydroxamic acid (SAHA, Vorinostat), have cleared clinical trials and emerged as anti-cancer drugs. However, SAHA inhibits all of the 11 metal iondependent HDAC proteins. Therefore, we synthesized several libraries of small molecule HDAC inhibitors based on SAHA to help understand the structural requirements of inhibitory potency and isoform selectivity.



www.manaraa.com

acid displayed decreased inhibitory activity compared to the parent compound, SAHA. The lack of potency of the C2 library indicated that limited flexibility exists in the HDAC active site near the hydroxamic acid. Therefore, we theorized the substituents on the C3, C4, C5, C6, and C7 positions would display more potent inhibition compared to the C2-SAHA library due to the more solvent exposed location. Interestingly, while the C2-SAHA analogues containing any substituents were poor potent, the C3-SAHA analogue with a methyl substituent displayed potency. The potency of the remaining analogues decreased with increasing size of the C3 substituents. Moreover, the C6-SAHA phenyl analogue even displayed potency in the submicromolar range. Finally, most of the C7-SAHA analogues displayed equal or greater potency compared to SAHA. The results indicate that more flexibility in the HDAC active site exists closer to the capping group region near the C6 and C7 positions, while only modest flexibility exists in the bottom of the active site near the C2 and C3 positions.

After analyzing the potency of SAHA analogues, isoform selective inhibition of the individual compounds was evaluated. Seven of the SAHA



analogues demonstrated selectivity. The C3-SAHA ethyl-substituted analogue showed preference for HDAC6 over HDAC1 and HDAC3 it even though displayed decreased potency.



The C6-SAHA analogues displayed diverse selectivity; the C6-SAHA methyl variant displayed preference for class I, *t*-butyl variant showed a dual-HDAC1 and HDAC6 selectivity, and 2-ethylhexyl variant showed HDAC3-selectivity. The C7-SAHA analogues displayed selective inhibition as well; the C7-SAHA pyridylmethyl and anthracenylmethyl variants displayed a dual-HDAC1 and HDAC6 selectivity, and naphthylmethyl variant showed HDAC3-selectivity. The interesting potency and selectivity of linker-modified SAHA analogues suggest that linker region substituents can be exploited in the design of new anti-cancer drugs.



AUTOBIOGRAPHICAL STATEMENT

SUN EA CHOI

Education

Wayne State University, Detroit, MI. (2006-2012) Ph.D., 2012

Cincinnati State College, Sung Kyun Kwan University, Tokyo Institute University A.D., B.A., R.A.

Research Experience

Graduate Student Studies September 2007-2012

Advisor: Prof. Mary Kay H. Pflum, Ph.D

Dissertation Title: 'Structural Requirements of Histone Deacetylase (HDAC) Inhibitors: Suberoylanilide Hydroxamic Acid (SAHA) Analogues Modified at the C3, C6, and C7 Positions Enhance Selectivity

Synthesis of SAHA analogues to elucidate the structural requirements of HDAC inhibitors

Determination IC₅₀ values of HDAC inhibitors using Fluor de Lys *in vitro* fluorescence activity assay kit (Enzo) using HeLa cell lysates as the source of HDAC activity

Research Student Studies August 2004-2006

Advisor: Prof. Martha Brosz Research title: Synthesis of Vitamin D Analogues

Affiliations/Honors

Member of American Chemical Society (**2010** to **present**) Member of Golden Key International Honor Society (**2007** to **present**) Member of Phi Lamda Upsilon-Honorary Chemical Society (**2007** to **present**) Honor Students Scholarship (**2005** to **2006**)

Publications

Sun Ea Choi, Sujith V. W. Weerasinghe and Mary Kay H. Pflum. "The Structural Requirement of Histone Deacetylase (HDAC) Inhibitors: Suberoyl Anilide Hydroxamic Acid (SAHA) analogues at the C3 position display Class II Selectivity", *Bioorganic and Medicinal Chemistry Letter* **2011**, 21, 6139-6142.

Sun Ea Choi, and Mary Kay Pflum, "The Structural Requirement of Histone Deacetylase (HDAC) Inhibitors: Suberoyl Anilide Hydroxamic Acid (SAHA) analogues at the C6 position Enhance Selectivity" in preparation.

Sun Ea Choi, Anton V. Bieliauskas, V. W. Weerashinghe, Geetha Padige, Satish Garre V. R. and Mary Kay Pflum, "The Structural Requirement of Histone Deacetylase (HDAC) Inhibitors: Suberoyl Anilide Hydroxamic Acid (SAHA) analogues at the C7 position display Dual-Selectivity" in preparation.

