

**Epigenetics:
A pioneer area for drug discovery across
multiple therapeutic areas**

**Cheryl Arrowsmith
University of Toronto
Ontario Cancer Institute
Sept 30th 2010**



SGC Toronto



SGC Oxford



**Karolinska
Institutet**

SGC Stockholm

Public-private consortium funding pre-competitive protein-based science

- GSK, Merck, Novartis
- Canadian, Swedish granting agencies
- Wellcome Trust, UK

Goals: 3D protein structures for biological and drug discovery (~160/year)

Three sites: Toronto, Oxford, Stockholm

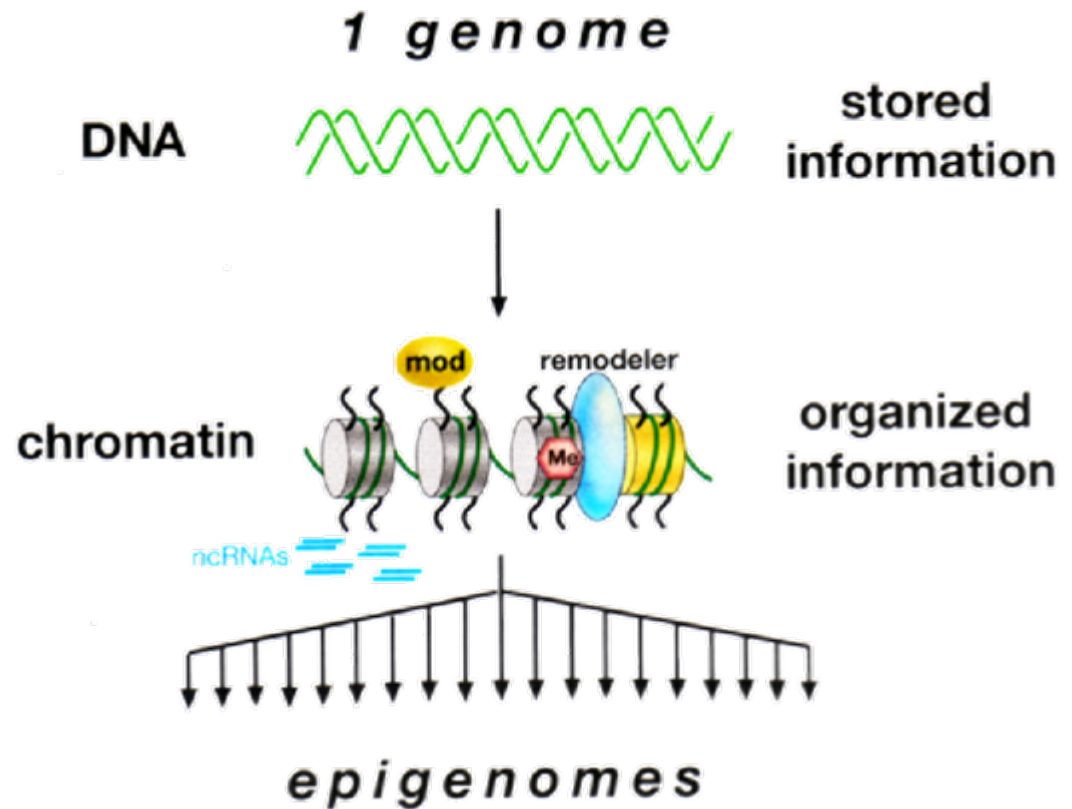
All data and reagents are made publicly available, without restriction on use

- 3D structures
- Protein expression clones
- Protocols for expression and crystallization
- Other protein-based protocols and methodologies
- www.TheSGC.org

New initiatives in developing chemical probes and protein capture reagents for biological discovery and potential new drug targets

Epigenetics

Heritable changes in phenotype caused by mechanisms other than changes in the underlying DNA sequence



Epigenetics: Pioneer Target Area

Biologically attractive, “pioneer target area”

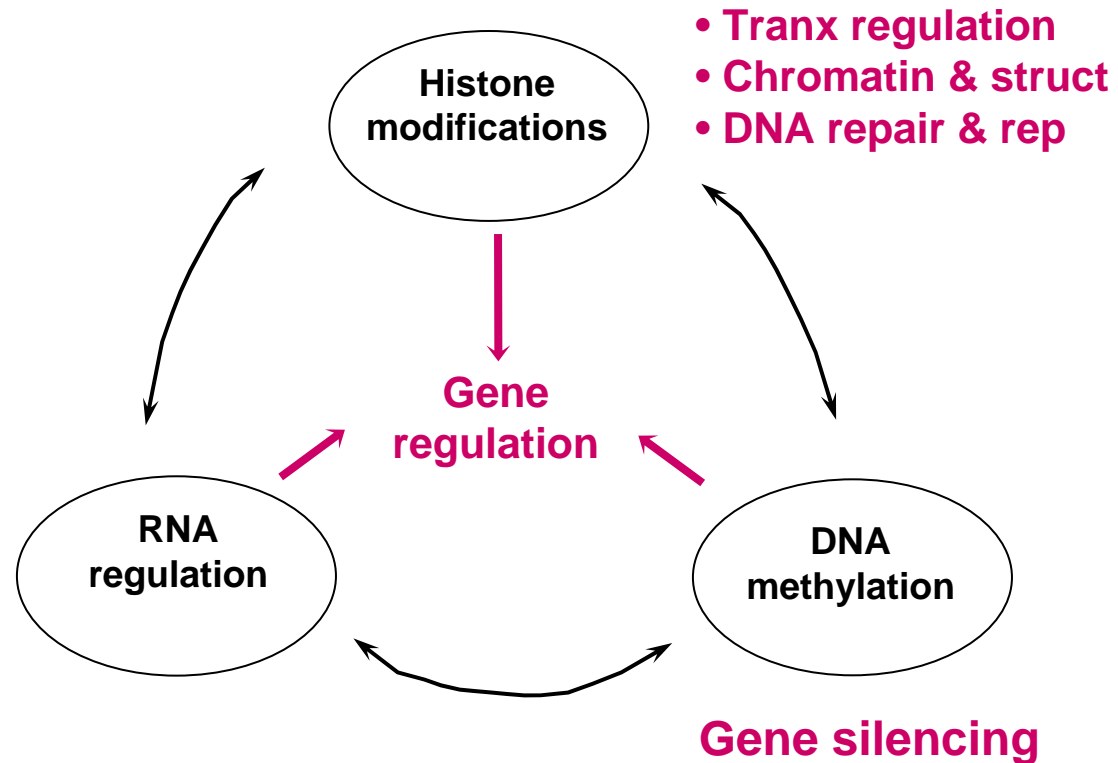
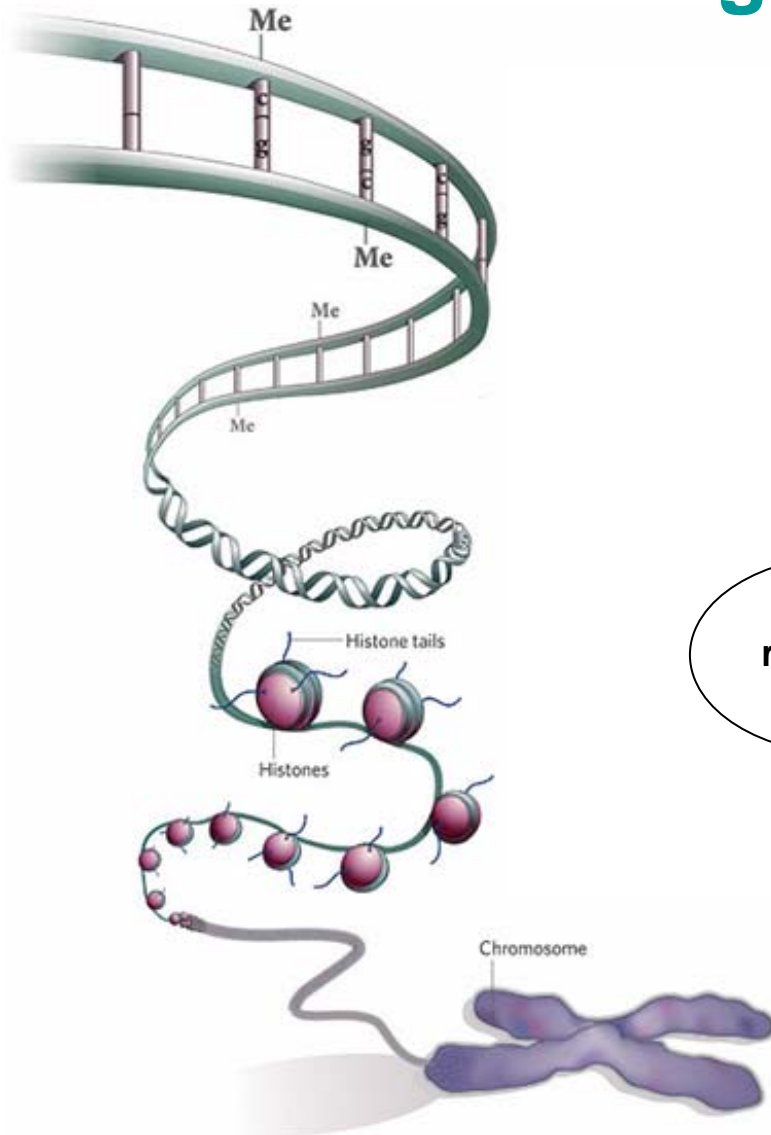
- Play a key role in development, differentiation and stem cell biology
- Underlie many chronic diseases: cancer, inflammation, psychiatric disorders
- Directly impact transcriptional programs, DNA repair & metabolism
- Intense area of research for which there is a receptive community to test chemical probes and protein capture reagents

Epigenetic targets appear to be Druggable

- SAHA (HDAC inhibitor) approved for cutaneous T-cell lymphoma
- Inhibitors of DNA MTases shown to reactivate silenced genes
- nM inhibitors of Bromo domains have been developed and can affect transcriptional programs.

Opportunity for discovery of new biology and new drug targets using chemical biology approaches

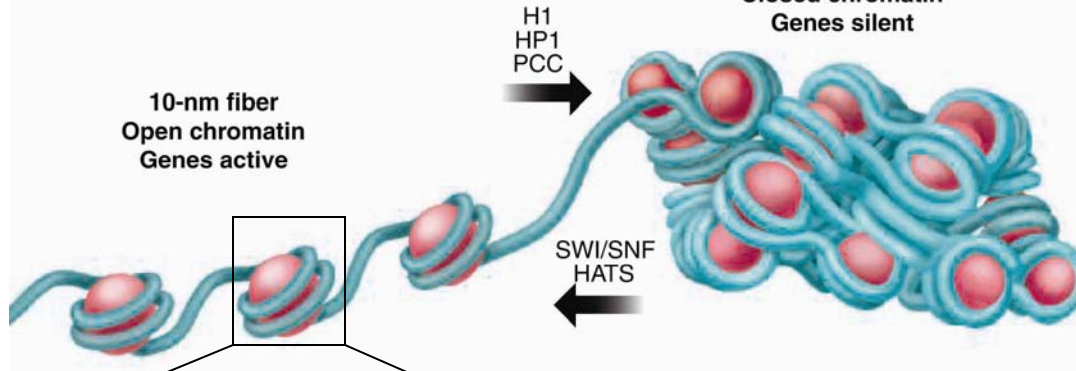
Three basic mechanisms of epigenetic regulation



Gene expression is regulated by chromatin structure and its covalent modifications

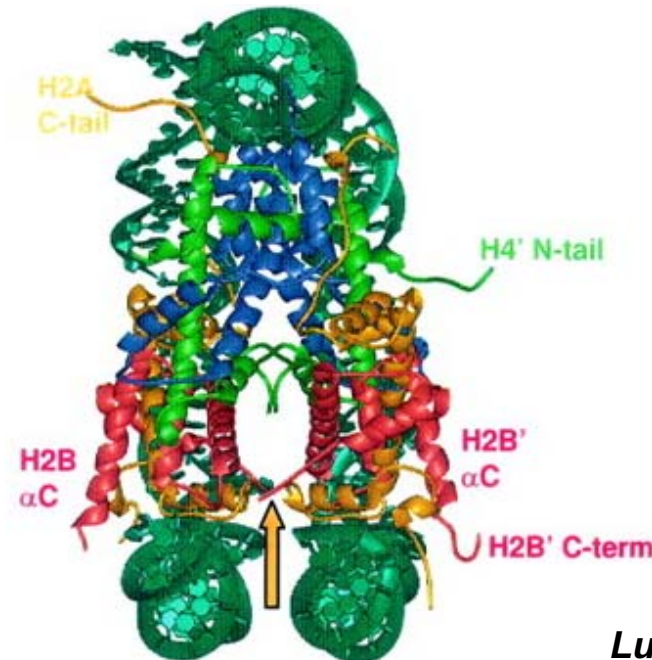
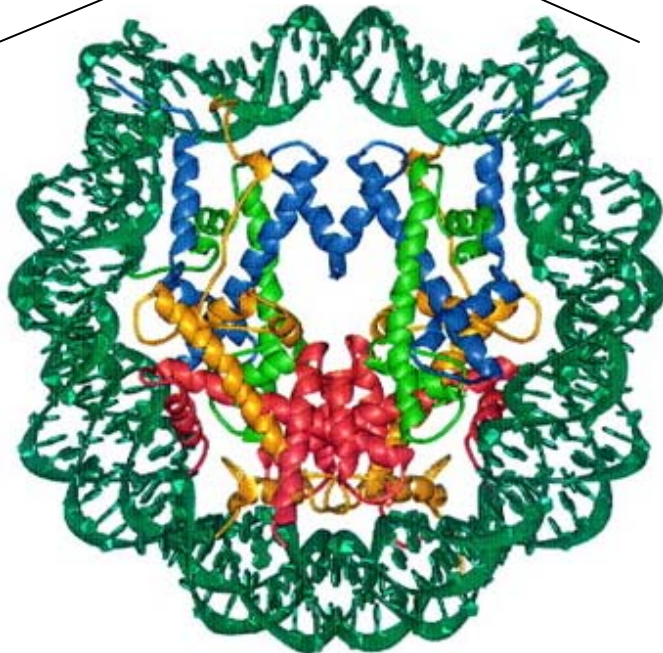
Mohd-Sarip et al, Science, 2004

30-nm fiber
Closed chromatin
Genes silent



Strahl & Allis, 2000

The “Histone Code” hypothesis:
Covalent modifications of histone tails encode heritable regulatory information

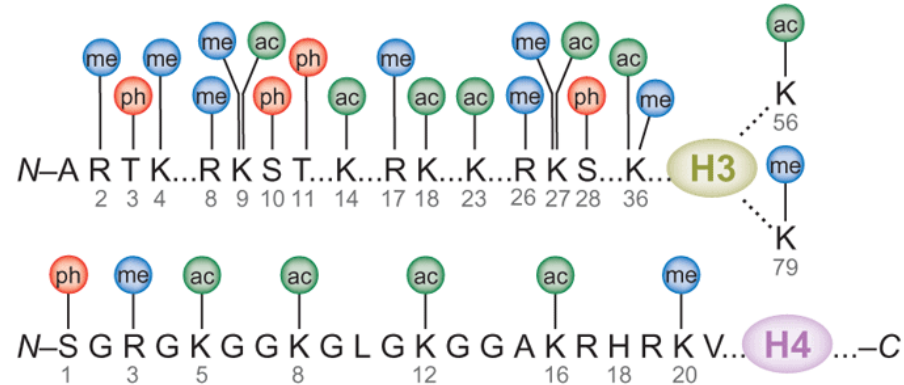
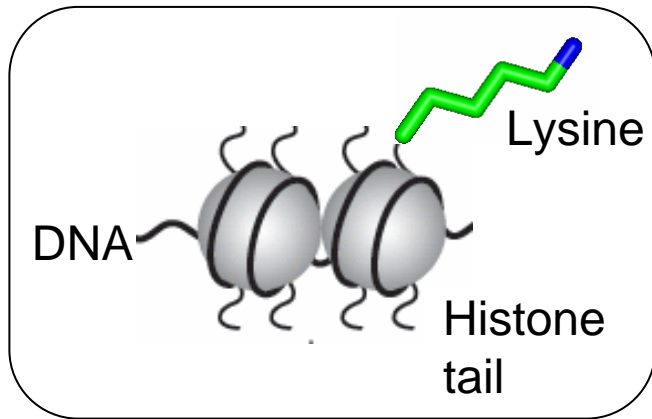


Histones

- H2A
- H2B
- H3
- H4

Luger et al., Nature, 1997

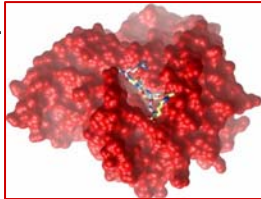
Acetyl- and methyl- lysines are an important component of the histone code



Lysine Modification	Write	Read	Erase	Oxford Toronto
	HAT	BROMO	HDAC	
Acetyl				
Methyl	HMT	Royal Family PHD	KDM	

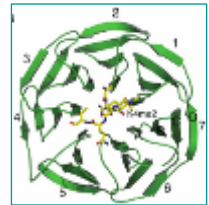
Readers, Writers and Erasers of Histone Marks: Key Focus of SGC Structural Effort

Ng et al, *Nature*. 2007, 448:87-91

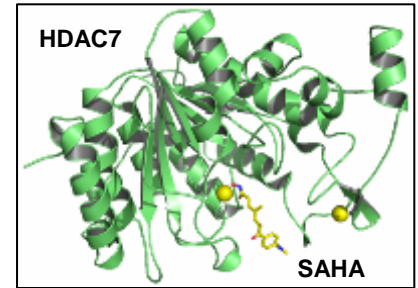
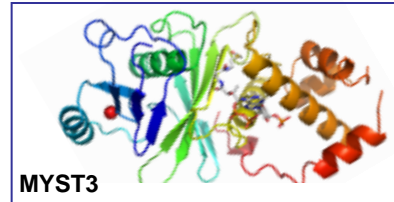
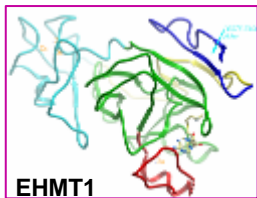


Histone Acetyltransferases: not so specific
HDACs: Sirt5 and HDAC7 - substrates unknown
Histone Methyltransferases: site specific
Readers: mixed specificity
Demethylase: specific

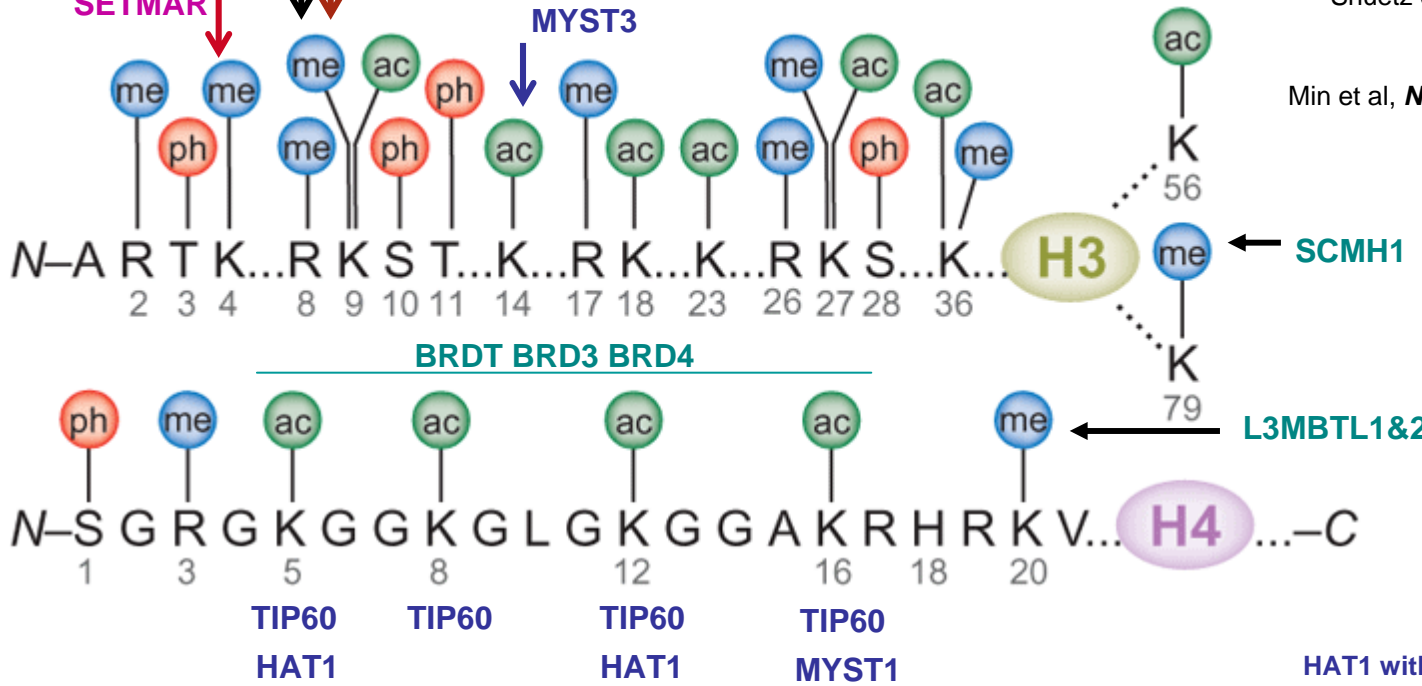
Shuetz et al, *EMBO J* 2006, 25:4245-52



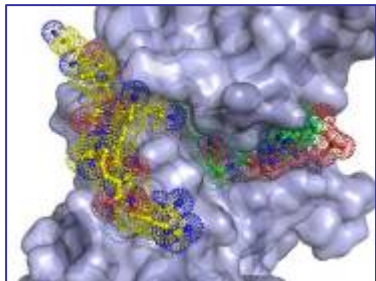
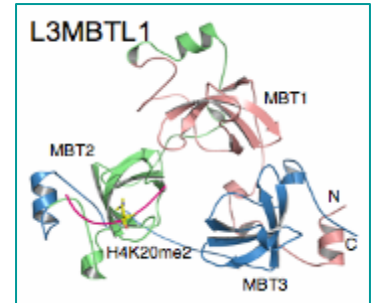
JMJD2
PRDM2
SUV39H2
EHMT1
EHMT2



Shuetz et al, *J. Biol Chem.* 2007, 283:11355

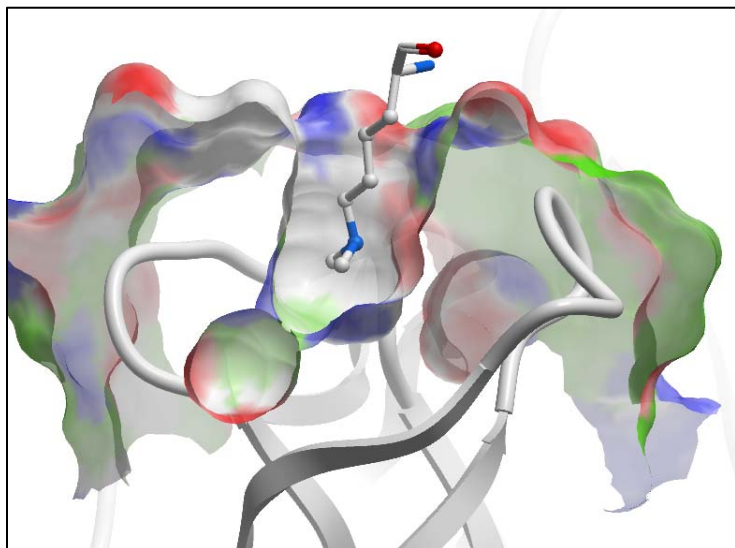


Min et al, *Nature Struct Mol. Biol* 2007, 14:1229

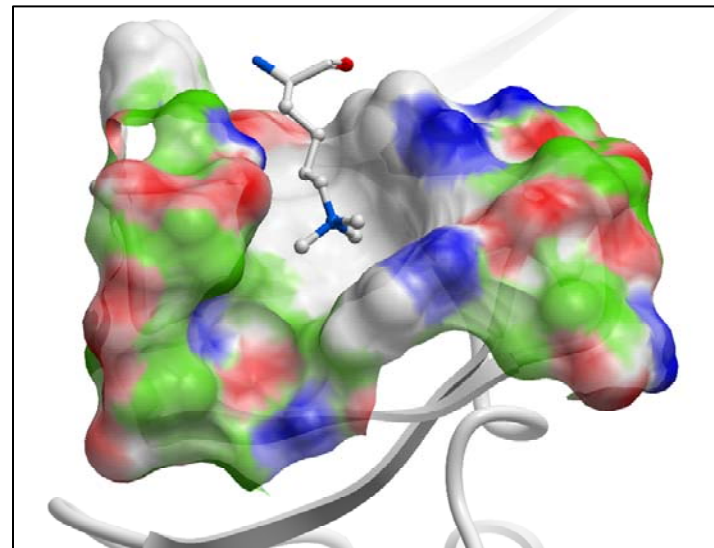


HAT1 with H4K12Ac and CoA

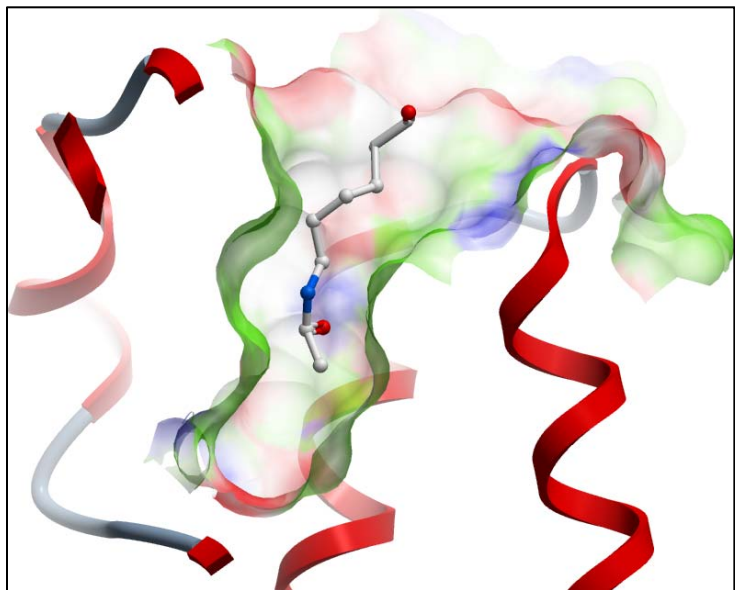
Can we exploit the variability in Lysine binding sites?



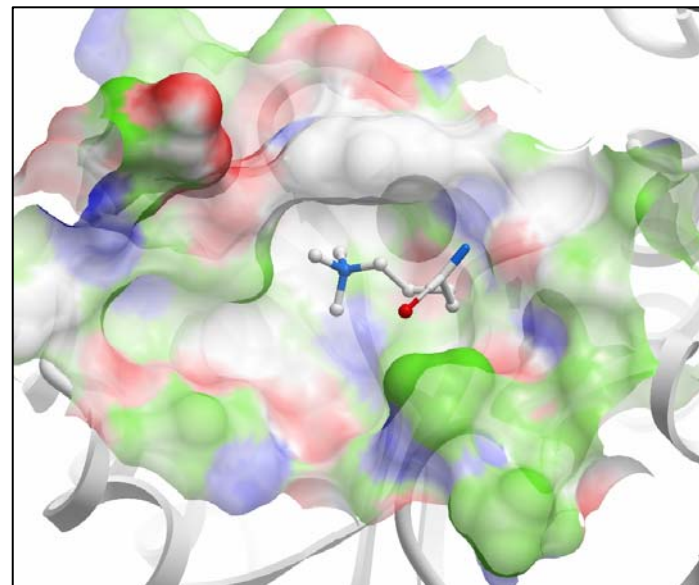
MBT Domain (mono & di-methyl)



Tudor Domain (di- & tri-methyl)



Bromo Domain (acetyl)



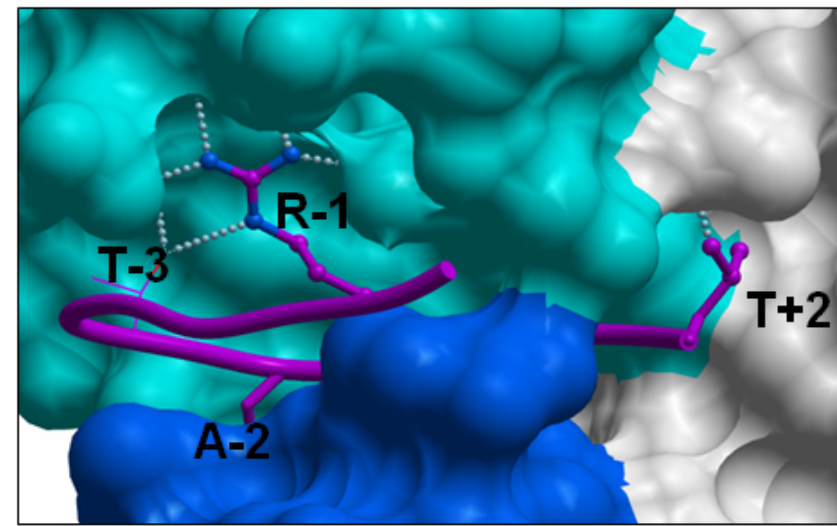
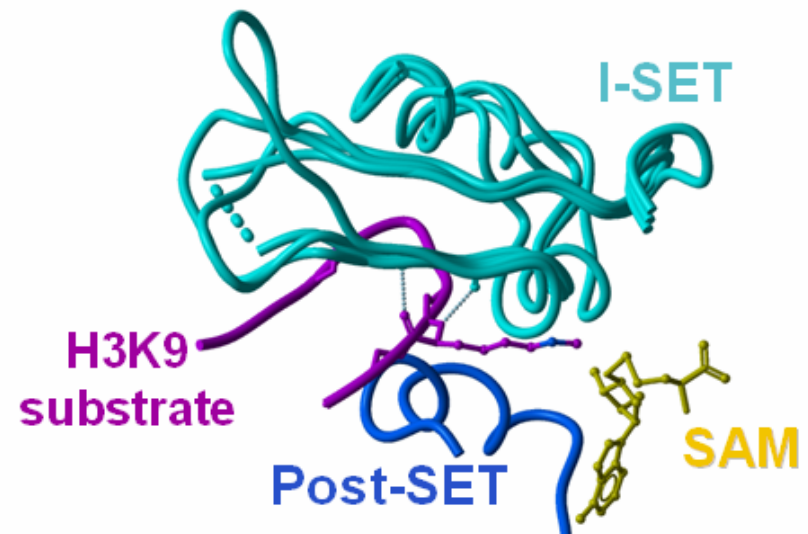
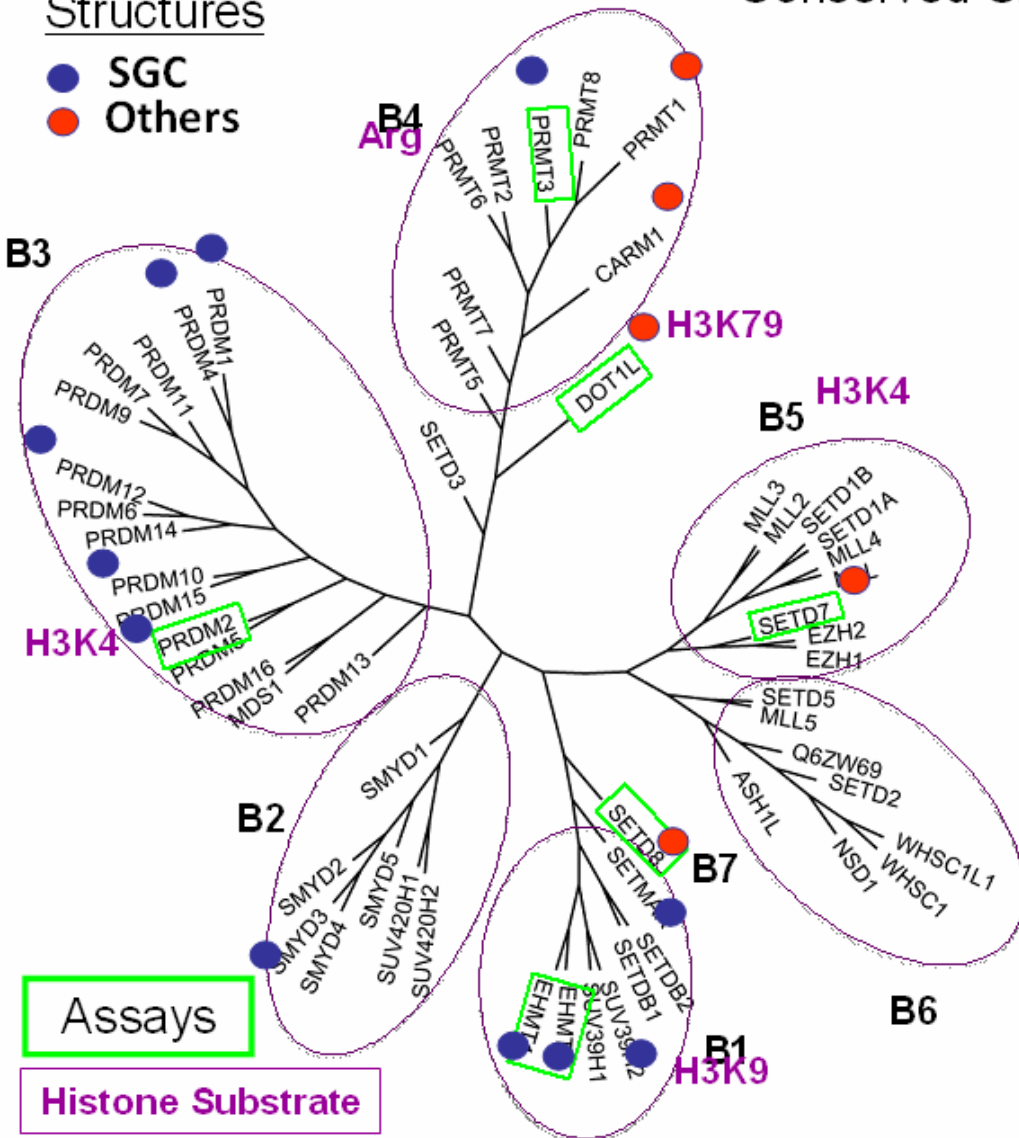
Chromo Domain (tri-methyl)

Histone Methyltransferase Family Approach: Opportunities for selectivity

Structures

- SGC
- Others

Conserved SET domain has unique substrate pockets



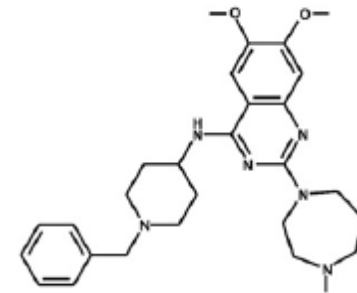
Case Study: G9a methyltransferase

Molecular Cell

Technique

Reversal of H3K9me2 by a Small-Molecule Inhibitor for the G9a Histone Methyltransferase

Stefan Kubicek,¹ Roderick J. O'Sullivan,¹ E. Michael August,² Eugene R. Hickey,² Qiang Zhang,² Miguel L. Teodoro,² Stephen Rea,^{1,3} Karl Mechtler,¹ Jennifer A. Kowalski,² Carol Ann Homon,² Terence A. Kelly,² and Thomas Jenuwein^{1,*}



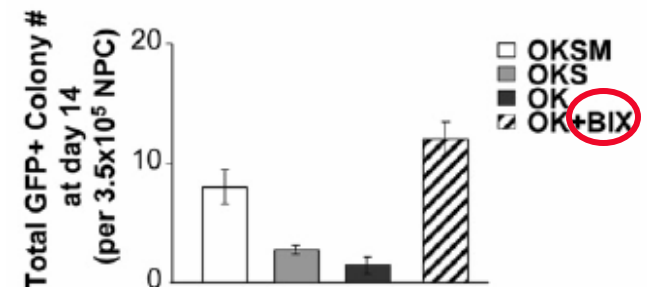
BIX-01294

Cell Stem Cell

Correspondence

A Combined Chemical and Genetic Approach for the Generation of Induced Pluripotent Stem Cells

Yan Shi,¹ Jeong Tae Do,² Caroline Desponts,¹ Heung Sik Hahm,¹ Hans R. Schöler,² and Sheng Ding^{1,*}



But, also implicated in Addiction, Cognition/Behavior, Viral Response and Cancer

SCIENCE VOL 327 8 JANUARY 2010

Essential Role of the Histone Methyltransferase G9a in Cocaine-Induced Plasticity

Ian Maze,¹ Herbert E. Covington III,¹ David M. Dietz,¹ Quincey LaPlant,^{1,2} William Renthal,² Scott J. Russo,¹ Max Mechanic,² Ezekiel Mouzon,¹ Rachael L. Neve,³ Stephen J. Haggarty,^{4,5} Yanhua Ren,¹ Srihari C. Sampath,⁶ Yasmin L. Hurd,¹ Paul Greengard,⁷ Alexander Tarakhovsky,⁶ Anne Schaefer,⁷ Eric J. Nestler^{1*}

678 *Neuron* 64, 678–691, December 10, 2009

Control of Cognition and Adaptive Behavior by the GLP/G9a Epigenetic Suppressor Complex

Anne Schaefer,^{1,4} Srihari C. Sampath,^{2,4,6} Adam Intrator,¹ Alice Min,¹ Tracy S. Gertler,³ D. James Summeier,³ Alexander Tarakhovsky,^{2,5,*} and Paul Greengard^{1,5,*}

J Biol Chem. 2010 Mar 24.

Involvement of histone H3 Lysine 9 (H3K9) methyltransferase G9a in the maintenance of HIV-1 latency and its reactivation by BIX01294. Imai K, Togami H, Okamoto T.

G9a and Glp Methylate Lysine 373 in the Tumor Suppressor p53^{*[5]}

Received for publication, September 8, 2009, and in revised form, January 5, 2010. Published, JBC Papers in Press, January 29, 2010, DOI 10.1074/jbc.M109.010744

Jing Huang^{†§1}, Jean Dorsey[§], Sergei Chuikov[§], Xinyue Zhang[†], Thomas Jenuwein^{||**}, Danny Reinberg^{§§} and Shelley L. Berger^{§§}

Mol Cancer Res 2009;7(6). June 2009

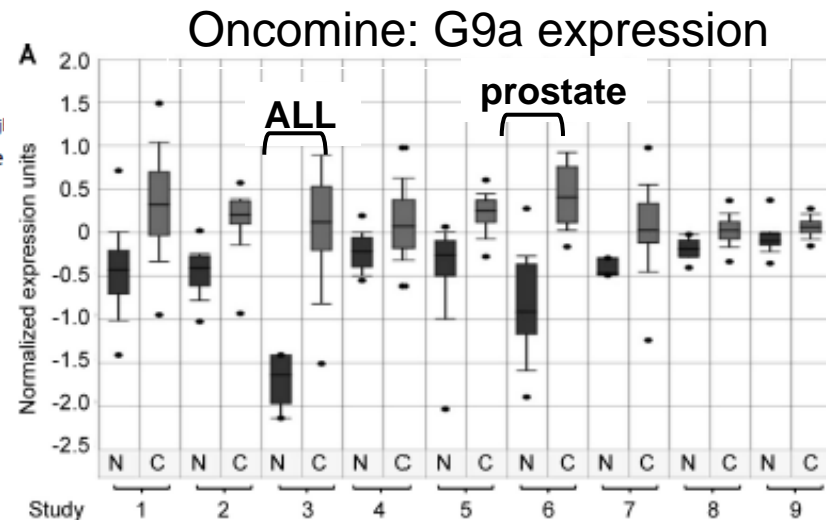
Distinct Roles for Histone Methyltransferases G9a and GLP in Cancer Germ-Line Antigen Gene Regulation in Human Cancer Cells and Murine Embryonic Stem Cells

Petra A. Link,¹ Omkaram Gangisetty,¹ Smitha R. James,¹ Anna Woloszynska-Read,¹ Makoto Tachibana,² Yoichi Shinkai,² and Adam R. Karpf¹

Leukemia (2010) 24, 81–88

EVI-1 interacts with histone methyltransferases SUV39H1 and G9a for transcriptional repression and bone marrow immortalization

S Goyama^{1,2}, E Nitta¹, T Yoshino¹, S Kako¹, N Watanabe-Okochi¹, M Shimabe¹, Y Imai¹, K Takahashi² and M Kurokawa¹



Chemical biology for target discovery/validation

Goal: Develop *well characterized* small molecules to be used to link pharmacological inhibition of an individual target (or small group of targets) with cellular biology/pathways/phenotype

- **Potent:** $IC_{50} < 100$ nM *in vitro*
- **Selective:** 30x over related proteins
- **Cell permeable:** $IC_{50} < 1$ uM in cell
- **Low/No *cellular* toxicity**

• **Make available to research community**

Unique Consortium: Epigenetics PPP

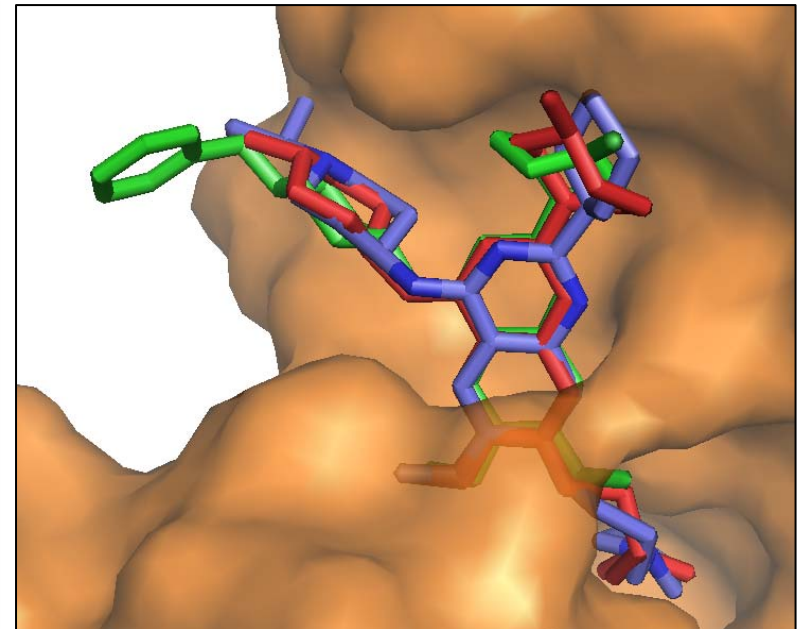
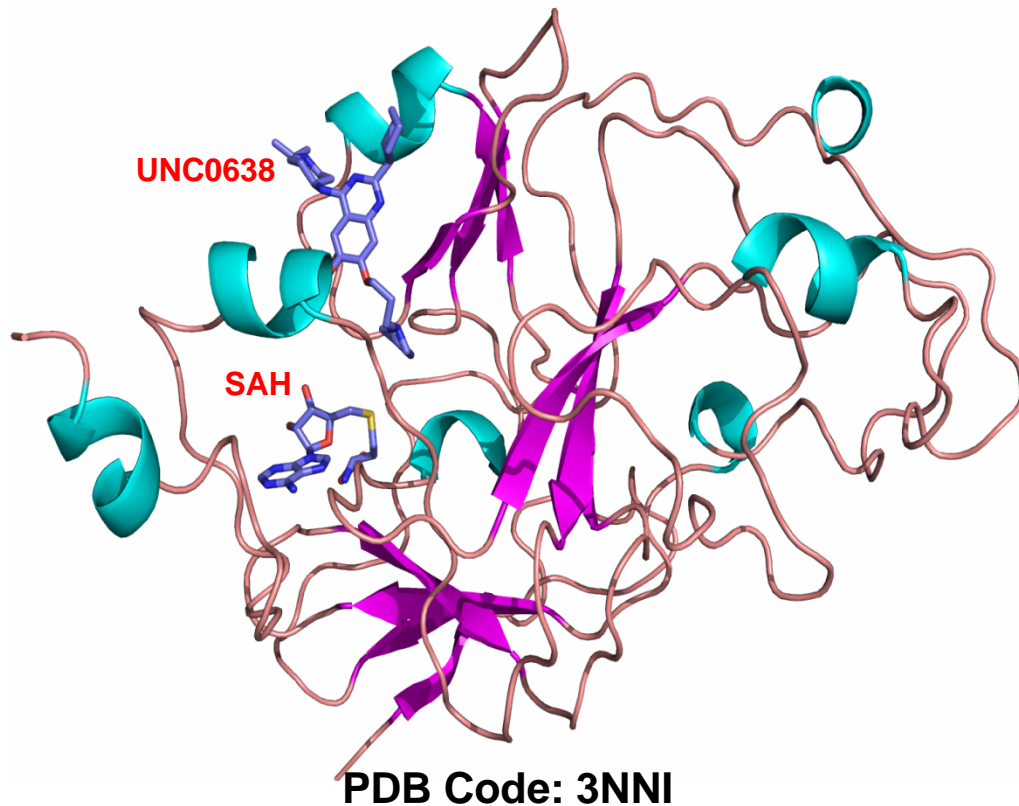
Objective: identify 40 probes and make compounds & data publicly available (no restriction on use) over 4 years

Participants:

Funder

- **SGC – Toronto (HMTs, Royal Family, HATs)** Ontario \$4.6M
- **SGC – Oxford (KDMs, Bromo domains)** Wellcome Trust \$8M
- **SGC – Stockholm (PARPs)** Swedish Sci. F. \$ 3M
- **GSK, Pfizer, Novartis Chemistry (8 med chemist FTEs each)**
 - commit to release “public probe” other compounds not disclosed
- **NIH Chemical Genomics Center (20 HTS slots – data public)**
- **Ontario Inst. Cancer Research (2 FTE med chemists)**
- **Frye Lab, University N. Carolina (4 FTE med chem/assay dev)**

Structure based design of potent and selective G9a antagonist



UNC0638 (PDB 3NNI)

UNC0224 (PDB 3K5K)

BIX-01294 (PDB 3FPD)

- UNC0638 occupies histone binding groove and does not interact with SAM binding pocket. Same binding mode as BIX01294 & UNC0224

Associated Data Published on SGC Website

Getting Started Latest Headlines

Probes for G9a/G...

Structural Genomics Consortium Datab...

www.TheSGC.org/chemical_probes/UNC0638

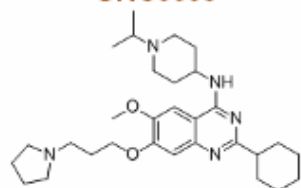
UNC0638: Selective chemical probe for G9a/GLP methyltransferases

UNC0638 Data Sheet

How to obtain this probe

UNC0638 released on June 1, 2010

UNC0638



Click on the **'Properties'** tab above for more details

Biology of the G9a/GLP methyltransferases

G9a (EHMT2) and GLP (EHMT1) catalyze the mono and dimethylation of lysine 9 of histone 3 (H3K9) and other non-histone substrates such as p53 and WIZ.

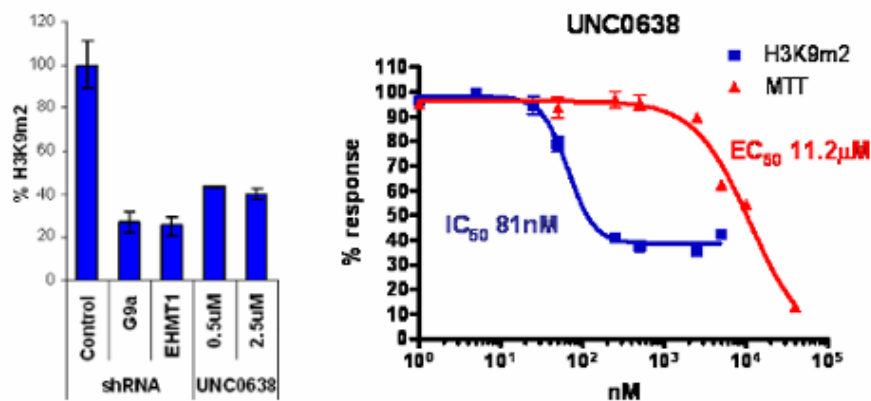
Selectivity Within Target Family

Protein	IC ₅₀ /nM (Activity)	Tm shift °C ¹
G9a (EHMT2)	<15	4
GLP (EHMT1)	19 ± 1	8
SETD7	>10,000	nt
SETD8	>10,000	nd
PRMT3	>10,000	nd
SUV39H2	>10,000	nt
DOT1L	nt	nd
PRDM1	nt	nd
PRDM10	nt	nd
PRDM12	nt	nd
SMYD3	nt	nd
JMJD2E	4660 (AlphaScreen)	nt
HTATIP	nt	nd

(nt=not tested, nd=not detected, ¹ singlicate determination @ 100 μM)

Cellular Activity

Significant reduction in H3K9 dimethylation at 100nM in MDA-MB231 cells as measured by fluorescence immunostaining without significant cellular toxicity.



Click on the **'Cell-based Assay Data'** tab above for more details

Selectivity Beyond Target Family

>30% Inhib @ 1 μM

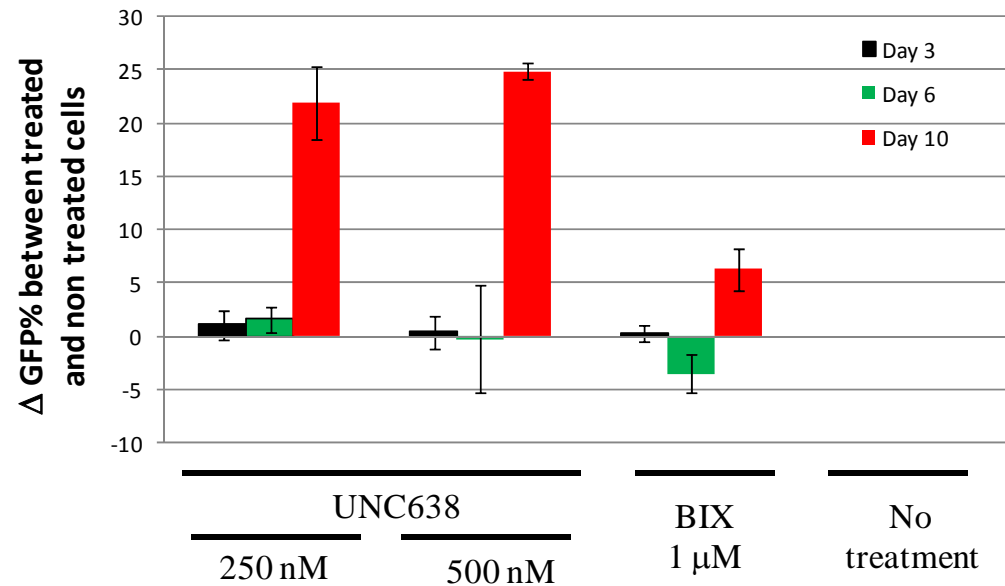
Functional consequences of G9a/GLP inhibition?

Well tolerated in variety of cancer cell lines

Cell Lines		IC ₅₀ (nM)	
		H3K9me2	MTT
Breast carcinoma	MDA231	81 ± 9	11,000 ± 710
	MCF7	70 ± 12	7,600
Prostate carcinoma	PC3	59	14,000
	22RV1	48	4,500
Colon carcinoma	HCT116 wt	210	11,000
	HCT116 p53 ^{-/-}	240	11,000
Human fibroblast	IMR90	120	2,300

Dalia Barsyte

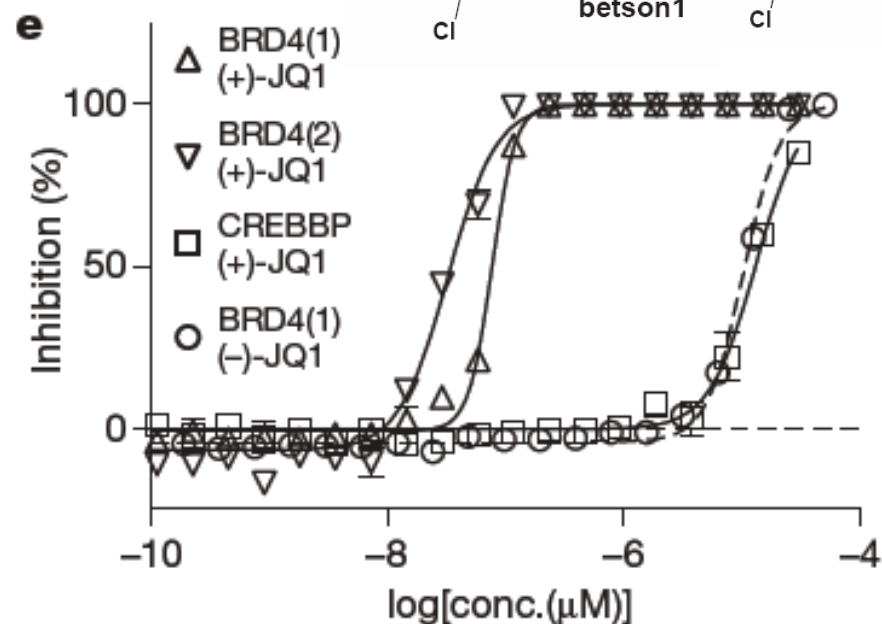
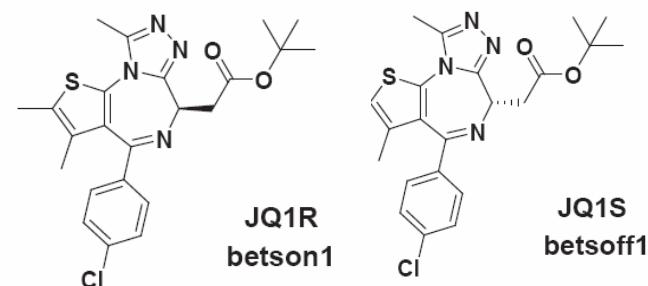
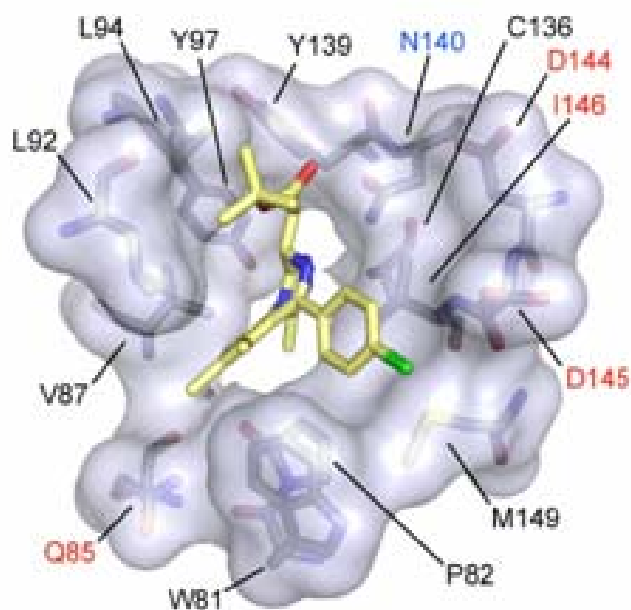
Re-activates expression of retroviral GFP reporter protein



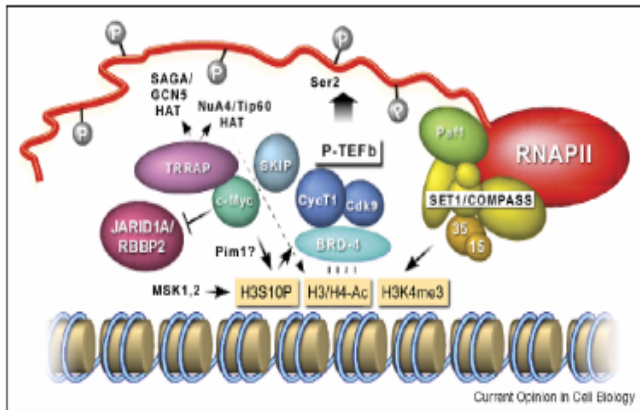
James Ellis, HSC

Selective inhibition of BET bromodomains

Panagis Filippakopoulos^{1*}, Jun Qi^{2*}, Sarah Picaud^{1*}, Yao Shen³, William B. Smith², Oleg Fedorov¹, Elizabeth M. Morse², Tracey Keates¹, Tyler T. Hickman⁴, Ildiko Felletar¹, Martin Philpott¹, Shonagh Munro⁵, Michael R. McKeown^{2,6}, Yuchuan Wang⁷, Amanda L. Christie⁸, Nathan West², Michael J. Cameron⁴, Brian Schwartz⁴, Tom D. Heightman¹, Nicholas La Thangue⁵, Christopher A. French⁴, Olaf Wiest³, Andrew L. Kung^{8,9}, Stefan Knapp^{1,5} & James E. Bradner^{2,6}



BET family of BRD proteins

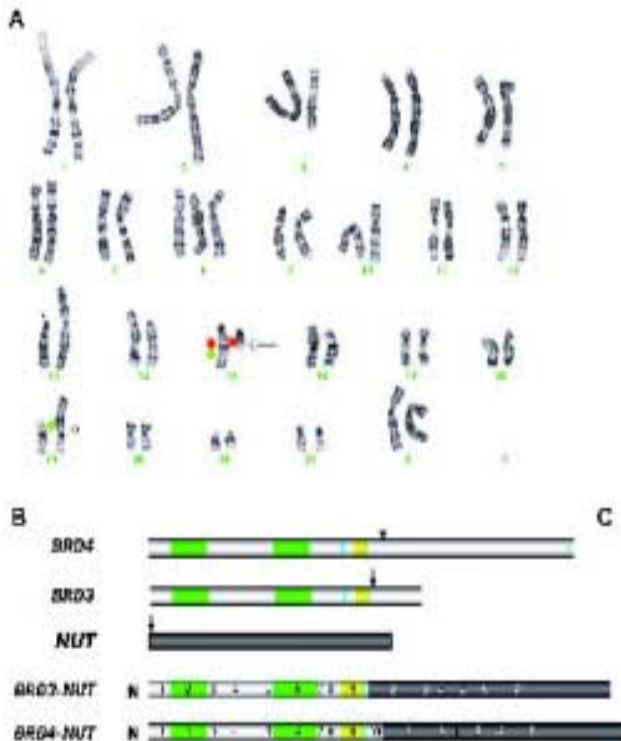


Regulation of P-Tefb(cdk9) mediated transcription

- KO of BRD4/2 results in G1 arrest and apoptosis and suppresses many genes required for growth
- P-TEFb and BRD functions with the oncogene c-Myc
- c-Myc interacts with the H3Kme3 specific demethylase JARID1A

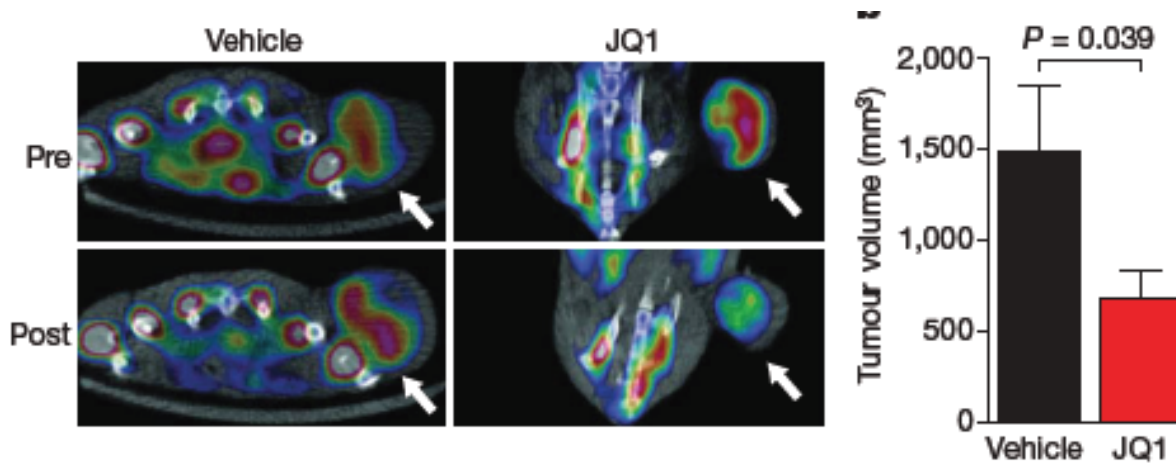
BET in Disease: NMC

- *NUT midline carcinoma (NMC)* is a rare, highly lethal cancer that occurs in children and adults.
- NMCs uniformly present in the midline, most commonly in the head, neck, or mediastinum, as poorly differentiated carcinomas
- Rearrangement of the Nuclear protein in testis (*NUT*) that creates a *BRD4-NUT* fusion gene
- Variant rearrangements, some involving the *BRD3* gene
- NMC is diagnosed by fluorescence *in situ* hybridization. However, most cases of NMC currently go unrecognized.



BET Probe: effective against NMC xenograft

Jay Bradner, Dana Farber



Cellular and *in vivo* studies

- Induces terminal differentiation of BRD4-NUT cell lines derived from MLC patients
- Anti-proliferative effects on cell lines that carry BRD-NUT fusion at 100nM
- Induces apoptosis in BRD-NUT cell lines
- Dissolves nuclear foci typically observed in BRD-NUT cell lines and biopsies
- Reduces tumour growth in xenograft models (50mg/kg IP, enantiomer)
- Displaces BRD4 from E-selectin and TNF α promoter in ChIP assays

- Open access research tools
 - Proteins, structural info, production protocols
 - Chemical Probes
 - Protein capture reagents
- Proactive engagement of community for
 - biological discovery
 - target validation
 - ultimately new therapeutics

ACKNOWLEDGEMENTS



www.TheSGC.org

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Johan Weigelt – Assoc. Dir, CS SGC–Stockholm, leader BioProbes Project

Chas Bountra – CS SGC–Oxford, leader Disease Association Project

Stefan Knapp – PI Kinome & Bromo Domains

Udo Opperman – PI Histone Lysine demethylases

Tom Heightman – PI Chemical Biology & Project Manager–Chem Probes

Peter Brown – Project Manager–Chemical Probes

Masoud Vedadi – PI Molecular Biophysics

Matthieu Schapira – PI Research Informatics/Comp Chem

Jinrong Min –PI Structural Chromatin Biology

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