Structural insights into the recognition of mono- and di-acetylated histones by the ATAD2B bromodomain

Supporting Information

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Supplementary Figure 1. Characterization of the ATAD2/B bromodomain binding curves for the dCypher assay. (A) The GST-tagged ATAD2 bromodomain (residues 981-1108) and (B) ATAD2B bromodomain (residues 953-1085) were titrated to control biotinylated histone peptides and binding curves determined on AlphaScreen[®] platform (i.e. dCypher[®] Phase A: see Methods). X-axes are log(protein concentration (M)) at constant peptide concentration (100 nM); Y-axes are AlphaScreen counts, representing relative strength of binding (n = 2; error bars are S.D.).



Supplementary Figure 2. ITC measurements of the interaction between acetylated histone ligands and the ATAD2B bromodomain. (A-S) Exothermic ITC enthalpy plots for the binding of the ATAD2B bromodomain to unmodified, mono- and di-acetylated histone ligands, as well as the ATAD2 bromodomain inhibitor compound 38. The calculated binding constants are indicated.



Supplementary Figure 3. Interaction of the ATAD2B bromodomain with acetylated histone ligands. (A) Superimposed ¹H-¹⁵N HSQC spectra of the ATAD2B bromodomain, collected during titrating in the indicated histone peptides. The spectra are color-coded according to the protein/peptide ratio. (B) 2D ¹H-¹⁵N HSQC spectra of ¹⁵N-labelled ATAD2B bromodomain with the complete HSQC assignments labeled.



Supplementary Figure 4. *ATAD2* and *ATAD2B* gene structures and splicing patterns. (A) Sashimi plots of splice junctions between *ATAD2* and *ATAD2B* are shown. The number of reads spanning each junction is indicated by the size of the sashimi plot curve, and the number of reads spanning novel junctions is indicated by red sashimi plot curves. Coverage plots for total mapped reads are shown (total exon coverages are shown on the y-axis). (B) RT-PCR Analysis of ATAD2 and ATAD2B exon 21-22 splicing patterns.



Supplementary Figure 5. ITC measurements of the interaction between acetylated histone ligands and mutant ATAD2B bromodomain proteins. (A-O) Exothermic ITC enthalpy plots for the binding of mutant ATAD2B bromodomain proteins to histone peptide ligands that are unmodified, mono- or di-acetylated. The calculated binding constants are indicated.



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Supplementary Figure 6. Analysis of ATAD2B splice isoform expression from RNAseq data. (A) Scatterplot comparing the normalized counts of reads that map to ATAD2B (x-axis) and ATAD2B_{short} (y-axis) isoforms across human breast cancer datasets from CCLE. Each dataset is colored by the breast cancer molecular subtype, the dashed line represents a 50:50 ratio of each isoform and the names of 4 cell lines with the highest expression of ATAD2B_{short} are labeled. (B) A plot showing the ranked expression of ATAD2B: ATAD2Bshort across human breast cancer cell lines. (C) A box plot of the ATAD2B: ATD2B_{short} ratios across human breast cancer molecular subtypes.



Supplementary Figure 7. Sequence alignment of the ATAD2 and ATAD2B bromodomains. Sequence alignment of the ATAD2 and ATAD2B bromodomain proteins corresponding to the amino acids in our ATAD2B bromodomain structure (residues 953-1085). Residues colored magenta are involved in hydrogen bonding to compound 38 for the ATAD2B bromodomain, and compound 42 for the ATAD2 bromodomain. Residues colored green are hydrophobic contacts. Residues that were mutated in this study are marked with a red vertical line. Sequence alignment was performed using the T-Coffee software ¹.

		962	972	982	992	
ATAD2B	953	EDQEENTLRELRLF	LRDVTKRLATD	KRFN <mark>I</mark> FSKP <mark>V</mark>	DIE <mark>EV</mark> SD <mark>Y</mark> LEVI	999
ATAD2	979	EEQEEDTFRELRIF	LRNVTHRLAID	KRFR <mark>V</mark> FTKP <mark>V</mark>	₽₽₽ <mark>₽₽₽₽₽</mark> ₽₽₽₽₽	K10250
		*:***:*:****	**:**:*** *	***。:*:***	* PDEXPDXVTV1	K 1026
		1009	1019	1029	1039	*
ATAD2B	1000	KEPMDLSTVITKID	KHNYLŤAKDFL	KDIDLICSNA	LE <mark>YN</mark> PDK <mark>D</mark> P <mark>GD</mark> K	1046
ATAD2	1026	KQPMDLSSVISKID	LHKYLTVKDYL	RDIDLICSNA	LE <mark>YN</mark> PDR <mark>D</mark> P <mark>GD</mark> F	1072
		* : * * * * * : * * : * * *	*:***.**:*	*******	***********	
		1056	1066	1076		
ATAD2B	1047	I <mark>I</mark> RH <mark>R</mark> ACTLKDTAH	AIIAAELDPEF	NKLCĚEIKEA	RIKR 1085	
ATAD2	1073	L <mark>I</mark> RH <mark>R</mark> ACALRDTAY	AIIKEELDEDF	EQLCEEIQES	RKKR 1111	
		• * * * * * * • * • * * * * * * * * * *	*** *** :*	::****:*:	* **	

1. Notredame, C., Higgins, D.G. & Heringa, J. T-Coffee: A novel method for fast and accurate multiple sequence alignment. *J Mol Biol* **302**, 205-17 (2000).

Data File C:\DATA\DCAUG10A\1FA-0301.D Sample Name: KG #1

H2AK5ac (1-12) HPLC report



Dilution : 1.0000 Use Multiplier & Dilution Factor with ISTDs

Signal 1: DAD1 C, Sig=210,8 Ref=360,100

Peak RetTime Type Width Area Height Area [min] [mAU*s] 8 # [min] [mAU] ----|-----|----|-----|-----|-----| 1 5.998 BB 0.1060 68.84024 9.55910 1.4777 2 9.312 VV 0.1266 4589.64307 543.08765 98.5223

H2AK5ac (1-12) MS report

#1

MW 1214



Mass (m/z)

10



Analysis Name:024-0501.DMethod:DC1M.MSample Name:H 4H 4PUREAnalysis Info:

Instrument: LC-MSD-Trap-SL Operator: Hodges

Print Date: 5/31/2011 3:26:41 PM Acq. Date: 5/31/2011 2:33:56 PM



H4K5ac (1-15) HPLC report

Sample Name:H4K5ac (1-15) Sample ID :U2819EJ240-1 Time Processed: 19:48:19 Month-Day-Year Processed :10/30/2019

Pump A : 0.065% trifluoroacetic in 100% water (v/v) Pump B : 0.05% trifluoroacetic in 100% acetonitrile (v/v) Total Flow:1 ml/min Wavelength:220 nm <<LC Time Program>> Time Module

Time	Module	Command	Value
0.01	Pumps	Pump A B.Conc	5
25.00	Pumps	Pump A B.Conc	65
25.01	Pumps	Pump A B.Conc	95
31.00	Pumps	Pump A B.Conc	95
31.01	Pumps	Pump A B.Conc	5
40.00	Pumps	Pump A B.Conc	5
40.01	Controller	Stop	
Column Borformon	1400		

<Column Performance>>
<Detector A>
Column : AlltimaTM C18 4.6 x 250 mm
Equipment:ZJ19010324



<Chromatogram>



<Peak Table>

Detector A Chann	el 1 220nm			
Peak#	Ret. Time	Area	Height	Area%
1	12.229	11546	1144	0.097
2	12.605	33865	3648	0.286
3	12.959	11807221	1149152	99.563
4	13.361	2802	621	0.024
5	13.578	1550	289	0.013
6	18.807	2072	383	0.017
Total		11859057	1155237	100.000

H4K5ac (1-15) MS report



H4K5ac (1-10) HPLC report

Sample Name: H4K5ac(1-10) Sample ID: U3559EH260-1 Time Processed : 8:43:45 Month-Day-Year Processed : 09/08/2019

Command Pump A B.Conc Stop



<Peak Table>

Peak#	Ret. Time	Area		
1	8.923	24054	Height	Area%
2	9.217	21854	2574	0.267
3	0.277	33068	5040	0.403
4	9.377	8098036	1075473	0.403
-	9.600	27857	6102	90.756
5	9.956	15390	1000	0.340
6	10.643	3877	1260	0.188
Total		0077	572	0.047

H4K5ac (1-10) MS report



16



Analysis Name:014-0901.DMethod:DC1M.MSample Name:K5Ac PUREAnalysis Info:

Instrument: LC-MSD-Trap-SL Operator: Hodges

Print Date: 5/10/2011 11:12:41 AM **Acq. Date:** 5/9/2011 8:21:14 PM



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H4K8ac (1-10) HPLC report





Analysis Name:	1EE-1801.D	Instrument:	LC-MSD-Trap-XCT	Print Date:	5/21/2017	5:45:54 PM
Method: DC2M.M		Operator:	Hodges	Acq. Date:	5/21/2017 2	2:51:17 PM
Sample Name: 67						
Analysis Info:						



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Instrument 1 5/10/2011 11:09:09 AM PK

Analysis Name:016-1101.DMethod:DC1M.MSample Name:K8Ac PUREAnalysis Info:

Instrument: LC-MSD-Trap-SL Operator: Hodges

Print Date: 5/10/2011 11:11:27 AM **Acq. Date:** 5/9/2011 9:28:16 PM



MSD Trap Report v 4 (Let-Opt2)

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H4K12ac (4-17) HPLC report



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HPLC REPORT

Sample Description: Structure:H4(4-17)K12ac GR-14 Lot No:P180117-CL633697 Column: 4.6mm*250mm, Inertsil ODS-SP Solvent A: 0.1%Trifluoroacetic in 100% Acetonirile Solvent B: 0.1%Trifluoroacetic in 100% Water Gradient: А В 0.01min 5% 95% 25.00min 30% 70% 25.01min 100% 0% 30.00min Stop

Flow rate:1.Oml/min

Wavelength:220nm Volume:10 µ 1

mV									
- 480									
- 420		7.582							
- 360									
- 300									
- 240									
- 180									
- 120									
- 60	4.594	1.079							
0									
- •60	2 4	6 8	10	12	14	16	18	20	min

Rank	Time	Conc.	Area	Height	
1 2 3	4.594 7.079 7.582	0. 7907 0. 7209 98. 49	49364 45008 6148640	6442 3761 402218	-
Total		100	6243012	412421	

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H4K12ac (4-17) MS report



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MS REPORT



H4K12ac (1-15) HPLC report



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HPLC Report

Sample Description: Structure:H4 SA-15 Lot NO. : P170620-MJ589927 Column:250*4.6mm, Boston Green ODS-AQ Solvent A:0.1%TFA in 100%water Solvent B:0.1%TFA in 100%acetonitrile Gradient : А В 0.1min 92 8 25min 67 ÷ 33 25.01min0 100

30min 0 Flow rate:1.0m1/min Wavelength(nm):220



100

Page 3 of 3



Mass Spectrometry Report



Page 2 of 3

Data File C:\DATA\DCAPR9D1\1AF-0801.D Sample Name: #5

H4K16ac (10-20) HPLC report



=======================================		=======================================	=========
Area	Percent	Report	
	========	=======================================	

Sorted By	:	Signal	
Multiplier	:	1.0000	
Dilution	:	1.0000	
Use Multiplier &	Dilution	Factor with	ISTDs

Signal 1: DAD1 C, Sig=210,8 Ref=360,100

Peak	RetTime	Type	Width	Area	Height	Area
#	[min]		[min]	[mAU*s]	[mAU]	20
1	10.711	BV	0.2268	1.25051e4	764.80334	98.2841
2	11.339	VV	0.1414	218.31677	22.85994	1.7159

Totals : 1.27234e4 787.66329

Analysis Name:	1AF-0801.d	Instrument:	LC-MSD-Trap-SL	Print Date:	4/9/2015	3:58:20 PM
Method: DC1M.m		Operator:	Hodges	Acq. Date:	4/9/2015 3:	12:56 PM
Sample Name: #5						
Analysis Info:						



MSD Trap Report v 4 (Let-Opt2)

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H4K5acK8ac (1-10) HPLC report

Sample Name :H4K5acK8ac(1-10) Sample ID :U3559EH260-3 Time Processed :8:35:14 AM Month-Day-Year Processed :09/04/2019

Pump A : 0.065% trifluoroacetic in 100% water (v/v)Pump B : 0.05% trifluoroacetic in 100% acetonitrile (v/v)Total Flow:1 ml/minWavelength:220 nm<<LC Time Program>>Time Module0.01 Pumps25.00 Pumps25.01 Pumps27.00 Pumps27.00 Pumps35.00 Pumps35.01 Controller<<Column Performance>><Detector A> Comr Solve Solve Solve Solve Solve Stop

mand	Value
ent B Conc.	5
ent B Conc.	65
ent B Conc.	95
ent B Conc.	95
ent B Conc.	5
ent B Conc.	5

mV

Column : Inertsil ODS-3 4.6 x 250 mm Equipment:ZJ17010508

<Chromatogram>



<Peak Table>

Detector A Chani	nel 1 220nm			
Peak#	Ret. Time	Area	Height	Area%
1	8.591	7220115	1087806	98.648
2	9.168	51513	8097	0.704
3	9.461	47441	8344	0.648
Total		7319069	1104247	100.000

H4K5acK8ac (1-10) MS report



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H4K5ac12ac (1-15) HPLC report

Sample Name :H4(1-15)K5acK12ac-A Sample ID :U291REE170-3 Time Processed :2:50:51 Month-Day-Year Processed :06/13/2019

Pump A : 0.065% trifluoroacetic in 100% water (v/v) Pump B : 0.05% trifluoroacetic in 100% acetonitrile (v/v) Total Flow: 1 ml/min Wavelength:220 nm Time Unit 0.01 Pumps

	Unit	Command	Value	Comment
0.01	Pumps	Pump B Conc	5	Comment
25.00	Pumps	Pump B Conc	65	
25.01	Pumps	Pump B Conc	95	
31.00	Pumps	Pump B Conc	95	
31.01	Pumps	Pump B Conc	5	
40.00	Pumps	Pump B Conc	5	
40.01	Controller	Stop	5	
		-		

<<Column Performance>> <Detector A> Column : Inertsil ODS-3 4.6 x 250 mm Equipment :SS-CM-0310



etector A Ch1 2	220nm			
Peak#	Ret. Time	Area	Height	Area %
1	8.725	101018	826	0.974
2	8.857	4764	625	0.874
3	8.958	2870	485	0.041
4	10.108	28279	229	0.025
5	10.796	18063	457	0.245
6	11.111	3432	265	0.030
7	11.539	11331469	1136910	0.050
8	12.642	3893	190	0.034
9	18.933	2296	140	0.034
10	24.108	38861	1287	0.020
11	24.926	19904	473	0.330
Total		11554848	1141887	100.000

Peak Table

H4K5ac12ac (1-15) MS report



H4K5ac16ac (1-24) HPLC report

		Sample Information	on	
Sample Name Sample ID Time Processed :15 Month-Day-Year Proc	:H4K5acK16ac res 1 :U7933DL110-1 5:31:34 essed :12/22/2018	-24		
Pump $\Delta : 0.065\%$ trifl	10r0acetic in 100% waters ()	<i></i>		
Pump B : 0.05% triflue	proacetic in 100% acetonitri	le (v/v)		
< <pump>> Flow</pump>	: 1.0000 mL/m	in		
< <detector a="">> Wavelength Ch1</detector>	: 220 nm			
< <lc program<="" td="" time=""><td>n>></td><td></td><td></td><td></td></lc>	n>>			
Time	Module	Command	Value	Comment
0.01	Pumps	Solvent B Conc.) 65	
25.00	Pumps	Solvent B Conc.	05	
27.00	Pumps	Solvent B Conc.	95	
27.00	Pumps	Solvent B Conc.	5	
35.00	Pumps	Solvent B Conc	5	
35.01	Controller	Stop	5	
< <column perform<br=""><detector a=""></detector></column>	ance>>	2.4.6 . 250		
Equipment:ZJ1701	: Inertsii ODS- 0210	3 4.6 x 250 mm		
		Chromatogram		
mV				
1		228		Detector A Channel 1 220nm
-		[∞]		
150-				
-				
100				
100-				
-				
-				
50-	~			
-	.25			
	2			
0	-			
-	V			
0.0	2.5 5.0 7	5 10.0 12.5	15.0 17	.5 20.0 22.5 25.0
		Dook Tabla		min
Detector A Channel	1 220nm	I Cak Table		
Peak#	Ret. Time	Height	Area	Area%
1	5.258	2192	20353	1.513

ι υακπ	Ket. Thile	noigin	Alca	Alca/0
1	5.258	2192	20353	1.513
2	8.228	179137	1324964	98.487
Total		181328	1345317	100.000

H4K5ac16ac (1-24) MS report Mass Spectrum



H4K8ac12ac (6-15) HPLC report

Data File C:\CHEM32\1\DATA\DC05212017\1FC-0701.D Sample Name: #4 pure



Analysis Name:	1FC-0701.D Ins	strument:	LC-MSD-Trap-XCT	Print Date:	5/21/2017	5:58:15 PM
Method: DC2M.M	Ор	erator:	Hodges	Acq. Date:	5/21/2017 1	1:45:14 AM
Sample Name: #4	pure					
Analysis Info:						



MSD Trap Report v 4 (Let-Opt2)

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H4K8ac16ac (1-20) HPLC report

Sample Name: H4K8acK16ac (res 1-20) Sample ID: U931EEK130-1 Time Processed :13:17:34 Month-Day-Year Processed :11/23/2019

Pump A : 0.065% trifluoroacetic in 100% water (v/v) Pump B : 0.05% trifluoroacetic in 100% acetonitrile (v/v) Total Flow:1 ml/min Wavelength:220 nm Time 0.01 25.00 25.01 32.00 32.01 Unit Command Command Pump A B.Conc Stop Pumps Pumps Pumps Pumps Pumps

Pumps Controller

40.00 40.00

<<Column Performance>> <Detector A> Column : Inertsil ODS-3 4.6 x 250 mm Equipment: GK1101009



Value

Detector A Ch1 220nm Peak# Ret. Time Area Height Area % 1 12.721 18139 2080 0.434 13.125 2 4133139 476832 98.840 13.400 3 23275 5808 0.557 13.895 4 1355 216 0.032 5 14.257 5738 82 0.137 Total 4181647 485016 100.000

Comment

H4K8ac16ac (1-20) MS report





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HPLC Report



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Mass Spectrometry Report



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Analysis Name: Method: DC1	003-0501.D M.M	Instrument: Operator:	LC-MSD-Trap-SL Hodges	Print Date: Acq. Date:	5/9/2011 3:43:22 PM 5/6/2011 5:01:31 PM
Sample Name:	H3 nat. pure			_	
Analysis Info:	Zorbax C18 300SB SI 15-30%B over 15min WJH3002 Control Per	N USFS003194 Dtide for D16			



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MSD Trap Report v 4 (Let-Opt2)

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H3K14ac (8-19) HPLC report



Analysis Name:	1CB-3101.D	Instrument:	LC-MSD-Trap-XCT	Print Date:	5/21/2017	8:25:59 AM
Method: DC2M.M		Operator:	Hodges	Acq. Date:	5/20/2017 7	':53:19 PM
Sample Name: #1	pure					
Analysis Info:						



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¹H NMR (500 MHz, CD₃OD)

