

Tiziana Bonaldi

List of Publications by Year in descending order

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98
papers

9,723
citations

81900
39
h-index

45317
90
g-index

102
all docs

102
docs citations

102
times ranked

14602
citing authors

#	ARTICLE	IF	CITATIONS
1	Loss of acetylation at Lys16 and trimethylation at Lys20 of histone H4 is a common hallmark of human cancer. <i>Nature Genetics</i> , 2005, 37, 391-400.	21.4	1,710
2	Monocytic cells hyperacetylate chromatin protein HMGB1 to redirect it towards secretion. <i>EMBO Journal</i> , 2003, 22, 5551-5560.	7.8	1,071
3	Identification of a specific inhibitor of the histone methyltransferase SU(VAR)3-9. , 2005, 1, 143-145.		462
4	The High Mobility Group (Hmg) Boxes of the Nuclear Protein Hmg1 Induce Chemotaxis and Cytoskeleton Reorganization in Rat Smooth Muscle Cells. <i>Journal of Cell Biology</i> , 2001, 152, 1197-1206.	5.2	435
5	Polycomb-Dependent H3K27me1 and H3K27me2 Regulate Active Transcription and Enhancer Fidelity. <i>Molecular Cell</i> , 2014, 53, 49-62.	9.7	403
6	NEW EMBO MEMBERS' REVIEW: The double life of HMGB1 chromatin protein: architectural factor and extracellular signal. <i>EMBO Journal</i> , 2001, 20, 4337-4340.	7.8	381
7	PTMs on H3 Variants before Chromatin Assembly Potentiate Their Final Epigenetic State. <i>Molecular Cell</i> , 2006, 24, 309-316.	9.7	361
8	Microbiota derived short chain fatty acids promote histone crotonylation in the colon through histone deacetylases. <i>Nature Communications</i> , 2018, 9, 105.	12.8	326
9	Tet Proteins Connect the O-Linked N-acetylglucosamine Transferase Ogt to Chromatin in Embryonic Stem Cells. <i>Molecular Cell</i> , 2013, 49, 645-656.	9.7	285
10	Iodoacetamide-induced artifact mimics ubiquitination in mass spectrometry. <i>Nature Methods</i> , 2008, 5, 459-460.	19.0	268
11	The DNA chaperone HMGB1 facilitates ACF/CHRAC-dependent nucleosome sliding. <i>EMBO Journal</i> , 2002, 21, 6865-6873.	7.8	219
12	The EGFR-specific antibody cetuximab combined with chemotherapy triggers immunogenic cell death. <i>Nature Medicine</i> , 2016, 22, 624-631.	30.7	214
13	The HP1±â€“CAF1±â€“SetDB1±â€“containing complex provides H3K9me1 for Suv39±â€“mediated K9me3 in pericentric heterochromatin. <i>EMBO Reports</i> , 2009, 10, 769-775.	4.5	201
14	Substantial Histone Reduction Modulates Genomewide Nucleosomal Occupancy and Global Transcriptional Output. <i>PLoS Biology</i> , 2011, 9, e1001086.	5.6	193
15	Therapeutic Targeting of RNA Splicing Catalysis through Inhibition of Protein Arginine Methylation. <i>Cancer Cell</i> , 2019, 36, 194-209.e9.	16.8	184
16	Threshold-controlled ubiquitination of the EGFR directs receptor fate. <i>EMBO Journal</i> , 2013, 32, 2140-2157.	7.8	156
17	Mass spectrometry-based identification and characterisation of lysine and arginine methylation in the human proteome. <i>Molecular BioSystems</i> , 2013, 9, 2231.	2.9	141
18	Functional Landscape of PCGF Proteins Reveals Both RING1A/B-Dependent-and RING1A/B-Independent-Specific Activities. <i>Molecular Cell</i> , 2019, 74, 1037-1052.e7.	9.7	128

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19	Reticulon 3â€“dependent ER-PM contact sites control EGFR nonclathrin endocytosis. <i>Science</i> , 2017, 356, 617-624.	12.6	118
20	Proteomics profiling of arginine methylation defines PRMT5 substrate specificity. <i>Science Signaling</i> , 2019, 12, .	3.6	114
21	The RAG1 Homeodomain Recruits HMG1 and HMG2 To Facilitate Recombination Signal Sequence Binding and To Enhance the Intrinsic DNA-Bending Activity of RAG1-RAG2. <i>Molecular and Cellular Biology</i> , 1999, 19, 6532-6542.	2.3	112
22	A combination of different mass spectroscopic techniques for the analysis of dynamic changes of histone modifications. <i>Proteomics</i> , 2004, 4, 1382-1396.	2.2	102
23	The Long Acidic Tail of High Mobility Group Box 1 (HMGB1) Protein Forms an Extended and Flexible Structure That Interacts with Specific Residues within and between the HMG Boxes. <i>Biochemistry</i> , 2004, 43, 11992-11997.	2.5	94
24	Systems-wide Analysis of a Phosphatase Knock-down by Quantitative Proteomics and Phosphoproteomics. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1908-1920.	3.8	94
25	Yin Yang 1 extends the Myc-related transcription factors network in embryonic stem cells. <i>Nucleic Acids Research</i> , 2012, 40, 3403-3418.	14.5	94
26	Combined Use of RNAi and Quantitative Proteomics to Study Gene Function in <i>Drosophila</i> . <i>Molecular Cell</i> , 2008, 31, 762-772.	9.7	93
27	miR-17-92 fine-tunes MYC expression and function to ensure optimal B cell lymphoma growth. <i>Nature Communications</i> , 2015, 6, 8725.	12.8	88
28	Extracellular vesicle-mediated transfer of CLIC1 protein is a novel mechanism for the regulation of glioblastoma growth. <i>Oncotarget</i> , 2015, 6, 31413-31427.	1.8	87
29	DEPDC1B Coordinates De-adhesion Events and Cell-Cycle Progression at Mitosis. <i>Developmental Cell</i> , 2014, 31, 420-433.	7.0	76
30	Quantitative proteomics as a new piece of the systems biology puzzle. <i>Journal of Proteomics</i> , 2008, 71, 357-367.	2.4	73
31	SILAC-based proteomic analysis to dissect the â€œhistone modification signatureâ€•of human breast cancer cells. <i>Amino Acids</i> , 2011, 41, 387-399.	2.7	71
32	PARP14 Controls the Nuclear Accumulation of a Subset of Type I IFNâ€“Inducible Proteins. <i>Journal of Immunology</i> , 2018, 200, 2439-2454.	0.8	70
33	Methylation of CenH3 arginine 37 regulates kinetochore integrity and chromosome segregation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 9029-9034.	7.1	62
34	Cell Reprogramming Requires Silencing of a Core Subset of Polycomb Targets. <i>PLoS Genetics</i> , 2013, 9, e1003292.	3.5	59
35	Targeting the scaffolding role of LSD1 (KDM1A) poises acute myeloid leukemia cells for retinoic acidâ€“induced differentiation. <i>Science Advances</i> , 2020, 6, eaax2746.	10.3	56
36	The Proteomic Investigation of Chromatin Functional Domains Reveals Novel Synergisms among Distinct Heterochromatin Components. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 764-780.	3.8	54

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37	Design of KDM4 Inhibitors with Antiproliferative Effects in Cancer Models. ACS Medicinal Chemistry Letters, 2017, 8, 869-874.	2.8	50
38	High constitutive activity of a broad panel of housekeeping and tissue-specific <i>cis</i>-regulatory elements depends on a subset of ETS proteins. Genes and Development, 2017, 31, 399-412.	5.9	48
39	The Use of Mass Spectrometry for the Analysis of Histone Modifications. Methods in Enzymology, 2003, 377, 111-130.	1.0	42
40	The N-Terminus of Drosophila SU(VAR)3â~9 Mediates Dimerization and Regulates Its Methyltransferase Activityâ€. Biochemistry, 2004, 43, 3740-3749.	2.5	42
41	Pathology Tissue-quantitative Mass Spectrometry Analysis to Profile Histone Post-translational Modification Patterns in Patient Samples. Molecular and Cellular Proteomics, 2016, 15, 866-877.	3.8	41
42	Site-specific acetylation of ISWI by GCN5. BMC Molecular Biology, 2007, 8, 73.	3.0	40
43	PRMT1 Is Recruited via DNA-PK to Chromatin Where It Sustains the Senescence-Associated Secretory Phenotype in Response to Cisplatin. Cell Reports, 2020, 30, 1208-1222.e9.	6.4	40
44	ARGONAUTE2 cooperates with SWI/SNF complex to determine nucleosome occupancy at human Transcription Start Sites. Nucleic Acids Research, 2015, 43, 1498-1512.	14.5	37
45	The kinetochore module Okp1 ^{CENPâ€Q} /Ame1 ^{CENPâ€U} is a reader for Nâ€terminal modifications on the centromeric histone Cse4 ^{CENPâ€A}. EMBO Journal, 2019, 38, .	7.8	34
46	Mass Spectrometry-Based Proteomics for the Analysis of Chromatin Structure and Dynamics. International Journal of Molecular Sciences, 2013, 14, 5402-5431.	4.1	31
47	Extensive and systematic rewiring of histone post-translational modifications in cancer model systems. Nucleic Acids Research, 2018, 46, 3817-3832.	14.5	31
48	The contribution of mass spectrometry-based proteomics to understanding epigenetics. Epigenomics, 2016, 8, 429-445.	2.1	30
49	Improved bottomâ€up strategy to efficiently separate hypermodified histone peptides through ultraâ€HPLC separation on a bench top Orbitrap instrument. Proteomics, 2014, 14, 2212-2225.	2.2	28
50	Chromatin proteomics reveals novel combinatorial histone modification signatures that mark distinct subpopulations of macrophage enhancers. Nucleic Acids Research, 2017, 45, 12195-12213.	14.5	26
51	Profiling of Epigenetic Features in Clinical Samples Reveals Novel Widespread Changes in Cancer. Cancers, 2019, 11, 723.	3.7	26
52	Advances in enrichment methods for mass spectrometry-based proteomics analysis of post-translational modifications. Journal of Chromatography A, 2022, 1678, 463352.	3.7	25
53	Zc3h10 is a novel mitochondrial regulator. EMBO Reports, 2018, 19, .	4.5	23
54	Enrichment of histones from patient samples for mass spectrometry-based analysis of post-translational modifications. Methods, 2020, 184, 19-28.	3.8	23

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55	PRMT1-mediated methylation of the microprocessor-associated proteins regulates microRNA biogenesis. <i>Nucleic Acids Research</i> , 2020, 48, 96-115.	14.5	22
56	The ChroP Approach Combines ChIP and Mass Spectrometry to Dissect Locus-specific Proteomic Landscapes of Chromatin. <i>Journal of Visualized Experiments</i> , 2014, , .	0.3	21
57	Intestinal differentiation involves cleavage of histone H3 N-terminal tails by multiple proteases. <i>Nucleic Acids Research</i> , 2021, 49, 791-804.	14.5	21
58	Long non-coding RNA TINCR suppresses metastatic melanoma dissemination by preventing ATF4 translation. <i>EMBO Reports</i> , 2021, 22, e50852.	4.5	21
59	A role for CENP-A/Cse4 phosphorylation on serine 33 in deposition at the centromere. <i>FEMS Yeast Research</i> , 2018, 18, .	2.3	20
60	FAM46C and FNDC3A Are Multiple Myeloma Tumor Suppressors That Act in Concert to Impair Clearing of Protein Aggregates and Autophagy. <i>Cancer Research</i> , 2020, 80, 4693-4706.	0.9	20
61	Mass spectrometry-based characterization of histones in clinical samples: applications, progress, and challenges. <i>FEBS Journal</i> , 2022, 289, 1191-1213.	4.7	20
62	A Super-SILAC Strategy for the Accurate and Multiplexed Profiling of Histone Posttranslational Modifications. <i>Methods in Enzymology</i> , 2017, 586, 311-332.	1.0	18
63	LSD1-directed therapy affects glioblastoma tumorigenicity by deregulating the protective ATF4-dependent integrated stress response. <i>Science Translational Medicine</i> , 2021, 13, eabf7036.	12.4	18
64	Reply to "Chaetocin is a nonspecific inhibitor of histone lysine methyltransferases". <i>Nature Chemical Biology</i> , 2013, 9, 137-137.	8.0	17
65	Biochemical systems approaches for the analysis of histone modification readout. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2014, 1839, 657-668.	1.9	17
66	PAT-H-MS coupled with laser microdissection to study histone post-translational modifications in selected cell populations from pathology samples. <i>Clinical Epigenetics</i> , 2017, 9, 69.	4.1	17
67	Pharmacological inhibition of LSD1 triggers myeloid differentiation by targeting GSE1 oncogenic functions in AML. <i>Oncogene</i> , 2022, 41, 878-894.	5.9	17
68	Mass Spectrometry-Based Proteomics to Unveil the Non-coding RNA World. <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 90.	3.5	15
69	Spatial epi-proteomics enabled by histone post-translational modification analysis from low-abundance clinical samples. <i>Clinical Epigenetics</i> , 2021, 13, 145.	4.1	15
70	Quantitative Chemical Proteomics Identifies Novel Targets of the Anti-cancer Multi-kinase Inhibitor E-3810. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1495-1509.	3.8	14
71	Clinical Application of Mass Spectrometry-Based Proteomics in Lung Cancer Early Diagnosis. <i>Proteomics - Clinical Applications</i> , 2020, 14, 1900138.	1.6	14
72	Chromatomics—the analysis of the chromatome. <i>Molecular BioSystems</i> , 2005, 1, 112-116.	2.9	13

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73	hmSEEKER: Identification of hmSILAC Doublets in MaxQuant Output Data. <i>Proteomics</i> , 2019, 19, e1800300.	2.2	13
74	hSWATH: Unlocking SWATHâ€™s Full Potential for an Untargeted Histone Perspective. <i>Journal of Proteome Research</i> , 2019, 18, 3840-3849.	3.7	12
75	Alternative digestion approaches improve histone modification mapping by mass spectrometry in clinical samples. <i>Proteomics - Clinical Applications</i> , 2019, 13, 1700166.	1.6	11
76	Nanoelectrospray peptide mapping revisited: Composite survey spectra allow high dynamic range protein characterization without LCMS on an orbitrap mass spectrometer. <i>International Journal of Mass Spectrometry</i> , 2007, 268, 158-167.	1.5	10
77	Epigenetic drug target deconvolution by mass spectrometryâ€‘based technologies. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 854-857.	8.2	9
78	Systems Biology â€œOn-the-Flyâ€‘ SILAC-Based Quantitative Proteomics and RNAi Approach in <i>Drosophila melanogaster</i> . <i>Methods in Molecular Biology</i> , 2010, 662, 59-78.	0.9	9
79	Label-Free Mass Spectrometry-Based Quantification of Linker Histone H1 Variants in Clinical Samples. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7330.	4.1	8
80	Systematic Analysis of the Impact of R-Methylation on RBPs-RNA Interactions: A Proteomic Approach. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 688973.	3.5	8
81	Biochemical and Computational Approaches for the Large-Scale Analysis of Protein Arginine Methylation by Mass Spectrometry. <i>Current Protein and Peptide Science</i> , 2020, 21, 725-739.	1.4	8
82	Quantitative assessment of chemical artefacts produced by propionylation of histones prior to mass spectrometry analysis. <i>Proteomics</i> , 2016, 16, 1952-1954.	2.2	7
83	Mass-spectrometry analysis of histone post-translational modifications in pathology tissue using the PAT-H-MS approach. <i>Data in Brief</i> , 2016, 7, 188-194.	1.0	6
84	SILAC-Based Quantitative Strategies for Accurate Histone Posttranslational Modification Profiling Across Multiple Biological Samples. <i>Methods in Molecular Biology</i> , 2017, 1528, 97-119.	0.9	6
85	Proteomics Meets Genetics: SILAC Labeling of <i>Drosophila melanogaster</i> Larvae and Cells for In Vivo Functional Studies. <i>Methods in Molecular Biology</i> , 2014, 1188, 293-311.	0.9	4
86	Recent advances in mass spectrometry analysis of histone post-translational modifications: potential clinical impact of the PAT-H-MS approach. <i>Expert Review of Proteomics</i> , 2016, 13, 245-250.	3.0	3
87	Dual role of PRMT1-dependent arginine methylation in cellular responses to genotoxic stress. <i>Molecular and Cellular Oncology</i> , 2020, 7, 1743808.	0.7	3
88	Software Options for the Analysis of MS-Proteomic Data. <i>Methods in Molecular Biology</i> , 2021, 2361, 35-59.	0.9	3
89	ProMetheusDB: An In-Depth Analysis of the High-Quality Human Methyl-proteome. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100243.	3.8	3
90	MS-analysis of SILAC-labeled MYC-driven B lymphoma cells overexpressing miR-17-19b. <i>Data in Brief</i> , 2016, 7, 349-353.	1.0	2

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91	Native Chromatin Proteomics (N-ChroP) to Characterize Histone Post-translational Modification (PTM) Combinatorics at Distinct Genomic Regions. Methods in Molecular Biology, 2021, 2351, 251-274.	0.9	1
92	Mass Spectrometry for the Identification of Posttranslational Modifications in Histones and Its Application in Clinical Epigenetics. , 2016, , 195-214.		1
93	Mass Spectrometry and Epigenetics. , 2017, , 1-18.		1
94	HMGB1 MOLECULAR BIOLOGY IN MYELOID CELLS. Shock, 2004, 21, 36.	2.1	0
95	Spatiotemporal plasticity of miRNAs functions: The miR-17-92 case. Molecular and Cellular Oncology, 2016, 3, e1156216.	0.7	0
96	MYC/miR-17-92 interplay maintains B-lymphoma cell homeostasis. Cell Cycle, 2016, 15, 1025-1026.	2.6	0
97	Mass Spectrometry and Epigenetics. , 2019, , 2251-2268.		0
98	Abstract 4731: Therapeutic targeting of RNA splicing through inhibition of protein arginine methylation. , 2019, , .		0