Tiziana Bonaldi

List of Publications by Year
in descending order

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98 papers	9,723 citations	81743 39 h-index	45213 90 g-index
102 all docs	102 docs citations	102 times ranked	14602 citing authors

#	Article	IF	Citations
1	Mass spectrometryâ€based characterization of histones in clinical samples: applications, progress, and challenges. FEBS Journal, 2022, 289, 1191-1213.	2.2	20
2	Pharmacological inhibition of LSD1 triggers myeloid differentiation by targeting GSE1 oncogenic functions in AML. Oncogene, 2022, 41, 878-894.	2.6	17
3	ProMetheusDB: An In-Depth Analysis of the High-Quality Human Methyl-proteome. Molecular and Cellular Proteomics, 2022, 21, 100243.	2.5	3
4	Advances in enrichment methods for mass spectrometry-based proteomics analysis of post-translational modifications. Journal of Chromatography A, 2022, 1678, 463352.	1.8	25
5	Intestinal differentiation involves cleavage of histone H3 N-terminal tails by multiple proteases. Nucleic Acids Research, 2021, 49, 791-804.	6.5	21
6	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.	0.4	1
7	Software Options for the Analysis of MS-Proteomic Data. Methods in Molecular Biology, 2021, 2361, 35-59.	0.4	3
8	Long nonâ€coding RNA TINCR suppresses metastatic melanoma dissemination by preventing ATF4 translation. EMBO Reports, 2021, 22, e50852.	2.0	21
9	Spatial epi-proteomics enabled by histone post-translational modification analysis from low-abundance clinical samples. Clinical Epigenetics, 2021, 13, 145.	1.8	15
10	Systematic Analysis of the Impact of R-Methylation on RBPs-RNA Interactions: A Proteomic Approach. Frontiers in Molecular Biosciences, 2021, 8, 688973.	1.6	8
11	LSD1-directed therapy affects glioblastoma tumorigenicity by deregulating the protective ATF4-dependent integrated stress response. Science Translational Medicine, 2021, 13, eabf7036.	5.8	18
12	Enrichment of histones from patient samples for mass spectrometry-based analysis of post-translational modifications. Methods, 2020, 184, 19-28.	1.9	23
13	PRMT1-mediated methylation of the microprocessor-associated proteins regulates microRNA biogenesis. Nucleic Acids Research, 2020, 48, 96-115.	6.5	22
14	Label-Free Mass Spectrometry-Based Quantification of Linker Histone H1 Variants in Clinical Samples. International Journal of Molecular Sciences, 2020, 21, 7330.	1.8	8
15	Dual role of PRMT1-dependent arginine methylation in cellular responses to genotoxic stress. Molecular and Cellular Oncology, 2020, 7, 1743808.	0.3	3
16	FAM46C and FNDC3A Are Multiple Myeloma Tumor Suppressors That Act in Concert to Impair Clearing of Protein Aggregates and Autophagy. Cancer Research, 2020, 80, 4693-4706.	0.4	20
17	Clinical Application of Mass Spectrometryâ€Based Proteomics in Lung Cancer Early Diagnosis. Proteomics - Clinical Applications, 2020, 14, 1900138.	0.8	14
18	Targeting the scaffolding role of LSD1 (KDM1A) poises acute myeloid leukemia cells for retinoic acidâ€“induced differentiation. Science Advances, 2020, 6, eaax2746.	4.7	56

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19	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.	2.9	40
20	Biochemical and Computational Approaches for the Large-Scale Analysis of Protein Arginine Methylation by Mass Spectrometry. Current Protein and Peptide Science, 2020, 21, 725-739.	0.7	8
21	hSWATH: Unlocking SWATHâ€™s Full Potential for an Untargeted Histone Perspective. Journal of Proteome Research, 2019, 18, 3840-3849.	1.8	12
22	Therapeutic Targeting of RNA Splicing Catalysis through Inhibition of Protein Arginine Methylation. Cancer Cell, 2019, 36, 194-209.e9.	7.7	184
23	Epigenetic drug target deconvolution by mass spectrometryâ€“based technologies. Nature Structural and Molecular Biology, 2019, 26, 854-857.	3.6	9
24	hmSEEKER: Identification of hmSILAC Doublets in MaxQuant Output Data. Proteomics, 2019, 19, e1800300.	1.3	13
25	Profiling of Epigenetic Features in Clinical Samples Reveals Novel Widespread Changes in Cancer. Cancers, 2019, 11, 723.	1.7	26
26	Functional Landscape of PCGF Proteins Reveals Both RING1A/B-Dependent-and RING1A/B-Independent-Specific Activities. Molecular Cell, 2019, 74, 1037-1052.e7.	4.5	128
27	Proteomics profiling of arginine methylation defines PRMT5 substrate specificity. Science Signaling, 2019, 12, .	1.6	114
28	Mass Spectrometry and Epigenetics. , 2019, , 2251-2268.		0
29	Alternative digestion approaches improve histone modification mapping by mass spectrometry in clinical samples. Proteomics - Clinical Applications, 2019, 13, 1700166.	0.8	11
30	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, .	3.5	34
31	Abstract 4731: Therapeutic targeting of RNA splicing through inhibition of protein arginine methylation. , 2019, , .		0
32	Zc3h10 is a novel mitochondrial regulator. EMBO Reports, 2018, 19, .	2.0	23
33	PARP14 Controls the Nuclear Accumulation of a Subset of Type I IFNâ€“Inducible Proteins. Journal of Immunology, 2018, 200, 2439-2454.	0.4	70
34	Extensive and systematic rewiring of histone post-translational modifications in cancer model systems. Nucleic Acids Research, 2018, 46, 3817-3832.	6.5	31
35	Microbiota derived short chain fatty acids promote histone crotonylation in the colon through histone deacetylases. Nature Communications, 2018, 9, 105.	5.8	326
36	A role for CENP-A/Cse4 phosphorylation on serine 33 in deposition at the centromere. FEMS Yeast Research, 2018, 18, .	1.1	20

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37	Mass Spectrometry-Based Proteomics to Unveil the Non-coding RNA World. Frontiers in Molecular Biosciences, 2018, 5, 90.	1.6	15
38	High constitutive activity of a broad panel of housekeeping and tissue-specific cis-regulatory elements depends on a subset of ETS proteins. Genes and Development, 2017, 31, 399-412.	2.7	48
39	Reticulon 3â€“dependent ER-PM contact sites control EGFR nonclathrin endocytosis. Science, 2017, 356, 617-624.	6.0	118
40	Chromatin proteomics reveals novel combinatorial histone modification signatures that mark distinct subpopulations of macrophage enhancers. Nucleic Acids Research, 2017, 45, 12195-12213.	6.5	26
41	Design of KDM4 Inhibitors with Antiproliferative Effects in Cancer Models. ACS Medicinal Chemistry Letters, 2017, 8, 869-874.	1.3	50
42	SILAC-Based Quantitative Strategies for Accurate Histone Posttranslational Modification Profiling Across Multiple Biological Samples. Methods in Molecular Biology, 2017, 1528, 97-119.	0.4	6
43	A Super-SILAC Strategy for the Accurate and Multiplexed Profiling of Histone Posttranslational Modifications. Methods in Enzymology, 2017, 586, 311-332.	0.4	18
44	PAT-H-MS coupled with laser microdissection to study histone post-translational modifications in selected cell populations from pathology samples. Clinical Epigenetics, 2017, 9, 69.	1.8	17
45	Mass Spectrometry and Epigenetics. , 2017, , 1-18.		1
46	Mass-spectrometry analysis of histone post-translational modifications in pathology tissue using the PAT-H-MS approach. Data in Brief, 2016, 7, 188-194.	0.5	6
47	MS-analysis of SILAC-labeled MYC-driven B lymphoma cells overexpressing miR-17-19b. Data in Brief, 2016, 7, 349-353.	0.5	2
48	The EGFR-specific antibody cetuximab combined with chemotherapy triggers immunogenic cell death. Nature Medicine, 2016, 22, 624-631.	15.2	214
49	Quantitative assessment of chemical artefacts produced by propionylation of histones prior to mass spectrometry analysis. Proteomics, 2016, 16, 1952-1954.	1.3	7
50	Spatiotemporal plasticity of miRNAs functions: The miR-17-92 case. Molecular and Cellular Oncology, 2016, 3, e1156216.	0.3	0
51	MYC/miR-17-92 interplay maintains B-lymphoma cell homeostasis. Cell Cycle, 2016, 15, 1025-1026.	1.3	0
52	The contribution of mass spectrometry-based proteomics to understanding epigenetics. Epigenomics, 2016, 8, 429-445.	1.0	30
53	Recent advances in mass spectrometry analysis of histone post-translational modifications: potential clinical impact of the PAT-H-MS approach. Expert Review of Proteomics, 2016, 13, 245-250.	1.3	3
54	Pathology Tissue-quantitative Mass Spectrometry Analysis to Profile Histone Post-translational Modification Patterns in Patient Samples. Molecular and Cellular Proteomics, 2016, 15, 866-877.	2.5	41

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55	Mass Spectrometry for the Identification of Posttranslational Modifications in Histones and Its Application in Clinical Epigenetics. , 2016, , 195-214.		1
56	miR-17-92 fine-tunes MYC expression and function to ensure optimal B cell lymphoma growth. Nature Communications, 2015, 6, 8725.	5.8	88
57	ARGONAUTE2 cooperates with SWI/SNF complex to determine nucleosome occupancy at human Transcription Start Sites. Nucleic Acids Research, 2015, 43, 1498-1512.	6.5	37
58	Extracellular vesicle-mediated transfer of CLIC1 protein is a novel mechanism for the regulation of glioblastoma growth. Oncotarget, 2015, 6, 31413-31427.	0.8	87
59	DEPDC1B Coordinates De-adhesion Events and Cell-Cycle Progression at Mitosis. Developmental Cell, 2014, 31, 420-433.	3.1	76
60	Biochemical systems approaches for the analysis of histone modification readout. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2014, 1839, 657-668.	0.9	17
61	Polycomb-Dependent H3K27me1 and H3K27me2 Regulate Active Transcription and Enhancer Fidelity. Molecular Cell, 2014, 53, 49-62.	4.5	403
62	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.	1.3	28
63	Proteomics Meets Genetics: SILAC Labeling of Drosophila melanogaster Larvae and Cells for In Vivo Functional Studies. Methods in Molecular Biology, 2014, 1188, 293-311.	0.4	4
64	Quantitative Chemical Proteomics Identifies Novel Targets of the Anti-cancer Multi-kinase Inhibitor E-3810. Molecular and Cellular Proteomics, 2014, 13, 1495-1509.	2.5	14
65	The ChroP Approach Combines ChIP and Mass Spectrometry to Dissect Locus-specific Proteomic Landscapes of Chromatin. Journal of Visualized Experiments, 2014, , .	0.2	21
66	Mass spectrometry-based identification and characterisation of lysine and arginine methylation in the human proteome. Molecular BioSystems, 2013, 9, 2231.	2.9	141
67	Threshold-controlled ubiquitination of the EGFR directs receptor fate. EMBO Journal, 2013, 32, 2140-2157.	3.5	156
68	The Proteomic Investigation of Chromatin Functional Domains Reveals Novel Synergisms among Distinct Heterochromatin Components. Molecular and Cellular Proteomics, 2013, 12, 764-780.	2.5	54
69	Tet Proteins Connect the O-Linked N-acetylglucosamine Transferase Ogt to Chromatin in Embryonic Stem Cells. Molecular Cell, 2013, 49, 645-656.	4.5	285
70	Cell Reprogramming Requires Silencing of a Core Subset of Polycomb Targets. PLoS Genetics, 2013, 9, e1003292.	1.5	59
71	Mass Spectrometry-Based Proteomics for the Analysis of Chromatin Structure and Dynamics. International Journal of Molecular Sciences, 2013, 14, 5402-5431.	1.8	31
72	Reply to "Chaetocin is a nonspecific inhibitor of histone lysine methyltransferases". Nature Chemical Biology, 2013, 9, 137-137.	3.9	17

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73	Methylation of CenH3 arginine 37 regulates kinetochore integrity and chromosome segregation. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 9029-9034.	3.3	62
74	Yin Yang 1 extends the Myc-related transcription factors network in embryonic stem cells. Nucleic Acids Research, 2012, 40, 3403-3418.	6.5	94
75	SILAC-based proteomic analysis to dissect the â€œhistone modification signatureâ€•of human breast cancer cells. Amino Acids, 2011, 41, 387-399.	1.2	71
76	Substantial Histone Reduction Modulates Genomewide Nucleosomal Occupancy and Global Transcriptional Output. PLoS Biology, 2011, 9, e1001086.	2.6	193
77	Systems Biology â€œOn-the-Flyâ€• SILAC-Based Quantitative Proteomics and RNAi Approach in Drosophila melanogaster. Methods in Molecular Biology, 2010, 662, 59-78.	0.4	9
78	Systems-wide Analysis of a Phosphatase Knock-down by Quantitative Proteomics and Phosphoproteomics. Molecular and Cellular Proteomics, 2009, 8, 1908-1920.	2.5	94
79	The HP1Î±â€“CAF1â€“SetDB1â€•containing complex provides H3K9me1 for Suv39â€•mediated K9me3 in pericentric heterochromatin. EMBO Reports, 2009, 10, 769-775.	2.0	201
80	Quantitative proteomics as a new piece of the systems biology puzzle. Journal of Proteomics, 2008, 71, 357-367.	1.2	73
81	Iodoacetamide-induced artifact mimics ubiquitination in mass spectrometry. Nature Methods, 2008, 5, 459-460.	9.0	268
82	Combined Use of RNAi and Quantitative Proteomics to Study Gene Function in Drosophila. Molecular Cell, 2008, 31, 762-772.	4.5	93
83	Nanoelectrospray peptide mapping revisited: Composite survey spectra allow high dynamic range protein characterization without LCMS on an orbitrap mass spectrometer. International Journal of Mass Spectrometry, 2007, 268, 158-167.	0.7	10
84	Site-specific acetylation of ISWI by GCN5. BMC Molecular Biology, 2007, 8, 73.	3.0	40
85	PTMs on H3 Variants before Chromatin Assembly Potentiate Their Final Epigenetic State. Molecular Cell, 2006, 24, 309-316.	4.5	361
86	Identification of a specific inhibitor of the histone methyltransferase SU(VAR)3-9. , 2005, 1, 143-145.		462
87	Loss of acetylation at Lys16 and trimethylation at Lys20 of histone H4 is a common hallmark of human cancer. Nature Genetics, 2005, 37, 391-400.	9.4	1,710
88	â€œChromatomicsâ€•the analysis of the chromatome. Molecular BioSystems, 2005, 1, 112-116.	2.9	13
89	A combination of different mass spectroscopic techniques for the analysis of dynamic changes of histone modifications. Proteomics, 2004, 4, 1382-1396.	1.3	102
90	The N-Terminus of Drosophila SU(VAR)3â^'9 Mediates Dimerization and Regulates Its Methyltransferase Activityâ€. Biochemistry, 2004, 43, 3740-3749.	1.2	42

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91	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. Biochemistry, 2004, 43, 11992-11997.	1.2	94
92	HMGBI MOLECULAR BIOLOGY IN MYELOID CELLS. Shock, 2004, 21, 36.	1.0	0
93	Monocytic cells hyperacetylate chromatin protein HMGB1 to redirect it towards secretion. EMBO Journal, 2003, 22, 5551-5560.	3.5	1,071
94	The Use of Mass Spectrometry for the Analysis of Histone Modifications. Methods in Enzymology, 2003, 377, 111-130.	0.4	42
95	The DNA chaperone HMGB1 facilitates ACF/CHRAC-dependent nucleosome sliding. EMBO Journal, 2002, 21, 6865-6873.	3.5	219
96	NEW EMBO MEMBERS' REVIEW: The double life of HMGB1 chromatin protein: architectural factor and extracellular signal. EMBO Journal, 2001, 20, 4337-4340.	3.5	381
97	The High Mobility Group (Hmg) Boxes of the Nuclear Protein Hmg1 Induce Chemotaxis and Cytoskeleton Reorganization in Rat Smooth Muscle Cells. Journal of Cell Biology, 2001, 152, 1197-1206.	2.3	435
98	The RAG1 Homeodomain Recruits HMG1 and HMG2 To Facilitate Recombination Signal Sequence Binding and To Enhance the Intrinsic DNA-Bending Activity of RAG1-RAG2. Molecular and Cellular Biology, 1999, 19, 6532-6542.	1.1	112