Peter A Dimaggio Jr

List of Publications by Year
in descending order

43 papers	2,201 citations	304743 22 h-index	276875 41 g-index
43 all docs	43 docs citations	43 times ranked	3560 citing authors

#	Article	IF	Citations
1	A chemical probe selectively inhibits G9a and GLP methyltransferase activity in cells. Nature Chemical Biology, 2011, 7, 566-574.	8.0	465
2	High Throughput Characterization of Combinatorial Histone Codes. Molecular and Cellular Proteomics, 2009, 8, 2266-2284.	3.8	271
3	A quantitative atlas of histone modification signatures from human cancer cells. Epigenetics and Chromatin, 2013, 6, 20.	3.9	128
4	Global turnover of histone post-translational modifications and variants in human cells. Epigenetics and Chromatin, 2010, 3, 22.	3.9	114
5	Histone H3 Lysine 56 Methylation Regulates DNA Replication through Its Interaction with PCNA. Molecular Cell, 2012, 46, 7-17.	9.7	108
6	Quantitative Dynamics of the Link between Cellular Metabolism and Histone Acetylation. Journal of Biological Chemistry, 2013, 288, 12142-12151.	3.4	98
7	The significance, development and progress of high-throughput combinatorial histone code analysis. Cellular and Molecular Life Sciences, 2010, 67, 3983-4000.	5.4	90
8	Proteogenomic characterization and mapping of nucleosomes decoded by Brd and HP1 proteins. Genome Biology, 2012, 13, R68.	9.6	81
9	Novel protein identification methods for biomarker discovery via a proteomic analysis of periodontally healthy and diseased gingival crevicular fluid samples. Journal of Clinical Periodontology, 2012, 39, 203-212.	4.9	80
10	A Mixed Integer Linear Optimization Framework for the Identification and Quantification of Targeted Post-translational Modifications of Highly Modified Proteins Using Multiplexed Electron Transfer Dissociation Tandem Mass Spectrometry. Molecular and Cellular Proteomics, 2009, 8, 2527-2543.	3.8	77
11	Biologically-active laminin-111 fragment that modulates the epithelial-to-mesenchymal transition in embryonic stem cells. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 5908-5913.	7.1	63
12	On the Histone Lysine Methyltransferase Activity of Fungal Metabolite Chaetocin. Journal of Medicinal Chemistry, 2013, 56, 8616-8625.	6.4	54
13	Biclustering via optimal re-ordering of data matrices in systems biology: rigorous methods and comparative studies. BMC Bioinformatics, 2008, 9, 458.	2.6	52
14	De Novo Peptide Identification via Tandem Mass Spectrometry and Integer Linear Optimization. Analytical Chemistry, 2007, 79, 1433-1446.	6.5	47
15	Fullerene oxidation and clustering in solution induced by light. Journal of Colloid and Interface Science, 2015, 446, 24-30.	9.4	43
16	A Novel Framework for Predicting In Vivo Toxicities from In Vitro Data Using Optimal Methods for Dense and Sparse Matrix Reordering and Logistic Regression. Toxicological Sciences, 2010, 118, 251-265.	3.1	42
17	A Novel Approach for Untargeted Post-translational Modification Identification Using Integer Linear Optimization and Tandem Mass Spectrometry. Molecular and Cellular Proteomics, 2010, 9, 764-779.	3.8	42
18	Quantitative proteomics reveals direct and indirect alterations in the histone code following methyltransferase knockdown. Molecular BioSystems, 2010, 6, 1719.	2.9	36

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19	Proteomics in epigenetics: new perspectives for cancer research. Briefings in Functional Genomics, 2013, 12, 205-218.	2.7	29
20	Quantitative Proteomic Discovery of Dynamic Epigenome Changes that Control Human Cytomegalovirus (HCMV) Infection. Molecular and Cellular Proteomics, 2014, 13, 2399-2410.	3.8	28
21	Plasmodium falciparum PfSET7: enzymatic characterization and cellular localization of a novel protein methyltransferase in sporozoite, liver and erythrocytic stage parasites. Scientific Reports, 2016, 6, 21802.	3.3	27
22	An Integrated Chemical Proteomics Approach for Quantitative Profiling of Intracellular ADP-Ribosylation. Scientific Reports, 2019, 9, 6655.	3.3	26
23	Multiple Levels of Control Determine How E4bp4/Nfil3 Regulates NK Cell Development. Journal of Immunology, 2018, 200, 1370-1381.	0.8	25
24	Descriptor-free molecular discovery in large libraries by adaptive substituent reordering. Bioorganic and Medicinal Chemistry Letters, 2008, 18, 5967-5970.	2.2	19
25	Collective mass spectrometry approaches reveal broad and combinatorial modification of high mobility group protein A1a. Journal of the American Society for Mass Spectrometry, 2010, 21, 960-970.	2.8	19
26	Novel Phosphorylation Sites in the *S. cerevisiae* Cdc13 Protein Reveal New Targets for Telomere Length Regulation. Journal of Proteome Research, 2013, 12, 316-327.	3.7	19
27	A Hybrid Method for Peptide Identification Using Integer Linear Optimization, Local Database Search, and Quadrupole Time-of-Flight or OrbiTrap Tandem Mass Spectrometry. Journal of Proteome Research, 2008, 7, 1584-1593.	3.7	18
28	The phase behavior of n-alkane systems. Computers and Chemical Engineering, 2005, 29, 2363-2379.	3.8	16
29	Selecting High Quality Protein Structures from Diverse Conformational Ensembles. Biophysical Journal, 2009, 97, 1728-1736.	0.5	15
30	Accelerating Students' Learning of Chromatography with an Experiential Module on Process Development and Scaleup. Journal of Chemical Education, 2020, 97, 1001-1007.	2.3	13
31	A network flow model for biclustering via optimal re-ordering of data matrices. Journal of Global Optimization, 2010, 47, 343-354.	1.8	12
32	A mixed-integer optimization framework for de novo peptide identification. AICHE Journal, 2007, 53, 160-173.	3.6	10
33	PILOT_PROTEIN: Identification of Unmodified and Modified Proteins via High-Resolution Mass Spectrometry and Mixed-Integer Linear Optimization. Journal of Proteome Research, 2012, 11, 4615-4629.	3.7	8
34	Unbiased Mass Spectrometry Elucidation of the Targets and Mechanisms of Activity-Based Probes: A Case Study Involving Sulfonyl Fluorides. ACS Chemical Biology, 2018, 13, 2897-2907.	3.4	7
35	Paired single residue-transposed Lys-N and Lys-C digestions for label-free identification of N-terminal and C-terminal MS/MS peptide product ions: ultrahigh resolution Fourier transform ion cyclotron resonance mass spectrometry and tandem mass spectrometr. Rapid Communications in Mass Spectrometry, 2015, 29, 659-666.	1.5	5
36	Mathematical modeling and efficient optimization methods for the distance-dependent rearrangement clustering problem. Journal of Global Optimization, 2009, 45, 111.	1.8	4

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37	Metabolic pathway analysis using a nash equilibrium approach. Journal of Global Optimization, 2018, 71, 537-550.	1.8	4
38	Mass Spectrometry Based Proteomics for Interrogating the Histone Code. Current Proteomics, 2010, 7, 177-187.	0.3	3
39	Multi-scale optimization. Computer Aided Chemical Engineering, 2004, 18, 1093-1098.	0.5	1
40	Biclustering of data matrices in systems biology via optimal re-ordering. Computer Aided Chemical Engineering, 2008, 25, 569-574.	0.5	1
41	Enhancing molecular discovery using descriptor‒free rearrangement clustering techniques for sparse data sets. AICHE Journal, 2010, 56, 405-418.	3.6	1
42	HiLight-PTM: an online application to aid matching peptide pairs with isotopically labelled PTMs. Bioinformatics, 2019, 36, 938-939.	4.1	0
43	Novel Biclustering Methods for Re-ordering Data Matrices. Fields Institute Communications, 2013, , 1-39.	1.3	0