

Gene Hart-Smith

List of Publications by Year in descending order

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53
papers

1,546
citations

218677

26
h-index

330143

37
g-index

56
all docs

56
docs citations

56
times ranked

2292
citing authors

#	ARTICLE	IF	CITATIONS
1	Systematic investigation of PRMT6 substrate recognition reveals broad specificity with a preference for an RG motif or basic and bulky residues. <i>FEBS Journal</i> , 2021, 288, 5668-5691.	4.7	7
2	Twin enzymes, divergent control: The cholesterologenic enzymes DHCR14 and LBR are differentially regulated transcriptionally and post-translationally. <i>Journal of Biological Chemistry</i> , 2020, 295, 2850-2865.	3.4	23
3	Crosstalk of Phosphorylation and Arginine Methylation in Disordered SRGG Repeats of <i>Saccharomyces cerevisiae</i> Fibrillar and Its Association with Nucleolar Localization. <i>Journal of Molecular Biology</i> , 2020, 432, 448-466.	4.2	22
4	Phenotypic screen for oxygen consumption rate identifies an anti-cancer naphthoquinone that induces mitochondrial oxidative stress. <i>Redox Biology</i> , 2020, 28, 101374.	9.0	9
5	Analytical Guidelines for co-fractionation Mass Spectrometry Obtained through Global Profiling of Gold Standard <i>Saccharomyces cerevisiae</i> Protein Complexes. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1876-1895.	3.8	14
6	Novel Antioxidant Therapy with the Immediate Precursor to Glutathione, γ -L-Glutamylcysteine (GGC), Ameliorates LPS-Induced Cellular Stress in In Vitro 3D-Differentiated Airway Model from Primary Cystic Fibrosis Human Bronchial Cells. <i>Antioxidants</i> , 2020, 9, 1204.	5.1	11
7	Combining Targeted and Untargeted Data Acquisition to Enhance Quantitative Plant Proteomics Experiments. <i>Methods in Molecular Biology</i> , 2020, 2139, 169-178.	0.9	2
8	MS2-Deisotoper: A Tool for Deisotoping High-Resolution MS/MS Spectra in Normal and Heavy Isotope-Labeled Samples. <i>Proteomics</i> , 2019, 19, 1800444.	2.2	4
9	Non-canonical ubiquitination of the cholesterol-regulated degron of squalene monooxygenase. <i>Journal of Biological Chemistry</i> , 2019, 294, 8134-8147.	3.4	36
10	Control of Cognate Sense mRNA Translation by cis-Natural Antisense RNAs. <i>Plant Physiology</i> , 2019, 180, 305-322.	4.8	41
11	MethylQuant: A Tool for Sensitive Validation of Enzyme-Mediated Protein Methylation Sites from Heavy-Methyl SILAC Data. <i>Journal of Proteome Research</i> , 2018, 17, 359-373.	3.7	11
12	Characterization of Protein Methyltransferases Rkm1, Rkm4, Efm4, Efm7, Set5 and Hmt1 Reveals Extensive Post-Translational Modification. <i>Journal of Molecular Biology</i> , 2018, 430, 102-118.	4.2	17
13	Light-sheet microscopy as a tool to understanding the behaviour of Polyion complex micelles for drug delivery. <i>Chemical Communications</i> , 2018, 54, 12618-12621.	4.1	21
14	Knockout of the Hmt1p Arginine Methyltransferase in <i>Saccharomyces cerevisiae</i> Leads to the Dysregulation of Phosphate-associated Genes and Processes. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2462-2479.	3.8	8
15	Genomic Location of PRMT6-Dependent H3R2 Methylation Is Linked to the Transcriptional Outcome of Associated Genes. <i>Cell Reports</i> , 2018, 24, 3339-3352.	6.4	38
16	Characterization of the Interaction between Arginine Methyltransferase Hmt1 and Its Substrate Npl3: Use of Multiple Cross-Linkers, Mass Spectrometric Approaches, and Software Platforms. <i>Analytical Chemistry</i> , 2018, 90, 9101-9108.	6.5	17
17	Improved Quantitative Plant Proteomics via the Combination of Targeted and Untargeted Data Acquisition. <i>Frontiers in Plant Science</i> , 2017, 8, 1669.	3.6	18
18	A new link between transcriptional initiation and pre-mRNA splicing: The RNA binding histone variant H2A.B. <i>PLoS Genetics</i> , 2017, 13, e1006633.	3.5	42

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19	The activity of a yeast Family 16 methyltransferase, Efm2, is affected by a conserved tryptophan and its N-terminal region. <i>FEBS Open Bio</i> , 2016, 6, 1320-1330.	2.3	5
20	Protein substrates of the arginine methyltransferase Hmt1 identified by proteome arrays. <i>Proteomics</i> , 2016, 16, 465-476.	2.2	8
21	Albumin-polymer conjugate nanoparticles and their interactions with prostate cancer cells in 2D and 3D culture: comparison between PMMA and PCL. <i>Journal of Materials Chemistry B</i> , 2016, 4, 2017-2027.	5.8	36
22	Large Scale Mass Spectrometry-based Identifications of Enzyme-mediated Protein Methylation Are Subject to High False Discovery Rates. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 989-1006.	3.8	65
23	Novel N-terminal and Lysine Methyltransferases That Target Translation Elongation Factor 1A in Yeast and Human. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 164-176.	3.8	57
24	Gene regulation by translational inhibition is determined by Dicer partnering proteins. <i>Nature Plants</i> , 2015, 1, 14027.	9.3	85
25	Yeast proteins Gar1p, Nop1p, Npl3p, Nsr1p, and Rps2p are natively methylated and are substrates of the arginine methyltransferase Hmt1p. <i>Proteomics</i> , 2015, 15, 3209-3218.	2.2	31
26	Proteomic Validation of Transcript Isoforms, Including Those Assembled from RNA-Seq Data. <i>Journal of Proteome Research</i> , 2015, 14, 3541-3554.	3.7	13
27	Lysine methylation modulates the protein-protein interactions of yeast cytochrome C Cyc1p. <i>Proteomics</i> , 2015, 15, 2166-2176.	2.2	13
28	The terminal enzymes of cholesterol synthesis, DHCR24 and DHCR7, interact physically and functionally. <i>Journal of Lipid Research</i> , 2015, 56, 888-897.	4.2	63
29	Polymer-Albumin Conjugate for the Facilitated Delivery of Macromolecular Platinum Drugs. <i>Macromolecular Rapid Communications</i> , 2015, 36, 890-897.	3.9	32
30	MicroRNA Regulatory Mechanisms Play Different Roles in Arabidopsis. <i>Journal of Proteome Research</i> , 2015, 14, 4743-4751.	3.7	22
31	Proteogenomic Discovery of a Small, Novel Protein in Yeast Reveals a Strategy for the Detection of Unannotated Short Open Reading Frames. <i>Journal of Proteome Research</i> , 2015, 14, 5038-5047.	3.7	25
32	Stoichiometry of <i>Saccharomyces cerevisiae</i> Lysine Methylation: Insights into Non-histone Protein Lysine Methyltransferase Activity. <i>Journal of Proteome Research</i> , 2014, 13, 1744-1756.	3.7	22
33	Albumin-micelles via a one-pot technology platform for the delivery of drugs. <i>Chemical Communications</i> , 2014, 50, 6394.	4.1	44
34	Tools to Covisualize and Coanalyze Proteomic Data with Genomes and Transcriptomes: Validation of Genes and Alternative mRNA Splicing. <i>Journal of Proteome Research</i> , 2014, 13, 84-98.	3.7	40
35	Elongation factor methyltransferase 3 - A novel eukaryotic lysine methyltransferase. <i>Biochemical and Biophysical Research Communications</i> , 2014, 451, 229-234.	2.1	20
36	A review of electron-capture and electron-transfer dissociation tandem mass spectrometry in polymer chemistry. <i>Analytica Chimica Acta</i> , 2014, 808, 44-55.	5.4	25

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37	The <i>Saccharomyces cerevisiae</i> poly(A)-binding protein is subject to multiple post-translational modifications, including the methylation of glutamic acid. <i>Biochemical and Biophysical Research Communications</i> , 2014, 443, 543-548.	2.1	5
38	Interactions Affected by Arginine Methylation in the Yeast Protein-Protein Interaction Network. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3184-3198.	3.8	33
39	A conditional two-hybrid (C2H) system for the detection of protein-protein interactions that are mediated by post-translational modification. <i>Proteomics</i> , 2013, 13, 1059-1064.	2.2	13
40	Analysis of the Proteome of <i>Saccharomyces cerevisiae</i> for Methylarginine. <i>Journal of Proteome Research</i> , 2013, 12, 3884-3899.	3.7	26
41	The methylproteome and the intracellular methylation network. <i>Proteomics</i> , 2012, 12, 564-586.	2.2	73
42	Enhanced Methylarginine Characterization by Post-Translational Modification-Specific Targeted Data Acquisition and Electron-Transfer Dissociation Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2012, 23, 1376-1389.	2.8	35
43	Detection and Characterization of Low Abundance Glycopeptides Via Higher-Energy C-Trap Dissociation and Orbitrap Mass Analysis. <i>Journal of the American Society for Mass Spectrometry</i> , 2012, 23, 124-140.	2.8	68
44	Degradation of Poly(methyl methacrylate) Model Compounds Under Extreme Environmental Conditions. <i>Macromolecular Chemistry and Physics</i> , 2010, 211, 1083-1097.	2.2	31
45	Contemporary Mass Spectrometry and the Analysis of Synthetic Polymers: Trends, Techniques and Untapped Potential. <i>Macromolecular Chemistry and Physics</i> , 2010, 211, 1507-1529.	2.2	43
46	ATRP poly(acrylate) star formation: A comparative study between MALDI and ESI mass spectrometry. <i>Polymer</i> , 2009, 50, 1986-2000.	3.8	27
47	The incorporation of metal cations into polymer backbones: An important consideration in the interpretation of ESI-MS spectra. <i>Polymer</i> , 2009, 50, 5175-5180.	3.8	11
48	Living star polymer formation (RAFT) studied via electrospray ionization mass spectrometry. <i>Journal of Polymer Science Part A</i> , 2008, 46, 1873-1892.	2.3	29
49	Living Star Polymer Formation: Detailed Assessment of Poly(acrylate) Radical Reaction Pathways via ESI-MS. <i>Macromolecules</i> , 2008, 41, 3023-3041.	4.8	33
50	Enhanced Ionization in Electrospray Ionization Mass Spectrometry of Labile End-Group-Containing Polystyrenes Using Silver(I) Tetrafluoroborate as Doping Salt. <i>Macromolecules</i> , 2008, 41, 1966-1971.	4.8	50
51	Characterization of Oligo(vinyl phosphonate)s by High-Resolution Electrospray Ionization Mass Spectrometry: Implications for the Mechanism of Polymerization. <i>Macromolecules</i> , 2008, 41, 1634-1639.	4.8	41
52	Electrospray Ionization Mass Spectrometry Investigation of Reversible Addition Fragmentation Chain Transfer Mediated Acrylate Polymerizations Initiated via ^{60}Co γ -Irradiation: Mapping Reaction Pathways. <i>Macromolecules</i> , 2007, 40, 4142-4153.	4.8	44
53	Mapping Formation Pathways and End Group Patterns of Stimuli-Responsive Polymer Systems via High-Resolution Electrospray Ionization Mass Spectrometry. <i>Biomacromolecules</i> , 2007, 8, 2404-2415.	5.4	31