

Gene Hart-Smith

List of Publications by Year in descending order

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53
papers

1,546
citations

218381
26
h-index

329751
37
g-index

56
all docs

56
docs citations

56
times ranked

2292
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Gene regulation by translational inhibition is determined by Dicer partnering proteins. <i>Nature Plants</i> , 2015, 1, 14027. | 4.7 | 85 |
| 2 | The methylproteome and the intracellular methylation network. <i>Proteomics</i> , 2012, 12, 564-586. | 1.3 | 73 |
| 3 | 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. | 1.2 | 68 |
| 4 | 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. | 2.5 | 65 |
| 5 | The terminal enzymes of cholesterol synthesis, DHCR24 and DHCR7, interact physically and functionally. <i>Journal of Lipid Research</i> , 2015, 56, 888-897. | 2.0 | 63 |
| 6 | 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. | 2.5 | 57 |
| 7 | 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. | 2.2 | 50 |
| 8 | Electrospray Ionization Mass Spectrometry Investigation of Reversible Addition Fragmentation Chain Transfer Mediated Acrylate Polymerizations Initiated via ^{60}Co γ -Irradiation: A Mapping Reaction Pathways. <i>Macromolecules</i> , 2007, 40, 4142-4153. | 2.2 | 44 |
| 9 | Albumin-micelles via a one-pot technology platform for the delivery of drugs. <i>Chemical Communications</i> , 2014, 50, 6394. | 2.2 | 44 |
| 10 | Contemporary Mass Spectrometry and the Analysis of Synthetic Polymers: Trends, Techniques and Untapped Potential. <i>Macromolecular Chemistry and Physics</i> , 2010, 211, 1507-1529. | 1.1 | 43 |
| 11 | A new link between transcriptional initiation and pre-mRNA splicing: The RNA binding histone variant H2A.B. <i>PLoS Genetics</i> , 2017, 13, e1006633. | 1.5 | 42 |
| 12 | 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. | 2.2 | 41 |
| 13 | Control of Cognate Sense mRNA Translation by cis-Natural Antisense RNAs. <i>Plant Physiology</i> , 2019, 180, 305-322. | 2.3 | 41 |
| 14 | 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. | 1.8 | 40 |
| 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. | 2.9 | 38 |
| 16 | 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. | 2.9 | 36 |
| 17 | Non-canonical ubiquitination of the cholesterol-regulated degnon of squalene monooxygenase. <i>Journal of Biological Chemistry</i> , 2019, 294, 8134-8147. | 1.6 | 36 |
| 18 | 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. | 1.2 | 35 |

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|----|--|-----|-----------|
| 19 | Living Star Polymer Formation: Detailed Assessment of Poly(acrylate) Radical Reaction Pathways via ESI-MS. <i>Macromolecules</i> , 2008, 41, 3023-3041. | 2.2 | 33 |
| 20 | Interactions Affected by Arginine Methylation in the Yeast Protein-Protein Interaction Network. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3184-3198. | 2.5 | 33 |
| 21 | Polymer-Albumin Conjugate for the Facilitated Delivery of Macromolecular Platinum Drugs. <i>Macromolecular Rapid Communications</i> , 2015, 36, 890-897. | 2.0 | 32 |
| 22 | 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. | 2.6 | 31 |
| 23 | Degradation of Poly(methyl methacrylate) Model Compounds Under Extreme Environmental Conditions. <i>Macromolecular Chemistry and Physics</i> , 2010, 211, 1083-1097. | 1.1 | 31 |
| 24 | 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. | 1.3 | 31 |
| 25 | Living star polymer formation (RAFT) studied via electrospray ionization mass spectrometry. <i>Journal of Polymer Science Part A</i> , 2008, 46, 1873-1892. | 2.5 | 29 |
| 26 | ATRP poly(acrylate) star formation: A comparative study between MALDI and ESI mass spectrometry. <i>Polymer</i> , 2009, 50, 1986-2000. | 1.8 | 27 |
| 27 | Analysis of the Proteome of <i>Saccharomyces cerevisiae</i> for Methylarginine. <i>Journal of Proteome Research</i> , 2013, 12, 3884-3899. | 1.8 | 26 |
| 28 | A review of electron-capture and electron-transfer dissociation tandem mass spectrometry in polymer chemistry. <i>Analytica Chimica Acta</i> , 2014, 808, 44-55. | 2.6 | 25 |
| 29 | 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. | 1.8 | 25 |
| 30 | 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. | 1.6 | 23 |
| 31 | 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. | 1.8 | 22 |
| 32 | MicroRNA Regulatory Mechanisms Play Different Roles in Arabidopsis. <i>Journal of Proteome Research</i> , 2015, 14, 4743-4751. | 1.8 | 22 |
| 33 | 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. | 2.0 | 22 |
| 34 | 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. | 2.2 | 21 |
| 35 | Elongation factor methyltransferase 3 - A novel eukaryotic lysine methyltransferase. <i>Biochemical and Biophysical Research Communications</i> , 2014, 451, 229-234. | 1.0 | 20 |
| 36 | Improved Quantitative Plant Proteomics via the Combination of Targeted and Untargeted Data Acquisition. <i>Frontiers in Plant Science</i> , 2017, 8, 1669. | 1.7 | 18 |

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|----|--|-----|-----------|
| 37 | 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. | 2.0 | 17 |
| 38 | 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. | 3.2 | 17 |
| 39 | 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. | 2.5 | 14 |
| 40 | 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. | 1.3 | 13 |
| 41 | Proteomic Validation of Transcript Isoforms, Including Those Assembled from RNA-Seq Data. <i>Journal of Proteome Research</i> , 2015, 14, 3541-3554. | 1.8 | 13 |
| 42 | Lysine methylation modulates the protein-protein interactions of yeast cytochrome C Cyc1p. <i>Proteomics</i> , 2015, 15, 2166-2176. | 1.3 | 13 |
| 43 | 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. | 1.8 | 11 |
| 44 | 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. | 1.8 | 11 |
| 45 | 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. | 2.2 | 11 |
| 46 | Phenotypic screen for oxygen consumption rate identifies an anti-cancer naphthoquinone that induces mitochondrial oxidative stress. <i>Redox Biology</i> , 2020, 28, 101374. | 3.9 | 9 |
| 47 | Protein substrates of the arginine methyltransferase Hmt1 identified by proteome arrays. <i>Proteomics</i> , 2016, 16, 465-476. | 1.3 | 8 |
| 48 | 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. | 2.5 | 8 |
| 49 | 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. | 2.2 | 7 |
| 50 | 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. | 1.0 | 5 |
| 51 | 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. | 1.0 | 5 |
| 52 | MS2-Deisotoper: A Tool for Deisotoping High-Resolution MS/MS Spectra in Normal and Heavy Isotope-Labelled Samples. <i>Proteomics</i> , 2019, 19, 1800444. | 1.3 | 4 |
| 53 | Combining Targeted and Untargeted Data Acquisition to Enhance Quantitative Plant Proteomics Experiments. <i>Methods in Molecular Biology</i> , 2020, 2139, 169-178. | 0.4 | 2 |