

Lloyd M Smith

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174
papers

10,676
citations

49
h-index

100
g-index

221
ext. papers

12,295
ext. citations

10
avg, IF

6.2
L-index

| # | Paper | IF | Citations |
|-----|---|------|-----------|
| 174 | Fluorescence detection in automated DNA sequence analysis. <i>Nature</i> , 1986 , 321, 674-9 | 50.4 | 1309 |
| 173 | Proteoform: a single term describing protein complexity. <i>Nature Methods</i> , 2013 , 10, 186-7 | 21.6 | 857 |
| 172 | DNA-modified nanocrystalline diamond thin-films as stable, biologically active substrates. <i>Nature Materials</i> , 2002 , 1, 253-7 | 27 | 744 |
| 171 | Direct fluorescence analysis of genetic polymorphisms by hybridization with oligonucleotide arrays on glass supports. <i>Nucleic Acids Research</i> , 1994 , 22, 5456-65 | 20.1 | 456 |
| 170 | Synthesis and Characterization of DNA-Modified Silicon (111) Surfaces. <i>Journal of the American Chemical Society</i> , 2000 , 122, 1205-1209 | 16.4 | 409 |
| 169 | How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018 , 14, 206-214 | 11.7 | 324 |
| 168 | DNA computing on surfaces. <i>Nature</i> , 2000 , 403, 175-9 | 50.4 | 300 |
| 167 | The synthesis of oligonucleotides containing an aliphatic amino group at the 5' terminus: synthesis of fluorescent DNA primers for use in DNA sequence analysis. <i>Nucleic Acids Research</i> , 1985 , 13, 2399-412 | 20.1 | 276 |
| 166 | Covalent attachment of oligodeoxyribonucleotides to amine-modified Si (001) surfaces. <i>Nucleic Acids Research</i> , 2000 , 28, 3535-41 | 20.1 | 248 |
| 165 | Formaldehyde crosslinking: a tool for the study of chromatin complexes. <i>Journal of Biological Chemistry</i> , 2015 , 290, 26404-11 | 5.4 | 192 |
| 164 | DNA Attachment and Hybridization at the Silicon (100) Surface. <i>Langmuir</i> , 2002 , 18, 788-796 | 4 | 177 |
| 163 | Lectin arrays for profiling cell surface carbohydrate expression. <i>Journal of the American Chemical Society</i> , 2005 , 127, 9982-3 | 16.4 | 176 |
| 162 | Controlling charge states of large ions. <i>Science</i> , 1999 , 283, 194-7 | 33.3 | 146 |
| 161 | A universal method for the direct cloning of PCR amplified nucleic acid. <i>Nature Biotechnology</i> , 1991 , 9, 657-63 | 44.5 | 143 |
| 160 | Best practices and benchmarks for intact protein analysis for top-down mass spectrometry. <i>Nature Methods</i> , 2019 , 16, 587-594 | 21.6 | 137 |
| 159 | DNA-Modified Diamond Surfaces. <i>Langmuir</i> , 2003 , 19, 1938-1942 | 4 | 130 |
| 158 | Charge reduction electrospray mass spectrometry. <i>Analytical Chemistry</i> , 2000 , 72, 52-60 | 7.8 | 124 |

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| 157 | Enhanced Global Post-translational Modification Discovery with MetaMorpheus. <i>Journal of Proteome Research</i> , 2018 , 17, 1844-1851 | 5.6 | 123 |
| 156 | Enhanced discrimination of single nucleotide polymorphisms by artificial mismatch hybridization. <i>Nature Biotechnology</i> , 1997 , 15, 331-5 | 44.5 | 118 |
| 155 | Oligodeoxynucleotide Fragmentation in MALDI/TOF Mass Spectrometry Using 355-nm Radiation. <i>Journal of the American Chemical Society</i> , 1995 , 117, 6048-6056 | 16.4 | 105 |
| 154 | Genetic analysis by peptide nucleic acid affinity MALDI-TOF mass spectrometry. <i>Nature Biotechnology</i> , 1997 , 15, 1368-72 | 44.5 | 103 |
| 153 | Proteoforms as the next proteomics currency. <i>Science</i> , 2018 , 359, 1106-1107 | 33.3 | 101 |
| 152 | Immobilization of amine-modified oligonucleotides on aldehyde-terminated alkanethiol monolayers on gold. <i>Langmuir</i> , 2005 , 21, 266-71 | 4 | 101 |
| 151 | Corona discharge in charge reduction electrospray mass spectrometry. <i>Analytical Chemistry</i> , 2000 , 72, 5158-61 | 7.8 | 100 |
| 150 | Discovery and mass spectrometric analysis of novel splice-junction peptides using RNA-Seq. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 2341-53 | 7.6 | 96 |
| 149 | Covalent photochemical functionalization of amorphous carbon thin films for integrated real-time biosensing. <i>Langmuir</i> , 2006 , 22, 9598-605 | 4 | 90 |
| 148 | Proteomic analysis of naturally-sourced biological scaffolds. <i>Biomaterials</i> , 2016 , 75, 37-46 | 15.6 | 85 |
| 147 | The analysis of mock DNA sequencing reactions using matrix-assisted laser desorption/ionization mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 1993 , 7, 895-897 | 2.2 | 83 |
| 146 | POWERDRESS interacts with HISTONE DEACETYLASE 9 to promote aging in. <i>ELife</i> , 2016 , 5, | 8.9 | 83 |
| 145 | SUMOylome Profiling Reveals a Diverse Array of Nuclear Targets Modified by the SUMO Ligase SIZ1 during Heat Stress. <i>Plant Cell</i> , 2018 , 30, 1077-1099 | 11.6 | 81 |
| 144 | Identification and Quantification of Proteoforms by Mass Spectrometry. <i>Proteomics</i> , 2019 , 19, e18003614.8 | 14.8 | 77 |
| 143 | Chemical Modification and Patterning of Iodine-Terminated Silicon Surfaces Using Visible Light. <i>Journal of Physical Chemistry B</i> , 2002 , 106, 2656-2664 | 3.4 | 70 |
| 142 | Flexible and accessible workflows for improved proteogenomic analysis using the Galaxy framework. <i>Journal of Proteome Research</i> , 2014 , 13, 5898-908 | 5.6 | 69 |
| 141 | Rapid DNA sequencing by horizontal ultrathin gel electrophoresis. <i>Nucleic Acids Research</i> , 1991 , 19, 4121-26.1 | 26.1 | 68 |
| 140 | Proteogenomics: Integrating Next-Generation Sequencing and Mass Spectrometry to Characterize Human Proteomic Variation. <i>Annual Review of Analytical Chemistry</i> , 2016 , 9, 521-45 | 12.5 | 67 |

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| 139 | 2'-Fluoro modified nucleic acids: polymerase-directed synthesis, properties and stability to analysis by matrix-assisted laser desorption/ionization mass spectrometry. <i>Nucleic Acids Research</i> , 1997 , 25, 4581-8 | 20.1 | 65 |
| 138 | Controlling DNA Fragmentation in MALDI-MS by Chemical Modification. <i>Analytical Chemistry</i> , 1997 , 69, 302-12 | 7.8 | 65 |
| 137 | Large-scale mass spectrometric detection of variant peptides resulting from nonsynonymous nucleotide differences. <i>Journal of Proteome Research</i> , 2014 , 13, 228-40 | 5.6 | 64 |
| 136 | Alpha-Ketoisocaproate-induced hypersecretion of insulin by islets from diabetes-susceptible mice. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2005 , 289, E218-24 | 6 | 63 |
| 135 | Relative quantification of carboxylic acid metabolites by liquid chromatography-mass spectrometry using isotopic variants of cholamine. <i>Analytical Chemistry</i> , 2007 , 79, 5143-9 | 7.8 | 62 |
| 134 | Matrix-assisted laser desorption/ionization mass spectrometry of synthetic oligodeoxyribonucleotides. <i>Rapid Communications in Mass Spectrometry</i> , 1992 , 6, 369-372 | 2.2 | 61 |
| 133 | Using Galaxy-P to leverage RNA-Seq for the discovery of novel protein variations. <i>BMC Genomics</i> , 2014 , 15, 703 | 4.5 | 58 |
| 132 | EBS is a bivalent histone reader that regulates floral phase transition in Arabidopsis. <i>Nature Genetics</i> , 2018 , 50, 1247-1253 | 36.3 | 56 |
| 131 | Modifying the charge state distribution of proteins in electrospray ionization mass spectrometry by chemical derivatization. <i>Journal of the American Society for Mass Spectrometry</i> , 2009 , 20, 1617-25 | 3.5 | 56 |
| 130 | A tetrafluorophenyl activated ester self-assembled monolayer for the immobilization of amine-modified oligonucleotides. <i>Langmuir</i> , 2008 , 24, 69-75 | 4 | 55 |
| 129 | Global Post-Translational Modification Discovery. <i>Journal of Proteome Research</i> , 2017 , 16, 1383-1390 | 5.6 | 54 |
| 128 | Carbon-on-metal films for surface plasmon resonance detection of DNA arrays. <i>Journal of the American Chemical Society</i> , 2008 , 130, 8611-3 | 16.4 | 54 |
| 127 | A surface-based approach to DNA computation. <i>Journal of Computational Biology</i> , 1998 , 5, 255-67 | 1.7 | 54 |
| 126 | Invasive cleavage reactions on DNA-modified diamond surfaces. <i>Biopolymers</i> , 2004 , 73, 606-13 | 2.2 | 50 |
| 125 | Mass spectrometric analysis of DNA mixtures: instrumental effects responsible for decreased sensitivity with increasing mass. <i>Analytical Chemistry</i> , 2003 , 75, 5944-52 | 7.8 | 49 |
| 124 | A software system for data analysis in automated DNA sequencing. <i>Genome Research</i> , 1998 , 8, 644-65 | 9.7 | 49 |
| 123 | Bioengineered vocal fold mucosa for voice restoration. <i>Science Translational Medicine</i> , 2015 , 7, 314ra187 | 17.5 | 46 |
| 122 | O-Pair Search with MetaMorpheus for O-glycopeptide characterization. <i>Nature Methods</i> , 2020 , 17, 1133-1138 | 11.38 | 46 |

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| 121 | Identification of mammalian cell lines using MALDI-TOF and LC-ESI-MS/MS mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2006 , 17, 490-499 | 3.5 | 43 |
| 120 | The synthesis and use of fluorescent oligonucleotides in DNA sequence analysis. <i>Methods in Enzymology</i> , 1987 , 155, 260-301 | 1.7 | 42 |
| 119 | A model for the mobility of single-stranded DNA in capillary gel electrophoresis. <i>Electrophoresis</i> , 1993 , 14, 492-501 | 3.6 | 41 |
| 118 | Alkylating tryptic peptides to enhance electrospray ionization mass spectrometry analysis. <i>Analytical Chemistry</i> , 2010 , 82, 10135-42 | 7.8 | 40 |
| 117 | Specific capture of mammalian cells by cell surface receptor binding to ligand immobilized on gold thin films. <i>Journal of Proteome Research</i> , 2006 , 5, 1580-5 | 5.6 | 40 |
| 116 | An adaptive, object oriented strategy for base calling in DNA sequence analysis. <i>Nucleic Acids Research</i> , 1993 , 21, 4530-40 | 20.1 | 40 |
| 115 | Neutron-encoded mass signatures for quantitative top-down proteomics. <i>Analytical Chemistry</i> , 2014 , 86, 2314-9 | 7.8 | 39 |
| 114 | Analysis of single nucleotide polymorphisms by primer extension and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2000 , 14, 950-9 | 2.2 | 39 |
| 113 | Analyzing sequencing reactions from bacteriophage M13 by matrix-assisted laser desorption/ionization mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 1996 , 10, 1475-8 | 2.2 | 38 |
| 112 | Controlling gas-phase reactions for efficient charge reduction electrospray mass spectrometry of intact proteins. <i>Journal of the American Society for Mass Spectrometry</i> , 2005 , 16, 1876-87 | 3.5 | 37 |
| 111 | Ultrafast Peptide Label-Free Quantification with FlashLFQ. <i>Journal of Proteome Research</i> , 2018 , 17, 386-391 | 3.1 | 36 |
| 110 | Measuring the formaldehyde Protein-DNA cross-link reversal rate. <i>Analytical Chemistry</i> , 2014 , 86, 5678-81 | 1.8 | 35 |
| 109 | Global Identification of Protein Post-translational Modifications in a Single-Pass Database Search. <i>Journal of Proteome Research</i> , 2015 , 14, 4714-20 | 5.6 | 34 |
| 108 | HDA9-PWR-HOS15 Is a Core Histone Deacetylase Complex Regulating Transcription and Development. <i>Plant Physiology</i> , 2019 , 180, 342-355 | 6.6 | 34 |
| 107 | Positive ion formation in the ultraviolet matrix-assisted laser desorption / ionization analysis of oligonucleotides by using 2,5-dihydroxybenzoic acid. <i>Journal of the American Society for Mass Spectrometry</i> , 1997 , 8, 218-224 | 3.5 | 33 |
| 106 | Elucidating Proteoform Families from Proteoform Intact-Mass and Lysine-Count Measurements. <i>Journal of Proteome Research</i> , 2016 , 15, 1213-21 | 5.6 | 33 |
| 105 | High speed automated DNA sequencing in ultrathin slab gels. <i>Nature Biotechnology</i> , 1992 , 10, 78-81 | 44.5 | 32 |
| 104 | Interlaboratory Study for Characterizing Monoclonal Antibodies by Top-Down and Middle-Down Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2020 , 31, 1783-1802 | 3.5 | 32 |

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| 103 | Chemical derivatization of peptide carboxyl groups for highly efficient electron transfer dissociation. <i>Journal of the American Society for Mass Spectrometry</i> , 2013 , 24, 1710-21 | 3.5 | 31 |
| 102 | In situ oligonucleotide synthesis on carbon materials: stable substrates for microarray fabrication. <i>Nucleic Acids Research</i> , 2008 , 36, e7 | 20.1 | 30 |
| 101 | A Self-Assembled Matrix Monolayer for UV-MALDI Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 1996 , 118, 8639-8645 | 16.4 | 30 |
| 100 | Structure-specific DNA cleavage on surfaces. <i>Journal of the American Chemical Society</i> , 2002 , 124, 7924-3164 | 16.4 | 28 |
| 99 | ProForma: A Standard Proteoform Notation. <i>Journal of Proteome Research</i> , 2018 , 17, 1321-1325 | 5.6 | 27 |
| 98 | A DNA computing readout operation based on structure-specific cleavage. <i>Nature Biotechnology</i> , 2001 , 19, 1053-9 | 44.5 | 27 |
| 97 | Identification of MS-Cleavable and Noncleavable Chemically Cross-Linked Peptides with MetaMorpheus. <i>Journal of Proteome Research</i> , 2018 , 17, 2370-2376 | 5.6 | 27 |
| 96 | Analysis of single nucleotide polymorphisms with solid phase invasive cleavage reactions. <i>Nucleic Acids Research</i> , 2001 , 29, E77 | 20.1 | 26 |
| 95 | Proteoform Suite: Software for Constructing, Quantifying, and Visualizing Proteoform Families. <i>Journal of Proteome Research</i> , 2018 , 17, 568-578 | 5.6 | 26 |
| 94 | Elucidating Escherichia coli Proteoform Families Using Intact-Mass Proteomics and a Global PTM Discovery Database. <i>Journal of Proteome Research</i> , 2017 , 16, 4156-4165 | 5.6 | 25 |
| 93 | A five-level classification system for proteoform identifications. <i>Nature Methods</i> , 2019 , 16, 939-940 | 21.6 | 25 |
| 92 | Photolithographic Synthesis of High-Density DNA and RNA Arrays on Flexible, Transparent, and Easily Subdivided Plastic Substrates. <i>Analytical Chemistry</i> , 2015 , 87, 11420-8 | 7.8 | 25 |
| 91 | Mass Spectrometric Analyses Reveal a Central Role for Ubiquitylation in Remodeling the Arabidopsis Proteome during Photomorphogenesis. <i>Molecular Plant</i> , 2017 , 10, 846-865 | 14.4 | 24 |
| 90 | Comment on "A subset of HLA-I peptides are not genomically templated: Evidence for cis- and trans-spliced peptide ligands". <i>Science Immunology</i> , 2019 , 4, | 28 | 24 |
| 89 | Sequence-specific capture of protein-DNA complexes for mass spectrometric protein identification. <i>PLoS ONE</i> , 2011 , 6, e26217 | 3.7 | 24 |
| 88 | Global Identification of Post-Translationally Spliced Peptides with Neo-Fusion. <i>Journal of Proteome Research</i> , 2019 , 18, 349-358 | 5.6 | 24 |
| 87 | HyPR-MS for Multiplexed Discovery of MALAT1, NEAT1, and NORAD lncRNA Protein Interactomes. <i>Journal of Proteome Research</i> , 2018 , 17, 3022-3038 | 5.6 | 24 |
| 86 | Elucidating the in vivo interactome of HIV-1 RNA by hybridization capture and mass spectrometry. <i>Scientific Reports</i> , 2017 , 7, 16965 | 4.9 | 23 |

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| 85 | Fabrication and characterization of DNA arrays prepared on carbon-on-metal substrates. <i>Analytical Chemistry</i> , 2009 , 81, 6429-37 | 7.8 | 23 |
| 84 | Human Proteomic Variation Revealed by Combining RNA-Seq Proteogenomics and Global Post-Translational Modification (G-PTM) Search Strategy. <i>Journal of Proteome Research</i> , 2016 , 15, 800-8 | 5.6 | 22 |
| 83 | The Transcription Factor Nfatc2 Regulates Cell Proliferation and Genes Associated with Type 2 Diabetes in Mouse and Human Islets. <i>PLoS Genetics</i> , 2016 , 12, e1006466 | 6 | 22 |
| 82 | Canonical and Noncanonical Actions of Arabidopsis Histone Deacetylases in Ribosomal RNA Processing. <i>Plant Cell</i> , 2018 , 30, 134-152 | 11.6 | 21 |
| 81 | Enzymatic fabrication of high-density RNA arrays. <i>Angewandte Chemie - International Edition</i> , 2014 , 53, 13514-7 | 16.4 | 21 |
| 80 | Protein turnover during in vitro tissue engineering. <i>Biomaterials</i> , 2016 , 81, 104-113 | 15.6 | 20 |
| 79 | Automatic matrix determination in four dye fluorescence-based DNA sequencing. <i>Electrophoresis</i> , 1996 , 17, 1143-50 | 3.6 | 20 |
| 78 | Expanding Proteoform Identifications in Top-Down Proteomic Analyses by Constructing Proteoform Families. <i>Analytical Chemistry</i> , 2018 , 90, 1325-1333 | 7.8 | 20 |
| 77 | Controlling oligonucleotide surface density in light-directed DNA array fabrication. <i>Langmuir</i> , 2009 , 25, 6570-5 | 4 | 19 |
| 76 | Scoring single-nucleotide polymorphisms at the single-molecule level by counting individual DNA cleavage events on surfaces. <i>Analytical Chemistry</i> , 2005 , 77, 6594-600 | 7.8 | 19 |
| 75 | A cylindrical capacitor ionization source: droplet generation and controlled charge reduction for mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2001 , 15, 401-5 | 2.2 | 19 |
| 74 | The Human Proteoform Project: Defining the human proteome. <i>Science Advances</i> , 2021 , 7, eabk0734 | 14.3 | 19 |
| 73 | Improved Protein Inference from Multiple Protease Bottom-Up Mass Spectrometry Data. <i>Journal of Proteome Research</i> , 2019 , 18, 3429-3438 | 5.6 | 18 |
| 72 | Ion-Ion Reactions with Fixed-Charge Modified Proteins to Produce Ions in a Single, Very High Charge State. <i>International Journal of Mass Spectrometry</i> , 2008 , 276, 136-143 | 1.9 | 18 |
| 71 | Identification and Quantification of Murine Mitochondrial Proteoforms Using an Integrated Top-Down and Intact-Mass Strategy. <i>Journal of Proteome Research</i> , 2018 , 17, 3526-3536 | 5.6 | 18 |
| 70 | Methylation of yeast ribosomal protein S2 is elevated during stationary phase growth conditions. <i>Biochemical and Biophysical Research Communications</i> , 2014 , 445, 535-41 | 3.4 | 17 |
| 69 | Fabrication of oligonucleotide and protein arrays on rigid and flexible substrates coated with reactive polymer multilayers. <i>ACS Applied Materials & Interfaces</i> , 2013 , 5, 351-9 | 9.5 | 17 |
| 68 | Discovery of Chromatin-Associated Proteins via Sequence-Specific Capture and Mass Spectrometric Protein Identification in <i>Saccharomyces cerevisiae</i> . <i>Journal of Proteome Research</i> , 2014 , 13, 3810-25 | 5.6 | 16 |

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| 67 | Aldehyde-terminated amorphous carbon substrates for the fabrication of biomolecule arrays. <i>Langmuir</i> , 2008 , 24, 9198-203 | 4 | 15 |
| 66 | Progress toward demonstration of a surface based DNA computation: a one word approach to solve a model satisfiability problem. <i>BioSystems</i> , 1999 , 52, 25-33 | 1.9 | 15 |
| 65 | Lectin-modified microchannels for mammalian cell capture and purification. <i>Biomedical Microdevices</i> , 2007 , 9, 611-7 | 3.7 | 14 |
| 64 | Is charge reduction in ESI really necessary?. <i>Journal of the American Society for Mass Spectrometry</i> , 2008 , 19, 629-31 | 3.5 | 14 |
| 63 | Differentiated fibrocytes assume a functional mesenchymal phenotype with regenerative potential. <i>Science Advances</i> , 2019 , 5, eaav7384 | 14.3 | 13 |
| 62 | Constructing Human Proteoform Families Using Intact-Mass and Top-Down Proteomics with a Multi-Protease Global Post-Translational Modification Discovery Database. <i>Journal of Proteome Research</i> , 2019 , 18, 3671-3680 | 5.6 | 12 |
| 61 | Proteomics in non-human primates: utilizing RNA-Seq data to improve protein identification by mass spectrometry in vervet monkeys. <i>BMC Genomics</i> , 2017 , 18, 877 | 4.5 | 12 |
| 60 | High resolution characterization of DNA fragment ions produced by ultraviolet matrix-assisted laser desorption/ionization using linear and reflecting time-of-flight mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 1999 , 10, 423-429 | 3.5 | 12 |
| 59 | Mapping and Sequencing the Human Genome: How to Proceed. <i>Nature Biotechnology</i> , 1987 , 5, 933-939 | 44.5 | 12 |
| 58 | Spritz: A Proteogenomic Database Engine. <i>Journal of Proteome Research</i> , 2021 , 20, 1826-1834 | 5.6 | 12 |
| 57 | Compartmentalization of HP1 Proteins in Pluripotency Acquisition and Maintenance. <i>Stem Cell Reports</i> , 2018 , 10, 627-641 | 8 | 11 |
| 56 | DNA computing on surfaces: encoding information at the single base level. <i>Journal of Computational Biology</i> , 1998 , 5, 269-78 | 1.7 | 11 |
| 55 | Elucidating Protein-DNA Interactions in Human Alphoid Chromatin via Hybridization Capture and Mass Spectrometry. <i>Journal of Proteome Research</i> , 2017 , 16, 3433-3442 | 5.6 | 10 |
| 54 | In situ Synthesis of Oligonucleotide Arrays on Surfaces Coated with Crosslinked Polymer Multilayers. <i>Chemistry of Materials</i> , 2012 , 24, 939-945 | 9.6 | 10 |
| 53 | Characterization of vascular endothelial growth factor receptors on the endothelial cell surface during hypoxia using whole cell binding arrays. <i>Analytical Biochemistry</i> , 2007 , 369, 241-7 | 3.1 | 10 |
| 52 | A surface invasive cleavage assay for highly parallel SNP analysis. <i>Human Mutation</i> , 2002 , 19, 416-22 | 4.7 | 10 |
| 51 | Separating field strength, temperature, and pulsing effects in pulsed field electrophoresis. <i>Electrophoresis</i> , 1994 , 15, 1084-90 | 3.6 | 10 |
| 50 | Proteomic analysis of affinity-purified 26S proteasomes identifies a suite of assembly chaperones in. <i>Journal of Biological Chemistry</i> , 2019 , 294, 17570-17592 | 5.4 | 9 |

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| 49 | Intact-Mass Analysis Facilitating the Identification of Large Human Heart Proteoforms. <i>Analytical Chemistry</i> , 2019 , 91, 10937-10942 | 7.8 | 8 |
| 48 | RNA-mediated gene assembly from DNA arrays. <i>Angewandte Chemie - International Edition</i> , 2012 , 51, 4628-32 | 16.4 | 8 |
| 47 | Solid phase purification in automated DNA sequencing. <i>DNA Sequence</i> , 1993 , 4, 151-62 | | 8 |
| 46 | HyCCAPP as a tool to characterize promoter DNA-protein interactions in <i>Saccharomyces cerevisiae</i> . <i>Genomics</i> , 2016 , 107, 267-73 | 4.3 | 8 |
| 45 | Improving Proteoform Identifications in Complex Systems Through Integration of Bottom-Up and Top-Down Data. <i>Journal of Proteome Research</i> , 2020 , 19, 3510-3517 | 5.6 | 7 |
| 44 | Carbon Substrates: A Stable Foundation for Biomolecular Arrays. <i>Annual Review of Analytical Chemistry</i> , 2015 , 8, 263-85 | 12.5 | 7 |
| 43 | Identification of cell surface markers to differentiate rat endothelial and fibroblast cells using lectin arrays and LC-ESI-MS/MS. <i>Analytical Chemistry</i> , 2008 , 80, 8269-75 | 7.8 | 7 |
| 42 | The Human Proteoform Project: A Plan to Define the Human Proteome | | 7 |
| 41 | Complete chemical modification of amine and acid functional groups of peptides and small proteins. <i>Methods in Molecular Biology</i> , 2011 , 753, 77-91 | 1.4 | 7 |
| 40 | Comprehensive in vivo identification of the c-Myc mRNA protein interactome using HyPR-MS. <i>Rna</i> , 2019 , 25, 1337-1352 | 5.8 | 6 |
| 39 | Enzymatic Fabrication of High-Density RNA Arrays. <i>Angewandte Chemie</i> , 2014 , 126, 13732-13735 | 3.6 | 6 |
| 38 | Multiplexed programmable release of captured DNA. <i>ChemBioChem</i> , 2014 , 15, 2353-6 | 3.8 | 6 |
| 37 | Multiplexed Sequence-Specific Capture of Chromatin and Mass Spectrometric Discovery of Associated Proteins. <i>Analytical Chemistry</i> , 2017 , 89, 7841-7846 | 7.8 | 6 |
| 36 | Subthreshold field emission from thin silicon membranes. <i>Applied Physics Letters</i> , 2007 , 91, 183506 | 3.4 | 6 |
| 35 | Collision cross sections of gas phase DNA ions. <i>International Journal of Mass Spectrometry</i> , 2002 , 219, 161-170 | 1.9 | 6 |
| 34 | Spritz: A Proteogenomic Database Engine | | 6 |
| 33 | ProteaseGuru: A Tool for Protease Selection in Bottom-Up Proteomics. <i>Journal of Proteome Research</i> , 2021 , 20, 1936-1942 | 5.6 | 6 |
| 32 | Long Noncoding RNAs AC009014.3 and Newly Discovered XPLAID Differentiate Aggressive and Indolent Prostate Cancers. <i>Translational Oncology</i> , 2018 , 11, 808-814 | 4.9 | 5 |

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| 31 | Construction of Human Proteoform Families from 21 Tesla Fourier Transform Ion Cyclotron Resonance Mass Spectrometry Top-Down Proteomic Data. <i>Journal of Proteome Research</i> , 2021 , 20, 317-325 | 5.6 | 5 |
| 30 | Morpheus Spectral Counter: A computational tool for label-free quantitative mass spectrometry using the Morpheus search engine. <i>Proteomics</i> , 2016 , 16, 920-4 | 4.8 | 4 |
| 29 | A surface-based approach to DNA computation. <i>DIMACS Series in Discrete Mathematics and Theoretical Computer Science</i> , 1998 , 123-132 | | 4 |
| 28 | A Bayesian Null Interval Hypothesis Test Controls False Discovery Rates and Improves Sensitivity in Label-Free Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2020 , 19, 1975-1981 | 5.6 | 3 |
| 27 | Encrypted Oligonucleotide Arrays for Molecular Authentication. <i>ACS Combinatorial Science</i> , 2019 , 21, 562-567 | 3.9 | 3 |
| 26 | RNA-Mediated Gene Assembly from DNA Arrays. <i>Angewandte Chemie</i> , 2012 , 124, 4706-4710 | 3.6 | 3 |
| 25 | To understand the whole, you must know the parts: unraveling the roles of protein-DNA interactions in genome regulation. <i>Analyst, The</i> , 2011 , 136, 3060-5 | 5 | 3 |
| 24 | An atlas of protein turnover rates in mouse tissues. <i>Nature Communications</i> , 2021 , 12, 6778 | 17.4 | 3 |
| 23 | Advanced Strategies for Proton-Transfer Reactions Coupled with Parallel Ion Parking on a 21 T FT-ICR MS for Intact Protein Analysis. <i>Analytical Chemistry</i> , 2021 , 93, 9119-9128 | 7.8 | 3 |
| 22 | Identification of host proteins differentially associated with HIV-1 RNA splice variants. <i>ELife</i> , 2021 , 10, | 8.9 | 3 |
| 21 | An Algorithm to Improve the Speed of Semi and Non-Specific Enzyme Searches in Proteomics. <i>Current Bioinformatics</i> , 2020 , 15, 1065-1074 | 4.7 | 3 |
| 20 | Fused in sarcoma regulates DNA replication timing and kinetics. <i>Journal of Biological Chemistry</i> , 2021 , 297, 101049 | 5.4 | 3 |
| 19 | Putting Humpty Dumpty Back Together Again: What Does Protein Quantification Mean in Bottom-Up Proteomics?. <i>Journal of Proteome Research</i> , 2022 , | 5.6 | 3 |
| 18 | Enhanced protein isoform characterization through long-read proteogenomics.. <i>Genome Biology</i> , 2022 , 23, 69 | 18.3 | 3 |
| 17 | Advanced methods for the analysis of chromatin-associated proteins. <i>Physiological Genomics</i> , 2014 , 46, 441-7 | 3.6 | 2 |
| 16 | Parallel DNA Synthesis on Poly(ethylene terephthalate). <i>ChemBioChem</i> , 2017 , 18, 1914-1916 | 3.8 | 2 |
| 15 | A high throughput system for the preparation of single stranded templates grown in microculture. <i>DNA Sequence</i> , 1994 , 4, 253-7 | | 2 |
| 14 | Precursor Intensity-Based Label-Free Quantification Software Tools for Proteomic and Multi-Omic Analysis within the Galaxy Platform. <i>Proteomes</i> , 2020 , 8, | 4.6 | 2 |

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| 13 | Automated Assignment of Proteoform Classification Levels. <i>Journal of Proteome Research</i> , 2021 , 20, 4101-4105 | 5.6 | 2 |
| 12 | Mesh Fragmentation Improves Dissociation Efficiency in Top-down Proteomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2021 , 32, 1319-1325 | 3.5 | 2 |
| 11 | Reply to Comment on Hydroxycarboxylic Acid-Derived Organosulfates: Synthesis, Stability and Quantification in Ambient Aerosol. <i>Environmental Science & Technology</i> , 2011 , 45, 9111-9111 | 10.3 | 1 |
| 10 | Covalently-linked Adducts of Single-walled Nanotubes with Biomolecules: Synthesis, Hybridization, and Biologically-Directed Surface Assembly. <i>Materials Research Society Symposia Proceedings</i> , 2002 , 737, 581 | | 1 |
| 9 | Preparation and Electrochemical Characterization of DNA-modified Nanocrystalline Diamond Films. <i>Materials Research Society Symposia Proceedings</i> , 2002 , 737, 569 | | 1 |
| 8 | Proteomic pathways to metabolic disease and type 2 diabetes in the pancreatic islet. <i>IScience</i> , 2021 , 24, 103099 | 6.1 | 1 |
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| 6 | Identifying Protein Interactomes of Target RNAs Using HyPR-MS. <i>Methods in Molecular Biology</i> , 2022 , 2404, 219-244 | 1.4 | 0 |
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| 4 | Nanomembranes as Protein Mass Spectrometers 2016 , 257-270 | | |
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| 2 | Proteoform Analysis and Construction of Proteoform Families in Proteoform Suite. <i>Methods in Molecular Biology</i> , 2022 , 67-81 | 1.4 | |
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