

Lloyd M Smith

List of Publications by Year in descending order

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172
papers

13,786
citations

34105

52
h-index

23533

111
g-index

221
all docs

221
docs citations

221
times ranked

12436
citing authors

#	ARTICLE	IF	CITATIONS
1	Identifying Protein Interactomes of Target RNAs Using HyPR-MS. <i>Methods in Molecular Biology</i> , 2022, 2404, 219-244.	0.9	4
2	MetaNetwork Enhances Biological Insights from Quantitative Proteomics Differences by Combining Clustering and Enrichment Analyses. <i>Journal of Proteome Research</i> , 2022, 21, 410-419.	3.7	2
3	Towards an Ideal In Cell Hybridization-Based Strategy to Discover Protein Interactomes of Selected RNA Molecules. <i>International Journal of Molecular Sciences</i> , 2022, 23, 942.	4.1	0
4	Putting Humpty Dumpty Back Together Again: What Does Protein Quantification Mean in Bottom-Up Proteomics?. <i>Journal of Proteome Research</i> , 2022, 21, 891-898.	3.7	35
5	Discovery of Dehydroamino Acid Residues in the Capsid and Matrix Structural Proteins of HIV-1. <i>Journal of Proteome Research</i> , 2022, 21, 993-1001.	3.7	2
6	Enhanced protein isoform characterization through long-read proteogenomics. <i>Genome Biology</i> , 2022, 23, 69.	8.8	33
7	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.	3.7	8
8	Spritz: A Proteogenomic Database Engine. <i>Journal of Proteome Research</i> , 2021, 20, 1826-1834.	3.7	24
9	Identification of host proteins differentially associated with HIV-1 RNA splice variants. <i>ELife</i> , 2021, 10, .	6.0	19
10	An Algorithm to Improve the Speed of Semi and Non-specific Enzyme Searches in Proteomics. <i>Current Bioinformatics</i> , 2021, 15, 1065-1074.	1.5	5
11	Mesh Fragmentation Improves Dissociation Efficiency in Top-down Proteomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 1319-1325.	2.8	7
12	ProteaseGuru: A Tool for Protease Selection in Bottom-Up Proteomics. <i>Journal of Proteome Research</i> , 2021, 20, 1936-1942.	3.7	14
13	Binary Classifier for Computing Posterior Error Probabilities in MetaMorpheus. <i>Journal of Proteome Research</i> , 2021, 20, 1997-2004.	3.7	1
14	Automated Assignment of Proteoform Classification Levels. <i>Journal of Proteome Research</i> , 2021, 20, 4101-4105.	3.7	2
15	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.	6.5	10
16	Fused in sarcoma regulates DNA replication timing and kinetics. <i>Journal of Biological Chemistry</i> , 2021, 297, 101049.	3.4	7
17	Proteomic pathways to metabolic disease and type 2 diabetes in the pancreatic islet. <i>IScience</i> , 2021, 24, 103099.	4.1	12
18	Internal Fragment Ions Disambiguate and Increase Identifications in Top-Down Proteomics. <i>Journal of Proteome Research</i> , 2021, 20, 5412-5418.	3.7	8

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19	An atlas of protein turnover rates in mouse tissues. <i>Nature Communications</i> , 2021, 12, 6778.	12.8	25
20	The Human Proteoform Project: Defining the human proteome. <i>Science Advances</i> , 2021, 7, eabk0734.	10.3	106
21	Precursor Intensity-Based Label-Free Quantification Software Tools for Proteomic and Multi-Omic Analysis within the Galaxy Platform. <i>Proteomes</i> , 2020, 8, 15.	3.5	9
22	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.	2.8	67
23	O-Pair Search with MetaMorpheus for O-glycopeptide characterization. <i>Nature Methods</i> , 2020, 17, 1133-1138.	19.0	98
24	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.	3.7	25
25	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.	3.7	7
26	Intact-Mass Analysis Facilitating the Identification of Large Human Heart Proteoforms. <i>Analytical Chemistry</i> , 2019, 91, 10937-10942.	6.5	11
27	Improved Protein Inference from Multiple Protease Bottom-Up Mass Spectrometry Data. <i>Journal of Proteome Research</i> , 2019, 18, 3429-3438.	3.7	36
28	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, .	11.9	39
29	Encrypted Oligonucleotide Arrays for Molecular Authentication. <i>ACS Combinatorial Science</i> , 2019, 21, 562-567.	3.8	5
30	Comprehensive in vivo identification of the c-Myc mRNA protein interactome using HyPR-MS. <i>Rna</i> , 2019, 25, 1337-1352.	3.5	15
31	Proteomic analysis of affinity-purified 26S proteasomes identifies a suite of assembly chaperones in <i>Arabidopsis</i> . <i>Journal of Biological Chemistry</i> , 2019, 294, 17570-17592.	3.4	17
32	A five-level classification system for proteoform identifications. <i>Nature Methods</i> , 2019, 16, 939-940.	19.0	55
33	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.	3.7	21
34	Best practices and benchmarks for intact protein analysis for top-down mass spectrometry. <i>Nature Methods</i> , 2019, 16, 587-594.	19.0	241
35	Differentiated fibrocytes assume a functional mesenchymal phenotype with regenerative potential. <i>Science Advances</i> , 2019, 5, eaav7384.	10.3	21
36	Identification and Quantification of Proteoforms by Mass Spectrometry. <i>Proteomics</i> , 2019, 19, e1800361.	2.2	147

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37	HDA9-PWR-HOS15 Is a Core Histone Deacetylase Complex Regulating Transcription and Development. <i>Plant Physiology</i> , 2019, 180, 342-355.	4.8	52
38	Proteoforms as the next proteomics currency. <i>Science</i> , 2018, 359, 1106-1107.	12.6	205
39	ProForma: A Standard Proteoform Notation. <i>Journal of Proteome Research</i> , 2018, 17, 1321-1325.	3.7	35
40	Compartmentalization of HP1 Proteins in Pluripotency Acquisition and Maintenance. <i>Stem Cell Reports</i> , 2018, 10, 627-641.	4.8	20
41	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018, 14, 206-214.	8.0	580
42	Canonical and Noncanonical Actions of Arabidopsis Histone Deacetylases in Ribosomal RNA Processing. <i>Plant Cell</i> , 2018, 30, 134-152.	6.6	44
43	Long Noncoding RNAs AC009014.3 and Newly Discovered XPLAID Differentiate Aggressive and Indolent Prostate Cancers. <i>Translational Oncology</i> , 2018, 11, 808-814.	3.7	7
44	Enhanced Global Post-translational Modification Discovery with MetaMorpheus. <i>Journal of Proteome Research</i> , 2018, 17, 1844-1851.	3.7	206
45	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.	6.6	120
46	Ultrafast Peptide Label-Free Quantification with FlashLFQ. <i>Journal of Proteome Research</i> , 2018, 17, 386-391.	3.7	74
47	Expanding Proteoform Identifications in Top-Down Proteomic Analyses by Constructing Proteoform Families. <i>Analytical Chemistry</i> , 2018, 90, 1325-1333.	6.5	27
48	Proteoform Suite: Software for Constructing, Quantifying, and Visualizing Proteoform Families. <i>Journal of Proteome Research</i> , 2018, 17, 568-578.	3.7	40
49	Global Identification of Post-Translationally Spliced Peptides with Neo-Fusion. <i>Journal of Proteome Research</i> , 2018, 18, 349-358.	3.7	32
50	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.	3.7	23
51	Identification of MS-Cleavable and Noncleavable Chemically Cross-Linked Peptides with MetaMorpheus. <i>Journal of Proteome Research</i> , 2018, 17, 2370-2376.	3.7	40
52	HyPR-MS for Multiplexed Discovery of MALAT1, NEAT1, and NORAD lncRNA Protein Interactomes. <i>Journal of Proteome Research</i> , 2018, 17, 3022-3038.	3.7	49
53	EBS is a bivalent histone reader that regulates floral phase transition in Arabidopsis. <i>Nature Genetics</i> , 2018, 50, 1247-1253.	21.4	97
54	Adaptation of Hybridization Capture of Chromatin-associated Proteins for Proteomics to Mammalian Cells. <i>Journal of Visualized Experiments</i> , 2018, , .	0.3	0

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55	Mass Spectrometric Analyses Reveal a Central Role for Ubiquitylation in Remodeling the Arabidopsis Proteome during Photomorphogenesis. <i>Molecular Plant</i> , 2017, 10, 846-865.	8.3	31
56	Elucidating <i>Escherichia coli</i> Proteoform Families Using Intact-Mass Proteomics and a Global PTM Discovery Database. <i>Journal of Proteome Research</i> , 2017, 16, 4156-4165.	3.7	32
57	Parallel DNA Synthesis on Poly(ethylene terephthalate). <i>ChemBioChem</i> , 2017, 18, 1914-1916.	2.6	6
58	Elucidating the in vivo interactome of HIV-1 RNA by hybridization capture and mass spectrometry. <i>Scientific Reports</i> , 2017, 7, 16965.	3.3	36
59	Elucidating Protein-DNA Interactions in Human Aliphoid Chromatin via Hybridization Capture and Mass Spectrometry. <i>Journal of Proteome Research</i> , 2017, 16, 3433-3442.	3.7	12
60	Multiplexed Sequence-Specific Capture of Chromatin and Mass Spectrometric Discovery of Associated Proteins. <i>Analytical Chemistry</i> , 2017, 89, 7841-7846.	6.5	8
61	Global Post-Translational Modification Discovery. <i>Journal of Proteome Research</i> , 2017, 16, 1383-1390.	3.7	75
62	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.	2.8	17
63	POWERDRESS interacts with HISTONE DEACETYLASE 9 to promote aging in Arabidopsis. <i>ELife</i> , 2016, 5, .	6.0	143
64	The Transcription Factor Nfatc2 Regulates β -Cell Proliferation and Genes Associated with Type 2 Diabetes in Mouse and Human Islets. <i>PLoS Genetics</i> , 2016, 12, e1006466.	3.5	40
65	Proteogenomics: Integrating Next-Generation Sequencing and Mass Spectrometry to Characterize Human Proteomic Variation. <i>Annual Review of Analytical Chemistry</i> , 2016, 9, 521-545.	5.4	91
66	Elucidating Proteoform Families from Proteoform Intact-Mass and Lysine-Count Measurements. <i>Journal of Proteome Research</i> , 2016, 15, 1213-1221.	3.7	43
67	HyCCAPP as a tool to characterize promoter DNA-protein interactions in <i>Saccharomyces cerevisiae</i> . <i>Genomics</i> , 2016, 107, 267-273.	2.9	12
68	Morpheus Spectral Counter: A computational tool for label-free quantitative mass spectrometry using the Morpheus search engine. <i>Proteomics</i> , 2016, 16, 920-924.	2.2	7
69	Protein turnover during in vitro tissue engineering. <i>Biomaterials</i> , 2016, 81, 104-113.	11.4	24
70	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, 800-808.	3.7	29
71	Proteomic analysis of naturally-sourced biological scaffolds. <i>Biomaterials</i> , 2016, 75, 37-46.	11.4	115
72	Carbon Substrates: A Stable Foundation for Biomolecular Arrays. <i>Annual Review of Analytical Chemistry</i> , 2015, 8, 263-285.	5.4	9

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73	Formaldehyde Crosslinking: A Tool for the Study of Chromatin Complexes. <i>Journal of Biological Chemistry</i> , 2015, 290, 26404-26411.	3.4	290
74	Global Identification of Protein Post-translational Modifications in a Single-Pass Database Search. <i>Journal of Proteome Research</i> , 2015, 14, 4714-4720.	3.7	43
75	Bioengineered vocal fold mucosa for voice restoration. <i>Science Translational Medicine</i> , 2015, 7, 314ra187.	12.4	60
76	Photolithographic Synthesis of High-Density DNA and RNA Arrays on Flexible, Transparent, and Easily Subdivided Plastic Substrates. <i>Analytical Chemistry</i> , 2015, 87, 11420-11428.	6.5	27
77	Enzymatic Fabrication of High-Density RNA Arrays. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 13514-13517.	13.8	24
78	Large-Scale Mass Spectrometric Detection of Variant Peptides Resulting from Nonsynonymous Nucleotide Differences. <i>Journal of Proteome Research</i> , 2014, 13, 228-240.	3.7	81
79	Advanced methods for the analysis of chromatin-associated proteins. <i>Physiological Genomics</i> , 2014, 46, 441-447.	2.3	5
80	Flexible and Accessible Workflows for Improved Proteogenomic Analysis Using the Galaxy Framework. <i>Journal of Proteome Research</i> , 2014, 13, 5898-5908.	3.7	88
81	Measuring the Formaldehyde Protein-DNA Cross-Link Reversal Rate. <i>Analytical Chemistry</i> , 2014, 86, 5678-5681.	6.5	49
82	Using Galaxy-P to leverage RNA-Seq for the discovery of novel protein variations. <i>BMC Genomics</i> , 2014, 15, 703.	2.8	74
83	Neutron-Encoded Mass Signatures for Quantitative Top-Down Proteomics. <i>Analytical Chemistry</i> , 2014, 86, 2314-2319.	6.5	45
84	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, 3810-3825.	3.7	21
85	Methylation of yeast ribosomal protein S2 is elevated during stationary phase growth conditions. <i>Biochemical and Biophysical Research Communications</i> , 2014, 445, 535-541.	2.1	25
86	Multiplexed Programmable Release of Captured DNA. <i>ChemBioChem</i> , 2014, 15, 2353-2356.	2.6	8
87	Discovery and Mass Spectrometric Analysis of Novel Splice-junction Peptides Using RNA-Seq. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2341-2353.	3.8	115
88	Proteiform: a single term describing protein complexity. <i>Nature Methods</i> , 2013, 10, 186-187.	19.0	1,180
89	Fabrication of Oligonucleotide and Protein Arrays on Rigid and Flexible Substrates Coated with Reactive Polymer Multilayers. <i>ACS Applied Materials & Interfaces</i> , 2013, 5, 351-359.	8.0	21
90	Chemical Derivatization of Peptide Carboxyl Groups for Highly Efficient Electron Transfer Dissociation. <i>Journal of the American Society for Mass Spectrometry</i> , 2013, 24, 1710-1721.	2.8	37

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91	<i>In situ</i> Synthesis of Oligonucleotide Arrays on Surfaces Coated with Crosslinked Polymer Multilayers. <i>Chemistry of Materials</i> , 2012, 24, 938-945.	6.7	12
92	RNA-Mediated Gene Assembly from DNA Arrays. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 4628-4632.	13.8	8
93	To understand the whole, you must know the parts: unraveling the roles of protein-DNA interactions in genome regulation. <i>Analyst</i> , 2011, 136, 3060.	3.5	4
94	Reply to Comment on "Hydroxycarboxylic Acid-Derived Organosulfates: Synthesis, Stability and Quantification in Ambient Aerosols". <i>Environmental Science & Technology</i> , 2011, 45, 9111-9111.	10.0	1
95	Sequence-Specific Capture of Protein-DNA Complexes for Mass Spectrometric Protein Identification. <i>PLoS ONE</i> , 2011, 6, e26217.	2.5	30
96	Complete Chemical Modification of Amine and Acid Functional Groups of Peptides and Small Proteins. <i>Methods in Molecular Biology</i> , 2011, 753, 77-91.	0.9	10
97	Molecular robots on the move. <i>Nature</i> , 2010, 465, 167-168.	27.8	24
98	Alkylating Tryptic Peptides to Enhance Electrospray Ionization Mass Spectrometry Analysis. <i>Analytical Chemistry</i> , 2010, 82, 10135-10142.	6.5	43
99	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, 1617-1625.	2.8	65
100	Controlling Oligonucleotide Surface Density in Light-Directed DNA Array Fabrication. <i>Langmuir</i> , 2009, 25, 6570-6575.	3.5	21
101	Fabrication and Characterization of DNA Arrays Prepared on Carbon-on-Metal Substrates. <i>Analytical Chemistry</i> , 2009, 81, 6429-6437.	6.5	26
102	Is charge reduction in ESI really necessary?. <i>Journal of the American Society for Mass Spectrometry</i> , 2008, 19, 629-631.	2.8	16
103	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.	1.5	21
104	A Tetrafluorophenyl Activated Ester Self-Assembled Monolayer for the Immobilization of Amine-Modified Oligonucleotides. <i>Langmuir</i> , 2008, 24, 69-75.	3.5	62
105	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, 8269-8275.	6.5	9
106	Carbon-on-Metal Films for Surface Plasmon Resonance Detection of DNA Arrays. <i>Journal of the American Chemical Society</i> , 2008, 130, 8611-8613.	13.7	60
107	Aldehyde-Terminated Amorphous Carbon Substrates for the Fabrication of Biomolecule Arrays. <i>Langmuir</i> , 2008, 24, 9198-9203.	3.5	16
108	Subthreshold field emission from thin silicon membranes. <i>Applied Physics Letters</i> , 2007, 91, 183506.	3.3	6

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109	In situ oligonucleotide synthesis on carbon materials: stable substrates for microarray fabrication. <i>Nucleic Acids Research</i> , 2007, 36, e7-e7.	14.5	39
110	Relative Quantification of Carboxylic Acid Metabolites by Liquid Chromatography-Mass Spectrometry Using Isotopic Variants of Choline. <i>Analytical Chemistry</i> , 2007, 79, 5143-5149.	6.5	71
111	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, 241-247.	2.4	11
112	Lectin-modified microchannels for mammalian cell capture and purification. <i>Biomedical Microdevices</i> , 2007, 9, 611-617.	2.8	16
113	Covalent Photochemical Functionalization of Amorphous Carbon Thin Films for Integrated Real-Time Biosensing. <i>Langmuir</i> , 2006, 22, 9598-9605.	3.5	96
114	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, 1580-1585.	3.7	46
115	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.	2.8	50
116	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, 1876-1887.	2.8	38
117	β -Ketoisocaproate-induced hypersecretion of insulin by islets from diabetes-susceptible mice. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2005, 289, E218-E224.	3.5	78
118	Lectin Arrays for Profiling Cell Surface Carbohydrate Expression. <i>Journal of the American Chemical Society</i> , 2005, 127, 9982-9983.	13.7	188
119	Scoring Single-Nucleotide Polymorphisms at the Single-Molecule Level by Counting Individual DNA Cleavage Events on Surfaces. <i>Analytical Chemistry</i> , 2005, 77, 6594-6600.	6.5	19
120	Immobilization of Amine-Modified Oligonucleotides on Aldehyde-Terminated Alkanethiol Monolayers on Gold. <i>Langmuir</i> , 2005, 21, 266-271.	3.5	107
121	Invasive cleavage reactions on DNA-modified diamond surfaces. <i>Biopolymers</i> , 2004, 73, 606-613.	2.4	52
122	DNA-Modified Diamond Surfaces. <i>Langmuir</i> , 2003, 19, 1938-1942.	3.5	134
123	Mass Spectrometric Analysis of DNA Mixtures: Instrumental Effects Responsible for Decreased Sensitivity with Increasing Mass. <i>Analytical Chemistry</i> , 2003, 75, 5944-5952.	6.5	54
124	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.	0.1	1
125	Covalently-linked Adducts of Single-walled Nanotubes with Biomolecules: Synthesis, Hybridization, and Biologically-Directed Surface Assembly. <i>Materials Research Society Symposia Proceedings</i> , 2002, 761, 1.	0.1	0
126	DNA Attachment and Hybridization at the Silicon (100) Surface. <i>Langmuir</i> , 2002, 18, 788-796.	3.5	190

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127	Structure-Specific DNA Cleavage on Surfaces. <i>Journal of the American Chemical Society</i> , 2002, 124, 7924-7931.	13.7	29
128	Chemical Modification and Patterning of Iodine-Terminated Silicon Surfaces Using Visible Light. <i>Journal of Physical Chemistry B</i> , 2002, 106, 2656-2664.	2.6	74
129	Preparation and Electrochemical Characterization of DNA-modified Nanocrystalline Diamond Films. <i>Materials Research Society Symposia Proceedings</i> , 2002, 737, 569.	0.1	1
130	A surface invasive cleavage assay for highly parallel SNP analysis. <i>Human Mutation</i> , 2002, 19, 416-422.	2.5	12
131	Collision cross sections of gas phase DNA ions. <i>International Journal of Mass Spectrometry</i> , 2002, 219, 161-170.	1.5	7
132	DNA-modified nanocrystalline diamond thin-films as stable, biologically active substrates. <i>Nature Materials</i> , 2002, 1, 253-257.	27.5	802
133	A cylindrical capacitor ionization source: droplet generation and controlled charge reduction for mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2001, 15, 401-405.	1.5	20
134	A DNA computing readout operation based on structure-specific cleavage. <i>Nature Biotechnology</i> , 2001, 19, 1053-1059.	17.5	32
135	Analysis of single nucleotide polymorphisms with solid phase invasive cleavage reactions. <i>Nucleic Acids Research</i> , 2001, 29, 77e-77.	14.5	28
136	Analysis of single nucleotide polymorphisms by primer extension and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. , 2000, 14, 950-959.		48
137	DNA computing on surfaces. <i>Nature</i> , 2000, 403, 175-179.	27.8	409
138	Synthesis and Characterization of DNA-Modified Silicon (111) Surfaces. <i>Journal of the American Chemical Society</i> , 2000, 122, 1205-1209.	13.7	432
139	Covalent attachment of oligodeoxyribonucleotides to amine-modified Si (001) surfaces. <i>Nucleic Acids Research</i> , 2000, 28, 3535-3541.	14.5	272
140	Charge Reduction Electrospray Mass Spectrometry. <i>Analytical Chemistry</i> , 2000, 72, 52-60.	6.5	136
141	Corona Discharge in Charge Reduction Electrospray Mass Spectrometry. <i>Analytical Chemistry</i> , 2000, 72, 5158-5161.	6.5	110
142	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.	2.8	13
143	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.	2.0	22
144	Controlling Charge States of Large Ions. <i>Science</i> , 1999, 283, 194-197.	12.6	157

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145	A Surface-Based Approach to DNA Computation. <i>Journal of Computational Biology</i> , 1998, 5, 255-267.	1.6	69
146	DNA Computing on Surfaces: Encoding Information at the Single Base Level. <i>Journal of Computational Biology</i> , 1998, 5, 269-278.	1.6	15
147	A Software System for Data Analysis in Automated DNA Sequencing. <i>Genome Research</i> , 1998, 8, 644-665.	5.5	54
148	A surface-based approach to DNA computation. <i>DIMACS Series in Discrete Mathematics and Theoretical Computer Science</i> , 1998, , 123-132.	0.0	4
149	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, 4581-4588.	14.5	70
150	Controlling DNA Fragmentation in MALDI-MS by Chemical Modification. <i>Analytical Chemistry</i> , 1997, 69, 302-312.	6.5	69
151	Enhanced discrimination of single nucleotide polymorphisms by artificial mismatch hybridization. <i>Nature Biotechnology</i> , 1997, 15, 331-335.	17.5	134
152	Genetic analysis by peptide nucleic acid affinity MALDI-TOF mass spectrometry. <i>Nature Biotechnology</i> , 1997, 15, 1368-1372.	17.5	113
153	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.	2.8	35
154	A Self-Assembled Matrix Monolayer for UV-MALDI Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 1996, 118, 8639-8645.	13.7	35
155	Automatic matrix determination in four dye fluorescence-based DNA sequencing. <i>Electrophoresis</i> , 1996, 17, 1143-1150.	2.4	24
156	Analyzing Sequencing Reactions from Bacteriophage M13 by Matrix-assisted Laser Desorption/Ionization Mass Spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 1996, 10, 1475-1478.	1.5	39
157	Oligodeoxynucleotide Fragmentation in MALDI/TOF Mass Spectrometry Using 355-nm Radiation. <i>Journal of the American Chemical Society</i> , 1995, 117, 6048-6056.	13.7	109
158	Separating field strength, temperature, and pulsing effects in pulsed field electrophoresis. <i>Electrophoresis</i> , 1994, 15, 1084-1090.	2.4	10
159	Direct fluorescence analysis of genetic polymorphisms by hybridization with oligonucleotide arrays on glass supports. <i>Nucleic Acids Research</i> , 1994, 22, 5456-5465.	14.5	495
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