

Lloyd M Smith

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/5579551/lloyd-m-smith-publications-by-year.pdf>

Version: 2024-04-29

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Identifying Protein Interactomes of Target RNAs Using HyPR-MS. <i>Methods in Molecular Biology</i> , 2022 , 2404, 219-244	1.4	0
173	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
172	Enhanced protein isoform characterization through long-read proteogenomics.. <i>Genome Biology</i> , 2022 , 23, 69	18.3	3
171	Proteoform Analysis and Construction of Proteoform Families in Proteoform Suite. <i>Methods in Molecular Biology</i> , 2022 , 67-81	1.4	
170	Proteoforms and Proteoform Families: Past, Present, and Future. <i>Methods in Molecular Biology</i> , 2022 , 1-4	1.4	
169	Internal Fragment Ions Disambiguate and Increase Identifications in Top-Down Proteomics. <i>Journal of Proteome Research</i> , 2021 , 20, 5412-5418	5.6	0
168	An atlas of protein turnover rates in mouse tissues. <i>Nature Communications</i> , 2021 , 12, 6778	17.4	3
167	The Human Proteoform Project: Defining the human proteome. <i>Science Advances</i> , 2021 , 7, eabk0734	14.3	19
166	Binary Classifier for Computing Posterior Error Probabilities in MetaMorpheus. <i>Journal of Proteome Research</i> , 2021 , 20, 1997-2004	5.6	0
165	Automated Assignment of Proteoform Classification Levels. <i>Journal of Proteome Research</i> , 2021 , 20, 4101-4105	5.6	2
164	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
163	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
162	Spritz: A Proteogenomic Database Engine. <i>Journal of Proteome Research</i> , 2021 , 20, 1826-1834	5.6	12
161	Identification of host proteins differentially associated with HIV-1 RNA splice variants. <i>ELife</i> , 2021 , 10,	8.9	3
160	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
159	ProteaseGuru: A Tool for Protease Selection in Bottom-Up Proteomics. <i>Journal of Proteome Research</i> , 2021 , 20, 1936-1942	5.6	6
158	Fused in sarcoma regulates DNA replication timing and kinetics. <i>Journal of Biological Chemistry</i> , 2021 , 297, 101049	5.4	3

157	Proteomic pathways to metabolic disease and type 2 diabetes in the pancreatic islet. <i>IScience</i> , 2021 , 24, 103099	6.1	1
156	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
155	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
154	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
153	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
152	O-Pair Search with MetaMorpheus for O-glycopeptide characterization. <i>Nature Methods</i> , 2020 , 17, 1133-1138	11.38	46
151	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
150	A five-level classification system for proteoform identifications. <i>Nature Methods</i> , 2019 , 16, 939-940	21.6	25
149	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
148	Best practices and benchmarks for intact protein analysis for top-down mass spectrometry. <i>Nature Methods</i> , 2019 , 16, 587-594	21.6	137
147	Differentiated fibrocytes assume a functional mesenchymal phenotype with regenerative potential. <i>Science Advances</i> , 2019 , 5, eaav7384	14.3	13
146	Identification and Quantification of Proteoforms by Mass Spectrometry. <i>Proteomics</i> , 2019 , 19, e180036	14.8	77
145	Intact-Mass Analysis Facilitating the Identification of Large Human Heart Proteoforms. <i>Analytical Chemistry</i> , 2019 , 91, 10937-10942	7.8	8
144	Improved Protein Inference from Multiple Protease Bottom-Up Mass Spectrometry Data. <i>Journal of Proteome Research</i> , 2019 , 18, 3429-3438	5.6	18
143	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
142	Encrypted Oligonucleotide Arrays for Molecular Authentication. <i>ACS Combinatorial Science</i> , 2019 , 21, 562-567	3.9	3
141	Comprehensive in vivo identification of the c-Myc mRNA protein interactome using HyPR-MS. <i>Rna</i> , 2019 , 25, 1337-1352	5.8	6
140	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

139	HDA9-PWR-HOS15 Is a Core Histone Deacetylase Complex Regulating Transcription and Development. <i>Plant Physiology</i> , 2019 , 180, 342-355	6.6	34
138	Global Identification of Post-Translationally Spliced Peptides with Neo-Fusion. <i>Journal of Proteome Research</i> , 2019 , 18, 349-358	5.6	24
137	Proteoforms as the next proteomics currency. <i>Science</i> , 2018 , 359, 1106-1107	33.3	101
136	ProForma: A Standard Proteoform Notation. <i>Journal of Proteome Research</i> , 2018 , 17, 1321-1325	5.6	27
135	Compartmentalization of HP1 Proteins in Pluripotency Acquisition and Maintenance. <i>Stem Cell Reports</i> , 2018 , 10, 627-641	8	11
134	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018 , 14, 206-214	11.7	324
133	Canonical and Noncanonical Actions of Arabidopsis Histone Deacetylases in Ribosomal RNA Processing. <i>Plant Cell</i> , 2018 , 30, 134-152	11.6	21
132	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
131	Enhanced Global Post-translational Modification Discovery with MetaMorpheus. <i>Journal of Proteome Research</i> , 2018 , 17, 1844-1851	5.6	123
130	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
129	Ultrafast Peptide Label-Free Quantification with FlashLFQ. <i>Journal of Proteome Research</i> , 2018 , 17, 386-391	3.1	36
128	EBS is a bivalent histone reader that regulates floral phase transition in Arabidopsis. <i>Nature Genetics</i> , 2018 , 50, 1247-1253	36.3	56
127	Expanding Proteoform Identifications in Top-Down Proteomic Analyses by Constructing Proteoform Families. <i>Analytical Chemistry</i> , 2018 , 90, 1325-1333	7.8	20
126	Proteoform Suite: Software for Constructing, Quantifying, and Visualizing Proteoform Families. <i>Journal of Proteome Research</i> , 2018 , 17, 568-578	5.6	26
125	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
124	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
123	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
122	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

121	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
120	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
119	Parallel DNA Synthesis on Poly(ethylene terephthalate). <i>ChemBioChem</i> , 2017 , 18, 1914-1916	3.8	2
118	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
117	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
116	Multiplexed Sequence-Specific Capture of Chromatin and Mass Spectrometric Discovery of Associated Proteins. <i>Analytical Chemistry</i> , 2017 , 89, 7841-7846	7.8	6
115	Global Post-Translational Modification Discovery. <i>Journal of Proteome Research</i> , 2017 , 16, 1383-1390	5.6	54
114	Proteomic analysis of naturally-sourced biological scaffolds. <i>Biomaterials</i> , 2016 , 75, 37-46	15.6	85
113	Nanomembranes as Protein Mass Spectrometers 2016 , 257-270		
112	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
111	Protein turnover during in vitro tissue engineering. <i>Biomaterials</i> , 2016 , 81, 104-113	15.6	20
110	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
109	POWERDRESS interacts with HISTONE DEACETYLASE 9 to promote aging in. <i>ELife</i> , 2016 , 5,	8.9	83
108	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
107	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
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	HyCCAPP as a tool to characterize promoter DNA-protein interactions in Saccharomyces cerevisiae. <i>Genomics</i> , 2016 , 107, 267-73	4.3	8
104	Formaldehyde crosslinking: a tool for the study of chromatin complexes. <i>Journal of Biological Chemistry</i> , 2015 , 290, 26404-11	5.4	192

103	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
102	Bioengineered vocal fold mucosa for voice restoration. <i>Science Translational Medicine</i> , 2015 , 7, 314ra18717.5	17.5	46
101	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
100	Carbon Substrates: A Stable Foundation for Biomolecular Arrays. <i>Annual Review of Analytical Chemistry</i> , 2015 , 8, 263-85	12.5	7
99	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
98	Advanced methods for the analysis of chromatin-associated proteins. <i>Physiological Genomics</i> , 2014 , 46, 441-7	3.6	2
97	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
96	Measuring the formaldehyde Protein-DNA cross-link reversal rate. <i>Analytical Chemistry</i> , 2014 , 86, 5678-81.8	1.8	35
95	Using Galaxy-P to leverage RNA-Seq for the discovery of novel protein variations. <i>BMC Genomics</i> , 2014 , 15, 703	4.5	58
94	Neutron-encoded mass signatures for quantitative top-down proteomics. <i>Analytical Chemistry</i> , 2014 , 86, 2314-9	7.8	39
93	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
92	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
91	Enzymatic Fabrication of High-Density RNA Arrays. <i>Angewandte Chemie</i> , 2014 , 126, 13732-13735	3.6	6
90	Multiplexed programmable release of captured DNA. <i>ChemBioChem</i> , 2014 , 15, 2353-6	3.8	6
89	Enzymatic fabrication of high-density RNA arrays. <i>Angewandte Chemie - International Edition</i> , 2014 , 53, 13514-7	16.4	21
88	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
87	Proteoform: a single term describing protein complexity. <i>Nature Methods</i> , 2013 , 10, 186-7	21.6	857
86	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

85	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
84	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
83	RNA-Mediated Gene Assembly from DNA Arrays. <i>Angewandte Chemie</i> , 2012 , 124, 4706-4710	3.6	3
82	RNA-mediated gene assembly from DNA arrays. <i>Angewandte Chemie - International Edition</i> , 2012 , 51, 4628-32	16.4	8
81	Sequence-specific capture of protein-DNA complexes for mass spectrometric protein identification. <i>PLoS ONE</i> , 2011 , 6, e26217	3.7	24
80	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
79	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
78	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
77	Alkylating tryptic peptides to enhance electrospray ionization mass spectrometry analysis. <i>Analytical Chemistry</i> , 2010 , 82, 10135-42	7.8	40
76	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
75	Controlling oligonucleotide surface density in light-directed DNA array fabrication. <i>Langmuir</i> , 2009 , 25, 6570-5	4	19
74	Fabrication and characterization of DNA arrays prepared on carbon-on-metal substrates. <i>Analytical Chemistry</i> , 2009 , 81, 6429-37	7.8	23
73	A tetrafluorophenyl activated ester self-assembled monolayer for the immobilization of amine-modified oligonucleotides. <i>Langmuir</i> , 2008 , 24, 69-75	4	55
72	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
71	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
70	Aldehyde-terminated amorphous carbon substrates for the fabrication of biomolecule arrays. <i>Langmuir</i> , 2008 , 24, 9198-203	4	15
69	Is charge reduction in ESI really necessary?. <i>Journal of the American Society for Mass Spectrometry</i> , 2008 , 19, 629-31	3.5	14
68	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

67	In situ oligonucleotide synthesis on carbon materials: stable substrates for microarray fabrication. <i>Nucleic Acids Research</i> , 2008 , 36, e7	20.1	30
66	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
65	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
64	Lectin-modified microchannels for mammalian cell capture and purification. <i>Biomedical Microdevices</i> , 2007 , 9, 611-7	3.7	14
63	Subthreshold field emission from thin silicon membranes. <i>Applied Physics Letters</i> , 2007 , 91, 183506	3.4	6
62	Covalent photochemical functionalization of amorphous carbon thin films for integrated real-time biosensing. <i>Langmuir</i> , 2006 , 22, 9598-605	4	90
61	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
60	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
59	Lectin arrays for profiling cell surface carbohydrate expression. <i>Journal of the American Chemical Society</i> , 2005 , 127, 9982-3	16.4	176
58	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
57	Immobilization of amine-modified oligonucleotides on aldehyde-terminated alkanethiol monolayers on gold. <i>Langmuir</i> , 2005 , 21, 266-71	4	101
56	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
55	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
54	Invasive cleavage reactions on DNA-modified diamond surfaces. <i>Biopolymers</i> , 2004 , 73, 606-13	2.2	50
53	DNA-Modified Diamond Surfaces. <i>Langmuir</i> , 2003 , 19, 1938-1942	4	130
52	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
51	A surface invasive cleavage assay for highly parallel SNP analysis. <i>Human Mutation</i> , 2002 , 19, 416-22	4.7	10
50	Collision cross sections of gas phase DNA ions. <i>International Journal of Mass Spectrometry</i> , 2002 , 219, 161-170	1.9	6

49	DNA-modified nanocrystalline diamond thin-films as stable, biologically active substrates. <i>Nature Materials</i> , 2002 , 1, 253-7	27	744
48	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
47	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		
46	DNA Attachment and Hybridization at the Silicon (100) Surface. <i>Langmuir</i> , 2002 , 18, 788-796	4	177
45	Structure-specific DNA cleavage on surfaces. <i>Journal of the American Chemical Society</i> , 2002 , 124, 7924-316.4	28	
44	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
43	Preparation and Electrochemical Characterization of DNA-modified Nanocrystalline Diamond Films. <i>Materials Research Society Symposia Proceedings</i> , 2002 , 737, 569		1
42	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
41	A DNA computing readout operation based on structure-specific cleavage. <i>Nature Biotechnology</i> , 2001 , 19, 1053-9	44.5	27
40	Analysis of single nucleotide polymorphisms with solid phase invasive cleavage reactions. <i>Nucleic Acids Research</i> , 2001 , 29, E77	20.1	26
39	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
38	DNA computing on surfaces. <i>Nature</i> , 2000 , 403, 175-9	50.4	300
37	Synthesis and Characterization of DNA-Modified Silicon (111) Surfaces. <i>Journal of the American Chemical Society</i> , 2000 , 122, 1205-1209	16.4	409
36	Covalent attachment of oligodeoxyribonucleotides to amine-modified Si (001) surfaces. <i>Nucleic Acids Research</i> , 2000 , 28, 3535-41	20.1	248
35	Charge reduction electrospray mass spectrometry. <i>Analytical Chemistry</i> , 2000 , 72, 52-60	7.8	124
34	Corona discharge in charge reduction electrospray mass spectrometry. <i>Analytical Chemistry</i> , 2000 , 72, 5158-61	7.8	100
33	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
32	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

31	Controlling charge states of large ions. <i>Science</i> , 1999 , 283, 194-7	33.3	146
30	A surface-based approach to DNA computation. <i>Journal of Computational Biology</i> , 1998 , 5, 255-67	1.7	54
29	DNA computing on surfaces: encoding information at the single base level. <i>Journal of Computational Biology</i> , 1998 , 5, 269-78	1.7	11
28	A software system for data analysis in automated DNA sequencing. <i>Genome Research</i> , 1998 , 8, 644-65	9.7	49
27	A surface-based approach to DNA computation. <i>DIMACS Series in Discrete Mathematics and Theoretical Computer Science</i> , 1998 , 123-132		4
26	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
25	Controlling DNA Fragmentation in MALDI-MS by Chemical Modification. <i>Analytical Chemistry</i> , 1997 , 69, 302-12	7.8	65
24	Enhanced discrimination of single nucleotide polymorphisms by artificial mismatch hybridization. <i>Nature Biotechnology</i> , 1997 , 15, 331-5	44.5	118
23	Genetic analysis by peptide nucleic acid affinity MALDI-TOF mass spectrometry. <i>Nature Biotechnology</i> , 1997 , 15, 1368-72	44.5	103
22	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
21	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
20	Automatic matrix determination in four dye fluorescence-based DNA sequencing. <i>Electrophoresis</i> , 1996 , 17, 1143-50	3.6	20
19	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
18	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
17	Separating field strength, temperature, and pulsing effects in pulsed field electrophoresis. <i>Electrophoresis</i> , 1994 , 15, 1084-90	3.6	10
16	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
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	Solid phase purification in automated DNA sequencing. <i>DNA Sequence</i> , 1993 , 4, 151-62		8

13	An adaptive, object oriented strategy for base calling in DNA sequence analysis. <i>Nucleic Acids Research</i> , 1993 , 21, 4530-40	20.1	40
12	A model for the mobility of single-stranded DNA in capillary gel electrophoresis. <i>Electrophoresis</i> , 1993 , 14, 492-501	3.6	41
11	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
10	High speed automated DNA sequencing in ultrathin slab gels. <i>Nature Biotechnology</i> , 1992 , 10, 78-81	44.5	32
9	Matrix-assisted laser desorption/ionization mass spectrometry of synthetic oligodeoxyribonucleotides. <i>Rapid Communications in Mass Spectrometry</i> , 1992 , 6, 369-372	2.2	61
8	Rapid DNA sequencing by horizontal ultrathin gel electrophoresis. <i>Nucleic Acids Research</i> , 1991 , 19, 4121-4126	16.1	68
7	A universal method for the direct cloning of PCR amplified nucleic acid. <i>Nature Biotechnology</i> , 1991 , 9, 657-63	44.5	143
6	The synthesis and use of fluorescent oligonucleotides in DNA sequence analysis. <i>Methods in Enzymology</i> , 1987 , 155, 260-301	1.7	42
5	Mapping and Sequencing the Human Genome: How to Proceed. <i>Nature Biotechnology</i> , 1987 , 5, 933-939	44.5	12
4	Fluorescence detection in automated DNA sequence analysis. <i>Nature</i> , 1986 , 321, 674-9	50.4	1309
3	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
2	The Human Proteoform Project: A Plan to Define the Human Proteome		7
1	Spritz: A Proteogenomic Database Engine		6