

Forest M White

List of Publications by Year in descending order

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135
papers

12,257
citations

43973

48
h-index

29081

104
g-index

146
all docs

146
docs citations

146
times ranked

15983
citing authors

#	ARTICLE	IF	CITATIONS
1	Multimodal platform for assessing drug distribution and response in clinical trials. <i>Neuro-Oncology</i> , 2022, 24, 64-77.	0.6	4
2	Deciphering the immunopeptidome in vivo reveals new tumour antigens. <i>Nature</i> , 2022, 607, 149-155.	13.7	38
3	Quantitative Consequences of Protein Carriers in Immunopeptidomics and Tyrosine Phosphorylation MS2 Analyses. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100104.	2.5	23
4	High-Density, Targeted Monitoring of Tyrosine Phosphorylation Reveals Activated Signaling Networks in Human Tumors. <i>Cancer Research</i> , 2021, 81, 2495-2509.	0.4	41
5	Excision of mutagenic replication-blocking lesions suppresses cancer but promotes cytotoxicity and lethality in nitrosamine-exposed mice. <i>Cell Reports</i> , 2021, 34, 108864.	2.9	16
6	Quantitative Analysis of Tyrosine Phosphorylation from FFPE Tissues Reveals Patient-Specific Signaling Networks. <i>Cancer Research</i> , 2021, 81, 3930-3941.	0.4	16
7	Heterogeneous delivery across the blood-brain barrier limits the efficacy of an EGFR-targeting antibody drug conjugate in glioblastoma. <i>Neuro-Oncology</i> , 2021, 23, 2042-2053.	0.6	37
8	Quantitative phosphoproteomics uncovers dysregulated kinase networks in Alzheimer's disease. <i>Nature Aging</i> , 2021, 1, 550-565.	5.3	21
9	Leveraging Immunopeptidomics To Study and Combat Infectious Disease. <i>MSystems</i> , 2021, 6, e0031021.	1.7	3
10	Absolute quantification of tumor antigens using embedded MHC-I isotopologue calibrants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	25
11	Phosphoproteomics: a valuable tool for uncovering molecular signaling in cancer cells. <i>Expert Review of Proteomics</i> , 2021, 18, 661-674.	1.3	15
12	Global Cancer Risk From Unregulated Polycyclic Aromatic Hydrocarbons. <i>GeoHealth</i> , 2021, 5, e2021GH000401.	1.9	21
13	Peak learning of mass spectrometry imaging data using artificial neural networks. <i>Nature Communications</i> , 2021, 12, 5544.	5.8	43
14	1,2,3, MHC: a review of mass spectrometry-based immunopeptidomics methods for relative and absolute quantification of pMHCs. <i>Immuno-Oncology Technology</i> , 2021, , 100042.	0.2	7
15	Platform for micro-invasive membrane-free biochemical sampling of brain interstitial fluid. <i>Science Advances</i> , 2020, 6, .	4.7	11
16	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. <i>Cell</i> , 2020, 183, 1436-1456.e31.	13.5	273
17	Multiplexed relative and absolute quantitative immunopeptidomics reveals MHC I repertoire alterations induced by CDK4/6 inhibition. <i>Nature Communications</i> , 2020, 11, 2760.	5.8	61
18	Localized Metabolomic Gradients in Patient-Derived Xenograft Models of Glioblastoma. <i>Cancer Research</i> , 2020, 80, 1258-1267.	0.4	67

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19	Phosphoproteomics identifies microglial Siglec ϵ inflammatory response during neurodegeneration. <i>Molecular Systems Biology</i> , 2020, 16, e9819.	3.2	20
20	Light-regulated allosteric switch enables temporal and subcellular control of enzyme activity. <i>ELife</i> , 2020, 9, .	2.8	32
21	High-fat diet in a mouse insulin-resistant model induces widespread rewiring of the phosphotyrosine signaling network. <i>Molecular Systems Biology</i> , 2019, 15, e8849.	3.2	30
22	Systemic analysis of tyrosine kinase signaling reveals a common adaptive response program in a HER2-positive breast cancer. <i>Science Signaling</i> , 2019, 12, .	1.6	26
23	The Physics of Cancer. <i>Cancer Research</i> , 2019, 79, 2107-2110.	0.4	22
24	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. <i>Cell</i> , 2019, 177, 1035-1049.e19.	13.5	498
25	Exploration of CTCF post-translation modifications uncovers Serine-224 phosphorylation by PLK1 at pericentric regions during the G2/M transition. <i>ELife</i> , 2019, 8, .	2.8	18
26	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018, 14, 206-214.	3.9	580
27	A thermodynamic-based approach for the resolution and prediction of protein network structures. <i>Chemical Physics</i> , 2018, 514, 20-30.	0.9	9
28	Src homology 2 domains enhance tyrosine phosphorylation in vivo by protecting binding sites in their target proteins from dephosphorylation. <i>Journal of Biological Chemistry</i> , 2018, 293, 623-637.	1.6	23
29	Identifying and Targeting Sporadic Oncogenic Genetic Aberrations in Mouse Models of Triple-Negative Breast Cancer. <i>Cancer Discovery</i> , 2018, 8, 354-369.	7.7	62
30	Integrated mapping of pharmacokinetics and pharmacodynamics in a patient-derived xenograft model of glioblastoma. <i>Nature Communications</i> , 2018, 9, 4904.	5.8	62
31	A Proteomics Approach to Profiling the Temporal Translational Response to Stress and Growth. <i>IScience</i> , 2018, 9, 367-381.	1.9	39
32	Microtubule-Based Control of Motor-Clutch System Mechanics in Glioma Cell Migration. <i>Cell Reports</i> , 2018, 25, 2591-2604.e8.	2.9	37
33	Quantitative Analysis of Tyrosine Kinase Signaling Across Differentially Embedded Human Glioblastoma Tumors. <i>Methods in Molecular Biology</i> , 2018, 1711, 149-164.	0.4	1
34	Characterization of <i>In Vivo</i> Resistance to Osimertinib and JNJ-61186372, an EGFR/Met Bispecific Antibody, Reveals Unique and Consensus Mechanisms of Resistance. <i>Molecular Cancer Therapeutics</i> , 2017, 16, 2572-2585.	1.9	26
35	Hepatic Dysfunction Caused by Consumption of a High-Fat Diet. <i>Cell Reports</i> , 2017, 21, 3317-3328.	2.9	68
36	Camptothecin resistance is determined by the regulation of topoisomerase I degradation mediated by ubiquitin proteasome pathway. <i>Oncotarget</i> , 2017, 8, 43733-43751.	0.8	20

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37	Quantitative Phosphoproteomics Reveals Wee1 Kinase as a Therapeutic Target in a Model of Proneural Glioblastoma. <i>Molecular Cancer Therapeutics</i> , 2016, 15, 1332-1343.	1.9	14
38	Methods for the Analysis of Protein Phosphorylation-Mediated Cellular Signaling Networks. <i>Annual Review of Analytical Chemistry</i> , 2016, 9, 295-315.	2.8	27
39	Revealing disease-associated pathways by network integration of untargeted metabolomics. <i>Nature Methods</i> , 2016, 13, 770-776.	9.0	145
40	Network Modeling Identifies Patient-specific Pathways in Glioblastoma. <i>Scientific Reports</i> , 2016, 6, 28668.	1.6	25
41	A Thermodynamic-Based Interpretation of Protein Expression Heterogeneity in Different Glioblastoma Multiforme Tumors Identifies Tumor-Specific Unbalanced Processes. <i>Journal of Physical Chemistry B</i> , 2016, 120, 5990-5997.	1.2	11
42	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. <i>Cell</i> , 2016, 166, 755-765.	13.5	804
43	Quantitative Phosphoproteomics Reveals Wee1 Kinase as a Therapeutic Target in a Model of Proneural Glioblastoma. <i>Molecular Cancer Therapeutics</i> , 2016, 15, 1332-1343.	1.9	34
44	Early signaling dynamics of the epidermal growth factor receptor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 3114-3119.	3.3	64
45	Identification of Direct Kinase Substrates Using Analogue-Sensitive Alleles. <i>Methods in Molecular Biology</i> , 2016, 1355, 71-84.	0.4	8
46	Measurement of Phosphorylated Peptides with Absolute Quantification. <i>Methods in Molecular Biology</i> , 2016, 1410, 281-292.	0.4	3
47	Time-resolved multimodal analysis of Src Homology 2 (SH2) domain binding in signaling by receptor tyrosine kinases. <i>ELife</i> , 2016, 5, e11835.	2.8	20
48	Minor Changes in Expression of the Mismatch Repair Protein MSH2 Exert a Major Impact on Glioblastoma Response to Temozolomide. <i>Cancer Research</i> , 2015, 75, 3127-3138.	0.4	96
49	MARQUIS: A multiplex method for absolute quantification of peptides and posttranslational modifications. <i>Nature Communications</i> , 2015, 6, 5924.	5.8	39
50	Engineered bromodomains to explore the acetylproteome. <i>Proteomics</i> , 2015, 15, 1470-1475.	1.3	10
51	Phosphotyrosine Signaling Analysis in Human Tumors Is Confounded by Systemic Ischemia-Driven Artifacts and Intra-Specimen Heterogeneity. <i>Cancer Research</i> , 2015, 75, 1495-1503.	0.4	42
52	Quantitative Profiling of Lysine Acetylation Reveals Dynamic Crosstalk between Receptor Tyrosine Kinases and Lysine Acetylation. <i>PLoS ONE</i> , 2015, 10, e0126242.	1.1	14
53	System level dynamics of post-translational modifications. <i>Current Opinion in Biotechnology</i> , 2014, 28, 83-87.	3.3	22
54	Adaptive protein and phosphoprotein networks which promote therapeutic sensitivity or acquired resistance. <i>Biochemical Society Transactions</i> , 2014, 42, 758-764.	1.6	5

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55	Quantitative Analysis of Signaling Networks across Differentially Embedded Tumors Highlights Interpatient Heterogeneity in Human Glioblastoma. <i>Journal of Proteome Research</i> , 2014, 13, 4581-4593.	1.8	32
56	SirT1 is required in the male germ cell for differentiation and fecundity in mice. <i>Development (Cambridge)</i> , 2014, 141, 3495-3504.	1.2	79
57	Qualitatively Different T Cell Phenotypic Responses to IL-2 versus IL-15 Are Unified by Identical Dependences on Receptor Signal Strength and Duration. <i>Journal of Immunology</i> , 2014, 192, 123-135.	0.4	45
58	Computer aided manual validation of mass spectrometry-based proteomic data. <i>Methods</i> , 2013, 61, 219-226.	1.9	30
59	Phosphotyrosine Profiling of NSCLC Cells in Response to EGF and HGF Reveals Network Specific Mediators of Invasion. <i>Journal of Proteome Research</i> , 2013, 12, 1856-1867.	1.8	26
60	The bromodomain protein Brd4 insulates chromatin from DNA damage signalling. <i>Nature</i> , 2013, 498, 246-250.	13.7	278
61	Molecular network analysis of phosphotyrosine and lipid metabolism in hepatic PTP1b deletion mice. <i>Integrative Biology (United Kingdom)</i> , 2013, 5, 940.	0.6	19
62	A developmentally regulated translational control pathway establishes the meiotic chromosome segregation pattern. <i>Genes and Development</i> , 2013, 27, 2147-2163.	2.7	90
63	Vascular Endothelial Growth Factor (VEGF) and Platelet (PF-4) Factor 4 Inputs Modulate Human Microvascular Endothelial Signaling in a Three-Dimensional Matrix Migration Context. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3704-3718.	2.5	9
64	Labeling and Identification of Direct Kinase Substrates. <i>Science Signaling</i> , 2012, 5, pl3.	1.6	11
65	Epidermal growth factor receptor downregulation by small heterodimeric binding proteins. <i>Protein Engineering, Design and Selection</i> , 2012, 25, 47-57.	1.0	25
66	Expanding applications of chemical genetics in signal transduction. <i>Cell Cycle</i> , 2012, 11, 1903-1909.	1.3	5
67	Signaling for death: tyrosine phosphorylation in the response to glucose deprivation. <i>Molecular Systems Biology</i> , 2012, 8, 591.	3.2	4
68	Molecular Characterization of EGFR and EGFRvIII Signaling Networks in Human Glioblastoma Tumor Xenografts. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1724-1740.	2.5	79
69	Toward quantitative phosphotyrosine profiling in vivo. <i>Seminars in Cell and Developmental Biology</i> , 2012, 23, 854-862.	2.3	29
70	Systems-pharmacology dissection of a drug synergy in imatinib-resistant CML. <i>Nature Chemical Biology</i> , 2012, 8, 905-912.	3.9	96
71	Robust co-regulation of tyrosine phosphorylation sites on proteins reveals novel protein interactions. <i>Molecular BioSystems</i> , 2012, 8, 2771.	2.9	19
72	Reply to Comment on "Sloppy models, parameter uncertainty, and the role of experimental design". <i>Molecular BioSystems</i> , 2011, 7, 2523.	2.9	6

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73	Using Small Molecules and Chemical Genetics To Interrogate Signaling Networks. ACS Chemical Biology, 2011, 6, 75-85.	1.6	20
74	Large-Scale Discovery of ERK2 Substrates Identifies ERK-Mediated Transcriptional Regulation by ETV3. Science Signaling, 2011, 4, rs11.	1.6	125
75	The Potential Cost of High-Throughput Proteomics. Science Signaling, 2011, 4, pe8.	1.6	39
76	CUB-domain-containing protein 1 (CDCP1) activates Src to promote melanoma metastasis. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 1379-1384.	3.3	84
77	MCAM: Multiple Clustering Analysis Methodology for Deriving Hypotheses and Insights from High-Throughput Proteomic Datasets. PLoS Computational Biology, 2011, 7, e1002119.	1.5	28
78	Cancer Signaling Network Analysis by Quantitative Mass Spectrometry. , 2011, , 55-75.		0
79	Integrated data management and validation platform for phosphorylated tandem mass spectrometry data. Proteomics, 2010, 10, 3515-3524.	1.3	7
80	PTMScout, a Web Resource for Analysis of High Throughput Post-translational Proteomics Studies. Molecular and Cellular Proteomics, 2010, 9, 2558-2570.	2.5	39
81	Combination antibody treatment down-regulates epidermal growth factor receptor by inhibiting endosomal recycling. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 13252-13257.	3.3	135
82	Quantitative Phosphoproteomic Analysis of T Cell Receptor Signaling in Diabetes Prone and Resistant Mice. Journal of Proteome Research, 2010, 9, 3135-3145.	1.8	44
83	Quantifying oncogenic phosphotyrosine signaling networks through systems biology. Current Opinion in Genetics and Development, 2010, 20, 23-30.	1.5	31
84	Phosphotyrosine signaling analysis of site-specific mutations on EGFRvIII identifies determinants governing glioblastoma cell growth. Molecular BioSystems, 2010, 6, 1227.	2.9	40
85	Sloppy models, parameter uncertainty, and the role of experimental design. Molecular BioSystems, 2010, 6, 1890.	2.9	114
86	Biological Insights From Quantitative Analysis of Tyrosine Kinase Signaling Networks. FASEB Journal, 2010, 24, 306.2.	0.2	0
87	Mcl-1 Integrates the Opposing Actions of Signaling Pathways That Mediate Survival and Apoptosis. Molecular and Cellular Biology, 2009, 29, 3845-3852.	1.1	119
88	Mechanical Injury and Cytokines Cause Loss of Cartilage Integrity and Upregulate Proteins Associated with Catabolism, Immunity, Inflammation, and Repair. Molecular and Cellular Proteomics, 2009, 8, 1475-1489.	2.5	90
89	Oncogenic EGFR Signaling Networks in Glioma. Science Signaling, 2009, 2, re6.	1.6	299
90	An integrated comparative phosphoproteomic and bioinformatic approach reveals a novel class of MPM-2 motifs upregulated in EGFRvIII-expressing glioblastoma cells. Molecular BioSystems, 2009, 5, 59-67.	2.9	27

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91	Manual Validation of Peptide Sequence and Sites of Tyrosine Phosphorylation from MS/MS Spectra. <i>Methods in Molecular Biology</i> , 2009, 492, 143-160.	0.4	44
92	Combinatorial Therapeutic Strategies for Blocking Kinase Pathways in Brain Tumors. , 2009, , 953-975.		1
93	Quantitative phosphoproteomics by mass spectrometry: Past, present, and future. <i>Proteomics</i> , 2008, 8, 4433-4443.	1.3	151
94	Quantitative phosphoproteomic analysis of signaling network dynamics. <i>Current Opinion in Biotechnology</i> , 2008, 19, 404-409.	3.3	49
95	Phosphoproteomics: Unraveling the Signaling Web. <i>Molecular Cell</i> , 2008, 31, 777-781.	4.5	50
96	Illuminating signaling network functional biology through quantitative phosphoproteomic mass spectrometry. <i>Briefings in Functional Genomics & Proteomics</i> , 2008, 7, 383-394.	3.8	4
97	Stimulus Design for Model Selection and Validation in Cell Signaling. <i>PLoS Computational Biology</i> , 2008, 4, e30.	1.5	71
98	Uncovering Therapeutic Targets FOR Glioblastoma: A Systems Biology Approach. <i>Cell Cycle</i> , 2007, 6, 2750-2754.	1.3	63
99	Modeling HER2 Effects on Cell Behavior from Mass Spectrometry Phosphotyrosine Data. <i>PLoS Computational Biology</i> , 2007, 3, e4.	1.5	92
100	Multiple reaction monitoring for robust quantitative proteomic analysis of cellular signaling networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 5860-5865.	3.3	472
101	Signaling netwErks get the global treatment. <i>Genome Biology</i> , 2007, 8, 202.	3.8	12
102	Quantitative analysis of EGFRvIII cellular signaling networks reveals a combinatorial therapeutic strategy for glioblastoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 12867-12872.	3.3	365
103	On the iTRAQ of kinase inhibitors. <i>Nature Biotechnology</i> , 2007, 25, 994-996.	9.4	4
104	14-3-3 β controls mitotic translation to facilitate cytokinesis. <i>Nature</i> , 2007, 446, 329-332.	13.7	217
105	Quantitative Proteomic Analysis of Phosphotyrosine-Mediated Cellular Signaling Networks. <i>Methods in Molecular Biology</i> , 2007, 359, 203-212.	0.4	25
106	Regulation and Specificity of S-Nitrosylation and Denitrosylation. <i>ACS Chemical Biology</i> , 2006, 1, 615-618.	1.6	57
107	Phosphoproteomic Analysis of Rat Liver by High Capacity IMAC and LC-MS/MS. <i>Journal of Proteome Research</i> , 2006, 5, 98-104.	1.8	150
108	Collecting and organizing systematic sets of protein data. <i>Nature Reviews Molecular Cell Biology</i> , 2006, 7, 803-812.	16.1	98

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109	Phosphoproteomic approaches to elucidate cellular signaling networks. <i>Current Opinion in Biotechnology</i> , 2006, 17, 406-414.	3.3	144
110	Cell system perturbation for time-resolved quantification of tyrosine phosphorylation in complex samples. , 2006, 2006, 51-2.		0
111	Effects of HER2 overexpression on cell signaling networks governing proliferation and migration. <i>Molecular Systems Biology</i> , 2006, 2, 54.	3.2	217
112	Quantitative Analysis of Phosphotyrosine Signaling Networks Triggered by CD3 and CD28 Costimulation in Jurkat Cells. <i>Journal of Immunology</i> , 2006, 176, 2833-2843.	0.4	103
113	Temporal Dynamics of Tyrosine Phosphorylation in Insulin Signaling. <i>Diabetes</i> , 2006, 55, 2171-2179.	0.3	153
114	Quantification of isomers from a mixture of twelve heparin and heparan sulfate disaccharides using tandem mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2005, 19, 2553-2562.	0.7	39
115	Time-resolved Mass Spectrometry of Tyrosine Phosphorylation Sites in the Epidermal Growth Factor Receptor Signaling Network Reveals Dynamic Modules. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1240-1250.	2.5	494
116	Global Phosphoproteome of HT-29 Human Colon Adenocarcinoma Cells. <i>Journal of Proteome Research</i> , 2005, 4, 1339-1346.	1.8	107
117	Proteomic analysis of cellular signaling. <i>Expert Review of Proteomics</i> , 2004, 1, 343-354.	1.3	27
118	Weak agonist self-peptides promote selection and tuning of virus-specific T cells. <i>European Journal of Immunology</i> , 2003, 33, 685-696.	1.6	19
119	Analysis of MHC Class II Antigen Processing by Quantitation of Peptides that Constitute Nested Sets. <i>Journal of Immunology</i> , 2002, 169, 5089-5097.	0.4	88
120	Androgen Receptor Phosphorylation. <i>Journal of Biological Chemistry</i> , 2002, 277, 29304-29314.	1.6	299
121	Identification by Mass Spectrometry of CD8+-T-Cell Mycobacterium tuberculosis Epitopes within the Rv0341 Gene Product. <i>Infection and Immunity</i> , 2002, 70, 2926-2932.	1.0	43
122	Phosphoproteome analysis by mass spectrometry and its application to <i>Saccharomyces cerevisiae</i> . <i>Nature Biotechnology</i> , 2002, 20, 301-305.	9.4	1,725
123	Characterization and evolutionary relevance of the sperm nuclear basic proteins from stickleback fish. <i>Molecular Reproduction and Development</i> , 2000, 57, 185-193.	1.0	12
124	Phosphorylated Peptides Are Naturally Processed and Presented by Major Histocompatibility Complex Class I Molecules in Vivo. <i>Journal of Experimental Medicine</i> , 2000, 192, 1755-1762.	4.2	192
125	Matrix-shimmed ion cyclotron resonance ion trap simultaneously optimized for excitation, detection, quadrupolar axialization, and trapping. <i>Journal of the American Society for Mass Spectrometry</i> , 1999, 10, 759-769.	1.2	25
126	Application of micro-electrospray liquid chromatography techniques to FT-ICR MS to enable high-sensitivity biological analysis. <i>Journal of the American Society for Mass Spectrometry</i> , 1998, 9, 333-340.	1.2	187

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127	Resolution, Elemental Composition, and Simultaneous Monitoring by Fourier Transform Ion Cyclotron Resonance Mass Spectrometry of Organosulfur Species before and after Diesel Fuel Processing. <i>Analytical Chemistry</i> , 1998, 70, 4743-4750.	3.2	87
128	High-Resolution Inductively Coupled Plasma Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. <i>Analytical Chemistry</i> , 1997, 69, 3714-3721.	3.2	51
129	Gas-Phase Dehydrogenation of Saturated and Aromatic Cyclic Hydrocarbons by Pt ⁿ⁺ (n= 1-4). <i>Journal of the American Chemical Society</i> , 1997, 119, 7567-7572.	6.6	32
130	Electrospray Ionization Fourier Transform Ion Cyclotron Resonance at 9.4 T. , 1996, 10, 1824-1828.		200
131	An External Source 7 T Fourier Transform Ion Cyclotron Resonance Mass Spectrometer with Electrostatic Ion Guide. , 1996, 10, 1845-1849.		17
132	Electrospray Ionization Fourier Transform Ion Cyclotron Resonance at 9.4 T. , 1996, 10, 1824.		4
133	Attomole Biomolecule Mass Analysis by Matrix-Assisted Laser Desorption/Ionization Fourier Transform Ion Cyclotron Resonance. <i>Analytical Chemistry</i> , 1995, 67, 4139-4144.	3.2	84
134	Structural Characterization of Phospholipids by Matrix-Assisted Laser Desorption/Ionization Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. <i>Analytical Chemistry</i> , 1995, 67, 3979-3984.	3.2	132
135	Quantitative Proteomic Analysis of Phosphotyrosine-Mediated Cellular Signaling Networks. , 0, , 203-212.		0