Forest M White

List of Publications by Year
in descending order

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	Phosphoproteome analysis by mass spectrometry and its application to Saccharomyces cerevisiae. Nature Biotechnology, 2002, 20, 301-305.	9.4	1,725
2	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. Cell, 2016, 166, 755-765.	13.5	804
3	How many human proteoforms are there?. Nature Chemical Biology, 2018, 14, 206-214.	3.9	580
4	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. Cell, 2019, 177, 1035-1049.e19.	13.5	498
5	Time-resolved Mass Spectrometry of Tyrosine Phosphorylation Sites in the Epidermal Growth Factor Receptor Signaling Network Reveals Dynamic Modules. Molecular and Cellular Proteomics, 2005, 4, 1240-1250.	2.5	494
6	Multiple reaction monitoring for robust quantitative proteomic analysis of cellular signaling networks. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 5860-5865.	3.3	472
7	Quantitative analysis of EGFRvIII cellular signaling networks reveals a combinatorial therapeutic strategy for glioblastoma. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 12867-12872.	3.3	365
8	Androgen Receptor Phosphorylation. Journal of Biological Chemistry, 2002, 277, 29304-29314.	1.6	299
9	Oncogenic EGFR Signaling Networks in Glioma. Science Signaling, 2009, 2, re6.	1.6	299
10	The bromodomain protein Brd4 insulates chromatin from DNA damage signalling. Nature, 2013, 498, 246-250.	13.7	278
11	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. Cell, 2020, 183, 1436-1456.e31.	13.5	273
12	Effects of HER2 overexpression on cell signaling networks governing proliferation and migration. Molecular Systems Biology, 2006, 2, 54.	3.2	217
13	14-3-3ζ controls mitotic translation to facilitate cytokinesis. Nature, 2007, 446, 329-332.	13.7	217
14	Electrospray Ionization Fourier Transform Ion Cyclotron Resonance at 9.4 T. , 1996, 10, 1824-1828.		200
15	Phosphorylated Peptides Are Naturally Processed and Presented by Major Histocompatibility Complex Class I Molecules in Vivo. Journal of Experimental Medicine, 2000, 192, 1755-1762.	4.2	192
16	Application of micro-electrospray liquid chromatography techniques to FT-ICR MS to enable high-sensitivity biological analysis. Journal of the American Society for Mass Spectrometry, 1998, 9, 333-340.	1.2	187
17	Temporal Dynamics of Tyrosine Phosphorylation in Insulin Signaling. Diabetes, 2006, 55, 2171-2179.	0.3	153
18	Quantitative phosphoproteomics by mass spectrometry: Past, present, and future. Proteomics, 2008, 8, 4433-4443.	1.3	151

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19	Phosphoproteomic Analysis of Rat Liver by High Capacity IMAC and LCˆMS/MS. Journal of Proteome Research, 2006, 5, 98-104.	1.8	150
20	Revealing disease-associated pathways by network integration of untargeted metabolomics. Nature Methods, 2016, 13, 770-776.	9.0	145
21	Phosphoproteomic approaches to elucidate cellular signaling networks. Current Opinion in Biotechnology, 2006, 17, 406-414.	3.3	144
22	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
23	Structural Characterization of Phospholipids by Matrix-Assisted Laser Desorption/Ionization Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. Analytical Chemistry, 1995, 67, 3979-3984.	3.2	132
24	Large-Scale Discovery of ERK2 Substrates Identifies ERK-Mediated Transcriptional Regulation by ETV3. Science Signaling, 2011, 4, rs11.	1.6	125
25	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
26	Sloppy models, parameter uncertainty, and the role of experimental design. Molecular BioSystems, 2010, 6, 1890.	2.9	114
27	Global Phosphoproteome of HT-29 Human Colon Adenocarcinoma Cells. Journal of Proteome Research, 2005, 4, 1339-1346.	1.8	107
28	Quantitative Analysis of Phosphotyrosine Signaling Networks Triggered by CD3 and CD28 Costimulation in Jurkat Cells. Journal of Immunology, 2006, 176, 2833-2843.	0.4	103
29	Collecting and organizing systematic sets of protein data. Nature Reviews Molecular Cell Biology, 2006, 7, 803-812.	16.1	98
30	Systems-pharmacology dissection of a drug synergy in imatinib-resistant CML. Nature Chemical Biology, 2012, 8, 905-912.	3.9	96
31	Minor Changes in Expression of the Mismatch Repair Protein MSH2 Exert a Major Impact on Glioblastoma Response to Temozolomide. Cancer Research, 2015, 75, 3127-3138.	0.4	96
32	Modeling HER2 Effects on Cell Behavior from Mass Spectrometry Phosphotyrosine Data. PLoS Computational Biology, 2007, 3, e4.	1.5	92
33	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
34	A developmentally regulated translational control pathway establishes the meiotic chromosome segregation pattern. Genes and Development, 2013, 27, 2147-2163.	2.7	90
35	Analysis of MHC Class II Antigen Processing by Quantitation of Peptides that Constitute Nested Sets. Journal of Immunology, 2002, 169, 5089-5097.	0.4	88
36	Resolution, Elemental Composition, and Simultaneous Monitoring by Fourier Transform Ion Cyclotron Resonance Mass Spectrometry of Organosulfur Species before and after Diesel Fuel Processing. Analytical Chemistry, 1998, 70, 4743-4750.	3.2	87

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37	Attomole Biomolecule Mass Analysis by Matrix-Assisted Laser Desorption/Ionization Fourier Transform Ion Cyclotron Resonance. Analytical Chemistry, 1995, 67, 4139-4144.	3.2	84
38	CUB-domainâ€"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
39	Molecular Characterization of EGFR and EGFRvIII Signaling Networks in Human Glioblastoma Tumor Xenografts. Molecular and Cellular Proteomics, 2012, 11, 1724-1740.	2.5	79
40	SirT1 is required in the male germ cell for differentiation and fecundity in mice. Development (Cambridge), 2014, 141, 3495-3504.	1.2	79
41	Stimulus Design for Model Selection and Validation in Cell Signaling. PLoS Computational Biology, 2008, 4, e30.	1.5	71
42	Hepatic Dysfunction Caused by Consumption of a High-Fat Diet. Cell Reports, 2017, 21, 3317-3328.	2.9	68
43	Localized Metabolomic Gradients in Patient-Derived Xenograft Models of Glioblastoma. Cancer Research, 2020, 80, 1258-1267.	0.4	67
44	Early signaling dynamics of the epidermal growth factor receptor. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 3114-3119.	3.3	64
45	Uncovering Therapeutic Targets FOR Glioblastoma: A Systems Biology Approach. Cell Cycle, 2007, 6, 2750-2754.	1.3	63
46	Identifying and Targeting Sporadic Oncogenic Genetic Aberrations in Mouse Models of Triple-Negative Breast Cancer. Cancer Discovery, 2018, 8, 354-369.	7.7	62
47	Integrated mapping of pharmacokinetics and pharmacodynamics in a patient-derived xenograft model of glioblastoma. Nature Communications, 2018, 9, 4904.	5.8	62
48	Multiplexed relative and absolute quantitative immunopeptidomics reveals MHC I repertoire alterations induced by CDK4/6 inhibition. Nature Communications, 2020, 11, 2760.	5.8	61
49	Regulation and Specificity of S-Nitrosylation and Denitrosylation. ACS Chemical Biology, 2006, 1, 615-618.	1.6	57
50	High-Resolution Inductively Coupled Plasma Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. Analytical Chemistry, 1997, 69, 3714-3721.	3.2	51
51	Phosphoproteomics: Unraveling the Signaling Web. Molecular Cell, 2008, 31, 777-781.	4.5	50
52	Quantitative phosphoproteomic analysis of signaling network dynamics. Current Opinion in Biotechnology, 2008, 19, 404-409.	3.3	49
53	Qualitatively Different T Cell Phenotypic Responses to IL-2 versus IL-15 Are Unified by Identical Dependences on Receptor Signal Strength and Duration. Journal of Immunology, 2014, 192, 123-135.	0.4	45
54	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

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55	Manual Validation of Peptide Sequence and Sites of Tyrosine Phosphorylation from MS/MS Spectra. Methods in Molecular Biology, 2009, 492, 143-160.	0.4	44
56	Identification by Mass Spectrometry of CD8+-T-Cell Mycobacterium tuberculosis Epitopes within the Rv0341 Gene Product. Infection and Immunity, 2002, 70, 2926-2932.	1.0	43
57	Peak learning of mass spectrometry imaging data using artificial neural networks. Nature Communications, 2021, 12, 5544.	5.8	43
58	Phosphotyrosine Signaling Analysis in Human Tumors Is Confounded by Systemic Ischemia-Driven Artifacts and Intra-Specimen Heterogeneity. Cancer Research, 2015, 75, 1495-1503.	0.4	42
59	High-Density, Targeted Monitoring of Tyrosine Phosphorylation Reveals Activated Signaling Networks in Human Tumors. Cancer Research, 2021, 81, 2495-2509.	0.4	41
60	Phosphotyrosine signaling analysis of site-specific mutations on EGFRvIII identifies determinants governing glioblastoma cell growth. Molecular BioSystems, 2010, 6, 1227.	2.9	40
61	Quantification of isomers from a mixture of twelve heparin and heparan sulfate disaccharides using tandem mass spectrometry. Rapid Communications in Mass Spectrometry, 2005, 19, 2553-2562.	0.7	39
62	PTMScout, a Web Resource for Analysis of High Throughput Post-translational Proteomics Studies. Molecular and Cellular Proteomics, 2010, 9, 2558-2570.	2.5	39
63	The Potential Cost of High-Throughput Proteomics. Science Signaling, 2011, 4, pe8.	1.6	39
64	MARQUIS: A multiplex method for absolute quantification of peptides and posttranslational modifications. Nature Communications, 2015, 6, 5924.	5.8	39
65	A Proteomics Approach to Profiling the Temporal Translational Response to Stress and Growth. IScience, 2018, 9, 367-381.	1.9	39
66	Deciphering the immunopeptidome in vivo reveals new tumour antigens. Nature, 2022, 607, 149-155.	13.7	38
67	Microtubule-Based Control of Motor-Clutch System Mechanics in Glioma Cell Migration. Cell Reports, 2018, 25, 2591-2604.e8.	2.9	37
68	Heterogeneous delivery across the blood-brain barrier limits the efficacy of an EGFR-targeting antibody drug conjugate in glioblastoma. Neuro-Oncology, 2021, 23, 2042-2053.	0.6	37
69	Quantitative Phosphoproteomics Reveals Wee1 Kinase as a Therapeutic Target in a Model of Proneural Glioblastoma. Molecular Cancer Therapeutics, 2016, 15, 1332-1343.	1.9	34
70	Gas-Phase Dehydrogenation of Saturated and Aromatic Cyclic Hydrocarbons by Ptn+(n= 1â~4). Journal of the American Chemical Society, 1997, 119, 7567-7572.	6.6	32
71	Quantitative Analysis of Signaling Networks across Differentially Embedded Tumors Highlights Interpatient Heterogeneity in Human Glioblastoma. Journal of Proteome Research, 2014, 13, 4581-4593.	1.8	32
72	Light-regulated allosteric switch enables temporal and subcellular control of enzyme activity. ELife, 2020, 9, .	2.8	32

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73	Quantifying oncogenic phosphotyrosine signaling networks through systems biology. Current Opinion in Genetics and Development, 2010, 20, 23-30.	1.5	31
74	Computer aided manual validation of mass spectrometry-based proteomic data. Methods, 2013, 61, 219-226.	1.9	30
75	High‐fat diet in a mouse insulin‐resistant model induces widespread rewiring of the phosphotyrosine signaling network. Molecular Systems Biology, 2019, 15, e8849.	3.2	30
76	Toward quantitative phosphotyrosine profiling in vivo. Seminars in Cell and Developmental Biology, 2012, 23, 854-862.	2.3	29
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	Proteomic analysis of cellular signaling. Expert Review of Proteomics, 2004, 1, 343-354.	1.3	27
79	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
80	Methods for the Analysis of Protein Phosphorylation‐Mediated Cellular Signaling Networks. Annual Review of Analytical Chemistry, 2016, 9, 295-315.	2.8	27
81	Phosphotyrosine Profiling of NSCLC Cells in Response to EGF and HGF Reveals Network Specific Mediators of Invasion. Journal of Proteome Research, 2013, 12, 1856-1867.	1.8	26
82	Characterization of <i>In Vivo</i> Resistance to Osimertinib and JNJ-61186372, an EGFR/Met Bispecific Antibody, Reveals Unique and Consensus Mechanisms of Resistance. Molecular Cancer Therapeutics, 2017, 16, 2572-2585.	1.9	26
83	Systemic analysis of tyrosine kinase signaling reveals a common adaptive response program in a HER2-positive breast cancer. Science Signaling, 2019, 12, .	1.6	26
84	Matrix-shimmed ion cyclotron resonance ion trap simultaneously optimized for excitation, detection, quadrupolar axialization, and trapping. Journal of the American Society for Mass Spectrometry, 1999, 10, 759-769.	1.2	25
85	Epidermal growth factor receptor downregulation by small heterodimeric binding proteins. Protein Engineering, Design and Selection, 2012, 25, 47-57.	1.0	25
86	Network Modeling Identifies Patient-specific Pathways in Glioblastoma. Scientific Reports, 2016, 6, 28668.	1.6	25
87	Absolute quantification of tumor antigens using embedded MHC-I isotopologue calibrants. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	25
88	Quantitative Proteomic Analysis of Phosphotyrosine-Mediated Cellular Signaling Networks. Methods in Molecular Biology, 2007, 359, 203-212.	0.4	25
89	Src homology 2 domains enhance tyrosine phosphorylation in vivo by protecting binding sites in their target proteins from dephosphorylation. Journal of Biological Chemistry, 2018, 293, 623-637.	1.6	23
90	Quantitative Consequences of Protein Carriers in Immunopeptidomics and Tyrosine Phosphorylation MS2 Analyses. Molecular and Cellular Proteomics, 2021, 20, 100104.	2.5	23

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91	System level dynamics of post-translational modifications. Current Opinion in Biotechnology, 2014, 28, 83-87.	3.3	22
92	The Physics of Cancer. Cancer Research, 2019, 79, 2107-2110.	0.4	22
93	Quantitative phosphoproteomics uncovers dysregulated kinase networks in Alzheimer's disease. Nature Aging, 2021, 1, 550-565.	5.3	21
94	Global Cancer Risk From Unregulated Polycyclic Aromatic Hydrocarbons. GeoHealth, 2021, 5, e2021GH000401.	1.9	21
95	Using Small Molecules and Chemical Genetics To Interrogate Signaling Networks. ACS Chemical Biology, 2011, 6, 75-85.	1.6	20
96	Phosphoproteomics identifies microglial Siglec-F inflammatory response during neurodegeneration. Molecular Systems Biology, 2020, 16, e9819.	3.2	20
97	Camptothecin resistance is determined by the regulation of topoisomerase I degradation mediated by ubiquitin proteasome pathway. Oncotarget, 2017, 8, 43733-43751.	0.8	20
98	Time-resolved multimodal analysis of Src Homology 2 (SH2) domain binding in signaling by receptor tyrosine kinases. ELife, 2016, 5, e11835.	2.8	20
99	Weak agonist self-peptides promote selection and tuning of virus-specific T cells. European Journal of Immunology, 2003, 33, 685-696.	1.6	19
100	Robust co-regulation of tyrosine phosphorylation sites on proteins reveals novel protein interactions. Molecular BioSystems, 2012, 8, 2771.	2.9	19
101	Molecular network analysis of phosphotyrosine and lipid metabolism in hepatic PTP1b deletion mice. Integrative Biology (United Kingdom), 2013, 5, 940.	0.6	19
102	Exploration of CTCF post-translation modifications uncovers Serine-224 phosphorylation by PLK1 at pericentric regions during the G2/M transition. ELife, 2019, 8, .	2.8	18
103	An External Source 7 T Fourier Transform Ion Cyclotron Resonance Mass Spectrometer with Electrostatic Ion Guide. , 1996, 10, 1845-1849.		17
104	Excision of mutagenic replication-blocking lesions suppresses cancer but promotes cytotoxicity and lethality in nitrosamine-exposed mice. Cell Reports, 2021, 34, 108864.	2.9	16
105	Quantitative Analysis of Tyrosine Phosphorylation from FFPE Tissues Reveals Patient-Specific Signaling Networks. Cancer Research, 2021, 81, 3930-3941.	0.4	16
106	Phosphoproteomics: a valuable tool for uncovering molecular signaling in cancer cells. Expert Review of Proteomics, 2021, 18, 661-674.	1.3	15
107	Quantitative Phosphoproteomics Reveals Wee1 Kinase as a Therapeutic Target in a Model of Proneural Glioblastoma. Molecular Cancer Therapeutics, 2016, 15, 1332-1343.	1.9	14
108	Quantitative Profiling of Lysine Acetylation Reveals Dynamic Crosstalk between Receptor Tyrosine Kinases and Lysine Acetylation. PLoS ONE, 2015, 10, e0126242.	1.1	14

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109	Characterization and evolutionary relevance of the sperm nuclear basic proteins from stickleback fish. Molecular Reproduction and Development, 2000, 57, 185-193.	1.0	12
110	Signaling netwErks get the global treatment. Genome Biology, 2007, 8, 202.	3.8	12
111	Labeling and Identification of Direct Kinase Substrates. Science Signaling, 2012, 5, pl3.	1.6	11
112	A Thermodynamic-Based Interpretation of Protein Expression Heterogeneity in Different Glioblastoma Multiforme Tumors Identifies Tumor-Specific Unbalanced Processes. Journal of Physical Chemistry B, 2016, 120, 5990-5997.	1.2	11
113	Platform for micro-invasive membrane-free biochemical sampling of brain interstitial fluid. Science Advances, 2020, 6, .	4.7	11
114	Engineered bromodomains to explore the acetylproteome. Proteomics, 2015, 15, 1470-1475.	1.3	10
115	Vascular Endothelial Growth Factor (VEGF) and Platelet (PF-4) Factor 4 Inputs Modulate Human Microvascular Endothelial Signaling in a Three-Dimensional Matrix Migration Context. Molecular and Cellular Proteomics, 2013, 12, 3704-3718.	2.5	9
116	A thermodynamic-based approach for the resolution and prediction of protein network structures. Chemical Physics, 2018, 514, 20-30.	0.9	9
117	Identification of Direct Kinase Substrates Using Analogue-Sensitive Alleles. Methods in Molecular Biology, 2016, 1355, 71-84.	0.4	8
118	Integrated data management and validation platform for phosphorylated tandem mass spectrometry data. Proteomics, 2010, 10, 3515-3524.	1.3	7
119	1,2,3, MHC: a review of mass spectrometry-based immunopeptidomics methods for relative and absolute quantification of pMHCs. Immuno-Oncology Technology, 2021, , 100042.	0.2	7
120	Reply to Comment on â€œSloppy models, parameter uncertainty, and the role of experimental designâ€• Molecular BioSystems, 2011, 7, 2523.	2.9	6
121	Expanding applications of chemical genetics in signal transduction. Cell Cycle, 2012, 11, 1903-1909.	1.3	5
122	Adaptive protein and phosphoprotein networks which promote therapeutic sensitivity or acquired resistance. Biochemical Society Transactions, 2014, 42, 758-764.	1.6	5
123	On the iTRAQ of kinase inhibitors. Nature Biotechnology, 2007, 25, 994-996.	9.4	4
124	Illuminating signaling network functional biology through quantitative phosphoproteomic mass spectrometry. Briefings in Functional Genomics & Proteomics, 2008, 7, 383-394.	3.8	4
125	Signaling for death: tyrosine phosphorylation in the response to glucose deprivation. Molecular Systems Biology, 2012, 8, 591.	3.2	4
126	Multimodal platform for assessing drug distribution and response in clinical trials. Neuro-Oncology, 2022, 24, 64-77.	0.6	4

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127	Electrospray Ionization Fourier Transform Ion Cyclotron Resonance at 9.4â€‰T. , 1996, 10, 1824.		4
128	Leveraging Immunopeptidomics To Study and Combat Infectious Disease. MSystems, 2021, 6, e0031021.	1.7	3
129	Measurement of Phosphorylated Peptides with Absolute Quantification. Methods in Molecular Biology, 2016, 1410, 281-292.	0.4	3
130	Combinatorial Therapeutic Strategies for Blocking Kinase Pathways in Brain Tumors. , 2009, , 953-975.		1
131	Quantitative Analysis of Tyrosine Kinase Signaling Across Differentially Embedded Human Glioblastoma Tumors. Methods in Molecular Biology, 2018, 1711, 149-164.	0.4	1
132	Cell system perturbation for time-resolved quantification of tyrosine phosphorylation in complex samples. , 2006, 2006, 51-2.		0
133	Biological Insights From Quantitative Analysis of Tyrosine Kinase Signaling Networks. FASEB Journal, 2010, 24, 306.2.	0.2	0
134	Cancer Signaling Network Analysis by Quantitative Mass Spectrometry. , 2011, , 55-75.		0
135	Quantitative Proteomic Analysis of Phosphotyrosine-Mediated Cellular Signaling Networks. , 0, , 203-212.		0