John M Koomen

List of Publications by Year in descending order

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94 papers

5,169 citations

38 h-index 95266 68 g-index

96 all docs 96 docs citations

96 times ranked 9235 citing authors

#	Article	IF	CITATIONS
1	The non-canonical target PARP16 contributes to polypharmacology of the PARP inhibitor talazoparib and its synergy with WEE1 inhibitors. Cell Chemical Biology, 2022, 29, 202-214.e7.	5.2	19
2	Integrated Proteomics-Based Physical and Functional Mapping of AXL Kinase Signaling Pathways and Inhibitors Define Its Role in Cell Migration. Molecular Cancer Research, 2022, 20, 542-555.	3.4	2
3	Disrupting the MYC-TFEB Circuit Impairs Amino Acid Homeostasis and Provokes Metabolic Anergy. Cancer Research, 2022, 82, 1234-1250.	0.9	8
4	Deubiquitinase Vulnerabilities Identified through Activity-Based Protein Profiling in Non-Small Cell Lung Cancer. ACS Chemical Biology, 2022, 17, 776-784.	3.4	1
5	Macrophages use apoptotic cell-derived methionine and DNMT3A during efferocytosis to promote tissue resolution. Nature Metabolism, 2022, 4, 444-457.	11.9	56
6	Single-cell Characterization of the Cellular Landscape of Acral Melanoma Identifies Novel Targets for Immunotherapy. Clinical Cancer Research, 2022, 28, 2131-2146.	7.0	36
7	Noncanonical EphA2 Signaling Is a Driver of Tumor-Endothelial Cell Interactions and Metastatic Dissemination in BRAF Inhibitorâ€'Resistant Melanoma. Journal of Investigative Dermatology, 2021, 141, 840-851.e4.	0.7	19
8	Cell Type–specific Adaptive Signaling Responses to KRASG12C Inhibition. Clinical Cancer Research, 2021, 27, 2533-2548.	7.0	46
9	Global Phosphoproteomics Reveal CDK Suppression as a Vulnerability to KRas Addiction in Pancreatic Cancer. Clinical Cancer Research, 2021, 27, 4012-4024.	7.0	20
10	A Mutational Survey of Acral Nevi. JAMA Dermatology, 2021, 157, 831-835.	4.1	13
10	A Mutational Survey of Acral Nevi. JAMA Dermatology, 2021, 157, 831-835. Metabolic Changes Are Associated with Melphalan Resistance in Multiple Myeloma. Journal of Proteome Research, 2021, 20, 3134-3149.	3.7	13
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11	Metabolic Changes Are Associated with Melphalan Resistance in Multiple Myeloma. Journal of Proteome Research, 2021, 20, 3134-3149. Fucosylated Proteome Profiling Identifies a Fucosylated, Non-Ribosomal, Stress-Responsive Species of	3.7	11
11 12	Metabolic Changes Are Associated with Melphalan Resistance in Multiple Myeloma. Journal of Proteome Research, 2021, 20, 3134-3149. Fucosylated Proteome Profiling Identifies a Fucosylated, Non-Ribosomal, Stress-Responsive Species of Ribosomal Protein S3. Cells, 2021, 10, 1310. Targeted mass-spectrometry-based assays enable multiplex quantification of receptor tyrosine kinase,	3.7 4.1	11 4
11 12 13	Metabolic Changes Are Associated with Melphalan Resistance in Multiple Myeloma. Journal of Proteome Research, 2021, 20, 3134-3149. Fucosylated Proteome Profiling Identifies a Fucosylated, Non-Ribosomal, Stress-Responsive Species of Ribosomal Protein S3. Cells, 2021, 10, 1310. Targeted mass-spectrometry-based assays enable multiplex quantification of receptor tyrosine kinase, MAP kinase, and AKT signaling. Cell Reports Methods, 2021, 1, 100015. Macrophage-Derived Cholesterol Contributes to Therapeutic Resistance in Prostate Cancer. Cancer	3.7 4.1 2.9	11 4
11 12 13	Metabolic Changes Are Associated with Melphalan Resistance in Multiple Myeloma. Journal of Proteome Research, 2021, 20, 3134-3149. Fucosylated Proteome Profiling Identifies a Fucosylated, Non-Ribosomal, Stress-Responsive Species of Ribosomal Protein S3. Cells, 2021, 10, 1310. Targeted mass-spectrometry-based assays enable multiplex quantification of receptor tyrosine kinase, MAP kinase, and AKT signaling. Cell Reports Methods, 2021, 1, 100015. Macrophage-Derived Cholesterol Contributes to Therapeutic Resistance in Prostate Cancer. Cancer Research, 2021, 81, 5477-5490. Tumor-infiltrating lymphocyte treatment for anti-PD-1-resistant metastatic lung cancer: a phase 1 trial.	3.7 4.1 2.9 0.9	11 4 10 48
11 12 13 14	Metabolic Changes Are Associated with Melphalan Resistance in Multiple Myeloma. Journal of Proteome Research, 2021, 20, 3134-3149. Fucosylated Proteome Profiling Identifies a Fucosylated, Non-Ribosomal, Stress-Responsive Species of Ribosomal Protein S3. Cells, 2021, 10, 1310. Targeted mass-spectrometry-based assays enable multiplex quantification of receptor tyrosine kinase, MAP kinase, and AKT signaling. Cell Reports Methods, 2021, 1, 100015. Macrophage-Derived Cholesterol Contributes to Therapeutic Resistance in Prostate Cancer. Cancer Research, 2021, 81, 5477-5490. Tumor-infiltrating lymphocyte treatment for anti-PD-1-resistant metastatic lung cancer: a phase 1 trial. Nature Medicine, 2021, 27, 1410-1418. Managing a Large-Scale Multiomics Project: A Team Science Case Study in Proteogenomics. Methods in	3.7 4.1 2.9 0.9	11 4 10 48 168

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19	Translational pathology, genomics and the development of systemic therapies for acral melanoma. Seminars in Cancer Biology, 2020, 61, 149-157.	9.6	30
20	Proteomic Analysis of CSF from Patients with Leptomeningeal Melanoma Metastases Identifies Signatures Associated with Disease Progression and Therapeutic Resistance. Clinical Cancer Research, 2020, 26, 2163-2175.	7.0	39
21	Cereblon harnesses Myc-dependent bioenergetics and activity of CD8+ T lymphocytes. Blood, 2020, 136, 857-870.	1.4	18
22	Lowering Sample Requirements to Study Tyrosine Kinase Signaling Using Phosphoproteomics with the TMT Calibrator Approach. Proteomics, 2020, 20, e2000116.	2.2	12
23	Macrophage Metabolism of Apoptotic Cell-Derived Arginine Promotes Continual Efferocytosis and Resolution of Injury. Cell Metabolism, 2020, 31, 518-533.e10.	16.2	235
24	HDAC11 deficiency disrupts oncogene-induced hematopoiesis in myeloproliferative neoplasms. Blood, 2020, 135, 191-207.	1.4	40
25	TAp63-Regulated miRNAs Suppress Cutaneous Squamous Cell Carcinoma through Inhibition of a Network of Cell-Cycle Genes. Cancer Research, 2020, 80, 2484-2497.	0.9	16
26	Proteogenomic landscape of squamous cell lung cancer. Nature Communications, 2019, 10, 3578.	12.8	84
27	Divergent Polypharmacology-Driven Cellular Activity of Structurally Similar Multi-Kinase Inhibitors through Cumulative Effects on Individual Targets. Cell Chemical Biology, 2019, 26, 1240-1252.e11.	5.2	15
28	HDAC Inhibition Enhances the <i>In Vivo</i> Efficacy of MEK Inhibitor Therapy in Uveal Melanoma. Clinical Cancer Research, 2019, 25, 5686-5701.	7.0	75
29	Proteometabolomics of Melphalan Resistance in Multiple Myeloma. Methods in Molecular Biology, 2019, 1996, 273-296.	0.9	6
30	BCL2 Amplicon Loss and Transcriptional Remodeling Drives ABT-199 Resistance in B Cell Lymphoma Models. Cancer Cell, 2019, 35, 752-766.e9.	16.8	56
31	K27-linked ubiquitination of BRAF by ITCH engages cytokine response to maintain MEK-ERK signaling. Nature Communications, 2019, 10, 1870.	12.8	61
32	HDAC8 Regulates a Stress Response Pathway in Melanoma to Mediate Escape from BRAF Inhibitor Therapy. Cancer Research, 2019, 79, 2947-2961.	0.9	59
33	An immunoproteomic approach to characterize the CAR interactome and signalosome. Science Signaling, 2019, 12, .	3.6	109
34	<i>PTPN11</i> Plays Oncogenic Roles and Is a Therapeutic Target for <i>BRAF</i> Wild-Type Melanomas. Molecular Cancer Research, 2019, 17, 583-593.	3.4	34
35	Combined BRAF and HSP90 Inhibition in Patients with Unresectable <i>BRAF</i> V600E-Mutant Melanoma. Clinical Cancer Research, 2018, 24, 5516-5524.	7.0	55
36	Comparison of Quantitative Mass Spectrometry Platforms for Monitoring Kinase ATP Probe Uptake in Lung Cancer. Journal of Proteome Research, 2018, 17, 63-75.	3.7	18

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37	Cytokeratin-8 in Anaplastic Thyroid Carcinoma: More Than a Simple Structural Cytoskeletal Protein. International Journal of Molecular Sciences, 2018, 19, 577.	4.1	13
38	PLK1 stabilizes a MYC-dependent kinase network in aggressive B cell lymphomas. Journal of Clinical Investigation, 2018, 128, 5517-5530.	8.2	67
39	Quantitative proteomics of breast tumors: Tissue quality assessment to clinical biomarkers. Proteomics, 2017, 17, 1600335.	2.2	8
40	Relative protein quantification and accessible biology in lung tumor proteomes from four LCâ€MS/MS discovery platforms. Proteomics, 2017, 17, 1600300.	2.2	15
41	Unification of de novo and acquired ibrutinib resistance in mantle cell lymphoma. Nature Communications, 2017, 8, 14920.	12.8	122
42	Polypharmacology-based ceritinib repurposing using integrated functional proteomics. Nature Chemical Biology, 2017, 13, 1222-1231.	8.0	60
43	Multiplexed Liquid Chromatography-Multiple Reaction Monitoring Mass Spectrometry Quantification of Cancer Signaling Proteins. Methods in Molecular Biology, 2017, 1647, 19-45.	0.9	5
44	Quantification of Breast Cancer Protein Biomarkers at Different Expression Levels in Human Tumors. Methods in Molecular Biology, 2017, 1788, 251-268.	0.9	2
45	Inhibition of PI3K/Akt/mTOR signaling in PI3KR2-overexpressing colon cancer stem cells reduces tumor growth due to apoptosis. Oncotarget, 2017, 8, 50476-50488.	1.8	43
46	Activity-Based Proteomics Reveals Heterogeneous Kinome and ATP-Binding Proteome Responses to MEK Inhibition in KRAS Mutant Lung Cancer. Proteomes, 2016, 4, 16.	3.5	5
47	Tyrosine Kinase Signaling in Clear Cell and Papillary Renal Cell Carcinoma Revealed by Mass Spectrometry–Based Phosphotyrosine Proteomics. Clinical Cancer Research, 2016, 22, 5605-5616.	7.0	19
48	APOSTL: An Interactive Galaxy Pipeline for Reproducible Analysis of Affinity Proteomics Data. Journal of Proteome Research, 2016, 15, 4747-4754.	3.7	16
49	Activity-Based Protein Profiling Shows Heterogeneous Signaling Adaptations to BRAF Inhibition. Journal of Proteome Research, 2016, 15, 4476-4489.	3.7	16
50	Phosphoproteomics Reveals MAPK Inhibitors Enhance MET- and EGFR-Driven AKT Signaling in <i>KRAS</i> -Mutant Lung Cancer. Molecular Cancer Research, 2016, 14, 1019-1029.	3.4	53
51	Proteome-wide Profiling of Clinical PARP Inhibitors Reveals Compound-Specific Secondary Targets. Cell Chemical Biology, 2016, 23, 1490-1503.	5.2	80
52	Target Identification in Small Cell Lung Cancer via Integrated Phenotypic Screening and Activity-Based Protein Profiling. Molecular Cancer Therapeutics, 2016, 15, 334-342.	4.1	19
53	Identification of Target Pathways Induced By the Multiple Myeloma Tumor Microenvironment Using Activity-Based Protein Profiling and Ex Vivo Protein Kinase Inhibitor Screening. Blood, 2016, 128, 3288-3288.	1.4	0
54	Chronic acidosis in the tumour microenvironment selects for overexpression of LAMP2 in the plasma membrane. Nature Communications, 2015, 6, 8752.	12.8	151

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55	Inhibition of Shp2 suppresses mutant EGFR-induced lung tumors in transgenic mouse model of lung adenocarcinoma. Oncotarget, 2015, 6, 6191-6202.	1.8	39
56	Quantitative analysis of immunoglobulin subclasses and subclass specific glycosylation by LC–MS–MRM in liver disease. Journal of Proteomics, 2015, 116, 24-33.	2.4	67
57	Ligand-Independent EPHA2 Signaling Drives the Adoption of a Targeted Therapy–Mediated Metastatic Melanoma Phenotype. Cancer Discovery, 2015, 5, 264-273.	9.4	82
58	Evaluating kinase ATP uptake and tyrosine phosphorylation using multiplexed quantification of chemically labeled and post-translationally modified peptides. Methods, 2015, 81, 41-49.	3.8	11
59	Ubiquitinated Sirtuin 1 (SIRT1) Function Is Modulated during DNA Damage-induced Cell Death and Survival. Journal of Biological Chemistry, 2015, 290, 8904-8912.	3.4	50
60	A Pilot Proteogenomic Study with Data Integration Identifies MCT1 and GLUT1 as Prognostic Markers in Lung Adenocarcinoma. PLoS ONE, 2015, 10, e0142162.	2.5	31
61	Evaluating Melanoma Drug Response and Therapeutic Escape with Quantitative Proteomics. Molecular and Cellular Proteomics, 2014, 13, 1844-1854.	3.8	52
62	Adaptive Responses to Dasatinib-Treated Lung Squamous Cell Cancer Cells Harboring DDR2 Mutations. Cancer Research, 2014, 74, 7217-7228.	0.9	43
63	Tyrosine Phosphoproteomics Identifies Both Codrivers and Cotargeting Strategies for T790M-Related EGFR-TKI Resistance in Non–Small Cell Lung Cancer. Clinical Cancer Research, 2014, 20, 4059-4074.	7.0	95
64	Quantification of peptides from immunoglobulin constant and variable regions by LCâ€MRM MS for assessment of multiple myeloma patients. Proteomics - Clinical Applications, 2014, 8, 783-795.	1.6	33
65	Amuvatinib has cytotoxic effects against NRAS-mutant melanoma but not BRAF-mutant melanoma. Melanoma Research, 2014, 24, 448-453.	1.2	14
66	Immunoglobulins: Expanding the Role for Mass Spectrometry in Protein Biomarker Quantification. Clinical Chemistry, 2014, 60, 1034-1035.	3.2	2
67	Inhibition of Wee1, AKT, and CDK4 Underlies the Efficacy of the HSP90 Inhibitor XL888 in an <i>In Vivo</i> Model of <i>NRAS</i> -Mutant Melanoma. Molecular Cancer Therapeutics, 2013, 12, 901-912.	4.1	52
68	Dissection of TBK1 signaling via phosphoproteomics in lung cancer cells. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 12414-12419.	7.1	88
69	The HSP90 Inhibitor XL888 Overcomes BRAF Inhibitor Resistance Mediated through Diverse Mechanisms. Clinical Cancer Research, 2012, 18, 2502-2514.	7.0	145
70	GSK3 \hat{l}^2 Inhibition Blocks Melanoma Cell/Host Interactions by Downregulating N-Cadherin Expression and Decreasing FAK Phosphorylation. Journal of Investigative Dermatology, 2012, 132, 2818-2827.	0.7	37
71	An ET-CURE Pilot Project Supporting Undergraduate Training in Cancer Research, Emerging Technology, and Health Disparities. Journal of Cancer Education, 2012, 27, 418-427.	1.3	4
72	Evaluation of Direct Infusion-Multiple Reaction Monitoring Mass Spectrometry for Quantification of Heat Shock Proteins. Analytical Chemistry, 2012, 84, 1981-1986.	6.5	12

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73	A mass spectrometryâ€based method to screen for αâ€amidated peptides. Proteomics, 2012, 12, 173-182.	2.2	13
74	Evaluation of protein quantification using standard peptides containing single conservative amino acid replacements. Journal of Mass Spectrometry, 2012, 47, 188-194.	1.6	13
75	Mass Spectrometry Mapping of Epidermal Growth Factor Receptor Phosphorylation Related to Oncogenic Mutations and Tyrosine Kinase Inhibitor Sensitivity. Journal of Proteome Research, 2011, 10, 305-319.	3.7	56
76	A database of reaction monitoring mass spectrometry assays for elucidating the rapeutic response in cancer. Proteomics - Clinical Applications, $2011, 5, 383-396$.	1.6	48
77	PTEN Loss Confers BRAF Inhibitor Resistance to Melanoma Cells through the Suppression of BIM Expression. Cancer Research, 2011, 71, 2750-2760.	0.9	488
78	Monitoring a Nuclear Factor-κB Signature of Drug Resistance in Multiple Myeloma. Molecular and Cellular Proteomics, 2011, 10, M110.005520.	3.8	30
79	Methods for investigation of targeted kinase inhibitor therapy using chemical proteomics and phosphorylation profiling. Biochemical Pharmacology, 2010, 80, 739-747.	4.4	15
80	A chemical and phosphoproteomic characterization of dasatinib action in lung cancer. Nature Chemical Biology, 2010, 6, 291-299.	8.0	254
81	Urine Collection and Processing for Protein Biomarker Discovery and Quantification. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 953-959.	2.5	110
82	IKKÏμ Phosphorylation of Estrogen Receptor α Ser-167 and Contribution to Tamoxifen Resistance in Breast Cancer. Journal of Biological Chemistry, 2010, 285, 3676-3684.	3.4	48
83	Critical Role of Shp2 in Tumor Growth Involving Regulation of c-Myc. Genes and Cancer, 2010, 1, 994-1007.	1.9	28
84	Quantification of \hat{l}^2 -Catenin Signaling Components in Colon Cancer Cell Lines, Tissue Sections, and Microdissected Tumor Cells using Reaction Monitoring Mass Spectrometry. Journal of Proteome Research, 2010, 9, 4215-4227.	3.7	45
85	IPEP: an <i>in silico</i> tool to examine proteolytic peptides for mass spectrometry. Bioinformatics, 2008, 24, 2801-2802.	4.1	11
86	Proteomic Contributions to Personalized Cancer Care. Molecular and Cellular Proteomics, 2008, 7, 1780-1794.	3.8	89
87	Proteome Analysis of Isolated Perfused Organ Effluent as a Novel Model for Protein Biomarker Discovery. Journal of Proteome Research, 2006, 5, 177-182.	3.7	23
88	Diagnostic protein discovery using liquid chromatography/mass spectrometry for proteolytic peptide targeting. Rapid Communications in Mass Spectrometry, 2005, 19, 1624-1636.	1.5	15
89	Understanding the Characteristics of Mass Spectrometry Data through the use of Simulation. Cancer Informatics, 2005, 1, 117693510500100.	1.9	42
90	Direct Tandem Mass Spectrometry Reveals Limitations in Protein Profiling Experiments for Plasma Biomarker Discovery. Journal of Proteome Research, 2005, 4, 972-981.	3.7	210

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91	Developing an Understanding of Proteomics: An Introduction to Biological Mass Spectrometry. Cancer Investigation, 2005, 23, 47-59.	1.3	13
92	Plasma protein profiling for diagnosis of pancreatic cancer reveals the presence of host response proteins. Clinical Cancer Research, 2005, 11 , $1110-8$.	7.0	125
93	Developing an understanding of proteomics: an introduction to biological mass spectrometry. Cancer Investigation, 2005, 23, 47-59.	1.3	1
94	Diagnostic protein discovery using proteolytic peptide targeting and identification. Rapid Communications in Mass Spectrometry, 2004, 18, 2537-2548.	1.5	26