John M Koomen

List of Publications by Year
in descending order

94 papers	5,169 citations	87888 38 h-index	95266 68 g-index
96 all docs	96 docs citations	96 times ranked	9235 citing authors

#	Article	IF	Citations
1	PTEN Loss Confers BRAF Inhibitor Resistance to Melanoma Cells through the Suppression of BIM Expression. Cancer Research, 2011, 71, 2750-2760.	0.9	488
2	A chemical and phosphoproteomic characterization of dasatinib action in lung cancer. Nature Chemical Biology, 2010, 6, 291-299.	8.0	254
3	Macrophage Metabolism of Apoptotic Cell-Derived Arginine Promotes Continual Efferocytosis and Resolution of Injury. Cell Metabolism, 2020, 31, 518-533.e10.	16.2	235
4	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
5	Tumor-infiltrating lymphocyte treatment for anti-PD-1-resistant metastatic lung cancer: a phase 1 trial. Nature Medicine, 2021, 27, 1410-1418.	30.7	168
6	Chronic acidosis in the tumour microenvironment selects for overexpression of LAMP2 in the plasma membrane. Nature Communications, 2015, 6, 8752.	12.8	151
7	The HSP90 Inhibitor XL888 Overcomes BRAF Inhibitor Resistance Mediated through Diverse Mechanisms. Clinical Cancer Research, 2012, 18, 2502-2514.	7.0	145
8	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
9	Unification of de novo and acquired ibrutinib resistance in mantle cell lymphoma. Nature Communications, 2017, 8, 14920.	12.8	122
10	Urine Collection and Processing for Protein Biomarker Discovery and Quantification. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 953-959.	2.5	110
11	An immunoproteomic approach to characterize the CAR interactome and signalosome. Science Signaling, 2019, 12, .	3.6	109
12	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
13	Proteomic Contributions to Personalized Cancer Care. Molecular and Cellular Proteomics, 2008, 7, 1780-1794.	3.8	89
14	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
15	Proteogenomic landscape of squamous cell lung cancer. Nature Communications, 2019, 10, 3578.	12.8	84
16	Ligand-Independent EPHA2 Signaling Drives the Adoption of a Targeted Therapy–Mediated Metastatic Melanoma Phenotype. Cancer Discovery, 2015, 5, 264-273.	9.4	82
17	Proteome-wide Profiling of Clinical PARP Inhibitors Reveals Compound-Specific Secondary Targets. Cell Chemical Biology, 2016, 23, 1490-1503.	5.2	80
18	HDAC Inhibition Enhances the In Vivo Efficacy of MEK Inhibitor Therapy in Uveal Melanoma. Clinical Cancer Research, 2019, 25, 5686-5701.	7.0	75

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19	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
20	PLK1 stabilizes a MYC-dependent kinase network in aggressive B cell lymphomas. Journal of Clinical Investigation, 2018, 128, 5517-5530.	8.2	67
21	K27-linked ubiquitination of BRAF by ITCH engages cytokine response to maintain MEK-ERK signaling. Nature Communications, 2019, 10, 1870.	12.8	61
22	Polypharmacology-based ceritinib repurposing using integrated functional proteomics. Nature Chemical Biology, 2017, 13, 1222-1231.	8.0	60
23	HDAC8 Regulates a Stress Response Pathway in Melanoma to Mediate Escape from BRAF Inhibitor Therapy. Cancer Research, 2019, 79, 2947-2961.	0.9	59
24	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
25	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
26	Macrophages use apoptotic cell-derived methionine and DNMT3A during efferocytosis to promote tissue resolution. Nature Metabolism, 2022, 4, 444-457.	11.9	56
27	Combined BRAF and HSP90 Inhibition in Patients with Unresectable *BRAF*V600E-Mutant Melanoma. Clinical Cancer Research, 2018, 24, 5516-5524.	7.0	55
28	Phosphoproteomics Reveals MAPK Inhibitors Enhance MET- and EGFR-Driven AKT Signaling in *KRAS*-Mutant Lung Cancer. Molecular Cancer Research, 2016, 14, 1019-1029.	3.4	53
29	Inhibition of Wee1, AKT, and CDK4 Underlies the Efficacy of the HSP90 Inhibitor XL888 in an *In Vivo* Model of *NRAS*-Mutant Melanoma. Molecular Cancer Therapeutics, 2013, 12, 901-912.	4.1	52
30	Evaluating Melanoma Drug Response and Therapeutic Escape with Quantitative Proteomics. Molecular and Cellular Proteomics, 2014, 13, 1844-1854.	3.8	52
31	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
32	IKKϵ 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
33	A database of reaction monitoring mass spectrometry assays for elucidating therapeutic response in cancer. Proteomics - Clinical Applications, 2011, 5, 383-396.	1.6	48
34	Macrophage-Derived Cholesterol Contributes to Therapeutic Resistance in Prostate Cancer. Cancer Research, 2021, 81, 5477-5490.	0.9	48
35	Cell Type–specific Adaptive Signaling Responses to KRASG12C Inhibition. Clinical Cancer Research, 2021, 27, 2533-2548.	7.0	46
36	Quantification of β-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

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37	Adaptive Responses to Dasatinib-Treated Lung Squamous Cell Cancer Cells Harboring DDR2 Mutations. Cancer Research, 2014, 74, 7217-7228.	0.9	43
38	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
39	Understanding the Characteristics of Mass Spectrometry Data through the use of Simulation. Cancer Informatics, 2005, 1, 117693510500100.	1.9	42
40	HDAC11 deficiency disrupts oncogene-induced hematopoiesis in myeloproliferative neoplasms. Blood, 2020, 135, 191-207.	1.4	40
41	Inhibition of Shp2 suppresses mutant EGFR-induced lung tumors in transgenic mouse model of lung adenocarcinoma. Oncotarget, 2015, 6, 6191-6202.	1.8	39
42	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
43	GSK3β 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
44	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
45	<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
46	Quantification of peptides from immunoglobulin constant and variable regions by LC–MRM MS for assessment of multiple myeloma patients. Proteomics - Clinical Applications, 2014, 8, 783-795.	1.6	33
47	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
48	Monitoring a Nuclear Factor-κB Signature of Drug Resistance in Multiple Myeloma. Molecular and Cellular Proteomics, 2011, 10, M110.005520.	3.8	30
49	Translational pathology, genomics and the development of systemic therapies for acral melanoma. Seminars in Cancer Biology, 2020, 61, 149-157.	9.6	30
50	Critical Role of Shp2 in Tumor Growth Involving Regulation of c-Myc. Genes and Cancer, 2010, 1, 994-1007.	1.9	28
51	Diagnostic protein discovery using proteolytic peptide targeting and identification. Rapid Communications in Mass Spectrometry, 2004, 18, 2537-2548.	1.5	26
52	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
53	Global Phosphoproteomics Reveal CDK Suppression as a Vulnerability to KRas Addiction in Pancreatic Cancer. Clinical Cancer Research, 2021, 27, 4012-4024.	7.0	20
54	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

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55	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
56	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
57	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
58	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
59	Cereblon harnesses Myc-dependent bioenergetics and activity of CD8+ T lymphocytes. Blood, 2020, 136, 857-870.	1.4	18
60	APOSTL: An Interactive Galaxy Pipeline for Reproducible Analysis of Affinity Proteomics Data. Journal of Proteome Research, 2016, 15, 4747-4754.	3.7	16
61	Activity-Based Protein Profiling Shows Heterogeneous Signaling Adaptations to BRAF Inhibition. Journal of Proteome Research, 2016, 15, 4476-4489.	3.7	16
62	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
63	Diagnostic protein discovery using liquid chromatography/mass spectrometry for proteolytic peptide targeting. Rapid Communications in Mass Spectrometry, 2005, 19, 1624-1636.	1.5	15
64	Methods for investigation of targeted kinase inhibitor therapy using chemical proteomics and phosphorylation profiling. Biochemical Pharmacology, 2010, 80, 739-747.	4.4	15
65	Relative protein quantification and accessible biology in lung tumor proteomes from four LCâ€MS/MS discovery platforms. Proteomics, 2017, 17, 1600300.	2.2	15
66	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
67	Amuvatinib has cytotoxic effects against NRAS-mutant melanoma but not BRAF-mutant melanoma. Melanoma Research, 2014, 24, 448-453.	1.2	14
68	Developing an Understanding of Proteomics: An Introduction to Biological Mass Spectrometry. Cancer Investigation, 2005, 23, 47-59.	1.3	13
69	A mass spectrometryâ€based method to screen for Î±â€amidated peptides. Proteomics, 2012, 12, 173-182.	2.2	13
70	Evaluation of protein quantification using standard peptides containing single conservative amino acid replacements. Journal of Mass Spectrometry, 2012, 47, 188-194.	1.6	13
71	Cytokeratin-8 in Anaplastic Thyroid Carcinoma: More Than a Simple Structural Cytoskeletal Protein. International Journal of Molecular Sciences, 2018, 19, 577.	4.1	13
72	GMSimpute: a generalized two-step Lasso approach to impute missing values in label-free mass spectrum analysis. Bioinformatics, 2020, 36, 257-263.	4.1	13

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73	A Mutational Survey of Acral Nevi. JAMA Dermatology, 2021, 157, 831-835.	4.1	13
74	Evaluation of Direct Infusion-Multiple Reaction Monitoring Mass Spectrometry for Quantification of Heat Shock Proteins. Analytical Chemistry, 2012, 84, 1981-1986.	6.5	12
75	Lowering Sample Requirements to Study Tyrosine Kinase Signaling Using Phosphoproteomics with the TMT Calibrator Approach. Proteomics, 2020, 20, e2000116.	2.2	12
76	IPEP: an *in silico* tool to examine proteolytic peptides for mass spectrometry. Bioinformatics, 2008, 24, 2801-2802.	4.1	11
77	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
78	Metabolic Changes Are Associated with Melphalan Resistance in Multiple Myeloma. Journal of Proteome Research, 2021, 20, 3134-3149.	3.7	11
79	Targeted mass-spectrometry-based assays enable multiplex quantification of receptor tyrosine kinase, MAP kinase, and AKT signaling. Cell Reports Methods, 2021, 1, 100015.	2.9	10
80	Quantitative proteomics of breast tumors: Tissue quality assessment to clinical biomarkers. Proteomics, 2017, 17, 1600335.	2.2	8
81	Plasma cell dependence on histone/protein deacetylase 11 reveals a therapeutic target in multiple myeloma. JCI Insight, 2021, 6, .	5.0	8
82	Disrupting the MYC-TFEB Circuit Impairs Amino Acid Homeostasis and Provokes Metabolic Anergy. Cancer Research, 2022, 82, 1234-1250.	0.9	8
83	Proteometabolomics of Melphalan Resistance in Multiple Myeloma. Methods in Molecular Biology, 2019, 1996, 273-296.	0.9	6
84	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
85	Multiplexed Liquid Chromatography-Multiple Reaction Monitoring Mass Spectrometry Quantification of Cancer Signaling Proteins. Methods in Molecular Biology, 2017, 1647, 19-45.	0.9	5
86	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
87	Fucosylated Proteome Profiling Identifies a Fucosylated, Non-Ribosomal, Stress-Responsive Species of Ribosomal Protein S3. Cells, 2021, 10, 1310.	4.1	4
88	Immunoglobulins: Expanding the Role for Mass Spectrometry in Protein Biomarker Quantification. Clinical Chemistry, 2014, 60, 1034-1035.	3.2	2
89	Quantification of Breast Cancer Protein Biomarkers at Different Expression Levels in Human Tumors. Methods in Molecular Biology, 2017, 1788, 251-268.	0.9	2
90	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

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91	Developing an understanding of proteomics: an introduction to biological mass spectrometry. Cancer Investigation, 2005, 23, 47-59.	1.3	1
92	Deubiquitinase Vulnerabilities Identified through Activity-Based Protein Profiling in Non-Small Cell Lung Cancer. ACS Chemical Biology, 2022, 17, 776-784.	3.4	1
93	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
94	Managing a Large-Scale Multiomics Project: A Team Science Case Study in Proteogenomics. Methods in Molecular Biology, 2021, 2194, 187-221.	0.9	0