

# Michael Krauthammer

## List of Publications by Year in descending order

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Version: 2024-02-01

60  
papers

7,240  
citations

201575

27  
h-index

138417

58  
g-index

64  
all docs

64  
docs citations

64  
times ranked

13117  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , 2015, 161, 1681-1696.	13.5	2,562
2	Exome sequencing identifies recurrent somatic RAC1 mutations in melanoma. <i>Nature Genetics</i> , 2012, 44, 1006-1014.	9.4	1,052
3	InÂVivo Identification of Tumor- Suppressive PTEN ceRNAs in an Oncogenic BRAF-Induced Mouse Model of Melanoma. <i>Cell</i> , 2011, 147, 382-395.	13.5	602
4	Exome sequencing identifies recurrent mutations in NF1 and RASopathy genes in sun-exposed melanomas. <i>Nature Genetics</i> , 2015, 47, 996-1002.	9.4	348
5	PLX4032, a selective BRAF <sup>V600E</sup> kinase inhibitor, activates the ERK pathway and enhances cell migration and proliferation of BRAF <sup>WT</sup> melanoma cells. <i>Pigment Cell and Melanoma Research</i> , 2010, 23, 190-200.	1.5	315
6	GeneWays: a system for extracting, analyzing, visualizing, and integrating molecular pathway data. <i>Journal of Biomedical Informatics</i> , 2004, 37, 43-53.	2.5	230
7	Genome-wide screen of promoter methylation identifies novel markers in melanoma. <i>Genome Research</i> , 2009, 19, 1462-1470.	2.4	179
8	Using BLAST for identifying gene and protein names in journal articles. <i>Gene</i> , 2000, 259, 245-252.	1.0	177
9	Molecular triangulation: Bridging linkage and molecular-network information for identifying candidate genes in Alzheimer's disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 15148-15153.	3.3	152
10	Interlesional diversity of T cell receptors in melanoma with immune checkpoints enriched in tissue-resident memory T cells. <i>JCI Insight</i> , 2016, 1, e88955.	2.3	111
11	MEDME: An experimental and analytical methodology for the estimation of DNA methylation levels based on microarray derived MeDIP-enrichment. <i>Genome Research</i> , 2008, 18, 1652-1659.	2.4	105
12	Germline MC1R status influences somatic mutation burden in melanoma. <i>Nature Communications</i> , 2016, 7, 12064.	5.8	103
13	MicroRNA signatures differentiate melanoma subtypes. <i>Cell Cycle</i> , 2011, 10, 1845-1852.	1.3	98
14	Phosphoproteomic Screen Identifies Potential Therapeutic Targets in Melanoma. <i>Molecular Cancer Research</i> , 2011, 9, 801-812.	1.5	83
15	The state of melanoma: challenges and opportunities. <i>Pigment Cell and Melanoma Research</i> , 2016, 29, 404-416.	1.5	77
16	Type II p21-activated kinases (PAKs) are regulated by an autoinhibitory pseudosubstrate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 16107-16112.	3.3	73
17	Genomewide Linkage Scan for Nicotine Dependence: Identification of a Chromosome 5 Risk Locus. <i>Biological Psychiatry</i> , 2007, 61, 119-126.	0.7	72
18	Commensal Clostridiales strains mediate effective anti-cancer immune response against solid tumors. <i>Cell Host and Microbe</i> , 2021, 29, 1573-1588.e7.	5.1	71

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19	Rare SF3B1 R625 mutations in cutaneous melanoma. <i>Melanoma Research</i> , 2014, 24, 332-334.	0.6	64
20	Oncolytic virotherapy-mediated anti-tumor response: a single-cell perspective. <i>Cancer Cell</i> , 2021, 39, 394-406.e4.	7.7	63
21	Rare Nonsynonymous Variants in Alpha-4 Nicotinic Acetylcholine Receptor Gene Protect Against Nicotine Dependence. <i>Biological Psychiatry</i> , 2011, 70, 528-536.	0.7	62
22	Integrated analysis of multidimensional omics data on cutaneous melanoma prognosis. <i>Genomics</i> , 2016, 107, 223-230.	1.3	57
23	Integrative Analysis of Epigenetic Modulation in Melanoma Cell Response to Decitabine: Clinical Implications. <i>PLoS ONE</i> , 2009, 4, e4563.	1.1	56
24	Spitz nevi and Spitzoid melanomas: exome sequencing and comparison with conventional melanocytic nevi and melanomas. <i>Modern Pathology</i> , 2017, 30, 640-649.	2.9	55
25	Neural networks versus Logistic regression for 30-days all-cause readmission prediction. <i>Scientific Reports</i> , 2019, 9, 9277.	1.6	45
26	Decentralized provenance-aware publishing with nanopublications. <i>PeerJ Computer Science</i> , 0, 2, e78.	2.7	45
27	Complementary ensemble clustering of biomedical data. <i>Journal of Biomedical Informatics</i> , 2013, 46, 436-443.	2.5	35
28	Proteomic-Based Detection of a Protein Cluster Dysregulated during Cardiovascular Development Identifies Biomarkers of Congenital Heart Defects. <i>PLoS ONE</i> , 2009, 4, e4221.	1.1	32
29	RASopathy Gene Mutations in Melanoma. <i>Journal of Investigative Dermatology</i> , 2016, 136, 1755-1759.	0.3	26
30	Toward automated assessment of health Web page quality using the DISCERN instrument. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2017, 24, 481-487.	2.2	26
31	Lost in Anonymization â€” A Data Anonymization Reference Classification Merging Legal and Technical Considerations. <i>Journal of Law, Medicine and Ethics</i> , 2020, 48, 228-231.	0.4	19
32	AutoDiscern: rating the quality of online health information with hierarchical encoder attention-based neural networks. <i>BMC Medical Informatics and Decision Making</i> , 2020, 20, 104.	1.5	19
33	A semantic web framework to integrate cancer omics data with biological knowledge. <i>BMC Bioinformatics</i> , 2012, 13, S10.	1.2	17
34	Genome-wide methylation and expression profiling identifies promoter characteristics affecting demethylation-induced gene up-regulation in melanoma. <i>BMC Medical Genomics</i> , 2010, 3, 4.	0.7	16
35	Analyzing Patient Trajectories With Artificial Intelligence. <i>Journal of Medical Internet Research</i> , 2021, 23, e29812.	2.1	16
36	The Association of <i>MUC16</i> Mutation with Tumor Mutation Burden and Its Prognostic Implications in Cutaneous Melanoma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 1792-1799.	1.1	15

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37	AI support for ethical decision-making around resuscitation: proceed with care. <i>Journal of Medical Ethics</i> , 2022, 48, 175-183.	1.0	15
38	A novel anti-melanoma SRC-family kinase inhibitor. <i>Oncotarget</i> , 2019, 10, 2237-2251.	0.8	13
39	Enhancing Clustering by Exploiting Complementary Data Modalities in the Medical Domain. <i>International Federation for Information Processing</i> , 2012, 381, 357-367.	0.4	12
40	Adjusting for Background Mutation Frequency Biases Improves the Identification of Cancer Driver Genes. <i>IEEE Transactions on Nanobioscience</i> , 2013, 12, 150-157.	2.2	10
41	Reducing Annotation Burden Through Multimodal Learning. <i>Frontiers in Big Data</i> , 2020, 3, 19.	1.8	10
42	A semantic web approach to biological pathway data reasoning and integration. <i>Web Semantics</i> , 2006, 4, 207-215.	2.2	9
43	Modulation of Sox10, HIF-1 $\alpha$ , Survivin, and YAP by Minocycline in the Treatment of Neurodevelopmental Handicaps following Hypoxic Insult. <i>American Journal of Pathology</i> , 2015, 185, 2364-2378.	1.9	9
44	Differential immunomodulatory effect of PARP inhibition in BRCA1 deficient and competent tumor cells. <i>Biochemical Pharmacology</i> , 2021, 184, 114359.	2.0	8
45	MU2A $\alpha$ reconciling the genome and transcriptome to determine the effects of base substitutions. <i>Bioinformatics</i> , 2011, 27, 416-418.	1.8	7
46	Modeling the Neurovascular Niche: Unbiased Transcriptome Analysis of the Murine Subventricular Zone in Response to Hypoxic Insult. <i>PLoS ONE</i> , 2013, 8, e76265.	1.1	7
47	Prospective observational study of the role of the microbiome in BCG responsiveness prediction (SILENT-EMPIRE): a study protocol. <i>BMJ Open</i> , 2022, 12, e061421.	0.8	7
48	PySeqLab: an open source Python package for sequence labeling and segmentation. <i>Bioinformatics</i> , 2017, 33, 3497-3499.	1.8	5
49	Next Generation Cancer Data Discovery, Access, and Integration Using Prizms and Nanopublications. <i>Lecture Notes in Computer Science</i> , 2013, 7970, 105-112.	1.0	5
50	Boosting text extraction from biomedical images using text region detection. , 2011, , .		4
51	Global copy number profiling of cancer genomes. <i>Bioinformatics</i> , 2016, 32, 926-928.	1.8	4
52	Controlling testing volume for respiratory viruses using machine learning and text mining. <i>AMIA ... Annual Symposium proceedings</i> , 2016, 2016, 1910-1919.	0.2	4
53	Using Semantic Web Technologies to Annotate and Align Microarray Designs. <i>Cancer Informatics</i> , 2009, 8, CIN.S2335.	0.9	2
54	Unraveling the etiology of primary malignant melanoma of the esophagus. <i>Journal of Thoracic Disease</i> , 2018, 10, S1074-S1075.	0.6	2

#	ARTICLE	IF	CITATIONS
55	How to Synchronize Longitudinal Patient Data With the Underlying Disease Progression: A Pilot Study Using the Biomarker CRP for Timing COVID-19. <i>Frontiers in Medicine</i> , 2021, 8, 607594.	1.2	2
56	A Clinical Decision Support System for Monitoring Post-Colonoscopy Patient Follow-Up and Scheduling. <i>AMIA Summits on Translational Science Proceedings</i> , 2017, 2017, 295-301.	0.4	2
57	Mutadelic: mutation analysis using description logic inferencing capabilities. <i>Bioinformatics</i> , 2015, 31, btv467.	1.8	1
58	Collection and preprocessing of fine needle aspirate patient samples for single cell profiling and data analysis. <i>STAR Protocols</i> , 2021, 2, 100581.	0.5	1
59	Computational Analysis in Cancer Exome Sequencing. <i>Methods in Molecular Biology</i> , 2014, 1176, 219-227.	0.4	1
60	Estimating a gene's mutation burden by the number of observed synonymous base substitutions. , 2012, , .		0