Michael Krauthammer

List of Publications by Year
in descending order

60	7,240	201674 27	138484 58
papers	citations	h-index	g-index

64	64	64	13117
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genomic Classification of Cutaneous Melanoma. Cell, 2015, 161, 1681-1696.	28.9	2,562
2	Exome sequencing identifies recurrent somatic RAC1 mutations in melanoma. Nature Genetics, 2012, 44, 1006-1014.	21.4	1,052
3	InÂVivo Identification of Tumor- Suppressive PTEN ceRNAs in an Oncogenic BRAF-Induced Mouse Model of Melanoma. Cell, 2011, 147, 382-395.	28.9	602
4	Exome sequencing identifies recurrent mutations in NF1 and RASopathy genes in sun-exposed melanomas. Nature Genetics, 2015, 47, 996-1002.	21.4	348
5	PLX4032, a selective BRAF ^{V600E} kinase inhibitor, activates the ERK pathway and enhances cell migration and proliferation of BRAF ^{WT} melanoma cells. Pigment Cell and Melanoma Research, 2010, 23, 190-200.	3.3	315
6	GeneWays: a system for extracting, analyzing, visualizing, and integrating molecular pathway data. Journal of Biomedical Informatics, 2004, 37, 43-53.	4.3	230
7	Genome-wide screen of promoter methylation identifies novel markers in melanoma. Genome Research, 2009, 19, 1462-1470.	5.5	179
8	Using BLAST for identifying gene and protein names in journal articles. Gene, 2000, 259, 245-252.	2.2	177
9	Molecular triangulation: Bridging linkage and molecular-network information for identifying candidate genes in Alzheimer's disease. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 15148-15153.	7.1	152
10	Interlesional diversity of T cell receptors in melanoma with immune checkpoints enriched in tissue-resident memory T cells. JCI Insight, 2016, 1, e88955.	5.0	111
11	MEDME: An experimental and analytical methodology for the estimation of DNA methylation levels based on microarray derived MeDIP-enrichment. Genome Research, 2008, 18, 1652-1659.	5.5	105
12	Germline MC1R status influences somatic mutation burden in melanoma. Nature Communications, 2016, 7, 12064.	12.8	103
13	MicroRNA signatures differentiate melanoma subtypes. Cell Cycle, 2011, 10, 1845-1852.	2.6	98
14	Phosphoproteomic Screen Identifies Potential Therapeutic Targets in Melanoma. Molecular Cancer Research, 2011, 9, 801-812.	3.4	83
15	The state of melanoma: challenges and opportunities. Pigment Cell and Melanoma Research, 2016, 29, 404-416.	3.3	77
16	Type II p21-activated kinases (PAKs) are regulated by an autoinhibitory pseudosubstrate. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 16107-16112.	7.1	73
17	Genomewide Linkage Scan for Nicotine Dependence: Identification of a Chromosome 5 Risk Locus. Biological Psychiatry, 2007, 61, 119-126.	1.3	72
18	Commensal Clostridiales strains mediate effective anti-cancer immune response against solid tumors. Cell Host and Microbe, 2021, 29, 1573-1588.e7.	11.0	71

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19	Rare SF3B1 R625 mutations in cutaneous melanoma. Melanoma Research, 2014, 24, 332-334.	1.2	64
20	Oncolytic virotherapy-mediated anti-tumor response: a single-cell perspective. Cancer Cell, 2021, 39, 394-406.e4.	16.8	63
21	Rare Nonsynonymous Variants in Alpha-4 Nicotinic Acetylcholine Receptor Gene Protect Against Nicotine Dependence. Biological Psychiatry, 2011, 70, 528-536.	1.3	62
22	Integrated analysis of multidimensional omics data on cutaneous melanoma prognosis. Genomics, 2016, 107, 223-230.	2.9	57
23	Integrative Analysis of Epigenetic Modulation in Melanoma Cell Response to Decitabine: Clinical Implications. PLoS ONE, 2009, 4, e4563.	2.5	56
24	Spitz nevi and Spitzoid melanomas: exome sequencing and comparison with conventional melanocytic nevi and melanomas. Modern Pathology, 2017, 30, 640-649.	5.5	55
25	Neural networks versus Logistic regression for 30â€‰days all-cause readmission prediction. Scientific Reports, 2019, 9, 9277.	3.3	45
26	Decentralized provenance-aware publishing with nanopublications. PeerJ Computer Science, 0, 2, e78.	4.5	45
27	Complementary ensemble clustering of biomedical data. Journal of Biomedical Informatics, 2013, 46, 436-443.	4.3	35
28	Proteomic-Based Detection of a Protein Cluster Dysregulated during Cardiovascular Development Identifies Biomarkers of Congenital Heart Defects. PLoS ONE, 2009, 4, e4221.	2.5	32
29	RASopathy Gene Mutations in Melanoma. Journal of Investigative Dermatology, 2016, 136, 1755-1759.	0.7	26
30	Toward automated assessment of health Web page quality using the DISCERN instrument. Journal of the American Medical Informatics Association: JAMIA, 2017, 24, 481-487.	4.4	26
31	Lost in Anonymization â€” A Data Anonymization Reference Classification Merging Legal and Technical Considerations. Journal of Law, Medicine and Ethics, 2020, 48, 228-231.	0.9	19
32	AutoDiscern: rating the quality of online health information with hierarchical encoder attention-based neural networks. BMC Medical Informatics and Decision Making, 2020, 20, 104.	3.0	19
33	A semantic web framework to integrate cancer omics data with biological knowledge. BMC Bioinformatics, 2012, 13, S10.	2.6	17
34	Genome-wide methylation and expression profiling identifies promoter characteristics affecting demethylation-induced gene up-regulation in melanoma. BMC Medical Genomics, 2010, 3, 4.	1.5	16
35	Analyzing Patient Trajectories With Artificial Intelligence. Journal of Medical Internet Research, 2021, 23, e29812.	4.3	16
36	The Association of MUC16 Mutation with Tumor Mutation Burden and Its Prognostic Implications in Cutaneous Melanoma. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1792-1799.	2.5	15

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37	AI support for ethical decision-making around resuscitation: proceed with care. Journal of Medical Ethics, 2022, 48, 175-183.	1.8	15
38	A novel anti-melanoma SRC-family kinase inhibitor. Oncotarget, 2019, 10, 2237-2251.	1.8	13
39	Enhancing Clustering by Exploiting Complementary Data Modalities in the Medical Domain. International Federation for Information Processing, 2012, 381, 357-367.	0.4	12
40	Adjusting for Background Mutation Frequency Biases Improves the Identification of Cancer Driver Genes. IEEE Transactions on Nanobioscience, 2013, 12, 150-157.	3.3	10
41	Reducing Annotation Burden Through Multimodal Learning. Frontiers in Big Data, 2020, 3, 19.	2.9	10
42	A semantic web approach to biological pathway data reasoning and integration. Web Semantics, 2006, 4, 207-215.	2.9	9
43	Modulation of Sox10, HIF-1Î±, Survivin, and YAP by Minocycline in the Treatment of Neurodevelopmental Handicaps following Hypoxic Insult. American Journal of Pathology, 2015, 185, 2364-2378.	3.8	9
44	Differential immunomodulatory effect of PARP inhibition in BRCA1 deficient and competent tumor cells. Biochemical Pharmacology, 2021, 184, 114359.	4.4	8
45	MU2Aâ€"reconciling the genome and transcriptome to determine the effects of base substitutions. Bioinformatics, 2011, 27, 416-418.	4.1	7
46	Modeling the Neurovascular Niche: Unbiased Transcriptome Analysis of the Murine Subventricular Zone in Response to Hypoxic Insult. PLoS ONE, 2013, 8, e76265.	2.5	7
47	Prospective observational study of the role of the microbiome in BCG responsiveness prediction (SILENT-EMPIRE): a study protocol. BMJ Open, 2022, 12, e061421.	1.9	7
48	PySeqLab: an open source Python package for sequence labeling and segmentation. Bioinformatics, 2017, 33, 3497-3499.	4.1	5
49	Next Generation Cancer Data Discovery, Access, and Integration Using Prizms and Nanopublications. Lecture Notes in Computer Science, 2013, 7970, 105-112.	1.3	5
50	Boosting text extraction from biomedical images using text region detection. , 2011, , .		4
51	Global copy number profiling of cancer genomes. Bioinformatics, 2016, 32, 926-928.	4.1	4
52	Controlling testing volume for respiratory viruses using machine learning and text mining. AMIA ... Annual Symposium proceedings, 2016, 2016, 1910-1919.	0.2	4
53	Using Semantic Web Technologies to Annotate and Align Microarray Designs. Cancer Informatics, 2009, 8, CIN.S2335.	1.9	2
54	Unraveling the etiology of primary malignant melanoma of the esophagus. Journal of Thoracic Disease, 2018, 10, S1074-S1075.	1.4	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. Frontiers in Medicine, 2021, 8, 607594.	2.6	2
56	A Clinical Decision Support System for Monitoring Post-Colonoscopy Patient Follow-Up and Scheduling. AMIA Summits on Translational Science Proceedings, 2017, 2017, 295-301.	0.4	2
57	Mutadelic: mutation analysis using description logic inferencing capabilities. Bioinformatics, 2015, 31, btv467.	4.1	1
58	Collection and preprocessing of fine needle aspirate patient samples for single cell profiling and data analysis. STAR Protocols, 2021, 2, 100581.	1.2	1
59	Computational Analysis in Cancer Exome Sequencing. Methods in Molecular Biology, 2014, 1176, 219-227.	0.9	1
60	Estimating a gene's mutation burden by the number of observed synonymous base substitutions. , 2012, , .		0