Michael Krauthammer

List of Publications by Year
in descending order

60	7,240	201575 27	138417 58
papers	citations	h-index	g-index

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

#	Article	IF	Citations
1	AI support for ethical decision-making around resuscitation: proceed with care. Journal of Medical Ethics, 2022, 48, 175-183.	1.0	15
2	Prospective observational study of the role of the microbiome in BCG responsiveness prediction (SILENT-EMPIRE): a study protocol. BMJ Open, 2022, 12, e061421.	0.8	7
3	Differential immunomodulatory effect of PARP inhibition in BRCA1 deficient and competent tumor cells. Biochemical Pharmacology, 2021, 184, 114359.	2.0	8
4	Oncolytic virotherapy-mediated anti-tumor response: a single-cell perspective. Cancer Cell, 2021, 39, 394-406.e4.	7.7	63
5	Collection and preprocessing of fine needle aspirate patient samples for single cell profiling and data analysis. STAR Protocols, 2021, 2, 100581.	0.5	1
6	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.	1.2	2
7	Commensal Clostridiales strains mediate effective anti-cancer immune response against solid tumors. Cell Host and Microbe, 2021, 29, 1573-1588.e7.	5.1	71
8	Analyzing Patient Trajectories With Artificial Intelligence. Journal of Medical Internet Research, 2021, 23, e29812.	2.1	16
9	Lost in Anonymization â€" A Data Anonymization Reference Classification Merging Legal and Technical Considerations. Journal of Law, Medicine and Ethics, 2020, 48, 228-231.	0.4	19
10	Reducing Annotation Burden Through Multimodal Learning. Frontiers in Big Data, 2020, 3, 19.	1.8	10
11	AutoDiscern: rating the quality of online health information with hierarchical encoder attention-based neural networks. BMC Medical Informatics and Decision Making, 2020, 20, 104.	1.5	19
12	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.	1.1	15
13	Neural networks versus Logistic regression for 30â€‰days all-cause readmission prediction. Scientific Reports, 2019, 9, 9277.	1.6	45
14	A novel anti-melanoma SRC-family kinase inhibitor. Oncotarget, 2019, 10, 2237-2251.	0.8	13
15	Unraveling the etiology of primary malignant melanoma of the esophagus. Journal of Thoracic Disease, 2018, 10, S1074-S1075.	0.6	2
16	Spitz nevi and Spitzoid melanomas: exome sequencing and comparison with conventional melanocytic nevi and melanomas. Modern Pathology, 2017, 30, 640-649.	2.9	55
17	PySeqLab: an open source Python package for sequence labeling and segmentation. Bioinformatics, 2017, 33, 3497-3499.	1.8	5
18	Toward automated assessment of health Web page quality using the DISCERN instrument. Journal of the American Medical Informatics Association: JAMIA, 2017, 24, 481-487.	2.2	26

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19	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
20	Germline MC1R status influences somatic mutation burden in melanoma. Nature Communications, 2016, 7, 12064.	5.8	103
21	Integrated analysis of multidimensional omics data on cutaneous melanoma prognosis. Genomics, 2016, 107, 223-230.	1.3	57
22	The state of melanoma: challenges and opportunities. Pigment Cell and Melanoma Research, 2016, 29, 404-416.	1.5	77
23	RASopathy Gene Mutations in Melanoma. Journal of Investigative Dermatology, 2016, 136, 1755-1759.	0.3	26
24	Global copy number profiling of cancer genomes. Bioinformatics, 2016, 32, 926-928.	1.8	4
25	Interlesional diversity of T cell receptors in melanoma with immune checkpoints enriched in tissue-resident memory T cells. JCI Insight, 2016, 1, e88955.	2.3	111
26	Controlling testing volume for respiratory viruses using machine learning and text mining. AMIA ... Annual Symposium proceedings, 2016, 2016, 1910-1919.	0.2	4
27	Mutadelic: mutation analysis using description logic inferencing capabilities. Bioinformatics, 2015, 31, btv467.	1.8	1
28	Genomic Classification of Cutaneous Melanoma. Cell, 2015, 161, 1681-1696.	13.5	2,562
29	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.	1.9	9
30	Exome sequencing identifies recurrent mutations in NF1 and RASopathy genes in sun-exposed melanomas. Nature Genetics, 2015, 47, 996-1002.	9.4	348
31	Rare SF3B1 R625 mutations in cutaneous melanoma. Melanoma Research, 2014, 24, 332-334.	0.6	64
32	Computational Analysis in Cancer Exome Sequencing. Methods in Molecular Biology, 2014, 1176, 219-227.	0.4	1
33	Complementary ensemble clustering of biomedical data. Journal of Biomedical Informatics, 2013, 46, 436-443.	2.5	35
34	Adjusting for Background Mutation Frequency Biases Improves the Identification of Cancer Driver Genes. IEEE Transactions on Nanobioscience, 2013, 12, 150-157.	2.2	10
35	Next Generation Cancer Data Discovery, Access, and Integration Using Prizms and Nanopublications. Lecture Notes in Computer Science, 2013, 7970, 105-112.	1.0	5
36	Modeling the Neurovascular Niche: Unbiased Transcriptome Analysis of the Murine Subventricular Zone in Response to Hypoxic Insult. PLoS ONE, 2013, 8, e76265.	1.1	7

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37	Estimating a gene's mutation burden by the number of observed synonymous base substitutions. , 2012, , .		0
38	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.	3.3	73
39	Exome sequencing identifies recurrent somatic RAC1 mutations in melanoma. Nature Genetics, 2012, 44, 1006-1014.	9.4	1,052
40	Enhancing Clustering by Exploiting Complementary Data Modalities in the Medical Domain. International Federation for Information Processing, 2012, 381, 357-367.	0.4	12
41	A semantic web framework to integrate cancer omics data with biological knowledge. BMC Bioinformatics, 2012, 13, S10.	1.2	17
42	Rare Nonsynonymous Variants in Alpha-4 Nicotinic Acetylcholine Receptor Gene Protect Against Nicotine Dependence. Biological Psychiatry, 2011, 70, 528-536.	0.7	62
43	Boosting text extraction from biomedical images using text region detection. , 2011, , .		4
44	InÂVivo Identification of Tumor- Suppressive PTEN ceRNAs in an Oncogenic BRAF-Induced Mouse Model of Melanoma. Cell, 2011, 147, 382-395.	13.5	602
45	Phosphoproteomic Screen Identifies Potential Therapeutic Targets in Melanoma. Molecular Cancer Research, 2011, 9, 801-812.	1.5	83
46	MU2Aâ€"reconciling the genome and transcriptome to determine the effects of base substitutions. Bioinformatics, 2011, 27, 416-418.	1.8	7
47	MicroRNA signatures differentiate melanoma subtypes. Cell Cycle, 2011, 10, 1845-1852.	1.3	98
48	Genome-wide methylation and expression profiling identifies promoter characteristics affecting demethylation-induced gene up-regulation in melanoma. BMC Medical Genomics, 2010, 3, 4.	0.7	16
49	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.	1.5	315
50	Using Semantic Web Technologies to Annotate and Align Microarray Designs. Cancer Informatics, 2009, 8, CIN.S2335.	0.9	2
51	Proteomic-Based Detection of a Protein Cluster Dysregulated during Cardiovascular Development Identifies Biomarkers of Congenital Heart Defects. PLoS ONE, 2009, 4, e4221.	1.1	32
52	Integrative Analysis of Epigenetic Modulation in Melanoma Cell Response to Decitabine: Clinical Implications. PLoS ONE, 2009, 4, e4563.	1.1	56
53	Genome-wide screen of promoter methylation identifies novel markers in melanoma. Genome Research, 2009, 19, 1462-1470.	2.4	179
54	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.	2.4	105

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55	Genomewide Linkage Scan for Nicotine Dependence: Identification of a Chromosome 5 Risk Locus. Biological Psychiatry, 2007, 61, 119-126.	0.7	72
56	A semantic web approach to biological pathway data reasoning and integration. Web Semantics, 2006, 4, 207-215.	2.2	9
57	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.	3.3	152
58	GeneWays: a system for extracting, analyzing, visualizing, and integrating molecular pathway data. Journal of Biomedical Informatics, 2004, 37, 43-53.	2.5	230
59	Using BLAST for identifying gene and protein names in journal articles. Gene, 2000, 259, 245-252.	1.0	177
60	Decentralized provenance-aware publishing with nanopublications. PeerJ Computer Science, 0, 2, e78.	2.7	45