

List of Publications by Year in descending order

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56
papers

6,087
citations

172386

29
h-index

149623

56
g-index

64
all docs

64
docs citations

64
times ranked

12332
citing authors

#	ARTICLE	IF	CITATIONS
1	Impact of mutant p53 functional properties on TP53 mutation patterns and tumor phenotype: lessons from recent developments in the IARC TP53 database. <i>Human Mutation</i> , 2007, 28, 622-629.	1.1	1,441
2	MiR-21 is an EGFR-regulated anti-apoptotic factor in lung cancer in never-smokers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 12085-12090.	3.3	488
3	MYC-driven accumulation of 2-hydroxyglutarate is associated with breast cancer prognosis. <i>Journal of Clinical Investigation</i> , 2014, 124, 398-412.	3.9	348
4	MicroRNA Expression in Squamous Cell Carcinoma and Adenocarcinoma of the Esophagus: Associations with Survival. <i>Clinical Cancer Research</i> , 2009, 15, 6192-6200.	3.2	347
5	Interactome Maps of Mouse Gene Regulatory Domains Reveal Basic Principles of Transcriptional Regulation. <i>Cell</i> , 2013, 155, 1507-1520.	13.5	299
6	Computational approaches for predicting the biological effect of p53 missense mutations: a comparison of three sequence analysis based methods. <i>Nucleic Acids Research</i> , 2006, 34, 1317-1325.	6.5	295
7	p53 isoforms p133p53 and p53 ^{Δ12} are endogenous regulators of replicative cellular senescence. <i>Nature Cell Biology</i> , 2009, 11, 1135-1142.	4.6	276
8	B Cell Super-Enhancers and Regulatory Clusters Recruit AID Tumorigenic Activity. <i>Cell</i> , 2014, 159, 1524-1537.	13.5	234
9	The Association of MicroRNA Expression with Prognosis and Progression in Early-Stage, Non-Small Cell Lung Adenocarcinoma: A Retrospective Analysis of Three Cohorts. <i>Clinical Cancer Research</i> , 2011, 17, 1875-1882.	3.2	187
10	DNA damage defines sites of recurrent chromosomal translocations in B lymphocytes. <i>Nature</i> , 2012, 484, 69-74.	13.7	186
11	Myc Regulates Chromatin Decompaction and Nuclear Architecture during B Cell Activation. <i>Molecular Cell</i> , 2017, 67, 566-578.e10.	4.5	174
12	Association of Inflammation-Related and microRNA Gene Expression with Cancer-Specific Mortality of Colon Adenocarcinoma. <i>Clinical Cancer Research</i> , 2009, 15, 5878-5887.	3.2	171
13	Noninvasive Urinary Metabolomic Profiling Identifies Diagnostic and Prognostic Markers in Lung Cancer. <i>Cancer Research</i> , 2014, 74, 3259-3270.	0.4	140
14	TCRD and Pharos 2021: mining the human proteome for disease biology. <i>Nucleic Acids Research</i> , 2021, 49, D1334-D1346.	6.5	109
15	An Integrated Prognostic Classifier for Stage I Lung Adenocarcinoma Based on mRNA, microRNA, and DNA Methylation Biomarkers. <i>Journal of Thoracic Oncology</i> , 2015, 10, 1037-1048.	0.5	103
16	BRD4 Profiling Identifies Critical Chronic Lymphocytic Leukemia Oncogenic Circuits and Reveals Sensitivity to PLX51107, a Novel Structurally Distinct BET Inhibitor. <i>Cancer Discovery</i> , 2018, 8, 458-477.	7.7	101
17	Nitric Oxide Is a Key Component in Inflammation-Accelerated Tumorigenesis. <i>Cancer Research</i> , 2008, 68, 7130-7136.	0.4	97
18	A Review of Pulmonary Toxicity of Electronic Cigarettes in the Context of Smoking: A Focus on Inflammation. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017, 26, 1175-1191.	1.1	95

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19	The Consortium of Metabolomics Studies (COMETS): Metabolomics in 47 Prospective Cohort Studies. <i>American Journal of Epidemiology</i> , 2019, 188, 991-1012.	1.6	81
20	Metabolomics and Multi-Omics Integration: A Survey of Computational Methods and Resources. <i>Metabolites</i> , 2020, 10, 202.	1.3	69
21	The metaRbolomics Toolbox in Bioconductor and beyond. <i>Metabolites</i> , 2019, 9, 200.	1.3	64
22	Inflammatory and MicroRNA Gene Expression as Prognostic Classifier of Barrett's-Associated Esophageal Adenocarcinoma. <i>Clinical Cancer Research</i> , 2010, 16, 5824-5834.	3.2	62
23	Effects of Electronic Cigarette Constituents on the Human Lung: A Pilot Clinical Trial. <i>Cancer Prevention Research</i> , 2020, 13, 145-152.	0.7	60
24	Inflammation regulates microRNA expression in cooperation with p53 and nitric oxide. <i>International Journal of Cancer</i> , 2012, 131, 760-765.	2.3	48
25	Network analyses in microbiome based on high-throughput multi-omics data. <i>Briefings in Bioinformatics</i> , 2021, 22, 1639-1655.	3.2	48
26	Integration of Metabolomic and Other Omics Data in Population-Based Study Designs: An Epidemiological Perspective. <i>Metabolites</i> , 2019, 9, 117.	1.3	47
27	microRNA and inflammatory gene expression as prognostic marker for overall survival in esophageal squamous cell carcinoma. <i>International Journal of Cancer</i> , 2013, 132, 2901-2909.	2.3	44
28	Urinary Metabolite Risk Biomarkers of Lung Cancer: A Prospective Cohort Study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 978-986.	1.1	44
29	Biomarkers of Exposure and Effect in the Lungs of Smokers, Nonsmokers, and Electronic Cigarette Users. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 443-451.	1.1	43
30	IntLIM: integration using linear models of metabolomics and gene expression data. <i>BMC Bioinformatics</i> , 2018, 19, 81.	1.2	34
31	RaMP: A Comprehensive Relational Database of Metabolomics Pathways for Pathway Enrichment Analysis of Genes and Metabolites. <i>Metabolites</i> , 2018, 8, 16.	1.3	32
32	Metabolomics Analytics Workflow for Epidemiological Research: Perspectives from the Consortium of Metabolomics Studies (COMETS). <i>Metabolites</i> , 2019, 9, 145.	1.3	30
33	Electronic versus Combustible Cigarette Effects on Inflammasome Component Release into Human Lung. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2019, 199, 922-925.	2.5	28
34	Elucidation of Biological Networks across Complex Diseases Using Single-Cell Omics. <i>Trends in Genetics</i> , 2020, 36, 951-966.	2.9	23
35	Predicting the transactivation activity of p53 missense mutants using a four-body potential score derived from Delaunay tessellations. <i>Human Mutation</i> , 2006, 27, 163-172.	1.1	21
36	The Omics Revolution Continues: The Maturation of High-Throughput Biological Data Sources. <i>Yearbook of Medical Informatics</i> , 2018, 27, 211-222.	0.8	21

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37	Using in vitro ADME data for lead compound selection: An emphasis on PAMPA pH 5 permeability and oral bioavailability. <i>Bioorganic and Medicinal Chemistry</i> , 2022, 56, 116588.	1.4	20
38	Identification of transcription factor co-regulators that drive prostate cancer progression. <i>Scientific Reports</i> , 2020, 10, 20332.	1.6	19
39	NCATS Inxight Drugs: a comprehensive and curated portal for translational research. <i>Nucleic Acids Research</i> , 2022, 50, D1307-D1316.	6.5	16
40	Challenges in proteogenomics: a comparison of analysis methods with the case study of the DREAM proteogenomics sub-challenge. <i>BMC Bioinformatics</i> , 2019, 20, 669.	1.2	10
41	MDM2-Dependent Rewiring of Metabolomic and Lipidomic Profiles in Dedifferentiated Liposarcoma Models. <i>Cancers</i> , 2020, 12, 2157.	1.7	9
42	COMETS Analytics: An Online Tool for Analyzing and Meta-Analyzing Metabolomics Data in Large Research Consortia. <i>American Journal of Epidemiology</i> , 2022, 191, 147-158.	1.6	9
43	Integration of Metabolomics and Transcriptomics to Identify Gene-Metabolite Relationships Specific to Phenotype. <i>Methods in Molecular Biology</i> , 2019, 1928, 441-468.	0.4	7
44	Saliva and Lung Microbiome Associations with Electronic Cigarette Use and Smoking. <i>Cancer Prevention Research</i> , 2022, 15, 435-446.	0.7	6
45	Modeling the functional consequences of single residue replacements in bacteriophage f1 gene V protein. <i>Protein Engineering, Design and Selection</i> , 2009, 22, 665-671.	1.0	5
46	ALTRE: workflow for defining ALTERed Regulatory Elements using chromatin accessibility data. <i>Bioinformatics</i> , 2017, 33, 740-742.	1.8	3
47	The International Conference on Intelligent Biology and Medicine (ICIBM) 2019: bioinformatics methods and applications for human diseases. <i>BMC Bioinformatics</i> , 2019, 20, 676.	1.2	3
48	Structure Based Functional Analysis of Bacteriophage f1 Gene V Protein. , 2008, , .		2
49	Experimental and Study Design Considerations for Uncovering Oncometabolites. <i>Methods in Molecular Biology</i> , 2017, 1513, 37-47.	0.4	2
50	Matchmaking in Bioinformatics. <i>F1000Research</i> , 2018, 7, 171.	0.8	2
51	A Workflow of Integrated Resources to Catalyze Network Pharmacology Driven COVID-19 Research. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 718-729.	2.5	2
52	Electronic Cigarettes and the Lung Proteome. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2018, 198, 1350-1351.	2.5	1
53	The International Conference on Intelligent Biology and Medicine 2019: computational methods for drug interactions. <i>BMC Medical Informatics and Decision Making</i> , 2020, 20, 51.	1.5	1
54	The International Conference on Intelligent Biology and Medicine 2019 (ICIBM 2019): computational methods and applications in medical genomics. <i>BMC Medical Genomics</i> , 2020, 13, 47.	0.7	1

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55	Innovating Computational Biology and Intelligent Medicine: ICIBM 2019 Special Issue. <i>Genes</i> , 2020, 11, 437.	1.0	0
56	Self-organizing maps with variable neighborhoods facilitate learning of chromatin accessibility signal shapes associated with regulatory elements. <i>BMC Bioinformatics</i> , 2021, 22, 35.	1.2	0