

Ewy A Math

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

49
papers

4,772
citations

26
h-index

64
g-index

64
ext. papers

5,567
ext. citations

10.1
avg, IF

4.84
L-index

#	Paper	IF	Citations
49	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	3.4	1
48	Network analyses in microbiome based on high-throughput multi-omics data. <i>Briefings in Bioinformatics</i> , 2021 , 22, 1639-1655	13.4	17
47	TCRD and Pharos 2021: mining the human proteome for disease biology. <i>Nucleic Acids Research</i> , 2021 , 49, D1334-D1346	20.1	20
46	Self-organizing maps with variable neighborhoods facilitate learning of chromatin accessibility signal shapes associated with regulatory elements. <i>BMC Bioinformatics</i> , 2021 , 22, 35	3.6	
45	Metabolomics and Multi-Omics Integration: A Survey of Computational Methods and Resources. <i>Metabolites</i> , 2020 , 10,	5.6	33
44	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	3.6	0
43	An OpenData portal to share COVID-19 drug repurposing data in real time 2020 ,		42
42	Effects of Electronic Cigarette Constituents on the Human Lung: A Pilot Clinical Trial. <i>Cancer Prevention Research</i> , 2020 , 13, 145-152	3.2	33
41	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	4	20
40	Elucidation of Biological Networks across Complex Diseases Using Single-Cell Omics. <i>Trends in Genetics</i> , 2020 , 36, 951-966	8.5	12
39	Identification of transcription factor co-regulators that drive prostate cancer progression. <i>Scientific Reports</i> , 2020 , 10, 20332	4.9	7
38	MDM2-Dependent Rewiring of Metabolomic and Lipidomic Profiles in Dedifferentiated Liposarcoma Models. <i>Cancers</i> , 2020 , 12,	6.6	1
37	The metaRbolomics Toolbox in Bioconductor and beyond. <i>Metabolites</i> , 2019 , 9,	5.6	38
36	Integration of Metabolomic and Other Omics Data in Population-Based Study Designs: An Epidemiological Perspective. <i>Metabolites</i> , 2019 , 9,	5.6	31
35	The Consortium of Metabolomics Studies (COMETS): Metabolomics in 47 Prospective Cohort Studies. <i>American Journal of Epidemiology</i> , 2019 , 188, 991-1012	3.8	44
34	Integration of Metabolomics and Transcriptomics to Identify Gene-Metabolite Relationships Specific to Phenotype. <i>Methods in Molecular Biology</i> , 2019 , 1928, 441-468	1.4	4
33	Metabolomics Analytics Workflow for Epidemiological Research: Perspectives from the Consortium of Metabolomics Studies (COMETS). <i>Metabolites</i> , 2019 , 9,	5.6	16

32	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	3.6	3
31	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	10.2	15
30	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	24.4	67
29	IntLIM: integration using linear models of metabolomics and gene expression data. <i>BMC Bioinformatics</i> , 2018 , 19, 81	3.6	17
28	RaMP: A Comprehensive Relational Database of Metabolomics Pathways for Pathway Enrichment Analysis of Genes and Metabolites. <i>Metabolites</i> , 2018 , 8,	5.6	20
27	The Omics Revolution Continues: The Maturation of High-Throughput Biological Data Sources. <i>Yearbook of Medical Informatics</i> , 2018 , 27, 211-222	4	9
26	Electronic Cigarettes and the Lung Proteome. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2018 , 198, 1350-1351	10.2	1
25	Myc Regulates Chromatin Decompaction and Nuclear Architecture during B Cell Activation. <i>Molecular Cell</i> , 2017 , 67, 566-578.e10	17.6	102
24	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	4	72
23	Experimental and Study Design Considerations for Uncovering Oncometabolites. <i>Methods in Molecular Biology</i> , 2017 , 1513, 37-47	1.4	2
22	ALTRE: workflow for defining ALTERed Regulatory Elements using chromatin accessibility data. <i>Bioinformatics</i> , 2017 , 33, 740-742	7.2	1
21	Urinary Metabolite Risk Biomarkers of Lung Cancer: A Prospective Cohort Study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016 , 25, 978-86	4	26
20	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, 1037-48	8.9	86
19	MYC-driven accumulation of 2-hydroxyglutarate is associated with breast cancer prognosis. <i>Journal of Clinical Investigation</i> , 2014 , 124, 398-412	15.9	281
18	Noninvasive urinary metabolomic profiling identifies diagnostic and prognostic markers in lung cancer. <i>Cancer Research</i> , 2014 , 74, 3259-70	10.1	97
17	B cell super-enhancers and regulatory clusters recruit AID tumorigenic activity. <i>Cell</i> , 2014 , 159, 1524-37	56.2	186
16	Interactome maps of mouse gene regulatory domains reveal basic principles of transcriptional regulation. <i>Cell</i> , 2013 , 155, 1507-20	56.2	255
15	microRNA and inflammatory gene expression as prognostic marker for overall survival in esophageal squamous cell carcinoma. <i>International Journal of Cancer</i> , 2013 , 132, 2901-9	7.5	37

14	DNA damage defines sites of recurrent chromosomal translocations in B lymphocytes. <i>Nature</i> , 2012 , 484, 69-74	50.4	159
13	Inflammation regulates microRNA expression in cooperation with p53 and nitric oxide. <i>International Journal of Cancer</i> , 2012 , 131, 760-5	7.5	39
12	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, 1875-82	12.9	164
11	Inflammatory and microRNA gene expression as prognostic classifier of Barrett's-associated esophageal adenocarcinoma. <i>Clinical Cancer Research</i> , 2010 , 16, 5824-34	12.9	52
10	Modeling the functional consequences of single residue replacements in bacteriophage f1 gene V protein. <i>Protein Engineering, Design and Selection</i> , 2009 , 22, 665-71	1.9	5
9	MicroRNA expression in squamous cell carcinoma and adenocarcinoma of the esophagus: associations with survival. <i>Clinical Cancer Research</i> , 2009 , 15, 6192-200	12.9	316
8	Association of inflammation-related and microRNA gene expression with cancer-specific mortality of colon adenocarcinoma. <i>Clinical Cancer Research</i> , 2009 , 15, 5878-87	12.9	158
7	p53 isoforms Delta133p53 and p53beta are endogenous regulators of replicative cellular senescence. <i>Nature Cell Biology</i> , 2009 , 11, 1135-42	23.4	221
6	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, 12085-90	11.5	423
5	Structure Based Functional Analysis of Bacteriophage f1 Gene V Protein 2008 ,		1
4	Nitric oxide is a key component in inflammation-accelerated tumorigenesis. <i>Cancer Research</i> , 2008 , 68, 7130-6	10.1	87
3	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, 622-9	4.7	1269
2	Predicting the transactivation activity of p53 missense mutants using a four-body potential score derived from Delaunay tessellations. <i>Human Mutation</i> , 2006 , 27, 163-72	4.7	21
1	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, 1317-25	20.1	252