

Hai Fang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9077858/publications.pdf>

Version: 2024-02-01

66
papers

5,915
citations

186265

28
h-index

133252

59
g-index

68
all docs

68
docs citations

68
times ranked

12315
citing authors

#	ARTICLE	IF	CITATIONS
1	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	27.8	1,838
2	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013, 10, 221-227.	19.0	789
3	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016, 17, 184.	8.8	308
4	A predictive computational framework for direct reprogramming between human cell types. <i>Nature Genetics</i> , 2016, 48, 331-335.	21.4	263
5	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019, 20, 244.	8.8	261
6	Peripheral CD8+ T cell characteristics associated with durable responses to immune checkpoint blockade in patients with metastatic melanoma. <i>Nature Medicine</i> , 2020, 26, 193-199.	30.7	211
7	The association between endometriosis and autoimmune diseases: a systematic review and meta-analysis. <i>Human Reproduction Update</i> , 2019, 25, 486-503.	10.8	179
8	A blood atlas of COVID-19 defines hallmarks of disease severity and specificity. <i>Cell</i> , 2022, 185, 916-938.e58.	28.9	164
9	A genetics-led approach defines the drug target landscape of 30 immune-related traits. <i>Nature Genetics</i> , 2019, 51, 1082-1091.	21.4	157
10	SUPERFAMILY 1.75 including a domain-centric gene ontology method. <i>Nucleic Acids Research</i> , 2011, 39, D427-D434.	14.5	147
11	Sequential transcriptional changes dictate safe and effective antigen-specific immunotherapy. <i>Nature Communications</i> , 2014, 5, 4741.	12.8	147
12	PML/RAR α Targets Promoter Regions Containing PU.1 Consensus and RARE Half Sites in Acute Promyelocytic Leukemia. <i>Cancer Cell</i> , 2010, 17, 186-197.	16.8	143
13	XGR software for enhanced interpretation of genomic summary data, illustrated by application to immunological traits. <i>Genome Medicine</i> , 2016, 8, 129.	8.2	137
14	dcGO: database of domain-centric ontologies on functions, phenotypes, diseases and more. <i>Nucleic Acids Research</i> , 2013, 41, D536-D544.	14.5	98
15	Coordination of intrinsic, extrinsic, and endoplasmic reticulum-mediated apoptosis by imatinib mesylate combined with arsenic trioxide in chronic myeloid leukemia. <i>Blood</i> , 2006, 107, 1582-1590.	1.4	91
16	The SUPERFAMILY 1.75 database in 2014: a doubling of data. <i>Nucleic Acids Research</i> , 2015, 43, D227-D233.	14.5	74
17	Transcriptome Analysis of Early Organogenesis in Human Embryos. <i>Developmental Cell</i> , 2010, 19, 174-184.	7.0	69
18	The dnet α ™ approach promotes emerging research on cancer patient survival. <i>Genome Medicine</i> , 2014, 6, 64.	8.2	52

#	ARTICLE	IF	CITATIONS
19	Preferential eradication of acute myelogenous leukemia stem cells by fenretinide. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 5606-5611.	7.1	49
20	A daily-updated tree of (sequenced) life as a reference for genome research. Scientific Reports, 2013, 3, 2015.	3.3	47
21	A PML/RAR α direct target atlas redefines transcriptional deregulation in acute promyelocytic leukemia. Blood, 2021, 137, 1503-1516.	1.4	47
22	Identifying collagen VI as a target of fibrotic diseases regulated by CREBBP/EP300. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 20753-20763.	7.1	45
23	Genome-wide studies identify a novel interplay between AML1 and AML1/ETO in t(8;21) acute myeloid leukemia. Blood, 2016, 127, 233-242.	1.4	44
24	A domain-centric solution to functional genomics via dcGO Predictor. BMC Bioinformatics, 2013, 14, S9.	2.6	42
25	supraHex: An R/Bioconductor package for tabular omics data analysis using a supra-hexagonal map. Biochemical and Biophysical Research Communications, 2014, 443, 285-289.	2.1	37
26	Evolution of the Calcium-Based Intracellular Signaling System. Genome Biology and Evolution, 2016, 8, 2118-2132.	2.5	35
27	Converting Redox Signaling to Apoptotic Activities by Stress-Responsive Regulators HSF1 and NRF2 in Fenretinide Treated Cancer Cells. PLoS ONE, 2009, 4, e7538.	2.5	34
28	p21-Activated kinase 3 is overexpressed in thymic neuroendocrine tumors (carcinoids) with ectopic ACTH syndrome and participates in cell migration. Endocrine, 2010, 38, 38-47.	2.3	33
29	An Interferon-Related Signature in the Transcriptional Core Response of Human Macrophages to Mycobacterium tuberculosis Infection. PLoS ONE, 2012, 7, e38367.	2.5	29
30	The dnet^2 approach promotes emerging research on cancer patient survival. Genome Medicine, 2014, 6, 64.	8.2	25
31	Integrating longitudinal clinical laboratory tests with targeted proteomic and transcriptomic analyses reveal the landscape of host responses in COVID-19. Cell Discovery, 2021, 7, 42.	6.7	23
32	Gene expression profiles of thymic neuroendocrine tumors (carcinoids) with ectopic ACTH syndrome reveal novel molecular mechanism. Endocrine-Related Cancer, 2009, 16, 1273-1282.	3.1	22
33	Reactive oxygen species in eradicating acute myeloid leukemic stem cells. Stem Cell Investigation, 2014, 1, 13.	3.0	20
34	Transcriptome and Proteome Analyses of Drug Interactions with Natural Products. Current Drug Metabolism, 2008, 9, 1038-1048.	1.2	18
35	dcGOR: An R Package for Analysing Ontologies and Protein Domain Annotations. PLoS Computational Biology, 2014, 10, e1003929.	3.2	18
36	Transcriptome-wide subtyping of pediatric and adult T cell acute lymphoblastic leukemia in an international study of 707 cases. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2120787119.	7.1	18

#	ARTICLE	IF	CITATIONS
37	From genome-wide association studies to rational drug target prioritisation in inflammatory arthritis. <i>Lancet Rheumatology</i> , The, 2020, 2, e50-e62.	3.9	17
38	Integration of Genomic and Transcriptomic Markers Improves the Prognosis Prediction of Acute Promyelocytic Leukemia. <i>Clinical Cancer Research</i> , 2021, 27, 3683-3694.	7.0	16
39	Priority index: database of genetic targets in immune-mediated disease. <i>Nucleic Acids Research</i> , 2022, 50, D1358-D1367.	14.5	16
40	Identification of copy number variation-driven molecular subtypes informative for prognosis and treatment in pancreatic adenocarcinoma of a Chinese cohort. <i>EBioMedicine</i> , 2021, 74, 103716.	6.1	14
41	Endoplasmic reticulum stress-mediated apoptosis in imatinib-resistant leukemic K562-r cells triggered by AMN107 combined with arsenic trioxide. <i>Experimental Biology and Medicine</i> , 2013, 238, 932-942.	2.4	13
42	The Evolution of Human Cells in Terms of Protein Innovation. <i>Molecular Biology and Evolution</i> , 2014, 31, 1364-1374.	8.9	13
43	Distinct immune signatures discriminate between asymptomatic and presymptomatic SARS-CoV-2pos subjects. <i>Cell Research</i> , 2021, 31, 1148-1162.	12.0	12
44	A disease-drug-phenotype matrix inferred by walking on a functional domain network. <i>Molecular BioSystems</i> , 2013, 9, 1686.	2.9	10
45	Genomic Evidence Supports the Recognition of Endometriosis as an Inflammatory Systemic Disease and Reveals Disease-Specific Therapeutic Potentials of Targeting Neutrophil Degranulation. <i>Frontiers in Immunology</i> , 2022, 13, 758440.	4.8	10
46	Epigenomic analysis reveals a dynamic and context-specific macrophage enhancer landscape associated with innate immune activation and tolerance. <i>Genome Biology</i> , 2022, 23, .	8.8	9
47	Genomic Insights into Myasthenia Gravis Identify Distinct Immunological Mechanisms in Early and Late Onset Disease. <i>Annals of Neurology</i> , 2021, 90, 455-463.	5.3	8
48	A Topology-Preserving Selection and Clustering Approach to Multidimensional Biological Data. <i>OMICS A Journal of Integrative Biology</i> , 2011, 15, 483-494.	2.0	6
49	A <sc>P</sc>roteome <sc>Q</sc>uality <sc>I</sc>ndex. <i>Environmental Microbiology</i> , 2015, 17, 4-9.	3.8	6
50	Genetic Prioritization, Therapeutic Repositioning and Cross-Disease Comparisons Reveal Inflammatory Targets Tractable for Kidney Stone Disease. <i>Frontiers in Immunology</i> , 2021, 12, 687291.	4.8	6
51	Function-selective domain architecture plasticity potentials in eukaryotic genome evolution. <i>Biochimie</i> , 2015, 119, 269-277.	2.6	5
52	Oncogenic Mutations and Tumor Microenvironment Alterations of Older Patients With Diffuse Large B-Cell Lymphoma. <i>Frontiers in Immunology</i> , 2022, 13, 842439.	4.8	5
53	PiER: web-based facilities tailored for genetic target prioritisation harnessing human disease genetics, functional genomics and protein interactions. <i>Nucleic Acids Research</i> , 2022, 50, W583-W592.	14.5	5
54	Using Self-Organizing Maps to Visualize, Filter and Cluster Multidimensional Bio-Omics Data. , 0, , .		4

#	ARTICLE	IF	CITATIONS
55	A Derived Network-Based Interferon-Related Signature of Human Macrophages Responding to Mycobacterium tuberculosis. <i>BioMed Research International</i> , 2014, 2014, 1-16.	1.9	3
56	Transcriptomic Analysis of Inflammatory Cardiomyopathy Identifies Molecular Signatures of Disease and Informs in silico Prediction of a Network-Based Rationale for Therapy. <i>Frontiers in Immunology</i> , 2021, 12, 640837.	4.8	3
57	Hepatitis B virus-associated follicular lymphoma presents T cell inflamed phenotype and response to lenalidomide. <i>Cancer Communications</i> , 2022, 42, 170-174.	9.2	3
58	An organogenesis network-based comparative transcriptome analysis for understanding early human development in vivo and in vitro. <i>BMC Systems Biology</i> , 2011, 5, 108.	3.0	2
59	Regulatory Genomic Data Cubism. <i>IScience</i> , 2018, 3, 217-225.	4.1	2
60	I3: A Self-organising Learning Workflow for Intuitive Integrative Interpretation of Complex Genetic Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 503-510.	6.9	2
61	Connecting Biological Themes Using a Single Human Network of Gene Associations. , 2009, , .		0
62	Identification of Copy Number Variation-Driven Molecular Subtypes in Pancreatic Adenocarcinoma of Chinese Cohort. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
63	Genetic Interaction Network Interpretation: A Tidy Data Science Perspective. <i>Methods in Molecular Biology</i> , 2021, 2212, 347-376.	0.9	0
64	Coordination of Intrinsic, Extrinsic and Endoplasmic Reticulum-Mediated Apoptosis by Imatinib Mesylate Combined with Arsenic Trioxide in Chronic Myeloid Leukemia.. <i>Blood</i> , 2005, 106, 4841-4841.	1.4	0
65	Coordination of Fenretinide-Induced Apoptosis by Stress-Responsive Regulators in Leukemia Cells. <i>Blood</i> , 2008, 112, 4730-4730.	1.4	0
66	A Probabilistic Integrated Gene Network Model of Multiple Hematopoietic Lineage Specification. <i>Blood</i> , 2008, 112, 4767-4767.	1.4	0