

Hossein Khiabanian

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7873208/publications.pdf>

Version: 2024-02-01

74
papers

7,664
citations

109137

35
h-index

88477

70
g-index

84
all docs

84
docs citations

84
times ranked

13027
citing authors

#	ARTICLE	IF	CITATIONS
1	Promotion of Hepatocellular Carcinoma by the Intestinal Microbiota and TLR4. <i>Cancer Cell</i> , 2012, 21, 504-516.	7.7	1,051
2	Analysis of the chronic lymphocytic leukemia coding genome: role of <i>NOTCH1</i> mutational activation. <i>Journal of Experimental Medicine</i> , 2011, 208, 1389-1401.	4.2	565
3	Recurrent mutations in epigenetic regulators, RHOA and FYN kinase in peripheral T cell lymphomas. <i>Nature Genetics</i> , 2014, 46, 166-170.	9.4	534
4	Genetics of Follicular Lymphoma Transformation. <i>Cell Reports</i> , 2014, 6, 130-140.	2.9	471
5	Leukaemogenesis induced by an activating β -catenin mutation in osteoblasts. <i>Nature</i> , 2014, 506, 240-244.	13.7	455
6	Integrated mutational and cytogenetic analysis identifies new prognostic subgroups in chronic lymphocytic leukemia. <i>Blood</i> , 2013, 121, 1403-1412.	0.6	420
7	Mutations of the SF3B1 splicing factor in chronic lymphocytic leukemia: association with progression and fludarabine-refractoriness. <i>Blood</i> , 2011, 118, 6904-6908.	0.6	342
8	The mutational landscape of cutaneous T cell lymphoma and SÅ©zary syndrome. <i>Nature Genetics</i> , 2015, 47, 1465-1470.	9.4	322
9	Activating mutations in the NT5C2 nucleotidase gene drive chemotherapy resistance in relapsed ALL. <i>Nature Medicine</i> , 2013, 19, 368-371.	15.2	304
10	Clinical impact of small TP53 mutated subclones in chronic lymphocytic leukemia. <i>Blood</i> , 2014, 123, 2139-2147.	0.6	302
11	PHF6 mutations in T-cell acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2010, 42, 338-342.	9.4	282
12	Genetic lesions associated with chronic lymphocytic leukemia transformation to Richter syndrome. <i>Journal of Experimental Medicine</i> , 2013, 210, 2273-2288.	4.2	255
13	Geographic Dependence, Surveillance, and Origins of the 2009 Influenza A (H1N1) Virus. <i>New England Journal of Medicine</i> , 2009, 361, 115-119.	13.9	252
14	A Nondegenerate Code of Deleterious Variants in Mendelian Loci Contributes to Complex Disease Risk. <i>Cell</i> , 2013, 155, 70-80.	13.5	209
15	Mutational landscape, clonal evolution patterns, and role of RAS mutations in relapsed acute lymphoblastic leukemia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 11306-11311.	3.3	151
16	The genetics of nodal marginal zone lymphoma. <i>Blood</i> , 2016, 128, 1362-1373.	0.6	147
17	The Mass of the Coma Cluster from Weak Lensing in the Sloan Digital Sky Survey. <i>Astrophysical Journal</i> , 2007, 671, 1466-1470.	1.6	112
18	Pan-Cancer Analysis of <i>BRCA1</i> and <i>BRCA2</i> Genomic Alterations and Their Association With Genomic Instability as Measured by Genome-Wide Loss of Heterozygosity. <i>JCO Precision Oncology</i> , 2020, 4, 442-465.	1.5	103

#	ARTICLE	IF	CITATIONS
19	Activating mutations and translocations in the guanine exchange factor VAV1 in peripheral T-cell lymphomas. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 764-769.	3.3	100
20	Clonal evolution mechanisms in NT5C2 mutant-relapsed acute lymphoblastic leukaemia. <i>Nature</i> , 2018, 553, 511-514.	13.7	90
21	Genetic lesions associated with chronic lymphocytic leukemia chemo-refractoriness. <i>Blood</i> , 2014, 123, 2378-2388.	0.6	78
22	Complete Regression of Advanced Pancreatic Ductal Adenocarcinomas upon Combined Inhibition of EGFR and C-RAF. <i>Cancer Cell</i> , 2019, 35, 573-587.e6.	7.7	75
23	Alterations to the Esophageal Microbiome Associated with Progression from Barrett's Esophagus to Esophageal Adenocarcinoma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019, 28, 1687-1693.	1.1	68
24	Detection of clonal hematopoiesis of indeterminate potential in clinical sequencing of solid tumor specimens. <i>Blood</i> , 2018, 131, 2501-2505.	0.6	57
25	Evolutionary Dynamics of Pandemic Methicillin-Sensitive <i>Staphylococcus aureus</i> ST398 and Its International Spread via Routes of Human Migration. <i>MBio</i> , 2017, 8, .	1.8	56
26	Gamma Secretase Inhibition by BMS-906024 Enhances Efficacy of Paclitaxel in Lung Adenocarcinoma. <i>Molecular Cancer Therapeutics</i> , 2017, 16, 2759-2769.	1.9	50
27	<i>Lactobacillus rhamnosus</i> GG probiotic enteric regimen does not appreciably alter the gut microbiome or provide protection against GVHD after allogeneic hematopoietic stem cell transplantation. <i>Clinical Transplantation</i> , 2017, 31, e12947.	0.8	49
28	Barrett's esophagus is associated with a distinct oral microbiome. <i>Clinical and Translational Gastroenterology</i> , 2018, 9, e135.	1.3	49
29	Genetic and phenotypic attributes of splenic marginal zone lymphoma. <i>Blood</i> , 2022, 139, 732-747.	0.6	49
30	Reassortment Patterns in Swine Influenza Viruses. <i>PLoS ONE</i> , 2009, 4, e7366.	1.1	46
31	Differences in Patient Age Distribution between Influenza A Subtypes. <i>PLoS ONE</i> , 2009, 4, e6832.	1.1	43
32	Tumor evolutionary directed graphs and the history of chronic lymphocytic leukemia. <i>ELife</i> , 2014, 3, .	2.8	43
33	De novo transcriptome reconstruction and annotation of the Egyptian rousette bat. <i>BMC Genomics</i> , 2015, 16, 1033.	1.2	42
34	Increasing Dietary Fiber Intake Is Associated with a Distinct Esophageal Microbiome. <i>Clinical and Translational Gastroenterology</i> , 2018, 9, e199.	1.3	42
35	Discovering Disease Associations by Integrating Electronic Clinical Data and Medical Literature. <i>PLoS ONE</i> , 2011, 6, e21132.	1.1	41
36	Clinical impact of small subclones harboring <i>NOTCH1</i> , <i>SF3B1</i> or <i>BIRC3</i> mutations in chronic lymphocytic leukemia. <i>Haematologica</i> , 2016, 101, e135-e138.	1.7	34

#	ARTICLE	IF	CITATIONS
37	JAK/STAT of all trades: linking inflammation with cancer development, tumor progression and therapy resistance. <i>Carcinogenesis</i> , 2021, 42, 1411-1419.	1.3	30
38	Data-driven discovery of seasonally linked diseases from an Electronic Health Records system. <i>BMC Bioinformatics</i> , 2014, 15, S3.	1.2	27
39	Emerging Role of Genomic Rearrangements in Breast Cancer: Applying Knowledge from Other Cancers. <i>Biomarkers in Cancer</i> , 2016, 8s1, BIC.S34417.	3.6	27
40	DARK MATTER STRUCTURES IN THE DEEP LENS SURVEY. <i>Astrophysical Journal</i> , 2009, 702, 980-988.	1.6	23
41	High-resolution Genomic Surveillance of 2014 Ebolavirus Using Shared Subclonal Variants. <i>PLOS Currents</i> , 2015, 7, .	1.4	23
42	Somatic CLL mutations occur at multiple distinct hematopoietic maturation stages: documentation and cautionary note regarding cell fraction purity. <i>Leukemia</i> , 2018, 32, 1040-1043.	3.3	19
43	Subclonal NT5C2 mutations are associated with poor outcomes after relapse of pediatric acute lymphoblastic leukemia. <i>Blood</i> , 2020, 135, 921-933.	0.6	17
44	Inference of Germline Mutational Status and Evaluation of Loss of Heterozygosity in High-Depth, Tumor-Only Sequencing Data. <i>JCO Precision Oncology</i> , 2018, 2018, 1-15.	1.5	16
45	A Tumor Suppressor Enhancer of <i>PTEN</i> in T-cell Development and Leukemia. <i>Blood Cancer Discovery</i> , 2021, 2, 92-109.	2.6	15
46	All-FIT: allele-frequency-based imputation of tumor purity from high-depth sequencing data. <i>Bioinformatics</i> , 2020, 36, 2173-2180.	1.8	13
47	Signs of the 2009 Influenza Pandemic in the New York-Presbyterian Hospital Electronic Health Records. <i>PLoS ONE</i> , 2010, 5, e12658.	1.1	12
48	Tissue- and development-stage-specific mRNA and heterogeneous CNV signatures of human ribosomal proteins in normal and cancer samples. <i>Nucleic Acids Research</i> , 2020, 48, 7079-7098.	6.5	12
49	A novel and highly effective mitochondrial uncoupling drug in T-cell leukemia. <i>Blood</i> , 2021, 138, 1317-1330.	0.6	11
50	A Multiresolution Weak-Lensing Mass Reconstruction Method. <i>Astrophysical Journal</i> , 2008, 684, 794-803.	1.6	10
51	Transcriptome reconstruction and annotation of cynomolgus and African green monkey. <i>BMC Genomics</i> , 2014, 15, 846.	1.2	10
52	A Case of T-cell Acute Lymphoblastic Leukemia Relapsed As Myeloid Acute Leukemia. <i>Pediatric Blood and Cancer</i> , 2016, 63, 1660-1663.	0.8	10
53	Gene expression of adipokines and adipokine receptors in the tumor microenvironment: associations of lower expression with more aggressive breast tumor features. <i>Breast Cancer Research and Treatment</i> , 2021, 185, 785-798.	1.1	10
54	Germline Testing Data Validate Inferences of Mutational Status for Variants Detected From Tumor-Only Sequencing. <i>JCO Precision Oncology</i> , 2021, 5, 1749-1757.	1.5	10

#	ARTICLE	IF	CITATIONS
55	Viral diversity and clonal evolution from unphased genomic data. BMC Genomics, 2014, 15, S17.	1.2	9
56	Association of <i>JAK2</i> -V617F Mutations Detected by Solid Tumor Sequencing With Coexistent Myeloproliferative Neoplasms. JAMA Oncology, 2019, 5, 265.	3.4	9
57	On Statistical Modeling of Sequencing Noise in High Depth Data to Assess Tumor Evolution. Journal of Statistical Physics, 2018, 172, 143-155.	0.5	8
58	Moduli Spaces of Phylogenetic Trees Describing Tumor Evolutionary Patterns. Lecture Notes in Computer Science, 2014, , 528-539.	1.0	8
59	The Coding Genome of Nodal Marginal Zone Lymphoma Reveals Recurrent Molecular Alterations of PTPRD and Other Jak/Stat Signaling Genes. Blood, 2014, 124, 705-705.	0.6	8
60	TuBA: Tunable biclustering algorithm reveals clinically relevant tumor transcriptional profiles in breast cancer. GigaScience, 2019, 8, .	3.3	6
61	Mutational signatures reveal ternary relationships between homologous recombination repair, APOBEC, and mismatch repair in gynecological cancers. Journal of Translational Medicine, 2022, 20, 65.	1.8	6
62	MERIT reveals the impact of genomic context on sequencing error rate in ultra-deep applications. BMC Bioinformatics, 2018, 19, 219.	1.2	4
63	Leukemia's Clonal Evolution in Development, Progression, and Relapse. Current Stem Cell Reports, 2019, 5, 73-81.	0.7	3
64	Spleen plays a major role in DLL4-driven acute T-cell lymphoblastic leukemia. Theranostics, 2021, 11, 1594-1608.	4.6	3
65	Deep DNA Sequencing Identifies Small Mutations in Patients with Acute Myelogenous Leukemia (AML) and High-Risk Myelodysplastic Syndromes (MDS): Analysis of Intratumor Genomic Heterogeneity for Prediction of Disease Relapse. Blood, 2019, 134, 1445-1445.	0.6	3
66	Detection of Three Distinct Clonal Populations Using Circulating Cell-Free DNA: A Cautionary Note on the Use of Liquid Biopsy. JCO Precision Oncology, 2019, 3, 1-6.	1.5	2
67	Cilium Expression Score Predicts Glioma Survival. Frontiers in Genetics, 2021, 12, 758391.	1.1	2
68	ParMap, an algorithm for the identification of small genomic insertions and deletions in nextgen sequencing data. BMC Research Notes, 2010, 3, 147.	0.6	1
69	Recurrent Rhoa Mutations In Peripheral T-Cell Lymphoma. Blood, 2013, 122, 846-846.	0.6	1
70	Small Subclones Harboring NOTCH1, SF3B1 or BIRC3 Mutations Are Clinically Irrelevant in Chronic Lymphocytic Leukemia. Blood, 2014, 124, 295-295.	0.6	1
71	The Emergence of 2009 H1N1 Pandemic Influenza. , 2011, , 95-111.		0
72	Integrated Mutational and Cytogenetic Analysis Identifies New Prognostic Subgroups in Chronic Lymphocytic Leukemia. Blood, 2012, 120, 712-712.	0.6	0

#	ARTICLE	IF	CITATIONS
73	Post-Translational Mechanisms of NT5C2 Activation As Non-Genetic Drivers of Chemotherapy Resistance in Relapsed Acute Lymphoblastic Leukemia. <i>Blood</i> , 2019, 134, 728-728.	0.6	0
74	Reply to T. MÃ©nard. <i>JCO Precision Oncology</i> , 2022, , .	1.5	0