Hossein Khiabanian

List of Publications by Year
in descending order

74	7,664	109137 35	88477 70
papers	citations	h-index	g-index

84	84	84	13027
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genetic and phenotypic attributes of splenic marginal zone lymphoma. Blood, 2022, 139, 732-747.	0.6	49
2	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
3	Reply to T. MÃ©nard. JCO Precision Oncology, 2022, , .	1.5	0
4	A Tumor Suppressor Enhancer ofPTENin T-cell Development and Leukemia. Blood Cancer Discovery, 2021, 2, 92-109.	2.6	15
5	Gene expression of adipokines and adipokine receptors in the tumor microenvironment: associations of lower expression with more aggressive breast tumor features. Breast Cancer Research and Treatment, 2021, 185, 785-798.	1.1	10
6	Spleen plays a major role in DLL4-driven acute T-cell lymphoblastic leukemia. Theranostics, 2021, 11, 1594-1608.	4.6	3
7	A novel and highly effective mitochondrial uncoupling drug in T-cell leukemia. Blood, 2021, 138, 1317-1330.	0.6	11
8	JAK/STAT of all trades: linking inflammation with cancer development, tumor progression and therapy resistance. Carcinogenesis, 2021, 42, 1411-1419.	1.3	30
9	Cilium Expression Score Predicts Glioma Survival. Frontiers in Genetics, 2021, 12, 758391.	1.1	2
10	Germline Testing Data Validate Inferences of Mutational Status for Variants Detected From Tumor-Only Sequencing. JCO Precision Oncology, 2021, 5, 1749-1757.	1.5	10
11	All-FIT: allele-frequency-based imputation of tumor purity from high-depth sequencing data. Bioinformatics, 2020, 36, 2173-2180.	1.8	13
12	Pan-Cancer Analysis of BRCA1 and BRCA2 Genomic Alterations and Their Association With Genomic Instability as Measured by Genome-Wide Loss of Heterozygosity. JCO Precision Oncology, 2020, 4, 442-465.	1.5	103
13	Tissue- and development-stageâ€“specific mRNA and heterogeneous CNV signatures of human ribosomal proteins in normal and cancer samples. Nucleic Acids Research, 2020, 48, 7079-7098.	6.5	12
14	Subclonal NT5C2 mutations are associated with poor outcomes after relapse of pediatric acute lymphoblastic leukemia. Blood, 2020, 135, 921-933.	0.6	17
15	TuBA: Tunable biclustering algorithm reveals clinically relevant tumor transcriptional profiles in breast cancer. GigaScience, 2019, 8, .	3.3	6
16	Alterations to the Esophageal Microbiome Associated with Progression from Barrett's Esophagus to Esophageal Adenocarcinoma. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 1687-1693.	1.1	68
17	Leukemiaâ€™s Clonal Evolution in Development, Progression, and Relapse. Current Stem Cell Reports, 2019, 5, 73-81.	0.7	3
18	Complete Regression of Advanced Pancreatic Ductal Adenocarcinomas upon Combined Inhibition of EGFR and C-RAF. Cancer Cell, 2019, 35, 573-587.e6.	7.7	75

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19	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
20	Association of JAK2-V617F Mutations Detected by Solid Tumor Sequencing With Coexistent Myeloproliferative Neoplasms. JAMA Oncology, 2019, 5, 265.	3.4	9
21	Post-Translational Mechanisms of NT5C2 Activation As Non-Genetic Drivers of Chemotherapy Resistance in Relapsed Acute Lymphoblastic Leukemia. Blood, 2019, 134, 728-728.	0.6	0
22	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
23	Barrett's esophagus is associated with a distinct oral microbiome. Clinical and Translational Gastroenterology, 2018, 9, e135.	1.3	49
24	Detection of clonal hematopoiesis of indeterminate potential in clinical sequencing of solid tumor specimens. Blood, 2018, 131, 2501-2505.	0.6	57
25	Clonal evolution mechanisms in NT5C2 mutant-relapsed acute lymphoblastic leukaemia. Nature, 2018, 553, 511-514.	13.7	90
26	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
27	Inference of Germline Mutational Status and Evaluation of Loss of Heterozygosity in High-Depth, Tumor-Only Sequencing Data. JCO Precision Oncology, 2018, 2018, 1-15.	1.5	16
28	Increasing Dietary Fiber Intake Is Associated with a Distinct Esophageal Microbiome. Clinical and Translational Gastroenterology, 2018, 9, e199.	1.3	42
29	MERIT reveals the impact of genomic context on sequencing error rate in ultra-deep applications. BMC Bioinformatics, 2018, 19, 219.	1.2	4
30	Somatic CLL mutations occur at multiple distinct hematopoietic maturation stages: documentation and cautionary note regarding cell fraction purity. Leukemia, 2018, 32, 1040-1043.	3.3	19
31	Evolutionary Dynamics of Pandemic Methicillin-Sensitive Staphylococcus aureus ST398 and Its International Spread via Routes of Human Migration. MBio, 2017, 8, .	1.8	56
32	Activating mutations and translocations in the guanine exchange factor VAV1 in peripheral T-cell lymphomas. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 764-769.	3.3	100
33	Lactobacillus rhamnosus GG probiotic enteric regimen does not appreciably alter the gut microbiome or provide protection against GVHD after allogeneic hematopoietic stem cell transplantation. Clinical Transplantation, 2017, 31, e12947.	0.8	49
34	Gamma Secretase Inhibition by BMS-906024 Enhances Efficacy of Paclitaxel in Lung Adenocarcinoma. Molecular Cancer Therapeutics, 2017, 16, 2759-2769.	1.9	50
35	A Case of Tâ€cell Acute Lymphoblastic Leukemia Relapsed As Myeloid Acute Leukemia. Pediatric Blood and Cancer, 2016, 63, 1660-1663.	0.8	10
36	Clinical impact of small subclones harboring NOTCH1 , SF3B1 or BIRC3 mutations in chronic lymphocytic leukemia. Haematologica, 2016, 101, e135-e138.	1.7	34

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37	Mutational landscape, clonal evolution patterns, and role of RAS mutations in relapsed acute lymphoblastic leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 11306-11311.	3.3	151
38	The genetics of nodal marginal zone lymphoma. Blood, 2016, 128, 1362-1373.	0.6	147
39	Emerging Role of Genomic Rearrangements in Breast Cancer: Applying Knowledge from Other Cancers. Biomarkers in Cancer, 2016, 8s1, BIC.S34417.	3.6	27
40	De novo transcriptome reconstruction and annotation of the Egyptian rousette bat. BMC Genomics, 2015, 16, 1033.	1.2	42
41	The mutational landscape of cutaneous T cell lymphoma and SÃ©zary syndrome. Nature Genetics, 2015, 47, 1465-1470.	9.4	322
42	High-resolution Genomic Surveillance of 2014 Ebolavirus Using Shared Subclonal Variants. PLOS Currents, 2015, 7, .	1.4	23
43	Transcriptome reconstruction and annotation of cynomolgus and African green monkey. BMC Genomics, 2014, 15, 846.	1.2	10
44	Clinical impact of small TP53 mutated subclones in chronic lymphocytic leukemia. Blood, 2014, 123, 2139-2147.	0.6	302
45	Recurrent mutations in epigenetic regulators, RHOA and FYN kinase in peripheral T cell lymphomas. Nature Genetics, 2014, 46, 166-170.	9.4	534
46	Leukaemogenesis induced by an activating Î²-catenin mutation in osteoblasts. Nature, 2014, 506, 240-244.	13.7	455
47	Genetic lesions associated with chronic lymphocytic leukemia chemo-refractoriness. Blood, 2014, 123, 2378-2388.	0.6	78
48	Data-driven discovery of seasonally linked diseases from an Electronic Health Records system. BMC Bioinformatics, 2014, 15, S3.	1.2	27
49	Genetics of Follicular Lymphoma Transformation. Cell Reports, 2014, 6, 130-140.	2.9	471
50	Viral diversity and clonal evolution from unphased genomic data. BMC Genomics, 2014, 15, S17.	1.2	9
51	Moduli Spaces of Phylogenetic Trees Describing Tumor Evolutionary Patterns. Lecture Notes in Computer Science, 2014, , 528-539.	1.0	8
52	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
53	Tumor evolutionary directed graphs and the history of chronic lymphocytic leukemia. ELife, 2014, 3, .	2.8	43
54	Small Subclones Harboring NOTCH1, SF3B1 or BIRC3 Mutations Are Clinically Irrelevant in Chronic Lymphocytic Leukemia. Blood, 2014, 124, 295-295.	0.6	1

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55	A Nondegenerate Code of Deleterious Variants in Mendelian Loci Contributes to Complex Disease Risk. Cell, 2013, 155, 70-80.	13.5	209
56	Genetic lesions associated with chronic lymphocytic leukemia transformation to Richter syndrome. Journal of Experimental Medicine, 2013, 210, 2273-2288.	4.2	255
57	Integrated mutational and cytogenetic analysis identifies new prognostic subgroups in chronic lymphocytic leukemia. Blood, 2013, 121, 1403-1412.	0.6	420
58	Activating mutations in the NT5C2 nucleotidase gene drive chemotherapy resistance in relapsed ALL. Nature Medicine, 2013, 19, 368-371.	15.2	304
59	Recurrent Rhoa Mutations In Peripheral T-Cell Lymphoma. Blood, 2013, 122, 846-846.	0.6	1
60	Promotion of Hepatocellular Carcinoma by the Intestinal Microbiota and TLR4. Cancer Cell, 2012, 21, 504-516.	7.7	1,051
61	Integrated Mutational and Cytogenetic Analysis Identifies New Prognostic Subgroups in Chronic Lymphocytic Leukemia. Blood, 2012, 120, 712-712.	0.6	0
62	Analysis of the chronic lymphocytic leukemia coding genome: role of NOTCH1 mutational activation. Journal of Experimental Medicine, 2011, 208, 1389-1401.	4.2	565
63	Mutations of the SF3B1 splicing factor in chronic lymphocytic leukemia: association with progression and fludarabine-refractoriness. Blood, 2011, 118, 6904-6908.	0.6	342
64	Discovering Disease Associations by Integrating Electronic Clinical Data and Medical Literature. PLoS ONE, 2011, 6, e21132.	1.1	41
65	The Emergence of 2009 H1N1 Pandemic Influenza. , 2011, , 95-111.		0
66	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
67	PHF6 mutations in T-cell acute lymphoblastic leukemia. Nature Genetics, 2010, 42, 338-342.	9.4	282
68	Signs of the 2009 Influenza Pandemic in the New York-Presbyterian Hospital Electronic Health Records. PLoS ONE, 2010, 5, e12658.	1.1	12
69	DARK MATTER STRUCTURES IN THE DEEP LENS SURVEY. Astrophysical Journal, 2009, 702, 980-988.	1.6	23
70	Reassortment Patterns in Swine Influenza Viruses. PLoS ONE, 2009, 4, e7366.	1.1	46
71	Geographic Dependence, Surveillance, and Origins of the 2009 Influenza A (H1N1) Virus. New England Journal of Medicine, 2009, 361, 115-119.	13.9	252
72	Differences in Patient Age Distribution between Influenza A Subtypes. PLoS ONE, 2009, 4, e6832.	1.1	43

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73	A Multiresolution Weakâ€Lensing Mass Reconstruction Method. Astrophysical Journal, 2008, 684, 794-803.	1.6	10
74	The Mass of the Coma Cluster from Weak Lensing in the Sloan Digital Sky Survey. Astrophysical Journal, 2007, 671, 1466-1470.	1.6	112