

Naveed Ishaque

List of Publications by Year in Descending Order

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Version: 2024-04-20

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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

2,862
citations

24
h-index

53
g-index

61
ext. papers

4,307
ext. citations

14.3
avg, IF

4.49
L-index

#	Paper	IF	Citations
49	SSAM-lite: A Light-Weight Web App for Rapid Analysis of Spatially Resolved Transcriptomics Data.. <i>Frontiers in Genetics</i> , 2022 , 13, 785877	4.5	0
48	The genomic and transcriptional landscape of primary central nervous system lymphoma.. <i>Nature Communications</i> , 2022 , 13, 2558	17.4	4
47	MYCN mediates cysteine addiction and sensitizes neuroblastoma to ferroptosis.. <i>Nature Cancer</i> , 2022 , 3, 471-485	15.4	0
46	Single-cell analysis of patient-derived PDAC organoids reveals cell state heterogeneity and a conserved developmental hierarchy. <i>Nature Communications</i> , 2021 , 12, 5826	17.4	8
45	Single-Nucleus and In Situ RNA-Sequencing Reveal Cell Topographies in the Human Pancreas. <i>Gastroenterology</i> , 2021 , 160, 1330-1344.e11	13.3	41
44	CATCH: A Prospective Precision Oncology Trial in Metastatic Breast Cancer. <i>JCO Precision Oncology</i> , 2021 , 5,	3.6	5
43	Gene Expression in Solitary Fibrous Tumors (SFTs) Correlates with Anatomic Localization and NAB2-STAT6 Gene Fusion Variants. <i>American Journal of Pathology</i> , 2021 , 191, 602-617	5.8	9
42	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. <i>Leukemia</i> , 2021 , 35, 2002-2016	10.7	3
41	Cell segmentation-free inference of cell types from in situ transcriptomics data. <i>Nature Communications</i> , 2021 , 12, 3545	17.4	14
40	Super enhancers define regulatory subtypes and cell identity in neuroblastoma.. <i>Nature Cancer</i> , 2021 , 2, 114-128	15.4	15
39	Hypertension delays viral clearance and exacerbates airway hyperinflammation in patients with COVID-19. <i>Nature Biotechnology</i> , 2021 , 39, 705-716	44.5	65
38	Memory-like HCV-specific CD8 T cells retain a molecular scar after cure of chronic HCV infection. <i>Nature Immunology</i> , 2021 , 22, 229-239	19.1	27
37	Alternative lengthening of telomeres in childhood neuroblastoma from genome to proteome. <i>Nature Communications</i> , 2021 , 12, 1269	17.4	12
36	Lipomatous Solitary Fibrous Tumors Harbor Rare NAB2-STAT6 Fusion Variants and Show Up-Regulation of the Gene PPARG, Encoding for a Regulator of Adipocyte Differentiation. <i>American Journal of Pathology</i> , 2021 , 191, 1314-1324	5.8	3
35	Linker histone epitopes are hidden by in situ higher-order chromatin structure. <i>Epigenetics and Chromatin</i> , 2020 , 13, 26	5.8	1
34	Methylome-based cell-of-origin modeling (Methyl-COOM) identifies aberrant expression of immune regulatory molecules in CLL. <i>Genome Medicine</i> , 2020 , 12, 29	14.4	8
33	Integrative Analysis of Multi-omics Data Identified EGFR and PTGS2 as Key Nodes in a Gene Regulatory Network Related to Immune Phenotypes in Head and Neck Cancer. <i>Clinical Cancer Research</i> , 2020 , 26, 3616-3628	12.9	21

32	COVID-19 severity correlates with airway epithelium-immune cell interactions identified by single-cell analysis. <i>Nature Biotechnology</i> , 2020 , 38, 970-979	44.5	487
31	Whole-genome fingerprint of the DNA methylome during chemically induced differentiation of the human AML cell line HL-60/S4. <i>Biology Open</i> , 2020 , 9,	2.2	1
30	Follicular T helper cells shape the HCV-specific CD4+ T cell repertoire after virus elimination. <i>Journal of Clinical Investigation</i> , 2020 , 130, 998-1009	15.9	26
29	IL411 Is a Metabolic Immune Checkpoint that Activates the AHR and Promotes Tumor Progression. <i>Cell</i> , 2020 , 182, 1252-1270.e34	56.2	84
28	Enhancer hijacking activates oncogenic transcription factor NR4A3 in acinic cell carcinomas of the salivary glands. <i>Nature Communications</i> , 2019 , 10, 368	17.4	89
27	Somatic mutations and promotor methylation of the ryanodine receptor 2 is a common event in the pathogenesis of head and neck cancer. <i>International Journal of Cancer</i> , 2019 , 145, 3299-3310	7.5	19
26	Linking aberrant chromatin features in chronic lymphocytic leukemia to transcription factor networks. <i>Molecular Systems Biology</i> , 2019 , 15, e8339	12.2	20
25	Mutational patterns and regulatory networks in epigenetic subgroups of meningioma. <i>Acta Neuropathologica</i> , 2019 , 138, 295-308	14.3	27
24	Identification and Analyses of Extra-Cranial and Cranial Rhabdoid Tumor Molecular Subgroups Reveal Tumors with Cytotoxic T Cell Infiltration. <i>Cell Reports</i> , 2019 , 29, 2338-2354.e7	10.6	40
23	mediates the impact of prenatal bisphenol A exposure on long-term body weight development. <i>Clinical Epigenetics</i> , 2018 , 10, 58	7.7	40
22	EnrichedHeatmap: an R/Bioconductor package for comprehensive visualization of genomic signal associations. <i>BMC Genomics</i> , 2018 , 19, 234	4.5	67
21	Modeling of the Epigenome of the Cell-of-Origin Identifies Cancer-Specific DNA Methylation Patterns in CLL. <i>Blood</i> , 2018 , 132, 3885-3885	2.2	
20	Whole genome sequencing puts forward hypotheses on metastasis evolution and therapy in colorectal cancer. <i>Nature Communications</i> , 2018 , 9, 4782	17.4	51
19	A downy mildew effector evades recognition by polymorphism of expression and subcellular localization. <i>Nature Communications</i> , 2018 , 9, 5192	17.4	27
18	Succession of transiently active tumor-initiating cell clones in human pancreatic cancer xenografts. <i>EMBO Molecular Medicine</i> , 2017 , 9, 918-932	12	26
17	The whole-genome landscape of medulloblastoma subtypes. <i>Nature</i> , 2017 , 547, 311-317	50.4	472
16	Prenatal maternal stress and wheeze in children: novel insights into epigenetic regulation. <i>Scientific Reports</i> , 2016 , 6, 28616	4.9	44
15	Increased vitamin D levels at birth and in early infancy increase offspring allergy risk-evidence for involvement of epigenetic mechanisms. <i>Journal of Allergy and Clinical Immunology</i> , 2016 , 137, 610-3	11.5	32

14	Environment-induced epigenetic reprogramming in genomic regulatory elements in smoking mothers and their children. <i>Molecular Systems Biology</i> , 2016 , 12, 861	12.2	71
13	Mutations in the SIX1/2 pathway and the DROSHA/DGCR8 miRNA microprocessor complex underlie high-risk blastemal type Wilms tumors. <i>Cancer Cell</i> , 2015 , 27, 298-311	24.3	183
12	Retrotransposon Alu is enriched in the epichromatin of HL-60 cells. <i>Nucleus</i> , 2014 , 5, 237-46	3.9	17
11	Expression profiling during arabidopsis/downy mildew interaction reveals a highly-expressed effector that attenuates responses to salicylic acid. <i>PLoS Pathogens</i> , 2014 , 10, e1004443	7.6	61
10	Hypermethylation of the inactive X chromosome is a frequent event in cancer. <i>Cell</i> , 2013 , 155, 567-81	56.2	50
9	In planta effector competition assays detect <i>Hyaloperonospora arabidopsis</i> effectors that contribute to virulence and localize to different plant subcellular compartments. <i>Molecular Plant-Microbe Interactions</i> , 2013 , 26, 745-57	3.6	12
8	Clonal Evolution In Patients With Chronic Lymphocytic Leukemia (CLL) Developing Resistance To BTK Inhibition. <i>Blood</i> , 2013 , 122, 866-866	2.2	20
7	Subcellular localization of the Hpa RxLR effector repertoire identifies a tonoplast-associated protein HaRxL17 that confers enhanced plant susceptibility. <i>Plant Journal</i> , 2012 , 69, 252-65	6.9	123
6	Mechanisms of nuclear suppression of host immunity by effectors from the Arabidopsis downy mildew pathogen <i>Hyaloperonospora arabidopsis</i> (Hpa). <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2012 , 77, 285-93	3.9	15
5	Multiple candidate effectors from the oomycete pathogen <i>Hyaloperonospora arabidopsis</i> suppress host plant immunity. <i>PLoS Pathogens</i> , 2011 , 7, e1002348	7.6	150
4	Signatures of adaptation to obligate biotrophy in the <i>Hyaloperonospora arabidopsis</i> genome. <i>Science</i> , 2010 , 330, 1549-1551	33.3	353
3	Single-cell analysis of patient-derived PDAC organoids reveals cell state heterogeneity and a conserved developmental hierarchy		2
2	Single nucleus and in situ RNA sequencing reveals cell topographies in the human pancreas		6
1	Cell segmentation-free inference of cell types from in situ transcriptomics data		9