

Naveed Ishaque

List of Publications by Year in descending order

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Version: 2024-02-01

50
papers

5,216
citations

147801

31
h-index

214800

47
g-index

62
all docs

62
docs citations

62
times ranked

11057
citing authors

#	ARTICLE	IF	CITATIONS
1	COVID-19 severity correlates with airway epitheliumâ€‘immune cell interactions identified by single-cell analysis. <i>Nature Biotechnology</i> , 2020, 38, 970-979.	17.5	887
2	The whole-genome landscape of medulloblastoma subtypes. <i>Nature</i> , 2017, 547, 311-317.	27.8	787
3	Signatures of Adaptation to Obligate Biotrophy in the <i>Hyaloperonospora arabidopsidis</i> Genome. <i>Science</i> , 2010, 330, 1549-1551.	12.6	492
4	IL4I1 Is a Metabolic Immune Checkpoint that Activates the AHR and Promotes Tumor Progression. <i>Cell</i> , 2020, 182, 1252-1270.e34.	28.9	259
5	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.	16.8	248
6	Multiple Candidate Effectors from the Oomycete Pathogen <i>Hyaloperonospora arabidopsidis</i> Suppress Host Plant Immunity. <i>PLoS Pathogens</i> , 2011, 7, e1002348.	4.7	212
7	Subcellular localization of the Hpa RxLR effector repertoire identifies a tonoplastâ€‘associated protein HaRxL17 that confers enhanced plant susceptibility. <i>Plant Journal</i> , 2012, 69, 252-265.	5.7	198
8	Enhancer hijacking activates oncogenic transcription factor NR4A3 in acinic cell carcinomas of the salivary glands. <i>Nature Communications</i> , 2019, 10, 368.	12.8	153
9	EnrichedHeatmap: an R/Bioconductor package for comprehensive visualization of genomic signal associations. <i>BMC Genomics</i> , 2018, 19, 234.	2.8	152
10	Hypertension delays viral clearance and exacerbates airway hyperinflammation in patients with COVID-19. <i>Nature Biotechnology</i> , 2021, 39, 705-716.	17.5	129
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.	4.7	117
12	Single-Nucleus and In Situ RNAâ€‘Sequencing Reveal Cell Topographies in the Human Pancreas. <i>Gastroenterology</i> , 2021, 160, 1330-1344.e11.	1.3	112
13	Whole genome sequencing puts forward hypotheses on metastasis evolution and therapy in colorectal cancer. <i>Nature Communications</i> , 2018, 9, 4782.	12.8	103
14	Environmentâ€‘induced epigenetic reprogramming in genomic regulatory elements in smoking mothers and their children. <i>Molecular Systems Biology</i> , 2016, 12, 861.	7.2	97
15	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.	14.5	95
16	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.	6.4	74
17	Mutational patterns and regulatory networks in epigenetic subgroups of meningioma. <i>Acta Neuropathologica</i> , 2019, 138, 295-308.	7.7	74
18	Super enhancers define regulatory subtypes and cell identity in neuroblastoma. <i>Nature Cancer</i> , 2021, 2, 114-128.	13.2	73

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19	MYCN mediates cysteine addiction and sensitizes neuroblastoma to ferroptosis. <i>Nature Cancer</i> , 2022, 3, 471-485.	13.2	73
20	MEST mediates the impact of prenatal bisphenol A exposure on long-term body weight development. <i>Clinical Epigenetics</i> , 2018, 10, 58.	4.1	72
21	Hypermethylation of the Inactive X Chromosome Is a Frequent Event in Cancer. <i>Cell</i> , 2013, 155, 567-581.	28.9	67
22	Single-cell analysis of patient-derived PDAC organoids reveals cell state heterogeneity and a conserved developmental hierarchy. <i>Nature Communications</i> , 2021, 12, 5826.	12.8	59
23	Prenatal maternal stress and wheeze in children: novel insights into epigenetic regulation. <i>Scientific Reports</i> , 2016, 6, 28616.	3.3	55
24	Cell segmentation-free inference of cell types from in situ transcriptomics data. <i>Nature Communications</i> , 2021, 12, 3545.	12.8	52
25	The genomic and transcriptional landscape of primary central nervous system lymphoma. <i>Nature Communications</i> , 2022, 13, 2558.	12.8	52
26	Alternative lengthening of telomeres in childhood neuroblastoma from genome to proteome. <i>Nature Communications</i> , 2021, 12, 1269.	12.8	46
27	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, 610-613.	2.9	43
28	A downy mildew effector evades recognition by polymorphism of expression and subcellular localization. <i>Nature Communications</i> , 2018, 9, 5192.	12.8	40
29	Linking aberrant chromatin features in chronic lymphocytic leukemia to transcription factor networks. <i>Molecular Systems Biology</i> , 2019, 15, e8339.	7.2	39
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.	8.2	39
31	Succession of transiently active tumor-initiating cell clones in human pancreatic cancer xenografts. <i>EMBO Molecular Medicine</i> , 2017, 9, 918-932.	6.9	36
32	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.	5.1	34
33	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. <i>Leukemia</i> , 2021, 35, 2002-2016.	7.2	34
34	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.	7.0	31
35	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.	3.8	30
36	Clonal Evolution In Patients With Chronic Lymphocytic Leukemia (CLL) Developing Resistance To BTK Inhibition. <i>Blood</i> , 2013, 122, 866-866.	1.4	22

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37	CATCH: A Prospective Precision Oncology Trial in Metastatic Breast Cancer. <i>JCO Precision Oncology</i> , 2021, 5, 676-686.	3.0	20
38	Retrotransposon Alu is enriched in the epichromatin of HL-60 cells. <i>Nucleus</i> , 2014, 5, 237-246.	2.2	19
39	Mechanisms of Nuclear Suppression of Host Immunity by Effectors from the Arabidopsis Downy Mildew Pathogen <i>Hyaloperonospora arabidopsidis</i> (Hpa). <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2012, 77, 285-293.	1.1	17
40	In Planta Effector Competition Assays Detect <i>Hyaloperonospora arabidopsidis</i> Effectors That Contribute to Virulence and Localize to Different Plant Subcellular Compartments. <i>Molecular Plant-Microbe Interactions</i> , 2013, 26, 745-757.	2.6	16
41	Methylome-based cell-of-origin modeling (Methyl-COOM) identifies aberrant expression of immune regulatory molecules in CLL. <i>Genome Medicine</i> , 2020, 12, 29.	8.2	15
42	Lipomatous Solitary Fibrous Tumors Harbor Rare NAB2-STAT6 Fusion Variants and Show Up-Regulation of the Gene PPARC, Encoding for a Regulator of Adipocyte Differentiation. <i>American Journal of Pathology</i> , 2021, 191, 1314-1324.	3.8	5
43	Linker histone epitopes are hidden by in situ higher-order chromatin structure. <i>Epigenetics and Chromatin</i> , 2020, 13, 26.	3.9	4
44	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, .	1.2	3
45	SSAM-lite: A Light-Weight Web App for Rapid Analysis of Spatially Resolved Transcriptomics Data. <i>Frontiers in Genetics</i> , 2022, 13, 785877.	2.3	2
46	PS-032-Impact of antigen recognition on memory-like HCV-specific CD8+ T-cells. <i>Journal of Hepatology</i> , 2019, 70, e22-e23.	3.7	0
47	Abstract 27: Unravelling Cell-specific Interactions At The Preeclamptic Maternal-foetal Interface From Early To Late Pregnancy. <i>Hypertension</i> , 2021, 78, .	2.7	0
48	Abstract 1417: Clonal succession in pancreatic cancer progression is not driven by genetic instability. , 2015, , .		0
49	LSC Abstract â€œ Epigenetic modifications in cord blood associated with asthma development later in children's life. , 2016, , .		0
50	Modeling of the Epigenome of the Cell-of-Origin Identifies Cancer-Specific DNA Methylation Patterns in CLL. <i>Blood</i> , 2018, 132, 3885-3885.	1.4	0