

Ahmed Mahfouz

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

4,267
citations

279798

23
h-index

206112

48
g-index

79
all docs

79
docs citations

79
times ranked

8278
citing authors

#	ARTICLE	IF	CITATIONS
1	Cell type specificity of glucocorticoid signaling in the adult mouse hippocampus. <i>Journal of Neuroendocrinology</i> , 2022, 34, e13072.	2.6	20
2	Correcting Differential Gene Expression Analysis for Cytoarchitectural Alterations in Substantia Nigra of Parkinson's Disease Patients Reveals Known and Potential Novel Disease-Associated Genes and Pathways. <i>Cells</i> , 2022, 11, 198.	4.1	0
3	scMoC: single-cell multi-omics clustering. <i>Bioinformatics Advances</i> , 2022, 2, .	2.4	3
4	Single-Cell Analysis of Refractory Celiac Disease Demonstrates Inter- and Intra-Patient Aberrant Cell Heterogeneity. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2022, , .	4.5	3
5	Single-Cell Transcriptomics Reveals Discrete Steps in Regulatory T Cell Development in the Human Thymus. <i>Journal of Immunology</i> , 2022, 208, 384-395.	0.8	8
6	Identification and characterization of two consistent osteoarthritis subtypes by transcriptome and clinical data integration. <i>Rheumatology</i> , 2021, 60, 1166-1175.	1.9	23
7	A spatially resolved brain region- and cell type-specific isoform atlas of the postnatal mouse brain. <i>Nature Communications</i> , 2021, 12, 463.	12.8	109
8	Cingulate networks associated with gray matter loss in Parkinson's disease show high expression of cholinergic genes in the healthy brain. <i>European Journal of Neuroscience</i> , 2021, 53, 3727-3739.	2.6	5
9	Hierarchical progressive learning of cell identities in single-cell data. <i>Nature Communications</i> , 2021, 12, 2799.	12.8	25
10	Molecular characterization of the stress network in individuals at risk for schizophrenia. <i>Neurobiology of Stress</i> , 2021, 14, 100307.	4.0	5
11	Timing and localization of myasthenia gravis-related gene expression. <i>European Journal of Neuroscience</i> , 2021, 54, 5574-5585.	2.6	4
12	Transcriptomic Signatures Associated With Regional Cortical Thickness Changes in Parkinson's Disease. <i>Frontiers in Neuroscience</i> , 2021, 15, 733501.	2.8	2
13	Differential analysis of binarized single-cell RNA sequencing data captures biological variation. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab118.	3.2	8
14	Single-Cell Transcriptomics Links Loss of Human Pancreatic β -Cell Identity to ER Stress. <i>Cells</i> , 2021, 10, 3585.	4.1	3
15	High-dimensional cytometric analysis of colorectal cancer reveals novel mediators of antitumour immunity. <i>Gut</i> , 2020, 69, 691-703.	12.1	92
16	Untangling biological factors influencing trajectory inference from single cell data. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa053.	3.2	4
17	Unraveling the Complexity of the Cancer Microenvironment With Multidimensional Genomic and Cytometric Technologies. <i>Frontiers in Oncology</i> , 2020, 10, 1254.	2.8	45
18	SpaGE: Spatial Gene Enhancement using scRNA-seq. <i>Nucleic Acids Research</i> , 2020, 48, e107-e107.	14.5	94

#	ARTICLE	IF	CITATIONS
19	Transcriptomic signatures of brain regional vulnerability to Parkinson's disease. <i>Communications Biology</i> , 2020, 3, 101.	4.4	58
20	An educational guide for nanopore sequencing in the classroom. <i>PLoS Computational Biology</i> , 2020, 16, e1007314.	3.2	20
21	Eleven grand challenges in single-cell data science. <i>Genome Biology</i> , 2020, 21, 31.	8.8	742
22	The single-cell eQTLGen consortium. <i>ELife</i> , 2020, 9, .	6.0	150
23	SCHNEL: scalable clustering of high dimensional single-cell data. <i>Bioinformatics</i> , 2020, 36, i849-i856.	4.1	4
24	Conserved cell types with divergent features in human versus mouse cortex. <i>Nature</i> , 2019, 573, 61-68.	27.8	1,198
25	A comparison of automatic cell identification methods for single-cell RNA sequencing data. <i>Genome Biology</i> , 2019, 20, 194.	8.8	402
26	Early-Life Compartmentalization of Immune Cells in Human Fetal Tissues Revealed by High-Dimensional Mass Cytometry. <i>Frontiers in Immunology</i> , 2019, 10, 1932.	4.8	15
27	Corticosteroid Action in the Brain: The Potential of Selective Receptor Modulation. <i>Neuroendocrinology</i> , 2019, 109, 266-276.	2.5	41
28	Predicting Cell Populations in Single Cell Mass Cytometry Data. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2019, 95, 769-781.	1.5	54
29	CyTOFmerge: integrating mass cytometry data across multiple panels. <i>Bioinformatics</i> , 2019, 35, 4063-4071.	4.1	23
30	Functional genomics analysis of Phelan-McDermid syndrome 22q13 region during human neurodevelopment. <i>PLoS ONE</i> , 2019, 14, e0213921.	2.5	16
31	S191. Molecular Characterization of Stress Reactivity Regions in the Brain. <i>Biological Psychiatry</i> , 2019, 85, S371.	1.3	0
32	Single-cell RNA sequencing in facioscapulohumeral muscular dystrophy disease etiology and development. <i>Human Molecular Genetics</i> , 2019, 28, 1064-1075.	2.9	46
33	RNA sequencing data integration reveals an miRNA interactome of osteoarthritis cartilage. <i>Annals of the Rheumatic Diseases</i> , 2019, 78, 270-277.	0.9	130
34	P24: MAPPING OF NATRIURETIC PEPTIDES AND THEIR RECEPTORS IN THE BRAINS OF NON-DEMENTED HUMAN SUBJECTS AND PATIENTS WITH ALZHEIMER'S DISEASE. <i>Alzheimer's and Dementia</i> , 2018, 14, P782.	0.8	0
35	Natriuretic Peptides in Post-mortem Brain Tissue and Cerebrospinal Fluid of Non-demented Humans and Alzheimer's Disease Patients. <i>Frontiers in Neuroscience</i> , 2018, 12, 864.	2.8	13
36	A structural equation model for imaging genetics using spatial transcriptomics. <i>Brain Informatics</i> , 2018, 5, 13.	3.0	6

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37	Single-cell isoform RNA sequencing characterizes isoforms in thousands of cerebellar cells. <i>Nature Biotechnology</i> , 2018, 36, 1197-1202.	17.5	253
38	How Metabolic State May Regulate Fear: Presence of Metabolic Receptors in the Fear Circuitry. <i>Frontiers in Neuroscience</i> , 2018, 12, 594.	2.8	10
39	Cortical Spreading Depression Causes Unique Dysregulation of Inflammatory Pathways in a Transgenic Mouse Model of Migraine. <i>Molecular Neurobiology</i> , 2017, 54, 2986-2996.	4.0	37
40	NeuroD Factors Discriminate Mineralocorticoid From Glucocorticoid Receptor DNA Binding in the Male Rat Brain. <i>Endocrinology</i> , 2017, 158, 1511-1522.	2.8	56
41	BrainScope: interactive visual exploration of the spatial and temporal human brain transcriptome. <i>Nucleic Acids Research</i> , 2017, 45, gkx046.	14.5	29
42	Brain transcriptome atlases: a computational perspective. <i>Brain Structure and Function</i> , 2017, 222, 1557-1580.	2.3	19
43	Continuous infusion of manganese improves contrast and reduces side effects in manganese-enhanced magnetic resonance imaging studies. <i>NeuroImage</i> , 2017, 147, 1-9.	4.2	20
44	Timing and localization of human dystrophin isoform expression provide insights into the cognitive phenotype of Duchenne muscular dystrophy. <i>Scientific Reports</i> , 2017, 7, 12575.	3.3	123
45	Co-expression Patterns between ATN1 and ATXN2 Coincide with Brain Regions Affected in Huntingtonâ€™s Disease. <i>Frontiers in Molecular Neuroscience</i> , 2017, 10, 399.	2.9	9
46	Pan-cancer subtyping in a 2D-map shows substructures that are driven by specific combinations of molecular characteristics. <i>Scientific Reports</i> , 2016, 6, 24949.	3.3	21
47	Genome-wide coexpression of steroid receptors in the mouse brain: Identifying signaling pathways and functionally coordinated regions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 2738-2743.	7.1	73
48	Gene co-expression analysis identifies brain regions and cell types involved in migraine pathophysiology: a GWAS-based study using the Allen Human Brain Atlas. <i>Human Genetics</i> , 2016, 135, 425-439.	3.8	47
49	Hi-C Chromatin Interaction Networks Predict Co-expression in the Mouse Cortex. <i>PLoS Computational Biology</i> , 2015, 11, e1004221.	3.2	45
50	Shared Pathways Among Autism Candidate Genes Determined by Co-expression Network Analysis of the Developing Human Brain Transcriptome. <i>Journal of Molecular Neuroscience</i> , 2015, 57, 580-594.	2.3	54
51	Visualizing the spatial gene expression organization in the brain through non-linear similarity embeddings. <i>Methods</i> , 2015, 73, 79-89.	3.8	54
52	Genomic connectivity networks based on the BrainSpan atlas of the developing human brain. , 2014, , .		1
53	Identification of a Disease-Associated Network of Intestinal Immune Cells in Treatment-Naive Inflammatory Bowel Disease. <i>Frontiers in Immunology</i> , 0, 13, .	4.8	7