

Fayaz Seifuddin

List of Publications by Year in Descending Order

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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.

36
papers

439
citations

12
h-index

20
g-index

39
ext. papers

713
ext. citations

8.5
avg, IF

3.59
L-index

#	Paper	IF	Citations
36	Amygdala and anterior cingulate transcriptomes from individuals with bipolar disorder reveal downregulated neuroimmune and synaptic pathways.. <i>Nature Neuroscience</i> , 2022 , 25, 381-389	25.5	2
35	Pklr Is a Genetic Modifier of Sickle Cell Disease. <i>Blood</i> , 2021 , 138, 953-953	2.2	
34	Early Myeloid Derived Suppressor Cells (eMDSCs) Are Associated With High Donor Myeloid Chimerism Following Haploidentical HSCT for Sickle Cell Disease.. <i>Frontiers in Immunology</i> , 2021 , 12, 757279	8.4	0
33	Bioinformatics Approaches for Functional Prediction of Long Noncoding RNAs. <i>Methods in Molecular Biology</i> , 2021 , 2254, 1-13	1.4	1
32	Fasting-induced FOXO4 blunts human CD4 T helper cell responsiveness. <i>Nature Metabolism</i> , 2021 , 3, 318-326	14.6	3
31	Network Analysis and Transcriptome Profiling Identify Autophagic and Mitochondrial Dysfunctions in SARS-CoV-2 Infection. <i>Frontiers in Genetics</i> , 2021 , 12, 599261	4.5	31
30	Cell-free DNA maps COVID-19 tissue injury and risk of death and can cause tissue injury. <i>JCI Insight</i> , 2021 , 6,	9.9	18
29	Circulating mitochondrial DNA is a proinflammatory DAMP in sickle cell disease. <i>Blood</i> , 2021 , 137, 3116-3126	12	
28	Methylomic and transcriptomic predictors of one-month exposure to cortisol in healthy individuals. <i>Stress</i> , 2021 , 1-9	3	
27	Identification of human long noncoding RNAs associated with nonalcoholic fatty liver disease and metabolic homeostasis. <i>Journal of Clinical Investigation</i> , 2021 , 131,	15.9	6
26	Toward best practice in cancer mutation detection with whole-genome and whole-exome sequencing. <i>Nature Biotechnology</i> , 2021 , 39, 1141-1150	44.5	11
25	Establishing community reference samples, data and call sets for benchmarking cancer mutation detection using whole-genome sequencing. <i>Nature Biotechnology</i> , 2021 , 39, 1151-1160	44.5	5
24	NOTCH-mediated ex vivo expansion of human hematopoietic stem and progenitor cells by culture under hypoxia. <i>Stem Cell Reports</i> , 2021 , 16, 2336-2350	8	3
23	Apolipoprotein E Signals via TLR4 to Induce CXCL5 Secretion by Asthmatic Airway Epithelial Cells. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2020 , 63, 185-197	5.7	6
22	β87Q-Globin Gene Therapy Reduces Sickle Hemoglobin Production, Allowing for Anti-sickling Activity in Human Erythroid Cells. <i>Molecular Therapy - Methods and Clinical Development</i> , 2020 , 17, 912-921	6.4	10
21	Misregulation of ELK1, AP1, and E12 Transcription Factor Networks Is Associated with Melanoma Progression. <i>Cancers</i> , 2020 , 12,	6.6	1
20	Notch-Mediated Expansion of Human Hematopoietic Stem and Progenitor Cells By Culture Under Hypoxia. <i>Blood</i> , 2020 , 136, 28-29	2.2	

19	RNA Seq Profiles and Bioinformatics Validation in a Large Sample of Sickle Cell Disease Patients. <i>Blood</i> , 2020 , 136, 13-14	2.2	
18	Acetylation-mediated remodeling of the nucleolus regulates cellular acetyl-CoA responses. <i>PLoS Biology</i> , 2020 , 18, e3000981	9.7	8
17	Network Analysis and Transcriptome Profiling Identify Autophagic and Mitochondrial Dysfunctions in SARS-CoV-2 Infection 2020 ,		11
16	In vivo functional analysis of non-conserved human lncRNAs associated with cardiometabolic traits. <i>Nature Communications</i> , 2020 , 11, 45	17.4	29
15	lncRNAKB, a knowledgebase of tissue-specific functional annotation and trait association of long noncoding RNA. <i>Scientific Data</i> , 2020 , 7, 326	8.2	16
14	Genome-Wide Analysis of Off-Target CRISPR/Cas9 Activity in Single-Cell-Derived Human Hematopoietic Stem and Progenitor Cell Clones. <i>Genes</i> , 2020 , 11,	4.2	1
13	IKAP-Identifying K mAjor cell Population groups in single-cell RNA-sequencing analysis. <i>GigaScience</i> , 2019 , 8,	7.6	7
12	Neutrophil Subsets, Platelets, and Vascular Disease in Psoriasis. <i>JACC Basic To Translational Science</i> , 2019 , 4, 1-14	8.7	36
11	Evaluation of Early Biomarkers Associated with Graft Rejection in Patients with Sickle Cell Disease Undergoing Haploidentical Hematopoietic Stem Cell Transplantation. <i>Biology of Blood and Marrow Transplantation</i> , 2018 , 24, S298	4.7	
10	Effect of Genotype and Maternal Affective Disorder on Intronic Methylation of FK506 Binding Protein 5 in Cord Blood DNA. <i>Frontiers in Genetics</i> , 2018 , 9, 648	4.5	6
9	High density lipoprotein proteome is associated with cardiovascular risk factors and atherosclerosis burden as evaluated by coronary CT angiography. <i>Atherosclerosis</i> , 2018 , 278, 278-285	3.1	27
8	Genome-wide Methyl-Seq analysis of blood-brain targets of glucocorticoid exposure. <i>Epigenetics</i> , 2017 , 12, 637-652	5.7	23
7	Investigating the role of early childhood abuse and HPA axis genes in suicide attempters with bipolar disorder. <i>Psychiatric Genetics</i> , 2015 , 25, 106-11	2.9	16
6	Alterations in DNA methylation of Fkbp5 as a determinant of blood-brain correlation of glucocorticoid exposure. <i>Psychoneuroendocrinology</i> , 2014 , 44, 112-22	5	84
5	Converging Evidence for Epistasis between ANK3 and Potassium Channel Gene KCNQ2 in Bipolar Disorder. <i>Frontiers in Genetics</i> , 2013 , 4, 87	4.5	27
4	Association study of X chromosome SNPs in attempted suicide. <i>Psychiatry Research</i> , 2012 , 200, 1044-6	9.9	2
3	Data mining approaches for genome-wide association of mood disorders. <i>Psychiatric Genetics</i> , 2012 , 22, 55-61	2.9	18
2	Adaptation of the CHARM DNA methylation platform for the rat genome reveals novel brain region-specific differences. <i>Epigenetics</i> , 2011 , 6, 1378-90	5.7	17

1 Comprehensive Assessment of Somatic Copy Number Variation Calling Using Next-Generation Sequencing Data

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