Fayaz Seifuddin

List of Publications by Year
in descending order

36 papers	963 citations	516561 16 h-index	501076 28 g-index
39 all docs	39 docs citations	39 times ranked	1653 citing authors

#	Article	IF	Citations
1	Alterations in DNA methylation of Fkbp5 as a determinant of bloodâ€“brain correlation of glucocorticoid exposure. Psychoneuroendocrinology, 2014, 44, 112-122.	1.3	101
2	Cell-free DNA maps COVID-19 tissue injury and risk of death and can cause tissue injury. JCI Insight, 2021, 6, .	2.3	86
3	In vivo functional analysis of non-conserved human lncRNAs associated with cardiometabolic traits. Nature Communications, 2020, 11, 45.	5.8	69
4	Toward best practice in cancer mutation detection with whole-genome and whole-exome sequencing. Nature Biotechnology, 2021, 39, 1141-1150.	9.4	66
5	Network Analysis and Transcriptome Profiling Identify Autophagic and Mitochondrial Dysfunctions in SARS-CoV-2 Infection. Frontiers in Genetics, 2021, 12, 599261.	1.1	64
6	Neutrophil Subsets, Platelets, andÂVascular Disease in Psoriasis. JACC Basic To Translational Science, 2019, 4, 1-14.	1.9	56
7	Circulating mitochondrial DNA is a proinflammatory DAMP in sickle cell disease. Blood, 2021, 137, 3116-3126.	0.6	51
8	lncRNAKB, a knowledgebase of tissue-specific functional annotation and trait association of long noncoding RNA. Scientific Data, 2020, 7, 326.	2.4	40
9	Genome-wide Methyl-Seq analysis of blood-brain targets of glucocorticoid exposure. Epigenetics, 2017, 12, 637-652.	1.3	39
10	High density lipoprotein proteome is associated with cardiovascular risk factors and atherosclerosis burden as evaluated by coronary CT angiography. Atherosclerosis, 2018, 278, 278-285.	0.4	39
11	Establishing community reference samples, data and call sets for benchmarking cancer mutation detection using whole-genome sequencing. Nature Biotechnology, 2021, 39, 1151-1160.	9.4	39
12	Data mining approaches for genome-wide association of mood disorders. Psychiatric Genetics, 2012, 22, 55-61.	0.6	32
13	Converging evidence for epistasis between ANK3 and potassium channel gene KCNQ2 in bipolar disorder. Frontiers in Genetics, 2013, 4, 87.	1.1	31
14	Fasting-induced FOXO4 blunts human CD4+ T helper cell responsiveness. Nature Metabolism, 2021, 3, 318-326.	5.1	29
15	Amygdala and anterior cingulate transcriptomes from individuals with bipolar disorder reveal downregulated neuroimmune and synaptic pathways. Nature Neuroscience, 2022, 25, 381-389.	7.1	27
16	Identification of human long noncoding RNAs associated with nonalcoholic fatty liver disease and metabolic homeostasis. Journal of Clinical Investigation, 2021, 131, .	3.9	23
17	Investigating the role of early childhood abuse and HPA axis genes in suicide attempters with bipolar disorder. Psychiatric Genetics, 2015, 25, 106-111.	0.6	20
18	Acetylation-mediated remodeling of the nucleolus regulates cellular acetyl-CoA responses. PLoS Biology, 2020, 18, e3000981.	2.6	20

#	Article	IF	Citations
19	Adaptation of the CHARM DNA methylation platform for the rat genome reveals novel brain region-specific differences. Epigenetics, 2011, 6, 1378-1390.	1.3	17
20	IKAPâ€"Identifying K mAjor cell Population groups in single-cell RNA-sequencing analysis. GigaScience, 2019, 8, .	3.3	16
21	Genome-Wide Analysis of Off-Target CRISPR/Cas9 Activity in Single-Cell-Derived Human Hematopoietic Stem and Progenitor Cell Clones. Genes, 2020, 11, 1501.	1.0	14
22	Î²T87Q-Globin Gene Therapy Reduces Sickle Hemoglobin Production, Allowing for ExÂVivo Anti-sickling Activity in Human Erythroid Cells. Molecular Therapy - Methods and Clinical Development, 2020, 17, 912-921.	1.8	13
23	Apolipoprotein E Signals via TLR4 to Induce CXCL5 Secretion by Asthmatic Airway Epithelial Cells. American Journal of Respiratory Cell and Molecular Biology, 2020, 63, 185-197.	1.4	12
24	NOTCH-mediated exÂvivo expansion of human hematopoietic stem and progenitor cells by culture under hypoxia. Stem Cell Reports, 2021, 16, 2336-2350.	2.3	10
25	Effect of Genotype and Maternal Affective Disorder on Intronic Methylation of FK506 Binding Protein 5 in Cord Blood DNA. Frontiers in Genetics, 2018, 9, 648.	1.1	9
26	Genetic variants of PKLR are associated with acute pain in sickle cell disease. Blood Advances, 2022, 6, 3535-3540.	2.5	6
27	Misregulation of ELK1, AP1, and E12 Transcription Factor Networks Is Associated with Melanoma Progression. Cancers, 2020, 12, 458.	1.7	5
28	Early Myeloid Derived Suppressor Cells (eMDSCs) Are Associated With High Donor Myeloid Chimerism Following Haploidentical HSCT for Sickle Cell Disease. Frontiers in Immunology, 2021, 12, 757279.	2.2	5
29	Association study of X chromosome SNPs in attempted suicide. Psychiatry Research, 2012, 200, 1044-1046.	1.7	4
30	Bioinformatics Approaches for Functional Prediction of Long Noncoding RNAs. Methods in Molecular Biology, 2021, 2254, 1-13.	0.4	1
31	Association of the FTO Gene with Suboptimal Weight Loss Following Bariatric Surgery. Surgery for Obesity and Related Diseases, 2016, 12, S32.	1.0	0
32	Evaluation of Early Biomarkers Associated with Graft Rejection in Patients with Sickle Cell Disease Undergoing Haploidentical Hematopoietic Stem Cell Transplantation. Biology of Blood and Marrow Transplantation, 2018, 24, S298.	2.0	0
33	Methylomic and transcriptomic predictors of one-month exposure to cortisol in healthy individuals. Stress, 2021, 24, 840-848.	0.8	0
34	Pklr Is a Genetic Modifier of Sickle Cell Disease. Blood, 2021, 138, 953-953.	0.6	0
35	Notch-Mediated Expansion of Human Hematopoietic Stem and Progenitor Cells By Culture Under Hypoxia. Blood, 2020, 136, 28-29.	0.6	0
36	RNA Seq Profiles and Bioinformatics Validation in a Large Sample of Sickle Cell Disease Patients. Blood, 2020, 136, 13-14.	0.6	0