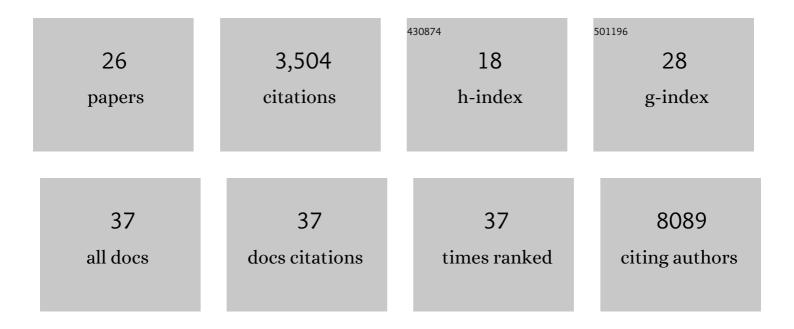
## Ikhlak Ahmed

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5150009/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Ensembl 2013. Nucleic Acids Research, 2012, 41, D48-D55.	14.5	856
2	Integrative epigenomic mapping defines four main chromatin states in Arabidopsis. EMBO Journal, 2011, 30, 1928-1938.	7.8	600
3	Mapping Human Genetic Diversity in Asia. Science, 2009, 326, 1541-1545.	12.6	557
4	Genetic landscape of the people of India: a canvas for disease gene exploration. Journal of Genetics, 2008, 87, 3-20.	0.7	282
5	Integrative Transcript and Metabolite Analysis of Nutritionally Enhanced <i>DE-ETIOLATED1</i> Downregulated Tomato Fruit. Plant Cell, 2010, 22, 1190-1215.	6.6	160
6	Altered expression pattern of circular RNAs in primary and metastatic sites of epithelial ovarian carcinoma. Oncotarget, 2016, 7, 36366-36381.	1.8	148
7	Genome-wide evidence for local DNA methylation spreading from small RNA-targeted sequences in Arabidopsis. Nucleic Acids Research, 2011, 39, 6919-6931.	14.5	142
8	Histone H2B Monoubiquitination Facilitates the Rapid Modulation of Gene Expression during Arabidopsis Photomorphogenesis. PLoS Genetics, 2012, 8, e1002825.	3.5	115
9	Insights into the role of DNA methylation in diatoms by genome-wide profiling in Phaeodactylum tricornutum. Nature Communications, 2013, 4, 2091.	12.8	113
10	Genus-wide sequencing supports a two-locus model for sex-determination in Phoenix. Nature Communications, 2018, 9, 3969.	12.8	86
11	Role of non-coding RNA networks in leukemia progression, metastasis and drug resistance. Molecular Cancer, 2020, 19, 57.	19.2	68
12	DET1-mediated degradation of a SAGA-like deubiquitination module controls H2Bub homeostasis. ELife, 2018, 7, .	6.0	63
13	Insights Into the Role of CircRNAs: Biogenesis, Characterization, Functional, and Clinical Impact in Human Malignancies. Frontiers in Cell and Developmental Biology, 2021, 9, 617281.	3.7	53
14	Ensembl regulation resources. Database: the Journal of Biological Databases and Curation, 2016, 2016, bav119.	3.0	45
15	Silencing of ANKRD12 circRNA induces molecular and functional changes associated with invasive phenotypes. BMC Cancer, 2019, 19, 565.	2.6	33
16	Qatar genome: Insights on genomics from the Middle East. Human Mutation, 2022, 43, 499-510.	2.5	29
17	Identification of human genetic variants controlling circular RNA expression. Rna, 2019, 25, 1765-1778.	3.5	23
18	A population study of clinically actionable genetic variation affecting drug response from the Middle East. Npj Genomic Medicine, 2022, 7, 10.	3.8	20

Ikhlak Ahmed

#	Article	IF	CITATIONS
19	Cell Type-Specific TGF-β Mediated EMT in 3D and 2D Models and Its Reversal by TGF-β Receptor Kinase Inhibitor in Ovarian Cancer Cell Lines. International Journal of Molecular Sciences, 2019, 20, 3568.	4.1	19
20	Regulation of Circular RNA CircNFATC3 in Cancer Cells Alters Proliferation, Migration, and Oxidative Phosphorylation. Frontiers in Cell and Developmental Biology, 2021, 9, 595156.	3.7	19
21	K-core decomposition of a protein domain co-occurrence network reveals lower cancer mutation rates for interior cores. Journal of Clinical Bioinformatics, 2015, 5, 1.	1.2	16
22	DNA DAMAGE BINDING PROTEIN2 Shapes the DNA Methylation Landscape. Plant Cell, 2016, 28, 2043-2059.	6.6	16
23	High-resolution protein–protein interaction mapping using all-versus-all sequencing (AVA-Seq). Journal of Biological Chemistry, 2019, 294, 11549-11558.	3.4	10
24	Melanocortinâ€4 receptor complexity in energy homeostasis,obesity and drug development strategies. Diabetes, Obesity and Metabolism, 2022, 24, 583-598.	4.4	8
25	Utilizing linkage disequilibrium information from Indian Genome Variation Database for mapping mutations: SCA12 case study. Journal of Genetics, 2009, 88, 55-60.	0.7	4
26	Characterization Of Circular Rnas In Ovarian Cancer. , 2014, , .		1