

# Osagie G Izuogu

## 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.

16 papers	4,917 citations	12 h-index	18 g-index
18 ext. papers	8,047 ext. citations	12 avg, IF	4.46 L-index

#	Paper	IF	Citations
16	Cell type-specific novel long non-coding RNA and circular RNA in the BLUEPRINT hematopoietic transcriptomes atlas. <i>Haematologica</i> , <b>2021</b> , 106, 2613-2623	6.6	5
15	Ensembl 2021. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, D884-D891	20.1	324
14	GENCODE 2021. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, D916-D923	20.1	82
13	LINE retrotransposons characterize mammalian tissue-specific and evolutionarily dynamic regulatory regions. <i>Genome Biology</i> , <b>2021</b> , 22, 62	18.3	9
12	An improved pig reference genome sequence to enable pig genetics and genomics research. <i>GigaScience</i> , <b>2020</b> , 9,	7.6	60
11	Ensembl 2020. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, D682-D688	20.1	645
10	Sequencing-based microsatellite instability testing using as few as six markers for high-throughput clinical diagnostics. <i>Human Mutation</i> , <b>2020</b> , 41, 332-341	4.7	12
9	An integrated transcriptional analysis of the developing human retina. <i>Development (Cambridge)</i> , <b>2019</b> , 146,	6.6	42
8	GENCODE reference annotation for the human and mouse genomes. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, D766-D773	20.1	1140
7	Ensembl 2019. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, D745-D751	20.1	554
6	Ensembl 2018. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, D754-D761	20.1	1822
5	Analysis of human ES cell differentiation establishes that the dominant isoforms of the lncRNAs RMST and FIRRE are circular. <i>BMC Genomics</i> , <b>2018</b> , 19, 276	4.5	27
4	PTESFinder: a computational method to identify post-transcriptional exon shuffling (PTES) events. <i>BMC Bioinformatics</i> , <b>2016</b> , 17, 31	3.6	32
3	Circular RNA enrichment in platelets is a signature of transcriptome degradation. <i>Blood</i> , <b>2016</b> , 127, e1-e11	11.1	141
2	Cell type specific novel lincRNAs and circRNAs in the BLUEPRINT haematopoietic transcriptomes atlas		3
1	An improved pig reference genome sequence to enable pig genetics and genomics research		15