

Suganthi Balasubramanian

List of Publications by Citations

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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.

38 papers	7,688 citations	27 h-index	41 g-index
41 ext. papers	9,783 ext. citations	19.9 avg, IF	4.46 L-index

#	Paper	IF	Citations
38	GENCODE: the reference human genome annotation for The ENCODE Project. <i>Genome Research</i> , 2012 , 22, 1760-74	9.7	3142
37	Personal omics profiling reveals dynamic molecular and medical phenotypes. <i>Cell</i> , 2012 , 148, 1293-307	56.2	921
36	A systematic survey of loss-of-function variants in human protein-coding genes. <i>Science</i> , 2012 , 335, 823-833	33.3	880
35	A Protein-Truncating HSD17B13 Variant and Protection from Chronic Liver Disease. <i>New England Journal of Medicine</i> , 2018 , 378, 1096-1106	59.2	350
34	Distribution and clinical impact of functional variants in 50,726 whole-exome sequences from the DiscovEHR study. <i>Science</i> , 2016 , 354,	33.3	320
33	Integrative annotation of variants from 1092 humans: application to cancer genomics. <i>Science</i> , 2013 , 342, 1235587	33.3	281
32	The GENCODE pseudogene resource. <i>Genome Biology</i> , 2012 , 13, R51	18.3	232
31	What makes a protein a protein? Hydrophobic core designs that specify stability and structural properties. <i>Protein Science</i> , 1996 , 5, 1584-93	6.3	166
30	Protein alchemy: changing beta-sheet into alpha-helix. <i>Nature Structural Biology</i> , 1997 , 4, 548-52		146
29	Molecular fossils in the human genome: identification and analysis of the pseudogenes in chromosomes 21 and 22. <i>Genome Research</i> , 2002 , 12, 272-80	9.7	144
28	Exome sequencing and characterization of 49,960 individuals in the UK Biobank. <i>Nature</i> , 2020 , 586, 749-756	35.6	122
27	Comprehensive analysis of amino acid and nucleotide composition in eukaryotic genomes, comparing genes and pseudogenes. <i>Nucleic Acids Research</i> , 2002 , 30, 2515-23	20.1	102
26	Defining the human reference protein-coding gene set. <i>Genome Biology</i> , 2010 , 11,	18.3	78
25	Comparative analysis of processed ribosomal protein pseudogenes in four mammalian genomes. <i>Genome Biology</i> , 2009 , 10, R2	18.3	72
24	Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. <i>Nature Communications</i> , 2015 , 6, 5903	17.4	56
23	Whole exome sequencing and characterization of coding variation in 49,960 individuals in the UK Biobank		56
22	VAT: a computational framework to functionally annotate variants in personal genomes within a cloud-computing environment. <i>Bioinformatics</i> , 2012 , 28, 2267-9	7.2	55

21	Comparative analysis of pseudogenes across three phyla. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 13361-6	11.5	54
20	Advancing human genetics research and drug discovery through exome sequencing of the UK Biobank. <i>Nature Genetics</i> , 2021 , 53, 942-948	36.3	42
19	Analysis of variable retroduplications in human populations suggests coupling of retrotransposition to cell division. <i>Genome Research</i> , 2013 , 23, 2042-52	9.7	41
18	Comprehensive analysis of the pseudogenes of glycolytic enzymes in vertebrates: the anomalously high number of GAPDH pseudogenes highlights a recent burst of retrotranspositional activity. <i>BMC Genomics</i> , 2009 , 10, 480	4.5	41
17	Transmuting alpha helices and beta sheets. <i>Folding & Design</i> , 1997 , 2, R71-9		41
16	A comprehensive catalog of predicted functional upstream open reading frames in humans. <i>Nucleic Acids Research</i> , 2018 , 46, 3326-3338	20.1	40
15	Profiling and Leveraging Relatedness in a Precision Medicine Cohort of 92,455 Exomes. <i>American Journal of Human Genetics</i> , 2018 , 102, 874-889	11	38
14	Concept and design of a genome-wide association genotyping array tailored for transplantation-specific studies. <i>Genome Medicine</i> , 2015 , 7, 90	14.4	38
13	Sequence variation in G-protein-coupled receptors: analysis of single nucleotide polymorphisms. <i>Nucleic Acids Research</i> , 2005 , 33, 1710-21	20.1	37
12	Exome sequencing and analysis of 454,787 UK Biobank participants. <i>Nature</i> , 2021 , 599, 628-634	50.4	34
11	Pan-ancestry exome-wide association analyses of COVID-19 outcomes in 586,157 individuals. <i>American Journal of Human Genetics</i> , 2021 , 108, 1350-1355	11	25
10	Gene inactivation and its implications for annotation in the era of personal genomics. <i>Genes and Development</i> , 2011 , 25, 1-10	12.6	23
9	Sequencing of 640,000 exomes identifies variants associated with protection from obesity. <i>Science</i> , 2021 , 373,	33.3	22
8	Using ALoFT to determine the impact of putative loss-of-function variants in protein-coding genes. <i>Nature Communications</i> , 2017 , 8, 382	17.4	19
7	Tertiary structure of uracil-DNA glycosylase inhibitor protein. <i>Journal of Biological Chemistry</i> , 1995 , 270, 16840-7	5.4	15
6	SNPs on human chromosomes 21 and 22 -- analysis in terms of protein features and pseudogenes. <i>Pharmacogenomics</i> , 2002 , 3, 393-402	2.6	14
5	Secondary structure of uracil-DNA glycosylase inhibitor protein. <i>Journal of Biological Chemistry</i> , 1995 , 270, 296-303	5.4	12
4	MAPPIN: a method for annotating, predicting pathogenicity and mode of inheritance for nonsynonymous variants. <i>Nucleic Acids Research</i> , 2017 , 45, 10393-10402	20.1	11

3	Polygenic Risk of Psychiatric Disorders Exhibits Cross-trait Associations in Electronic Health Record Data From European Ancestry Individuals. <i>Biological Psychiatry</i> , 2021 , 89, 236-245	7.9	8
2	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. <i>Kidney International</i> , 2021 , 99, 926-939	9.9	6
1	Analysis of rare genetic variation underlying cardiometabolic diseases and traits among 200,000 individuals in the UK Biobank.. <i>Nature Genetics</i> , 2022 ,	36.3	4