Suganthi Balasubramanian

List of Publications by Year
in descending order

37	10,916	159585	345221
papers	citations	30	36
		h-index	g-index

41	41	41	24499
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	GENCODE: The reference human genome annotation for The ENCODE Project. Genome Research, 2012, 22, 1760-1774.	5.5	4,217
2	Personal Omics Profiling Reveals Dynamic Molecular and Medical Phenotypes. Cell, 2012, 148, 1293-1307.	28.9	1,134
3	A Systematic Survey of Loss-of-Function Variants in Human Protein-Coding Genes. Science, 2012, 335, 823-828.	12.6	1,095
4	A Protein-Truncating *HSD17B13* Variant and Protection from Chronic Liver Disease. New England Journal of Medicine, 2018, 378, 1096-1106.	27.0	556
5	Distribution and clinical impact of functional variants in 50,726 whole-exome sequences from the DiscovEHR study. Science, 2016, 354, .	12.6	464
6	Exome sequencing and analysis of 454,787 UK Biobank participants. Nature, 2021, 599, 628-634.	27.8	377
7	Exome sequencing and characterization of 49,960 individuals in the UK Biobank. Nature, 2020, 586, 749-756.	27.8	369
8	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235587.	12.6	341
9	The GENCODE pseudogene resource. Genome Biology, 2012, 13, R51.	9.6	273
10	Advancing human genetics research and drug discovery through exome sequencing of the UK Biobank. Nature Genetics, 2021, 53, 942-948.	21.4	234
11	What makes a protein a protein? Hydrophobic core designs that specify stability and structural properties. Protein Science, 1996, 5, 1584-1593.	7.6	189
12	Molecular Fossils in the Human Genome: Identification and Analysis of the Pseudogenes in Chromosomes 21 and 22. Genome Research, 2002, 12, 272-280.	5.5	167
13	Protein alchemy: Changing Î²-sheet into Î±-helix. Nature Structural Biology, 1997, 4, 548-552.	9.7	164
14	Sequencing of 640,000 exomes identifies *GPR75* variants associated with protection from obesity. Science, 2021, 373, .	12.6	130
15	Comprehensive analysis of amino acid and nucleotide composition in eukaryotic genomes, comparing genes and pseudogenes. Nucleic Acids Research, 2002, 30, 2515-2523.	14.5	121
16	Comparative analysis of processed ribosomal protein pseudogenes in four mammalian genomes. Genome Biology, 2009, 10, R2.	9.6	87
17	A comprehensive catalog of predicted functional upstream open reading frames in humans. Nucleic Acids Research, 2018, 46, 3326-3338.	14.5	76
18	Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. Nature Communications, 2015, 6, 5903.	12.8	73

#	ARTICLE	IF	CITATIONS
19	Comparative analysis of pseudogenes across three phyla. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 13361-13366.	7.1	72
20	Pan-ancestry exome-wide association analyses of COVID-19 outcomes in 586,157 individuals. American Journal of Human Genetics, 2021, 108, 1350-1355.	6.2	72
21	Analysis of rare genetic variation underlying cardiometabolic diseases and traits among 200,000 individuals in the UK Biobank. Nature Genetics, 2022, 54, 240-250.	21.4	68
22	VAT: a computational framework to functionally annotate variants in personal genomes within a cloud-computing environment. Bioinformatics, 2012, 28, 2267-2269.	4.1	65
23	Profiling and Leveraging Relatedness in a Precision Medicine Cohort of 92,455 Exomes. American Journal of Human Genetics, 2018, 102, 874-889.	6.2	58
24	Analysis of variable retroduplications in human populations suggests coupling of retrotransposition to cell division. Genome Research, 2013, 23, 2042-2052.	5.5	52
25	Concept and design of a genome-wide association genotyping array tailored for transplantation-specific studies. Genome Medicine, 2015, 7, 90.	8.2	49
26	Comprehensive analysis of the pseudogenes of glycolytic enzymes in vertebrates: the anomalously high number of GAPDH pseudogenes highlights a recent burst of retrotrans-positional activity. BMC Genomics, 2009, 10, 480.	2.8	48
27	Transmuting α helices and β sheets. Folding & Design, 1997, 2, R71-R79.	4.5	43
28	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. Kidney International, 2021, 99, 926-939.	5.2	42
29	Using ALoFT to determine the impact of putative loss-of-function variants in protein-coding genes. Nature Communications, 2017, 8, 382.	12.8	40
30	Sequence variation in G-protein-coupled receptors: analysis of single nucleotide polymorphisms. Nucleic Acids Research, 2005, 33, 1710-1721.	14.5	37
31	Gene inactivation and its implications for annotation in the era of personal genomics. Genes and Development, 2011, 25, 1-10.	5.9	29
32	Polygenic Risk of Psychiatric Disorders Exhibits Cross-trait Associations in Electronic Health Record Data From European Ancestry Individuals. Biological Psychiatry, 2021, 89, 236-245.	1.3	26
33	Secondary Structure of Uracil-DNA Glycosylase Inhibitor Protein. Journal of Biological Chemistry, 1995, 270, 296-303.	3.4	20
34	SNPs on human chromosomes 21 and 22 – analysis in terms of protein features and pseudogenes. Pharmacogenomics, 2002, 3, 393-402.	1.3	16
35	Tertiary Structure of Uracil-DNA Glycosylase Inhibitor Protein. Journal of Biological Chemistry, 1995, 270, 16840-16847.	3.4	15
36	MAPPIN: a method for annotating, predicting pathogenicity and mode of inheritance for nonsynonymous variants. Nucleic Acids Research, 2017, 45, 10393-10402.	14.5	15

#	Article	IF	Citations
37	Defining the human reference protein-coding gene set. Genome Biology, 2010, 11, .	8.8	0