Suganthi Balasubramanian

List of Publications by Year in Descending Order

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	Analysis of rare genetic variation underlying cardiometabolic diseases and traits among 200,000 individuals in the UK Biobank.. *Nature Genetics*, **2022**,	36.3	4
37	Exome sequencing and analysis of 454,787 UK Biobank participants. *Nature*, **2021**, 599, 628-634	50.4	34
36	Advancing human genetics research and drug discovery through exome sequencing of the UK Biobank. *Nature Genetics*, **2021**, 53, 942-948	36.3	42
35	Pan-ancestry exome-wide association analyses of COVID-19 outcomes in 586,157 individuals. *American Journal of Human Genetics*, **2021**, 108, 1350-1355	11	25
34	Sequencing of 640,000 exomes identifies variants associated with protection from obesity. *Science*, **2021**, 373,	33.3	22
33	Polygenic Risk of Psychiatric Disorders Exhibits Cross-trait Associations in Electronic Health Record Data From European Ancestry Individuals. *Biological Psychiatry*, **2021**, 89, 236-245	7.9	8
32	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. *Kidney International*, **2021**, 99, 926-939	9.9	6
31	Exome sequencing and characterization of 49,960 individuals in the UK Biobank. *Nature*, **2020**, 586, 749-756	364	122
30	Profiling and Leveraging Relatedness in a Precision Medicine Cohort of 92,455 Exomes. *American Journal of Human Genetics*, **2018**, 102, 874-889	11	38
29	A Protein-Truncating HSD17B13 Variant and Protection from Chronic Liver Disease. *New England Journal of Medicine*, **2018**, 378, 1096-1106	59.2	350
28	A comprehensive catalog of predicted functional upstream open reading frames in humans. *Nucleic Acids Research*, **2018**, 46, 3326-3338	20.1	40
27	MAPPIN: a method for annotating, predicting pathogenicity and mode of inheritance for nonsynonymous variants. *Nucleic Acids Research*, **2017**, 45, 10393-10402	20.1	11
26	Using ALoFT to determine the impact of putative loss-of-function variants in protein-coding genes. *Nature Communications*, **2017**, 8, 382	17.4	19
25	Distribution and clinical impact of functional variants in 50,726 whole-exome sequences from the DiscovEHR study. *Science*, **2016**, 354,	33.3	320
24	Concept and design of a genome-wide association genotyping array tailored for transplantation-specific studies. *Genome Medicine*, **2015**, 7, 90	14.4	38
23	Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. *Nature Communications*, **2015**, 6, 5903	17.4	56
22	Comparative analysis of pseudogenes across three phyla. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 13361-6	11.5	54

21	Integrative annotation of variants from 1092 humans: application to cancer genomics. *Science*, **2013**, 342, 1235587	33.3	281
20	Analysis of variable retroduplications in human populations suggests coupling of retrotransposition to cell division. *Genome Research*, **2013**, 23, 2042-52	9.7	41
19	VAT: a computational framework to functionally annotate variants in personal genomes within a cloud-computing environment. *Bioinformatics*, **2012**, 28, 2267-9	7.2	55
18	The GENCODE pseudogene resource. *Genome Biology*, **2012**, 13, R51	18.3	232
17	GENCODE: the reference human genome annotation for The ENCODE Project. *Genome Research*, **2012**, 22, 1760-74	9.7	3142
16	Personal omics profiling reveals dynamic molecular and medical phenotypes. *Cell*, **2012**, 148, 1293-307	56.2	921
15	A systematic survey of loss-of-function variants in human protein-coding genes. *Science*, **2012**, 335, 823-8	33.3	880
14	Gene inactivation and its implications for annotation in the era of personal genomics. *Genes and Development*, **2011**, 25, 1-10	12.6	23
13	Defining the human reference protein-coding gene set. *Genome Biology*, **2010**, 11,	18.3	78
12	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	4.5	41
11	Comparative analysis of processed ribosomal protein pseudogenes in four mammalian genomes. *Genome Biology*, **2009**, 10, R2	18.3	72
10	Sequence variation in G-protein-coupled receptors: analysis of single nucleotide polymorphisms. *Nucleic Acids Research*, **2005**, 33, 1710-21	20.1	37
9	Molecular fossils in the human genome: identification and analysis of the pseudogenes in chromosomes 21 and 22. *Genome Research*, **2002**, 12, 272-80	9.7	144
8	SNPs on human chromosomes 21 and 22 -- analysis in terms of protein features and pseudogenes. *Pharmacogenomics*, **2002**, 3, 393-402	2.6	14
7	Comprehensive analysis of amino acid and nucleotide composition in eukaryotic genomes, comparing genes and pseudogenes. *Nucleic Acids Research*, **2002**, 30, 2515-23	20.1	102
6	Protein alchemy: changing beta-sheet into alpha-helix. *Nature Structural Biology*, **1997**, 4, 548-52		146
5	Transmuting alpha helices and beta sheets. *Folding & Design*, **1997**, 2, R71-9		41
4	What makes a protein a protein? Hydrophobic core designs that specify stability and structural properties. *Protein Science*, **1996**, 5, 1584-93	6.3	166

3	Tertiary structure of uracil-DNA glycosylase inhibitor protein. *Journal of Biological Chemistry*, **1995**, 270, 16840-7	5.4	15
2	Secondary structure of uracil-DNA glycosylase inhibitor protein. *Journal of Biological Chemistry*, **1995**, 270, 296-303	5.4	12
1	Whole exome sequencing and characterization of coding variation in 49,960 individuals in the UK Biobank		56