Suganthi Balasubramanian

List of Publications by Year
in descending order

37 papers	10,916 citations	159585 30 h-index	345221 36 g-index
41 all docs	41 docs citations	41 times ranked	24499 citing authors

#	Article	IF	Citations
1	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
2	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
3	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. Kidney International, 2021, 99, 926-939.	5.2	42
4	Advancing human genetics research and drug discovery through exome sequencing of the UK Biobank. Nature Genetics, 2021, 53, 942-948.	21.4	234
5	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
6	Sequencing of 640,000 exomes identifies GPR75 variants associated with protection from obesity. Science, 2021, 373, .	12.6	130
7	Exome sequencing and analysis of 454,787 UK Biobank participants. Nature, 2021, 599, 628-634.	27.8	377
8	Exome sequencing and characterization of 49,960 individuals in the UK Biobank. Nature, 2020, 586, 749-756.	27.8	369
9	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
10	A Protein-TruncatingHSD17B13Variant and Protection from Chronic Liver Disease. New England Journal of Medicine, 2018, 378, 1096-1106.	27.0	556
11	A comprehensive catalog of predicted functional upstream open reading frames in humans. Nucleic Acids Research, 2018, 46, 3326-3338.	14.5	76
12	MAPPIN: a method for annotating, predicting pathogenicity and mode of inheritance for nonsynonymous variants. Nucleic Acids Research, 2017, 45, 10393-10402.	14.5	15
13	Using ALoFT to determine the impact of putative loss-of-function variants in protein-coding genes. Nature Communications, 2017, 8, 382.	12.8	40
14	Distribution and clinical impact of functional variants in 50,726 whole-exome sequences from the DiscovEHR study. Science, 2016, 354, .	12.6	464
15	Concept and design of a genome-wide association genotyping array tailored for transplantation-specific studies. Genome Medicine, 2015, 7, 90.	8.2	49
16	Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. Nature Communications, 2015, 6, 5903.	12.8	73
17	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
18	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235587.	12.6	341

#	Article	IF	Citations
19	Analysis of variable retroduplications in human populations suggests coupling of retrotransposition to cell division. Genome Research, 2013, 23, 2042-2052.	5.5	52
20	VAT: a computational framework to functionally annotate variants in personal genomes within a cloud-computing environment. Bioinformatics, 2012, 28, 2267-2269.	4.1	65
21	The GENCODE pseudogene resource. Genome Biology, 2012, 13, R51.	9.6	273
22	GENCODE: The reference human genome annotation for The ENCODE Project. Genome Research, 2012, 22, 1760-1774.	5.5	4,217
23	Personal Omics Profiling Reveals Dynamic Molecular and Medical Phenotypes. Cell, 2012, 148, 1293-1307.	28.9	1,134
24	A Systematic Survey of Loss-of-Function Variants in Human Protein-Coding Genes. Science, 2012, 335, 823-828.	12.6	1,095
25	Gene inactivation and its implications for annotation in the era of personal genomics. Genes and Development, 2011, 25, 1-10.	5.9	29
26	Defining the human reference protein-coding gene set. Genome Biology, 2010, 11, .	8.8	0
27	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
28	Comparative analysis of processed ribosomal protein pseudogenes in four mammalian genomes. Genome Biology, 2009, 10, R2.	9.6	87
29	Sequence variation in G-protein-coupled receptors: analysis of single nucleotide polymorphisms. Nucleic Acids Research, 2005, 33, 1710-1721.	14.5	37
30	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
31	SNPs on human chromosomes 21 and 22 â€“ analysis in terms of protein features and pseudogenes. Pharmacogenomics, 2002, 3, 393-402.	1.3	16
32	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
33	Protein alchemy: Changing Î²-sheet into Î±-helix. Nature Structural Biology, 1997, 4, 548-552.	9.7	164
34	Transmuting Î± helices and Î² sheets. Folding & Design, 1997, 2, R71-R79.	4.5	43
35	What makes a protein a protein? Hydrophobic core designs that specify stability and structural properties. Protein Science, 1996, 5, 1584-1593.	7.6	189
36	Tertiary Structure of Uracil-DNA Glycosylase Inhibitor Protein. Journal of Biological Chemistry, 1995, 270, 16840-16847.	3.4	15

#	Article	IF	Citations
37	Secondary Structure of Uracil-DNA Glycosylase Inhibitor Protein. Journal of Biological Chemistry, 1995, 270, 296-303.	3.4	20