Fuli Yu

List of Publications by Year in descending order

54 papers	27,555 citations	236612 25 h-index	288905 40 g-index
56 all docs	56 docs citations	56 times ranked	46978 citing authors

#	Article	IF	Citations
1	Mutations in ASH1L confer susceptibility to Tourette syndrome. Molecular Psychiatry, 2020, 25, 476-490.	4.1	41
2	REDBot: Natural language process methods for clinical copy number variation reporting in prenatal and products of conception diagnosis. Molecular Genetics & Genomic Medicine, 2020, 8, e1488.	0.6	3
3	Reduced meiotic recombination in rhesus macaques and the origin of the human recombination landscape. PLoS ONE, 2020, 15, e0236285.	1.1	7
4	Spontaneous hyperactivity in Ash1l mutant mice, a new model for Tourette syndrome. Molecular Psychiatry, 2020, 25, 241-242.	4.1	1
5	Title is missing!. , 2020, 15, e0236285.		0
6	Title is missing!. , 2020, 15, e0236285.		0
7	Title is missing!. , 2020, 15, e0236285.		0
8	Title is missing!. , 2020, 15, e0236285.		0
9	Whole-Exome Sequencing Reveals Uncaptured Variation and Distinct Ancestry in the Southern African Population of Botswana. American Journal of Human Genetics, 2018, 102, 731-743.	2.6	38
10	Rho Guanine Nucleotide Exchange Factor ARHGEF17 Is a Risk Gene for Intracranial Aneurysms. Circulation Genomic and Precision Medicine, 2018, 11, e002099.	1.6	18
11	Prospective chromosome analysis of 3429 amniocentesis samples in China using copy number variation sequencing. American Journal of Obstetrics and Gynecology, 2018, 219, 287.e1-287.e18.	0.7	71
12	Allele-specific epigenome maps reveal sequence-dependent stochastic switching at regulatory loci. Science, 2018, 361, .	6.0	87
13	Practical Approaches for Whole-Genome Sequence Analysis of Heart- and Blood-Related Traits. American Journal of Human Genetics, 2017, 100, 205-215.	2.6	50
14	Characterization of chromosomal abnormalities in pregnancy losses reveals critical genes and loci for human early development. Human Mutation, 2017, 38, 669-677.	1.1	28
15	Extremely low-coverage whole genome sequencing in South Asians captures population genomics information. BMC Genomics, 2017, 18, 396.	1.2	26
16	Abstract P096: The Genetics Architecture of the Serum Metabolome. Circulation, 2017, 135, .	1.6	0
17	A hybrid computational strategy to address WGS variant analysis in >5000 samples. BMC Bioinformatics, 2016, 17, 361.	1.2	7
18	Base-Biased Evolution of Disease-Associated Mutations in the Human Genome. Human Mutation, 2016, 37, 1209-1214.	1.1	5

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19	An overview on cloud computing platform spark for Human Genome mining. , 2016, , .		8
20	The population genomics of rhesus macaques (Macaca mulatta) based on whole-genome sequences. Genome Research, 2016, 26, 1651-1662.	2.4	101
21	Multiallelic Positions in the Human Genome: Challenges for Genetic Analyses. Human Mutation, 2016, 37, 231-234.	1.1	18
22	Association of Single Nucleotide Polymorphisms in the ST3GAL4 Gene with VWF Antigen and Factor VIII Activity. PLoS ONE, 2016, 11, e0160757.	1.1	10
23	The distribution and mutagenesis of short coding INDELs from 1,128 whole exomes. BMC Genomics, 2015, 16, 143.	1.2	9
24	PacBio-LITS: a large-insert targeted sequencing method for characterization of human disease-associated chromosomal structural variations. BMC Genomics, 2015, 16, 214.	1.2	63
25	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
26	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	13.7	1,994
27	A fast and accurate SNP detection method on the cloud platform. , 2015, , .		0
28	Population Genomic Analysis of 962 Whole Genome Sequences of Humans Reveals Natural Selection in Non-Coding Regions. PLoS ONE, 2015, 10, e0121644.	1.1	13
29	Launching genomics into the cloud: deployment of Mercury, a next generation sequence analysis pipeline. BMC Bioinformatics, 2014, 15, 30.	1.2	199
30	Possible Race and Gender Divergence in Association of Genetic Variations with Plasma von Willebrand Factor: A Study of ARIC and 1000 Genome Cohorts. PLoS ONE, 2014, 9, e84810.	1.1	22
31	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235587.	6.0	341
32	Cloud processing of 1000 genomes sequencing data using Amazon Web Service. , 2013, , .		2
33	The 1000 Genomes Project: paving the way for personalized genomic medicine. Personalized Medicine, 2013, 10, 321-324.	0.8	4
34	Whole-genome sequenceâ€"based analysis of high-density lipoprotein cholesterol. Nature Genetics, 2013, 45, 899-901.	9.4	132
35	Sequence Alignment, Analysis, and Bioinformatic Pipelines. , 2013, , 59-77.		0
36	An integrative variant analysis suite for whole exome next-generation sequencing data. BMC Bioinformatics, 2012, 13, 8.	1.2	252

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37	Rare Coding Single Nucleotide Variants of ADAMTS13 Are Associated with Deep Vein Thrombosis in a Next-Generation Sequencing Association Study. Blood, 2012, 120, 107-107.	0.6	0
38	A novel approach for alignments output storage problem facing clinical scenarios. , 2011, , .		0
39	The functional spectrum of low-frequency coding variation. Genome Biology, 2011, 12, R84.	13.9	173
40	Characterization of single-nucleotide variation in Indian-origin rhesus macaques (Macaca mulatta). BMC Genomics, 2011, 12, 311.	1.2	30
41	Demographic history and rare allele sharing among human populations. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 11983-11988.	3.3	589
42	Enabling Atlas2 personal genome analysis on the cloud. , 2011, , .		3
43	Identification of DEEP Vein Thrombosis GENETIC RISK Variants by NEXT GENERATION Sequencing of Hemostatic Genes. Blood, 2011, 118, 710-710.	0.6	0
44	Integrating common and rare genetic variation in diverse human populations. Nature, 2010, 467, 52-58.	13.7	2,625
45	A SNP discovery method to assess variant allele probability from next-generation resequencing data. Genome Research, 2010, 20, 273-280.	2.4	168
46	Genetic diversity in India and the inference of Eurasian population expansion. Genome Biology, 2010, 11, R113.	3.8	60
47	Genetic Determinants of Plasma Von Willebrand Factor Antigen Levels: A Target Gene SNP and Haplotype Analysis of the ARIC Cohort. Blood, 2010, 116, 4310-4310.	0.6	0
48	Detecting natural selection by empirical comparison to random regions of the genome. Human Molecular Genetics, 2009, 18, 4853-4867.	1.4	27
49	Corrections and Clarifications. Science, 2007, 316, 370a-370a.	6.0	20
50	Genome-wide detection and characterization of positive selection in human populations. Nature, 2007, 449, 913-918.	13.7	1,788
51	A second generation human haplotype map of over 3.1 million SNPs. Nature, 2007, 449, 851-861.	13.7	4,137
52	Positive Selection of a Pre-Expansion CAG Repeat of the Human SCA2 Gene. PLoS Genetics, 2005, 1, e41.	1.5	49
53	Highly multiplexed molecular inversion probe genotyping: Over 10,000 targeted SNPs genotyped in a single tube assay. Genome Research, 2005, 15, 269-275.	2.4	276
54	Positive Selection of a Pre-expansion CAG Repeat of the Human SCA2 Gene. PLoS Genetics, 2005, preprint, e41.	1.5	0