Stacey Gabriel

List of Publications by Year
in descending order

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73 papers	90,275 citations	17440 63 h-index	76900 74 g-index
77 all docs	77 docs citations	77 times ranked	120030 citing authors

#	Article	IF	Citations
1	The Genome Analysis Toolkit: A MapReduce framework for analyzing next-generation DNA sequencing data. Genome Research, 2010, 20, 1297-1303.	5.5	21,358
2	EGFR Mutations in Lung Cancer: Correlation with Clinical Response to Gefitinib Therapy. Science, 2004, 304, 1497-1500.	12.6	9,038
3	Integrated Genomic Analysis Identifies Clinically Relevant Subtypes of Glioblastoma Characterized by Abnormalities in PDGFRA, IDH1, EGFR, and NF1. Cancer Cell, 2010, 17, 98-110.	16.8	6,138
4	From FastQ Data to Highâ€Confidence Variant Calls: The Genome Analysis Toolkit Best Practices Pipeline. Current Protocols in Bioinformatics, 2013, 43, 11.10.1-11.10.33.	25.8	4,796
5	The Somatic Genomic Landscape of Glioblastoma. Cell, 2013, 155, 462-477.	28.9	3,979
6	Sensitive detection of somatic point mutations in impure and heterogeneous cancer samples. Nature Biotechnology, 2013, 31, 213-219.	17.5	3,934
7	Age-Related Clonal Hematopoiesis Associated with Adverse Outcomes. New England Journal of Medicine, 2014, 371, 2488-2498.	27.0	3,474
8	The landscape of somatic copy-number alteration across human cancers. Nature, 2010, 463, 899-905.	27.8	3,331
9	Activating mutation in the tyrosine kinase JAK2 in polycythemia vera, essential thrombocythemia, and myeloid metaplasia with myelofibrosis. Cancer Cell, 2005, 7, 387-397.	16.8	2,695
10	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	27.0	2,582
11	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	21.4	2,421
12	Genomic correlates of response to CTLA-4 blockade in metastatic melanoma. Science, 2015, 350, 207-211.	12.6	2,275
13	Patterns and rates of exonic de novo mutations in autism spectrum disorders. Nature, 2012, 485, 242-245.	27.8	1,597
14	A polygenic burden of rare disruptive mutations in schizophrenia. Nature, 2014, 506, 185-190.	27.8	1,305
15	Solution hybrid selection with ultra-long oligonucleotides for massively parallel targeted sequencing. Nature Biotechnology, 2009, 27, 182-189.	17.5	1,267
16	Evolution and Impact of Subclonal Mutations in Chronic Lymphocytic Leukemia. Cell, 2013, 152, 714-726.	28.9	1,202
17	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
18	SF3B1 and Other Novel Cancer Genes in Chronic Lymphocytic Leukemia. New England Journal of Medicine, 2011, 365, 2497-2506.	27.0	1,021

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19	Advances in understanding cancer genomes through second-generation sequencing. Nature Reviews Genetics, 2010, 11, 685-696.	16.3	1,014
20	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
21	High-throughput oncogene mutation profiling in human cancer. Nature Genetics, 2007, 39, 347-351.	21.4	927
22	Genomic Characterization of Brain Metastases Reveals Branched Evolution and Potential Therapeutic Targets. Cancer Discovery, 2015, 5, 1164-1177.	9.4	821
23	Alzheimer's disease: early alterations in brain DNA methylation at ANK1, BIN1, RHBDF2 and other loci. Nature Neuroscience, 2014, 17, 1156-1163.	14.8	800
24	Diagnostic Yield and Clinical Utility of Sequencing Familial Hypercholesterolemia Genes in Patients With Severe Hypercholesterolemia. Journal of the American College of Cardiology, 2016, 67, 2578-2589.	2.8	723
25	A structural variation reference for medical and population genetics. Nature, 2020, 581, 444-451.	27.8	614
26	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. Nature, 2015, 518, 102-106.	27.8	581
27	A scalable, fully automated process for construction of sequence-ready human exome targeted capture libraries. Genome Biology, 2011, 12, R1.	9.6	547
28	Whole-exome sequencing and clinical interpretation of formalin-fixed, paraffin-embedded tumor samples to guide precision cancer medicine. Nature Medicine, 2014, 20, 682-688.	30.7	508
29	Somatic ERCC2 Mutations Correlate with Cisplatin Sensitivity in Muscle-Invasive Urothelial Carcinoma. Cancer Discovery, 2014, 4, 1140-1153.	9.4	506
30	Prognostically relevant gene signatures of high-grade serous ovarian carcinoma. Journal of Clinical Investigation, 2013, 123, 517-25.	8.2	462
31	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. Cell, 2019, 179, 964-983.e31.	28.9	430
32	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. Nature Genetics, 2014, 46, 357-363.	21.4	428
33	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. Cell, 2020, 182, 200-225.e35.	28.9	410
34	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	27.8	376
35	Distribution and Medical Impact of Loss-of-Function Variants in the Finnish Founder Population. PLoS Genetics, 2014, 10, e1004494.	3.5	351
36	ANGPTL3 Deficiency and Protection Against Coronary Artery Disease. Journal of the American College of Cardiology, 2017, 69, 2054-2063.	2.8	348

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37	Whole-genome and multisector exome sequencing of primary and post-treatment glioblastoma reveals patterns of tumor evolution. Genome Research, 2015, 25, 316-327.	5.5	343
38	Drug-sensitiveFGFR2mutations in endometrial carcinoma. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8713-8717.	7.1	329
39	Proteogenomic and metabolomic characterization of human glioblastoma. Cancer Cell, 2021, 39, 509-528.e20.	16.8	327
40	Epidermal Growth Factor Receptor Activation in Glioblastoma through Novel Missense Mutations in the Extracellular Domain. PLoS Medicine, 2006, 3, e485.	8.4	298
41	Proteogenomic Characterization of Endometrial Carcinoma. Cell, 2020, 180, 729-748.e26.	28.9	296
42	Human knockouts and phenotypic analysis in a cohort with a high rate of consanguinity. Nature, 2017, 544, 235-239.	27.8	292
43	Systematic identification of personal tumor-specific neoantigens in chronic lymphocytic leukemia. Blood, 2014, 124, 453-462.	1.4	286
44	Clonal evolution in patients with chronic lymphocytic leukaemia developing resistance to BTK inhibition. Nature Communications, 2016, 7, 11589.	12.8	285
45	Genomic sequencing of colorectal adenocarcinomas identifies a recurrent VTI1A-TCF7L2 fusion. Nature Genetics, 2011, 43, 964-968.	21.4	270
46	Genetic Interleukin 6 Signaling Deficiency Attenuates Cardiovascular Risk in Clonal Hematopoiesis. Circulation, 2020, 141, 124-131.	1.6	270
47	Structural Alterations Driving Castration-Resistant Prostate Cancer Revealed by Linked-Read Genome Sequencing. Cell, 2018, 174, 433-447.e19.	28.9	258
48	Genetic and Clonal Dissection of Murine Small Cell Lung Carcinoma Progression by Genome Sequencing. Cell, 2014, 156, 1298-1311.	28.9	241
49	Proteogenomic characterization of pancreatic ductal adenocarcinoma. Cell, 2021, 184, 5031-5052.e26.	28.9	236
50	Characterization and remediation of sample index swaps by non-redundant dual indexing on massively parallel sequencing platforms. BMC Genomics, 2018, 19, 332.	2.8	201
51	Proteogenomic insights into the biology and treatment of HPV-negative head and neck squamous cell carcinoma. Cancer Cell, 2021, 39, 361-379.e16.	16.8	189
52	Phenotypic Characterization of GeneticallyÂLowered Human Lipoprotein(a) Levels. Journal of the American College of Cardiology, 2016, 68, 2761-2772.	2.8	186
53	Association of Rare and Common Variation in the Lipoprotein Lipase Gene With Coronary Artery Disease. JAMA - Journal of the American Medical Association, 2017, 317, 937.	7.4	148
54	Association Between Titin Loss-of-Function Variants and Early-Onset Atrial Fibrillation. JAMA - Journal of the American Medical Association, 2018, 320, 2354.	7.4	144

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55	Genomic evolution and chemoresistance in germ-cell tumours. Nature, 2016, 540, 114-118.	27.8	139
56	Pangenomics enables genotyping of known structural variants in 5202 diverse genomes. Science, 2021, 374, abg8871.	12.6	132
57	Molecular Genetic Anatomy and Risk Profile of Hirschsprungâ€™s Disease. New England Journal of Medicine, 2019, 380, 1421-1432.	27.0	131
58	A missense variant in Mitochondrial Amidoxime Reducing Component 1 gene and protection against liver disease. PLoS Genetics, 2020, 16, e1008629.	3.5	101
59	Harmonizing Clinical Sequencing and Interpretation for the eMERGE III Network. American Journal of Human Genetics, 2019, 105, 588-605.	6.2	99
60	Identification and Functional Characterization of G6PC2 Coding Variants Influencing Glycemic Traits Define an Effector Transcript at the G6PC2-ABCB11 Locus. PLoS Genetics, 2015, 11, e1004876.	3.5	95
61	Analysis commons, a team approach to discovery in a big-data environment for genetic epidemiology. Nature Genetics, 2017, 49, 1560-1563.	21.4	93
62	Comparing strategies to fine-map the association of common SNPs at chromosome 9p21 with type 2 diabetes and myocardial infarction. Nature Genetics, 2011, 43, 801-805.	21.4	79
63	Analysis of predicted loss-of-function variants in UK Biobank identifies variants protective for disease. Nature Communications, 2018, 9, 1613.	12.8	78
64	Advances in genetics show the need for extending screening strategies for autosomal dominant hypercholesterolaemia. European Heart Journal, 2012, 33, 1360-1366.	2.2	76
65	Phenotypic extremes in rare variant study designs. European Journal of Human Genetics, 2016, 24, 924-930.	2.8	65
66	A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.6	47
67	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	5.3	31
68	DNA Sequence Variation in ACVR1C Encoding the Activin Receptor-Like Kinase 7 Influences Body Fat Distribution and Protects Against Type 2 Diabetes. Diabetes, 2019, 68, 226-234.	0.6	31
69	Combined tumor and immune signals from genomes or transcriptomes predict outcomes of checkpoint inhibition in melanoma. Cell Reports Medicine, 2022, 3, 100500.	6.5	13
70	Association of Exome Sequences With Cardiovascular Traits Among Blacks in the Jackson Heart Study. Circulation: Cardiovascular Genetics, 2016, 9, 368-374.	5.1	8
71	Variation in the Human Genome and the Inherited Basis of Common Disease. Seminars in Oncology, 2006, 33, 46-49.	2.2	7
72	Rare variant associations with waist-to-hip ratio in European-American and African-American women from the NHLBI-Exome Sequencing Project. European Journal of Human Genetics, 2016, 24, 1181-1187.	2.8	5

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73	Population Genetic Tools: Application to Cancer. Seminars in Oncology, 2007, 34, S21-S24.	2.2	1