Laura Clarke

List of Publications by Year
in descending order

69	53,677	44444 50	100535 70
papers	citations	h-index	g-index

78	78	78	83817
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
2	A map of human genome variation from population-scale sequencing. Nature, 2010, 467, 1061-1073.	13.7	7,209
3	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	13.7	7,199
4	Finishing the euchromatic sequence of the human genome. Nature, 2004, 431, 931-945.	13.7	4,232
5	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	13.7	1,994
6	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. Nature, 2004, 428, 493-521.	13.7	1,943
7	The Ensembl genome database project. Nucleic Acids Research, 2002, 30, 38-41.	6.5	1,411
8	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. Science, 2007, 316, 222-234.	6.0	1,283
9	A Systematic Survey of Loss-of-Function Variants in Human Protein-Coding Genes. Science, 2012, 335, 823-828.	6.0	1,095
10	The Ensembl gene annotation system. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw093.	1.4	912
11	Lineage-Specific Genome Architecture Links Enhancers and Non-coding Disease Variants to Target Gene Promoters. Cell, 2016, 167, 1369-1384.e19.	13.5	863
12	The Genome Sequence of Caenorhabditis briggsae: A Platform for Comparative Genomics. PLoS Biology, 2003, 1, e45.	2.6	812
13	Evaluation of GRCh38 and de novo haploid genome assemblies demonstrates the enduring quality of the reference assembly. Genome Research, 2017, 27, 849-864.	2.4	728
14	Genome analysis of the platypus reveals unique signatures of evolution. Nature, 2008, 453, 175-183.	13.7	657
15	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	5.8	636
16	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
17	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. Cell, 2016, 167, 1398-1414.e24.	13.5	573
18	Common genetic variation drives molecular heterogeneity in human iPSCs. Nature, 2017, 546, 370-375.	13.7	491

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19	Î²-Glucan Reverses the Epigenetic State of LPS-Induced Immunological Tolerance. Cell, 2016, 167, 1354-1368.e14.	13.5	467
20	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	13.5	404
21	An Overview of Ensembl. Genome Research, 2004, 14, 925-928.	2.4	391
22	The Ensembl Automatic Gene Annotation System. Genome Research, 2004, 14, 942-950.	2.4	352
23	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235587.	6.0	341
24	Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project. Genome Biology, 2015, 16, 57.	3.8	331
25	The 1000 Genomes Project: data management and community access. Nature Methods, 2012, 9, 459-462.	9.0	308
26	Whole-genome fingerprint of the DNA methylome during human B cell differentiation. Nature Genetics, 2015, 47, 746-756.	9.4	278
27	Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. Nature Genetics, 2016, 48, 593-599.	9.4	273
28	Deleterious- and Disease-Allele Prevalence in Healthy Individuals: Insights from Current Predictions, Mutation Databases, and Population-Scale Resequencing. American Journal of Human Genetics, 2012, 91, 1022-1032.	2.6	255
29	Transcriptional diversity during lineage commitment of human blood progenitors. Science, 2014, 345, 1251033.	6.0	253
30	Convergent genomic signatures of domestication in sheep and goats. Nature Communications, 2018, 9, 813.	5.8	220
31	Ensembl 2002: accommodating comparative genomics. Nucleic Acids Research, 2003, 31, 38-42.	6.5	216
32	The international Genome sample resource (IGSR): A worldwide collection of genome variation incorporating the 1000 Genomes Project data. Nucleic Acids Research, 2017, 45, D854-D859.	6.5	215
33	The origin, evolution, and functional impact of short insertionâ€“deletion variants identified in 179 human genomes. Genome Research, 2013, 23, 749-761.	2.4	206
34	The functional spectrum of low-frequency coding variation. Genome Biology, 2011, 12, R84.	13.9	173
35	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. Nature Medicine, 2018, 24, 868-880.	15.2	157
36	Increased DNA methylation variability in type 1 diabetes across three immune effector cell types. Nature Communications, 2016, 7, 13555.	5.8	142

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37	The BLUEPRINT Data Analysis Portal. Cell Systems, 2016, 3, 491-495.e5.	2.9	123
38	Whole-epigenome analysis in multiple myeloma reveals DNA hypermethylation of B cell-specific enhancers. Genome Research, 2015, 25, 478-487.	2.4	118
39	Characterizing neutral genomic diversity and selection signatures in indigenous populations of Moroccan goats (Capra hircus) using WGS data. Frontiers in Genetics, 2015, 6, 107.	1.1	108
40	Dynamics of Transcription Regulation in Human Bone Marrow Myeloid Differentiation to Mature Blood Neutrophils. Cell Reports, 2018, 24, 2784-2794.	2.9	104
41	The Ensembl Analysis Pipeline. Genome Research, 2004, 14, 934-941.	2.4	99
42	Repeat associated mechanisms of genome evolution and function revealed by the Mus caroli and Mus pahari genomes. Genome Research, 2018, 28, 448-459.	2.4	99
43	The Organoid Cell Atlas. Nature Biotechnology, 2021, 39, 13-17.	9.4	96
44	The human-induced pluripotent stem cell initiativeâ€”data resources for cellular genetics. Nucleic Acids Research, 2017, 45, D691-D697.	6.5	81
45	The European Nucleotide Archive in 2017. Nucleic Acids Research, 2018, 46, D36-D40.	6.5	79
46	<scp>FAANG</scp>, establishing metadata standards, validation and best practices for the farmed and companion animal community. Animal Genetics, 2018, 49, 520-526.	0.6	78
47	Expression Atlas update: gene and protein expression in multiple species. Nucleic Acids Research, 2022, 50, D129-D140.	6.5	78
48	Variant calling on the GRCh38 assembly with the data from phase three of the 1000 Genomes Project. Wellcome Open Research, 2019, 4, 50.	0.9	73
49	Functional variation in allelic methylomes underscores a strong genetic contribution and reveals novel epigenetic alterations in the human epigenome. Genome Biology, 2017, 18, 50.	3.8	71
50	European Nucleotide Archive in 2016. Nucleic Acids Research, 2017, 45, D32-D36.	6.5	68
51	Biopipe: A Flexible Framework for Protocol-Based Bioinformatics Analysis. Genome Research, 2003, 13, 1904-15.	2.4	65
52	<scp>GO</scp>â€<scp>FAANG</scp> meeting: a Gathering On Functional Annotation of <scp>An</scp>imal Genomes. Animal Genetics, 2016, 47, 528-533.	0.6	65
53	Distinct Trends of DNA Methylation Patterning in the Innate and Adaptive Immune Systems. Cell Reports, 2016, 17, 2101-2111.	2.9	54
54	A Standard Nomenclature for Referencing and Authentication of Pluripotent Stem Cells. Stem Cell Reports, 2018, 10, 1-6.	2.3	53

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55	Rapid establishment of the European Bank for induced Pluripotent Stem Cells (EBiSC) - the Hot Start experience. Stem Cell Research, 2017, 20, 105-114.	0.3	51
56	Platelet function is modified by common sequence variation in megakaryocyte super enhancers. Nature Communications, 2017, 8, 16058.	5.8	50
57	Alignment of 1000 Genomes Project reads to reference assembly GRCh38. GigaScience, 2017, 6, 1-8.	3.3	49
58	Report of the International Stem Cell Banking Initiative Workshop Activity: Current Hurdles and Progress in Seed-Stock Banking of Human Pluripotent Stem Cells. Stem Cells Translational Medicine, 2017, 6, 1956-1962.	1.6	42
59	Population-scale proteome variation in human induced pluripotent stem cells. ELife, 2020, 9, .	2.8	40
60	Chromatin-Based Classification of Genetically Heterogeneous AMLs into Two Distinct Subtypes with Diverse Stemness Phenotypes. Cell Reports, 2019, 26, 1059-1069.e6.	2.9	33
61	Genetic perturbation of PU.1 binding and chromatin looping at neutrophil enhancers associates with autoimmune disease. Nature Communications, 2021, 12, 2298.	5.8	32
62	An evaluation of sequencing coverage and genotyping strategies to assess neutral and adaptive diversity. Molecular Ecology Resources, 2019, 19, 1497-1515.	2.2	31
63	Guidelines for reporting single-cell RNA-seq experiments. Nature Biotechnology, 2020, 38, 1384-1386.	9.4	27
64	Variant calling on the GRCh38 assembly with the data from phase three of the 1000 Genomes Project. Wellcome Open Research, 2019, 4, 50.	0.9	26
65	Relationship between genome and epigenome - challenges and requirements for future research. BMC Genomics, 2014, 15, 487.	1.2	24
66	Multi-omics profiling reveals a distinctive epigenome signature for high-risk acute promyelocytic leukemia. Oncotarget, 2018, 9, 25647-25660.	0.8	13
67	Cell type-specific novel long non-coding RNA and circular RNA in the BLUEPRINT hematopoietic transcriptomes atlas. Haematologica, 2021, 106, 2613-2623.	1.7	12
68	Characterization of the DNA Methylome during Human B-Cell Differentiation. Blood, 2014, 124, 4346-4346.	0.6	0
69	Whole-Genome Epigenomic Analysis in Multiple Myeloma Reveals DNA Hypermethylation of B-Cell Specific Enhancers. Blood, 2014, 124, 2032-2032.	0.6	0