

# Laura Clarke

## List of Publications by Year in descending order

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Version: 2024-02-01

69  
papers

53,677  
citations

44444

50  
h-index

100535

70  
g-index

78  
all docs

78  
docs citations

78  
times ranked

83817  
citing authors

#	ARTICLE	IF	CITATIONS
1	Expression Atlas update: gene and protein expression in multiple species. <i>Nucleic Acids Research</i> , 2022, 50, D129-D140.	6.5	78
2	Cell type-specific novel long non-coding RNA and circular RNA in the BLUEPRINT hematopoietic transcriptomes atlas. <i>Haematologica</i> , 2021, 106, 2613-2623.	1.7	12
3	Genetic perturbation of PU.1 binding and chromatin looping at neutrophil enhancers associates with autoimmune disease. <i>Nature Communications</i> , 2021, 12, 2298.	5.8	32
4	The Organoid Cell Atlas. <i>Nature Biotechnology</i> , 2021, 39, 13-17.	9.4	96
5	Guidelines for reporting single-cell RNA-seq experiments. <i>Nature Biotechnology</i> , 2020, 38, 1384-1386.	9.4	27
6	Population-scale proteome variation in human induced pluripotent stem cells. <i>ELife</i> , 2020, 9, .	2.8	40
7	An evaluation of sequencing coverage and genotyping strategies to assess neutral and adaptive diversity. <i>Molecular Ecology Resources</i> , 2019, 19, 1497-1515.	2.2	31
8	Chromatin-Based Classification of Genetically Heterogeneous AMLs into Two Distinct Subtypes with Diverse Stemness Phenotypes. <i>Cell Reports</i> , 2019, 26, 1059-1069.e6.	2.9	33
9	Multi-platform discovery of haplotype-resolved structural variation in human genomes. <i>Nature Communications</i> , 2019, 10, 1784.	5.8	636
10	Variant calling on the GRCh38 assembly with the data from phase three of the 1000 Genomes Project. <i>Wellcome Open Research</i> , 2019, 4, 50.	0.9	26
11	Variant calling on the GRCh38 assembly with the data from phase three of the 1000 Genomes Project. <i>Wellcome Open Research</i> , 2019, 4, 50.	0.9	73
12	Convergent genomic signatures of domestication in sheep and goats. <i>Nature Communications</i> , 2018, 9, 813.	5.8	220
13	A Standard Nomenclature for Referencing and Authentication of Pluripotent Stem Cells. <i>Stem Cell Reports</i> , 2018, 10, 1-6.	2.3	53
14	The European Nucleotide Archive in 2017. <i>Nucleic Acids Research</i> , 2018, 46, D36-D40.	6.5	79
15	Repeat associated mechanisms of genome evolution and function revealed by the <i>Mus caroli</i> and <i>Mus pahari</i> genomes. <i>Genome Research</i> , 2018, 28, 448-459.	2.4	99
16	Multi-omics profiling reveals a distinctive epigenome signature for high-risk acute promyelocytic leukemia. <i>Oncotarget</i> , 2018, 9, 25647-25660.	0.8	13
17	<sc>FAANG</sc>, establishing metadata standards, validation and best practices for the farmed and companion animal community. <i>Animal Genetics</i> , 2018, 49, 520-526.	0.6	78
18	Dynamics of Transcription Regulation in Human Bone Marrow Myeloid Differentiation to Mature Blood Neutrophils. <i>Cell Reports</i> , 2018, 24, 2784-2794.	2.9	104

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19	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. <i>Nature Medicine</i> , 2018, 24, 868-880.	15.2	157
20	Functional variation in allelic methylomes underscores a strong genetic contribution and reveals novel epigenetic alterations in the human epigenome. <i>Genome Biology</i> , 2017, 18, 50.	3.8	71
21	Evaluation of GRCh38 and de novo haploid genome assemblies demonstrates the enduring quality of the reference assembly. <i>Genome Research</i> , 2017, 27, 849-864.	2.4	728
22	Common genetic variation drives molecular heterogeneity in human iPSCs. <i>Nature</i> , 2017, 546, 370-375.	13.7	491
23	Alignment of 1000 Genomes Project reads to reference assembly GRCh38. <i>GigaScience</i> , 2017, 6, 1-8.	3.3	49
24	Rapid establishment of the European Bank for induced Pluripotent Stem Cells (EBiSC) - the Hot Start experience. <i>Stem Cell Research</i> , 2017, 20, 105-114.	0.3	51
25	Report of the International Stem Cell Banking Initiative Workshop Activity: Current Hurdles and Progress in Seed-Stock Banking of Human Pluripotent Stem Cells. <i>Stem Cells Translational Medicine</i> , 2017, 6, 1956-1962.	1.6	42
26	Platelet function is modified by common sequence variation in megakaryocyte super enhancers. <i>Nature Communications</i> , 2017, 8, 16058.	5.8	50
27	The human-induced pluripotent stem cell initiative's data resources for cellular genetics. <i>Nucleic Acids Research</i> , 2017, 45, D691-D697.	6.5	81
28	The international Genome sample resource (IGSR): A worldwide collection of genome variation incorporating the 1000 Genomes Project data. <i>Nucleic Acids Research</i> , 2017, 45, D854-D859.	6.5	215
29	European Nucleotide Archive in 2016. <i>Nucleic Acids Research</i> , 2017, 45, D32-D36.	6.5	68
30	The Ensembl gene annotation system. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw093.	1.4	912
31	Increased DNA methylation variability in type 1 diabetes across three immune effector cell types. <i>Nature Communications</i> , 2016, 7, 13555.	5.8	142
32	Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. <i>Nature Genetics</i> , 2016, 48, 593-599.	9.4	273
33	The BLUEPRINT Data Analysis Portal. <i>Cell Systems</i> , 2016, 3, 491-495.e5.	2.9	123
34	FAANG meeting: a Gathering On Functional Annotation of Animal Genomes. <i>Animal Genetics</i> , 2016, 47, 528-533.	0.6	65
35	$\beta$ -Glucan Reverses the Epigenetic State of LPS-Induced Immunological Tolerance. <i>Cell</i> , 2016, 167, 1354-1368.e14.	13.5	467
36	Lineage-Specific Genome Architecture Links Enhancers and Non-coding Disease Variants to Target Gene Promoters. <i>Cell</i> , 2016, 167, 1369-1384.e19.	13.5	863

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37	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016, 167, 1145-1149.	13.5	404
38	Distinct Trends of DNA Methylation Patterning in the Innate and Adaptive Immune Systems. <i>Cell Reports</i> , 2016, 17, 2101-2111.	2.9	54
39	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. <i>Cell</i> , 2016, 167, 1398-1414.e24.	13.5	573
40	Characterizing neutral genomic diversity and selection signatures in indigenous populations of Moroccan goats ( <i>Capra hircus</i> ) using WGS data. <i>Frontiers in Genetics</i> , 2015, 6, 107.	1.1	108
41	Whole-genome fingerprint of the DNA methylome during human B cell differentiation. <i>Nature Genetics</i> , 2015, 47, 746-756.	9.4	278
42	Whole-epigenome analysis in multiple myeloma reveals DNA hypermethylation of B cell-specific enhancers. <i>Genome Research</i> , 2015, 25, 478-487.	2.4	118
43	Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project. <i>Genome Biology</i> , 2015, 16, 57.	3.8	331
44	A global reference for human genetic variation. <i>Nature</i> , 2015, 526, 68-74.	13.7	13,998
45	An integrated map of structural variation in 2,504 human genomes. <i>Nature</i> , 2015, 526, 75-81.	13.7	1,994
46	Relationship between genome and epigenome - challenges and requirements for future research. <i>BMC Genomics</i> , 2014, 15, 487.	1.2	24
47	Transcriptional diversity during lineage commitment of human blood progenitors. <i>Science</i> , 2014, 345, 1251033.	6.0	253
48	Characterization of the DNA Methylome during Human B-Cell Differentiation. <i>Blood</i> , 2014, 124, 4346-4346.	0.6	0
49	Whole-Genome Epigenomic Analysis in Multiple Myeloma Reveals DNA Hypermethylation of B-Cell Specific Enhancers. <i>Blood</i> , 2014, 124, 2032-2032.	0.6	0
50	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. <i>Science</i> , 2013, 342, 1235587.	6.0	341
51	The origin, evolution, and functional impact of short insertion-deletion variants identified in 179 human genomes. <i>Genome Research</i> , 2013, 23, 749-761.	2.4	206
52	The 1000 Genomes Project: data management and community access. <i>Nature Methods</i> , 2012, 9, 459-462.	9.0	308
53	An integrated map of genetic variation from 1,092 human genomes. <i>Nature</i> , 2012, 491, 56-65.	13.7	7,199
54	Deleterious- and Disease-Allele Prevalence in Healthy Individuals: Insights from Current Predictions, Mutation Databases, and Population-Scale Resequencing. <i>American Journal of Human Genetics</i> , 2012, 91, 1022-1032.	2.6	255

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55	A Systematic Survey of Loss-of-Function Variants in Human Protein-Coding Genes. <i>Science</i> , 2012, 335, 823-828.	6.0	1,095
56	The functional spectrum of low-frequency coding variation. <i>Genome Biology</i> , 2011, 12, R84.	13.9	173
57	Demographic history and rare allele sharing among human populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11983-11988.	3.3	589
58	A map of human genome variation from population-scale sequencing. <i>Nature</i> , 2010, 467, 1061-1073.	13.7	7,209
59	Genome analysis of the platypus reveals unique signatures of evolution. <i>Nature</i> , 2008, 453, 175-183.	13.7	657
60	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. <i>Science</i> , 2007, 316, 222-234.	6.0	1,283
61	The Ensembl Automatic Gene Annotation System. <i>Genome Research</i> , 2004, 14, 942-950.	2.4	352
62	An Overview of Ensembl. <i>Genome Research</i> , 2004, 14, 925-928.	2.4	391
63	The Ensembl Analysis Pipeline. <i>Genome Research</i> , 2004, 14, 934-941.	2.4	99
64	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	13.7	1,943
65	Finishing the euchromatic sequence of the human genome. <i>Nature</i> , 2004, 431, 931-945.	13.7	4,232
66	Ensembl 2002: accommodating comparative genomics. <i>Nucleic Acids Research</i> , 2003, 31, 38-42.	6.5	216
67	Biopipe: A Flexible Framework for Protocol-Based Bioinformatics Analysis. <i>Genome Research</i> , 2003, 13, 1904-15.	2.4	65
68	The Genome Sequence of <i>Caenorhabditis briggsae</i> : A Platform for Comparative Genomics. <i>PLoS Biology</i> , 2003, 1, e45.	2.6	812
69	The Ensembl genome database project. <i>Nucleic Acids Research</i> , 2002, 30, 38-41.	6.5	1,411