Laura Clarke

List of Publications by Year
in descending order

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69 papers	53,677 citations	38742 50 h-index	88630 70 g-index
78 all docs	78 docs citations	78 times ranked	76066 citing authors

#	Article	IF	Citations
1	Expression Atlas update: gene and protein expression in multiple species. Nucleic Acids Research, 2022, 50, D129-D140.	14.5	78
2	Cell type-specific novel long non-coding RNA and circular RNA in the BLUEPRINT hematopoietic transcriptomes atlas. Haematologica, 2021, 106, 2613-2623.	3.5	12
3	Genetic perturbation of PU.1 binding and chromatin looping at neutrophil enhancers associates with autoimmune disease. Nature Communications, 2021, 12, 2298.	12.8	32
4	The Organoid Cell Atlas. Nature Biotechnology, 2021, 39, 13-17.	17.5	96
5	Guidelines for reporting single-cell RNA-seq experiments. Nature Biotechnology, 2020, 38, 1384-1386.	17.5	27
6	Population-scale proteome variation in human induced pluripotent stem cells. ELife, 2020, 9, .	6.0	40
7	An evaluation of sequencing coverage and genotyping strategies to assess neutral and adaptive diversity. Molecular Ecology Resources, 2019, 19, 1497-1515.	4.8	31
8	Chromatin-Based Classification of Genetically Heterogeneous AMLs into Two Distinct Subtypes with Diverse Stemness Phenotypes. Cell Reports, 2019, 26, 1059-1069.e6.	6.4	33
9	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	12.8	636
10	Variant calling on the GRCh38 assembly with the data from phase three of the 1000 Genomes Project. Wellcome Open Research, 2019, 4, 50.	1.8	26
11	Variant calling on the GRCh38 assembly with the data from phase three of the 1000 Genomes Project. Wellcome Open Research, 2019, 4, 50.	1.8	73
12	Convergent genomic signatures of domestication in sheep and goats. Nature Communications, 2018, 9, 813.	12.8	220
13	A Standard Nomenclature for Referencing and Authentication of Pluripotent Stem Cells. Stem Cell Reports, 2018, 10, 1-6.	4.8	53
14	The European Nucleotide Archive in 2017. Nucleic Acids Research, 2018, 46, D36-D40.	14.5	79
15	Repeat associated mechanisms of genome evolution and function revealed by the Mus caroli and Mus pahari genomes. Genome Research, 2018, 28, 448-459.	5.5	99
16	Multi-omics profiling reveals a distinctive epigenome signature for high-risk acute promyelocytic leukemia. Oncotarget, 2018, 9, 25647-25660.	1.8	13
17	<scp>FAANG</scp>, establishing metadata standards, validation and best practices for the farmed and companion animal community. Animal Genetics, 2018, 49, 520-526.	1.7	78
18	Dynamics of Transcription Regulation in Human Bone Marrow Myeloid Differentiation to Mature Blood Neutrophils. Cell Reports, 2018, 24, 2784-2794.	6.4	104

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19	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. Nature Medicine, 2018, 24, 868-880.	30.7	157
20	Functional variation in allelic methylomes underscores a strong genetic contribution and reveals novel epigenetic alterations in the human epigenome. Genome Biology, 2017, 18, 50.	8.8	71
21	Evaluation of GRCh38 and de novo haploid genome assemblies demonstrates the enduring quality of the reference assembly. Genome Research, 2017, 27, 849-864.	5.5	728
22	Common genetic variation drives molecular heterogeneity in human iPSCs. Nature, 2017, 546, 370-375.	27.8	491
23	Alignment of 1000 Genomes Project reads to reference assembly GRCh38. GigaScience, 2017, 6, 1-8.	6.4	49
24	Rapid establishment of the European Bank for induced Pluripotent Stem Cells (EBiSC) - the Hot Start experience. Stem Cell Research, 2017, 20, 105-114.	0.7	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. Stem Cells Translational Medicine, 2017, 6, 1956-1962.	3.3	42
26	Platelet function is modified by common sequence variation in megakaryocyte super enhancers. Nature Communications, 2017, 8, 16058.	12.8	50
27	The human-induced pluripotent stem cell initiativeâ€”data resources for cellular genetics. Nucleic Acids Research, 2017, 45, D691-D697.	14.5	81
28	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.	14.5	215
29	European Nucleotide Archive in 2016. Nucleic Acids Research, 2017, 45, D32-D36.	14.5	68
30	The Ensembl gene annotation system. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw093.	3.0	912
31	Increased DNA methylation variability in type 1 diabetes across three immune effector cell types. Nature Communications, 2016, 7, 13555.	12.8	142
32	Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. Nature Genetics, 2016, 48, 593-599.	21.4	273
33	The BLUEPRINT Data Analysis Portal. Cell Systems, 2016, 3, 491-495.e5.	6.2	123
34	<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.	1.7	65
35	Î²-Glucan Reverses the Epigenetic State of LPS-Induced Immunological Tolerance. Cell, 2016, 167, 1354-1368.e14.	28.9	467
36	Lineage-Specific Genome Architecture Links Enhancers and Non-coding Disease Variants to Target Gene Promoters. Cell, 2016, 167, 1369-1384.e19.	28.9	863

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37	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	28.9	404
38	Distinct Trends of DNA Methylation Patterning in the Innate and Adaptive Immune Systems. Cell Reports, 2016, 17, 2101-2111.	6.4	54
39	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. Cell, 2016, 167, 1398-1414.e24.	28.9	573
40	Characterizing neutral genomic diversity and selection signatures in indigenous populations of Moroccan goats (Capra hircus) using WGS data. Frontiers in Genetics, 2015, 6, 107.	2.3	108
41	Whole-genome fingerprint of the DNA methylome during human B cell differentiation. Nature Genetics, 2015, 47, 746-756.	21.4	278
42	Whole-epigenome analysis in multiple myeloma reveals DNA hypermethylation of B cell-specific enhancers. Genome Research, 2015, 25, 478-487.	5.5	118
43	Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project. Genome Biology, 2015, 16, 57.	8.8	331
44	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	27.8	13,998
45	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	27.8	1,994
46	Relationship between genome and epigenome - challenges and requirements for future research. BMC Genomics, 2014, 15, 487.	2.8	24
47	Transcriptional diversity during lineage commitment of human blood progenitors. Science, 2014, 345, 1251033.	12.6	253
48	Characterization of the DNA Methylome during Human B-Cell Differentiation. Blood, 2014, 124, 4346-4346.	1.4	0
49	Whole-Genome Epigenomic Analysis in Multiple Myeloma Reveals DNA Hypermethylation of B-Cell Specific Enhancers. Blood, 2014, 124, 2032-2032.	1.4	0
50	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235587.	12.6	341
51	The origin, evolution, and functional impact of short insertionâ€“deletion variants identified in 179 human genomes. Genome Research, 2013, 23, 749-761.	5.5	206
52	The 1000 Genomes Project: data management and community access. Nature Methods, 2012, 9, 459-462.	19.0	308
53	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	27.8	7,199
54	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.	6.2	255

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55	A Systematic Survey of Loss-of-Function Variants in Human Protein-Coding Genes. Science, 2012, 335, 823-828.	12.6	1,095
56	The functional spectrum of low-frequency coding variation. Genome Biology, 2011, 12, R84.	9.6	173
57	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.	7.1	589
58	A map of human genome variation from population-scale sequencing. Nature, 2010, 467, 1061-1073.	27.8	7,209
59	Genome analysis of the platypus reveals unique signatures of evolution. Nature, 2008, 453, 175-183.	27.8	657
60	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. Science, 2007, 316, 222-234.	12.6	1,283
61	The Ensembl Automatic Gene Annotation System. Genome Research, 2004, 14, 942-950.	5.5	352
62	An Overview of Ensembl. Genome Research, 2004, 14, 925-928.	5.5	391
63	The Ensembl Analysis Pipeline. Genome Research, 2004, 14, 934-941.	5.5	99
64	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. Nature, 2004, 428, 493-521.	27.8	1,943
65	Finishing the euchromatic sequence of the human genome. Nature, 2004, 431, 931-945.	27.8	4,232
66	Ensembl 2002: accommodating comparative genomics. Nucleic Acids Research, 2003, 31, 38-42.	14.5	216
67	Biopipe: A Flexible Framework for Protocol-Based Bioinformatics Analysis. Genome Research, 2003, 13, 1904-15.	5.5	65
68	The Genome Sequence of Caenorhabditis briggsae: A Platform for Comparative Genomics. PLoS Biology, 2003, 1, e45.	5.6	812
69	The Ensembl genome database project. Nucleic Acids Research, 2002, 30, 38-41.	14.5	1,411