

Laura Clarke

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

74
papers

39,206
citations

46
h-index

78
g-index

78
ext. papers

48,254
ext. citations

21.1
avg, IF

6.89
L-index

#	Paper	IF	Citations
74	Expression Atlas update: gene and protein expression in multiple species. <i>Nucleic Acids Research</i> , 2021 ,	20.1	8
73	The Organoid Cell Atlas. <i>Nature Biotechnology</i> , 2021 , 39, 13-17	44.5	30
72	Cell type-specific novel long non-coding RNA and circular RNA in the BLUEPRINT hematopoietic transcriptomes atlas. <i>Haematologica</i> , 2021 , 106, 2613-2623	6.6	5
71	Genetic perturbation of PU.1 binding and chromatin looping at neutrophil enhancers associates with autoimmune disease. <i>Nature Communications</i> , 2021 , 12, 2298	17.4	7
70	Population-scale proteome variation in human induced pluripotent stem cells. <i>ELife</i> , 2020 , 9,	8.9	16
69	Guidelines for reporting single-cell RNA-seq experiments. <i>Nature Biotechnology</i> , 2020 , 38, 1384-1386	44.5	9
68	Chromatin-Based Classification of Genetically Heterogeneous AMLs into Two Distinct Subtypes with Diverse Stemness Phenotypes. <i>Cell Reports</i> , 2019 , 26, 1059-1069.e6	10.6	19
67	Multi-platform discovery of haplotype-resolved structural variation in human genomes. <i>Nature Communications</i> , 2019 , 10, 1784	17.4	346
66	An evaluation of sequencing coverage and genotyping strategies to assess neutral and adaptive diversity. <i>Molecular Ecology Resources</i> , 2019 , 19, 1497-1515	8.4	17
65	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	4.8	19
64	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	4.8	24
63	Convergent genomic signatures of domestication in sheep and goats. <i>Nature Communications</i> , 2018 , 9, 813	17.4	112
62	A Standard Nomenclature for Referencing and Authentication of Pluripotent Stem Cells. <i>Stem Cell Reports</i> , 2018 , 10, 1-6	8	39
61	The European Nucleotide Archive in 2017. <i>Nucleic Acids Research</i> , 2018 , 46, D36-D40	20.1	59
60	Repeat associated mechanisms of genome evolution and function revealed by the and genomes. <i>Genome Research</i> , 2018 , 28, 448-459	9.7	57
59	Multi-omics profiling reveals a distinctive epigenome signature for high-risk acute promyelocytic leukemia. <i>Oncotarget</i> , 2018 , 9, 25647-25660	3.3	11
58	FAANG, establishing metadata standards, validation and best practices for the farmed and companion animal community. <i>Animal Genetics</i> , 2018 , 49, 520-526	2.5	19

57	Dynamics of Transcription Regulation in Human Bone Marrow Myeloid Differentiation to Mature Blood Neutrophils. <i>Cell Reports</i> , 2018 , 24, 2784-2794	10.6	54
56	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. <i>Nature Medicine</i> , 2018 , 24, 868-880	50.5	103
55	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	18.3	57
54	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	9.7	365
53	Common genetic variation drives molecular heterogeneity in human iPSCs. <i>Nature</i> , 2017 , 546, 370-375	50.4	294
52	Alignment of 1000 Genomes Project reads to reference assembly GRCh38. <i>GigaScience</i> , 2017 , 6, 1-8	7.6	31
51	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	1.6	45
50	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	6.9	33
49	European Nucleotide Archive in 2016. <i>Nucleic Acids Research</i> , 2017 , 45, D32-D36	20.1	58
48	Platelet function is modified by common sequence variation in megakaryocyte super enhancers. <i>Nature Communications</i> , 2017 , 8, 16058	17.4	30
47	The human-induced pluripotent stem cell initiative-data resources for cellular genetics. <i>Nucleic Acids Research</i> , 2017 , 45, D691-D697	20.1	63
46	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	20.1	101
45	The BLUEPRINT Data Analysis Portal. <i>Cell Systems</i> , 2016 , 3, 491-495.e5	10.6	71
44	GO-FAANG meeting: a Gathering On Functional Annotation of Animal Genomes. <i>Animal Genetics</i> , 2016 , 47, 528-33	2.5	37
43	β-Glucan Reverses the Epigenetic State of LPS-Induced Immunological Tolerance. <i>Cell</i> , 2016 , 167, 1354-1368.e14	56.2	1483
42	Lineage-Specific Genome Architecture Links Enhancers and Non-coding Disease Variants to Target Gene Promoters. <i>Cell</i> , 2016 , 167, 1369-1384.e19	56.2	556
41	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016 , 167, 1145-1149	56.2	232
40	Distinct Trends of DNA Methylation Patterning in the Innate and Adaptive Immune Systems. <i>Cell Reports</i> , 2016 , 17, 2101-2111	10.6	42

39	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. <i>Cell</i> , 2016 , 167, 1398-1414. DOI: 10.1016/j.cell.2016.08.034	5.1	534
38	The Ensembl gene annotation system. <i>Database: the Journal of Biological Databases and Curation</i> , 2016 , 2016,	5	537
37	Increased DNA methylation variability in type 1 diabetes across three immune effector cell types. <i>Nature Communications</i> , 2016 , 7, 13555	17.4	95
36	Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. <i>Nature Genetics</i> , 2016 , 48, 593-9	36.3	204
35	Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project. <i>Genome Biology</i> , 2015 , 16, 57	18.3	196
34	A global reference for human genetic variation. <i>Nature</i> , 2015 , 526, 68-74	50.4	8599
33	An integrated map of structural variation in 2,504 human genomes. <i>Nature</i> , 2015 , 526, 75-81	50.4	1368
32	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	4.5	55
31	Whole-genome fingerprint of the DNA methylome during human B cell differentiation. <i>Nature Genetics</i> , 2015 , 47, 746-56	36.3	209
30	Whole-epigenome analysis in multiple myeloma reveals DNA hypermethylation of B cell-specific enhancers. <i>Genome Research</i> , 2015 , 25, 478-87	9.7	92
29	Relationship between genome and epigenome--challenges and requirements for future research. <i>BMC Genomics</i> , 2014 , 15, 487	4.5	21
28	Transcriptional diversity during lineage commitment of human blood progenitors. <i>Science</i> , 2014 , 345, 1251033	33.3	187
27	Characterization of the DNA Methylome during Human B-Cell Differentiation. <i>Blood</i> , 2014 , 124, 4346-4346	4.6	46
26	Whole-Genome Epigenomic Analysis in Multiple Myeloma Reveals DNA Hypermethylation of B-Cell Specific Enhancers. <i>Blood</i> , 2014 , 124, 2032-2032	2.2	2
25	Integrative annotation of variants from 1092 humans: application to cancer genomics. <i>Science</i> , 2013 , 342, 1235587	33.3	281
24	The origin, evolution, and functional impact of short insertion-deletion variants identified in 179 human genomes. <i>Genome Research</i> , 2013 , 23, 749-61	9.7	150
23	The 1000 Genomes Project: data management and community access. <i>Nature Methods</i> , 2012 , 9, 459-62	21.6	202
22	An integrated map of genetic variation from 1,092 human genomes. <i>Nature</i> , 2012 , 491, 56-65	50.4	6049

21	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, 1022-32	11	221
20	A systematic survey of loss-of-function variants in human protein-coding genes. <i>Science</i> , 2012 , 335, 823-833	83.3	880
19	The functional spectrum of low-frequency coding variation. <i>Genome Biology</i> , 2011 , 12, R84	18.3	161
18	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, 11983-8	11.5	455
17	A map of human genome variation from population-scale sequencing. <i>Nature</i> , 2010 , 467, 1061-73	50.4	6142
16	Genome analysis of the platypus reveals unique signatures of evolution. <i>Nature</i> , 2008 , 453, 175-83	50.4	545
15	Evolutionary and biomedical insights from the rhesus macaque genome. <i>Science</i> , 2007 , 316, 222-34	33.3	1072
14	The Ensembl automatic gene annotation system. <i>Genome Research</i> , 2004 , 14, 942-50	9.7	308
13	An overview of Ensembl. <i>Genome Research</i> , 2004 , 14, 925-8	9.7	316
12	The Ensembl analysis pipeline. <i>Genome Research</i> , 2004 , 14, 934-41	9.7	86
11	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004 , 428, 493-521	50.4	1689
10	Finishing the euchromatic sequence of the human genome. <i>Nature</i> , 2004 , 431, 931-45	50.4	3444
9	Biopipe: a flexible framework for protocol-based bioinformatics analysis. <i>Genome Research</i> , 2003 , 13, 1904-15	9.7	45
8	The genome sequence of <i>Caenorhabditis briggsae</i> : a platform for comparative genomics. <i>PLoS Biology</i> , 2003 , 1, E45	9.7	677
7	Ensembl 2002: accommodating comparative genomics. <i>Nucleic Acids Research</i> , 2003 , 31, 38-42	20.1	180
6	The Ensembl genome database project. <i>Nucleic Acids Research</i> , 2002 , 30, 38-41	20.1	1084
5	Multiple adaptive solutions to face climatic constraints: novel insights in the debate over the role of convergence in local adaptation		1
4	Variation in PU.1 binding and chromatin looping at neutrophil enhancers influences autoimmune disease susceptibility		1

3	Cell type specific novel lincRNAs and circRNAs in the BLUEPRINT haematopoietic transcriptomes atlas	3
2	Multi-platform discovery of haplotype-resolved structural variation in human genomes	26
1	Repeat associated mechanisms of genome evolution and function revealed by the <i>Mus caroli</i> and <i>Mus pahari</i> genomes	3