# Laura Clarke

## List of Publications by Citations



| | | | |
|---|---|---|---|
| 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 | A global reference for human genetic variation. *Nature*, **2015**, 526, 68-74 | 50.4 | 8599 |
| 73 | A map of human genome variation from population-scale sequencing. *Nature*, **2010**, 467, 1061-73 | 50.4 | 6142 |
| 72 | An integrated map of genetic variation from 1,092 human genomes. *Nature*, **2012**, 491, 56-65 | 50.4 | 6049 |
| 71 | Finishing the euchromatic sequence of the human genome. *Nature*, **2004**, 431, 931-45 | 50.4 | 3444 |
| 70 | Genome sequence of the Brown Norway rat yields insights into mammalian evolution. *Nature*, **2004**, 428, 493-521 | 50.4 | 1689 |
| 69 | An integrated map of structural variation in 2,504 human genomes. *Nature*, **2015**, 526, 75-81 | 50.4 | 1368 |
| 68 | The Ensembl genome database project. *Nucleic Acids Research*, **2002**, 30, 38-41 | 20.1 | 1084 |
| 67 | Evolutionary and biomedical insights from the rhesus macaque genome. *Science*, **2007**, 316, 222-34 | 33.3 | 1072 |
| 66 | A systematic survey of loss-of-function variants in human protein-coding genes. *Science*, **2012**, 335, 823-8 | 33.3 | 880 |
| 65 | The genome sequence of Caenorhabditis briggsae: a platform for comparative genomics. *PLoS Biology*, **2003**, 1, E45 | 9.7 | 677 |
| 64 | Lineage-Specific Genome Architecture Links Enhancers and Non-coding Disease Variants to Target Gene Promoters. *Cell*, **2016**, 167, 1369-1384.e19 | 56.2 | 556 |
| 63 | Genome analysis of the platypus reveals unique signatures of evolution. *Nature*, **2008**, 453, 175-83 | 50.4 | 545 |
| 62 | The Ensembl gene annotation system. *Database: the Journal of Biological Databases and Curation*, **2016**, 2016, | 5 | 537 |
| 61 | Demographic history and rare allele sharing among human populations. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 11983-8 | 11.5 | 455 |
| 60 | Evaluation of GRCh38 and de novo haploid genome assemblies demonstrates the enduring quality of the reference assembly. *Genome Research*, **2017**, 27, 849-864 | 9.7 | 365 |
| 59 | Multi-platform discovery of haplotype-resolved structural variation in human genomes. *Nature Communications*, **2019**, 10, 1784 | 17.4 | 346 |
| 58 | Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. *Cell*, **2016**, 167, 1398-1414.e24 | 56.2 | 339 |

| | | | |
|---|---|---|---|
| 57 | An overview of Ensembl. *Genome Research*, **2004**, 14, 925-8 | 9.7 | 316 |
| 56 | The Ensembl automatic gene annotation system. *Genome Research*, **2004**, 14, 942-50 | 9.7 | 308 |
| 55 | Common genetic variation drives molecular heterogeneity in human iPSCs. *Nature*, **2017**, 546, 370-375 | 50.4 | 294 |
| 54 | Glucan Reverses the Epigenetic State of LPS-Induced Immunological Tolerance. *Cell*, **2016**, 167, 1354-1368.e14 | 36.2 | 283 |
| 53 | Integrative annotation of variants from 1092 humans: application to cancer genomics. *Science*, **2013**, 342, 1235587 | 33.3 | 281 |
| 52 | The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. *Cell*, **2016**, 167, 1145-1149 | 56.2 | 232 |
| 51 | 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, 1022-32 | 11 | 221 |
| 50 | Whole-genome fingerprint of the DNA methylome during human B cell differentiation. *Nature Genetics*, **2015**, 47, 746-56 | 36.3 | 209 |
| 49 | Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. *Nature Genetics*, **2016**, 48, 593-9 | 36.3 | 204 |
| 48 | The 1000 Genomes Project: data management and community access. *Nature Methods*, **2012**, 9, 459-62 | 21.6 | 202 |
| 47 | Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project. *Genome Biology*, **2015**, 16, 57 | 18.3 | 196 |
| 46 | Transcriptional diversity during lineage commitment of human blood progenitors. *Science*, **2014**, 345, 1251033 | 33.3 | 187 |
| 45 | Ensembl 2002: accommodating comparative genomics. *Nucleic Acids Research*, **2003**, 31, 38-42 | 20.1 | 180 |
| 44 | The functional spectrum of low-frequency coding variation. *Genome Biology*, **2011**, 12, R84 | 18.3 | 161 |
| 43 | The origin, evolution, and functional impact of short insertion-deletion variants identified in 179 human genomes. *Genome Research*, **2013**, 23, 749-61 | 9.7 | 150 |
| 42 | Convergent genomic signatures of domestication in sheep and goats. *Nature Communications*, **2018**, 9, 813 | 17.4 | 112 |
| 41 | The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. *Nature Medicine*, **2018**, 24, 868-880 | 50.5 | 103 |
| 40 | 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 | 20.1 | 101 |

| | | | |
|---|---|---|---|
| 39 | Increased DNA methylation variability in type 1 diabetes across three immune effector cell types. *Nature Communications*, **2016**, 7, 13555 | 17.4 | 95 |
| 38 | Whole-epigenome analysis in multiple myeloma reveals DNA hypermethylation of B cell-specific enhancers. *Genome Research*, **2015**, 25, 478-87 | 9.7 | 92 |
| 37 | The Ensembl analysis pipeline. *Genome Research*, **2004**, 14, 934-41 | 9.7 | 86 |
| 36 | The BLUEPRINT Data Analysis Portal. *Cell Systems*, **2016**, 3, 491-495.e5 | 10.6 | 71 |
| 35 | The human-induced pluripotent stem cell initiative-data resources for cellular genetics. *Nucleic Acids Research*, **2017**, 45, D691-D697 | 20.1 | 63 |
| 34 | The European Nucleotide Archive in 2017. *Nucleic Acids Research*, **2018**, 46, D36-D40 | 20.1 | 59 |
| 33 | European Nucleotide Archive in 2016. *Nucleic Acids Research*, **2017**, 45, D32-D36 | 20.1 | 58 |
| 32 | Functional variation in allelic methylomes underscores a strong genetic contribution and reveals novel epigenetic alterations in the human epigenome. *Genome Biology*, **2017**, 18, 50 | 18.3 | 57 |
| 31 | Repeat associated mechanisms of genome evolution and function revealed by the and genomes. *Genome Research*, **2018**, 28, 448-459 | 9.7 | 57 |
| 30 | Characterizing neutral genomic diversity and selection signatures in indigenous populations of Moroccan goats (Capra hircus) using WGS data. *Frontiers in Genetics*, **2015**, 6, 107 | 4.5 | 55 |
| 29 | Dynamics of Transcription Regulation in Human Bone Marrow Myeloid Differentiation to Mature Blood Neutrophils. *Cell Reports*, **2018**, 24, 2784-2794 | 10.6 | 54 |
| 28 | Rapid establishment of the European Bank for induced Pluripotent Stem Cells (EBiSC) - the Hot Start experience. *Stem Cell Research*, **2017**, 20, 105-114 | 1.6 | 45 |
| 27 | Biopipe: a flexible framework for protocol-based bioinformatics analysis. *Genome Research*, **2003**, 13, 1904-15 | 9.7 | 45 |
| 26 | Distinct Trends of DNA Methylation Patterning in the Innate and Adaptive Immune Systems. *Cell Reports*, **2016**, 17, 2101-2111 | 10.6 | 42 |
| 25 | A Standard Nomenclature for Referencing and Authentication of Pluripotent Stem Cells. *Stem Cell Reports*, **2018**, 10, 1-6 | 8 | 39 |
| 24 | GO-FAANG meeting: a Gathering On Functional Annotation of Animal Genomes. *Animal Genetics*, **2016**, 47, 528-33 | 2.5 | 37 |
| 23 | 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 | 6.9 | 33 |
| 22 | Alignment of 1000 Genomes Project reads to reference assembly GRCh38. *GigaScience*, **2017**, 6, 1-8 | 7.6 | 31 |

| | | | |
|---|---|---|---|
| 21 | Platelet function is modified by common sequence variation in megakaryocyte super enhancers. *Nature Communications*, **2017**, 8, 16058 | 17.4 | 30 |
| 20 | The Organoid Cell Atlas. *Nature Biotechnology*, **2021**, 39, 13-17 | 44.5 | 30 |
| 19 | Multi-platform discovery of haplotype-resolved structural variation in human genomes | | 26 |
| 18 | Variant calling on the GRCh38 assembly with the data from phase three of the 1000 Genomes Project. *Wellcome Open Research*, **2019**, 4, 50 | 4.8 | 24 |
| 17 | Relationship between genome and epigenome--challenges and requirements for future research. *BMC Genomics*, **2014**, 15, 487 | 4.5 | 21 |
| 16 | Chromatin-Based Classification of Genetically Heterogeneous AMLs into Two Distinct Subtypes with Diverse Stemness Phenotypes. *Cell Reports*, **2019**, 26, 1059-1069.e6 | 10.6 | 19 |
| 15 | Variant calling on the GRCh38 assembly with the data from phase three of the 1000 Genomes Project. *Wellcome Open Research*, **2019**, 4, 50 | 4.8 | 19 |
| 14 | FAANG, establishing metadata standards, validation and best practices for the farmed and companion animal community. *Animal Genetics*, **2018**, 49, 520-526 | 2.5 | 19 |
| 13 | An evaluation of sequencing coverage and genotyping strategies to assess neutral and adaptive diversity. *Molecular Ecology Resources*, **2019**, 19, 1497-1515 | 8.4 | 17 |
| 12 | Population-scale proteome variation in human induced pluripotent stem cells. *ELife*, **2020**, 9, | 8.9 | 16 |
| 11 | Multi-omics profiling reveals a distinctive epigenome signature for high-risk acute promyelocytic leukemia. *Oncotarget*, **2018**, 9, 25647-25660 | 3.3 | 11 |
| 10 | Guidelines for reporting single-cell RNA-seq experiments. *Nature Biotechnology*, **2020**, 38, 1384-1386 | 44.5 | 9 |
| 9 | Expression Atlas update: gene and protein expression in multiple species. *Nucleic Acids Research*, **2021**, | 20.1 | 8 |
| 8 | Genetic perturbation of PU.1 binding and chromatin looping at neutrophil enhancers associates with autoimmune disease. *Nature Communications*, **2021**, 12, 2298 | 17.4 | 7 |
| 7 | Cell type-specific novel long non-coding RNA and circular RNA in the BLUEPRINT hematopoietic transcriptomes atlas. *Haematologica*, **2021**, 106, 2613-2623 | 6.6 | 5 |
| 6 | Cell type specific novel lincRNAs and circRNAs in the BLUEPRINT haematopoietic transcriptomes atlas | | 3 |
| 5 | Repeat associated mechanisms of genome evolution and function revealed by the Mus caroli and Mus pahari genomes | | 3 |
| 4 | Multiple adaptive solutions to face climatic constraints: novel insights in the debate over the role of convergence in local adaptation | | 1 |

| | | |
|---|---|---|
| 3 | Variation in PU.1 binding and chromatin looping at neutrophil enhancers influences autoimmune disease susceptibility | 1 |
| 2 | Characterization of the DNA Methylome during Human B-Cell Differentiation. *Blood*, **2014**, 124, 4346-4346 | |
| 1 | Whole-Genome Epigenomic Analysis in Multiple Myeloma Reveals DNA Hypermethylation of B-Cell Specific Enhancers. *Blood*, **2014**, 124, 2032-2032 | 2.2 |