

Javier Herrero

List of Publications by Year in descending order

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Version: 2024-02-01

120
papers

87,460
citations

14655

66
h-index

18130

120
g-index

139
all docs

139
docs citations

139
times ranked

117772
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Systematic Evaluation of the Immune Environment of Small Intestinal Neuroendocrine Tumors. <i>Clinical Cancer Research</i> , 2022, 28, 2657-2668. | 7.0 | 4 |
| 2 | A local human V α 1 T cell population is associated with survival in nonsmall-cell lung cancer. <i>Nature Cancer</i> , 2022, 3, 696-709. | 13.2 | 39 |
| 3 | Incorporating alignment uncertainty into Felsenstein's phylogenetic bootstrap to improve its reliability. <i>Bioinformatics</i> , 2021, 37, 1506-1514. | 4.1 | 7 |
| 4 | Increased Immune-Regulatory Receptor Expression on Effector T Cells as Early Indicators of Relapse Following Autologous Stem Cell Transplantation for Multiple Myeloma. <i>Frontiers in Immunology</i> , 2021, 12, 618610. | 4.8 | 7 |
| 5 | Meta-analysis of tumor- and T cell-intrinsic mechanisms of sensitization to checkpoint inhibition. <i>Cell</i> , 2021, 184, 596-614.e14. | 28.9 | 485 |
| 6 | Glioblastomas acquire myeloid-affiliated transcriptional programs via epigenetic immunoediting to elicit immune evasion. <i>Cell</i> , 2021, 184, 2454-2470.e26. | 28.9 | 165 |
| 7 | Chemotherapy induces canalization of cell state in childhood B-cell precursor acute lymphoblastic leukemia. <i>Nature Cancer</i> , 2021, 2, 835-852. | 13.2 | 25 |
| 8 | Nascent RNA antagonizes the interaction of a set of regulatory proteins with chromatin. <i>Molecular Cell</i> , 2021, 81, 2944-2959.e10. | 9.7 | 19 |
| 9 | The Th1 cell regulatory circuitry is largely conserved between human and mouse. <i>Life Science Alliance</i> , 2021, 4, e202101075. | 2.8 | 1 |
| 10 | Using DNA sequencing data to quantify T cell fraction and therapy response. <i>Nature</i> , 2021, 597, 555-560. | 27.8 | 36 |
| 11 | GenomeChronicler: The Personal Genome Project UK Genomic Report Generator Pipeline. <i>Frontiers in Genetics</i> , 2020, 11, 518644. | 2.3 | 4 |
| 12 | Escape from nonsense-mediated decay associates with anti-tumor immunogenicity. <i>Nature Communications</i> , 2020, 11, 3800. | 12.8 | 61 |
| 13 | EZH2-Deficient T-cell Acute Lymphoblastic Leukemia Is Sensitized to CHK1 Inhibition through Enhanced Replication Stress. <i>Cancer Discovery</i> , 2020, 10, 998-1017. | 9.4 | 29 |
| 14 | Marrow-Infiltrating Regulatory T Cells Correlate with the Presence of Dysfunctional CD4+PD-1+ Cells and Inferior Survival in Patients with Newly Diagnosed Multiple Myeloma. <i>Clinical Cancer Research</i> , 2020, 26, 3443-3454. | 7.0 | 33 |
| 15 | The T cell differentiation landscape is shaped by tumour mutations in lung cancer. <i>Nature Cancer</i> , 2020, 1, 546-561. | 13.2 | 74 |
| 16 | Enhancer accessibility and CTCF occupancy underlie asymmetric TAD architecture and cell type specific genome topology. <i>Nature Communications</i> , 2019, 10, 2908. | 12.8 | 81 |
| 17 | The Personal Genome Project-UK, an open access resource of human multi-omics data. <i>Scientific Data</i> , 2019, 6, 257. | 5.3 | 19 |
| 18 | Spatial heterogeneity of the T cell receptor repertoire reflects the mutational landscape in lung cancer. <i>Nature Medicine</i> , 2019, 25, 1549-1559. | 30.7 | 147 |

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|----|---|------|-----------|
| 19 | A clonal expression biomarker associates with lung cancer mortality. Nature Medicine, 2019, 25, 1540-1548. | 30.7 | 75 |
| 20 | G-tract RNA removes Polycomb repressive complex 2 from genes. Nature Structural and Molecular Biology, 2019, 26, 899-909. | 8.2 | 86 |
| 21 | Neoantigen-directed immune escape in lung cancer evolution. Nature, 2019, 567, 479-485. | 27.8 | 639 |
| 22 | Abstract 2678: A clonal expression biomarker improves prognostic accuracy: TRACERx lung. , 2019, , . | | 0 |
| 23 | Deterministic Evolutionary Trajectories Influence Primary Tumor Growth: TRACERx Renal. Cell, 2018, 173, 595-610.e11. | 28.9 | 472 |
| 24 | A Human IPS Model Implicates Embryonic B-Myeloid Fate Restriction as Developmental Susceptibility to B-Cell Acute Lymphoblastic Leukemia-Associated ETV6-RUNX1. Developmental Cell, 2018, 44, 362-377.e7. | 7.0 | 65 |
| 25 | Fc Effector Function Contributes to the Activity of Human Anti-CTLA-4 Antibodies. Cancer Cell, 2018, 33, 649-663.e4. | 16.8 | 448 |
| 26 | Aequatus: an open-source homology browser. GigaScience, 2018, 7, . | 6.4 | 1 |
| 27 | Personal Genome Project UK (PGP-UK): a research and citizen science hybrid project in support of personalized medicine. BMC Medical Genomics, 2018, 11, 108. | 1.5 | 34 |
| 28 | Generation of a cancer testis antigen mCherry reporter HCT116 colorectal carcinoma cell line. Heliyon, 2018, 4, e00858. | 3.2 | 0 |
| 29 | RNA-seq of newly diagnosed patients in the PADIMAC study leads to a bortezomib/lenalidomide decision signature. Blood, 2018, 132, 2154-2165. | 1.4 | 14 |
| 30 | <scp>KAP</scp> 1 regulates endogenous retroviruses in adult human cells and contributes to innate immune control. EMBO Reports, 2018, 19, . | 4.5 | 88 |
| 31 | The HUSH complex cooperates with TRIM28 to repress young retrotransposons and new genes. Genome Research, 2018, 28, 836-845. | 5.5 | 141 |
| 32 | Fc-Optimized Anti-CD25 Depletes Tumor-Infiltrating Regulatory T Cells and Synergizes with PD-1 Blockade to Eradicate Established Tumors. Immunity, 2017, 46, 577-586. | 14.3 | 323 |
| 33 | Phylogenetic ctDNA analysis depicts early-stage lung cancer evolution. Nature, 2017, 545, 446-451. | 27.8 | 1,287 |
| 34 | Tracking the Evolution of Non-Small-Cell Lung Cancer. New England Journal of Medicine, 2017, 376, 2109-2121. | 27.0 | 1,786 |
| 35 | Allele-Specific HLA Loss and Immune Escape in Lung Cancer Evolution. Cell, 2017, 171, 1259-1271.e11. | 28.9 | 968 |
| 36 | H3.3K27M Cooperates with Trp53 Loss and PDGFRA Gain in Mouse Embryonic Neural Progenitor Cells to Induce Invasive High-Grade Gliomas. Cancer Cell, 2017, 32, 684-700.e9. | 16.8 | 192 |

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|----|---|------|-----------|
| 37 | A human ips model implicates embryonic B-myeloid fate restriction as a developmental susceptibility to ETV6-RUNX1. <i>Experimental Hematology</i> , 2017, 53, S45. | 0.4 | 0 |
| 38 | A novel requirement for DROSHA in maintenance of mammalian CG methylation. <i>Nucleic Acids Research</i> , 2017, 45, 9398-9412. | 14.5 | 9 |
| 39 | Intratumoural evolutionary landscape of high-risk prostate cancer: the PROGENY study of genomic and immune parameters. <i>Annals of Oncology</i> , 2017, 28, 2472-2480. | 1.2 | 45 |
| 40 | Deciphering Genetic Intratumor Heterogeneity and Its Impact on Cancer Evolution. <i>Annual Review of Cancer Biology</i> , 2017, 1, 223-240. | 4.5 | 20 |
| 41 | A 3-way hybrid approach to generate a new high-quality chimpanzee reference genome (Pan_tro_3.0). <i>GigaScience</i> , 2017, 6, 1-6. | 6.4 | 17 |
| 42 | Herpesviruses shape tumour microenvironment through exosomal transfer of viral microRNAs. <i>PLoS Pathogens</i> , 2017, 13, e1006524. | 4.7 | 73 |
| 43 | Genetic variants alter T-bet binding and gene expression in mucosal inflammatory disease. <i>PLoS Genetics</i> , 2017, 13, e1006587. | 3.5 | 40 |
| 44 | Quantification of tumour evolution and heterogeneity via Bayesian epiallele detection. <i>BMC Bioinformatics</i> , 2017, 18, 354. | 2.6 | 15 |
| 45 | Clonal Evolutionary Analysis during HER2 Blockade in HER2-Positive Inflammatory Breast Cancer: A Phase II Open-Label Clinical Trial of Afatinib +/- Vinorelbine. <i>PLoS Medicine</i> , 2016, 13, e1002136. | 8.4 | 28 |
| 46 | Ensembl comparative genomics resources. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, bav096. | 3.0 | 344 |
| 47 | TALEN-Mediated Inactivation of PD-1 in Tumor-Reactive Lymphocytes Promotes Intratumoral T-cell Persistence and Rejection of Established Tumors. <i>Cancer Research</i> , 2016, 76, 2087-2093. | 0.9 | 67 |
| 48 | eFORGE: A Tool for Identifying Cell Type-Specific Signal in Epigenomic Data. <i>Cell Reports</i> , 2016, 17, 2137-2150. | 6.4 | 102 |
| 49 | CORALINA: a universal method for the generation of gRNA libraries for CRISPR-based screening. <i>BMC Genomics</i> , 2016, 17, 917. | 2.8 | 16 |
| 50 | Saturation analysis for whole-genome bisulfite sequencing data. <i>Nature Biotechnology</i> , 2016, 34, 691-693. | 17.5 | 26 |
| 51 | Modelling the in-utero initiation of ETV6-RUNX1 in childhood acute lymphoblastic leukaemia using human pluripotent stem cells. <i>Lancet, The</i> , 2016, 387, S86. | 13.7 | 0 |
| 52 | deconstructSigs: delineating mutational processes in single tumors distinguishes DNA repair deficiencies and patterns of carcinoma evolution. <i>Genome Biology</i> , 2016, 17, 31. | 8.8 | 917 |
| 53 | ncRNA orthologies in the vertebrate lineage. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, bav127. | 3.0 | 19 |
| 54 | The pig X and Y Chromosomes: structure, sequence, and evolution. <i>Genome Research</i> , 2016, 26, 130-139. | 5.5 | 69 |

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|----|--|------|-----------|
| 55 | Abstract 2692: ETV6-RUNX1 targets a developmentally restricted embryonic human B-myeloid progenitor. , 2016, , . | | 0 |
| 56 | Single-Cell Analysis of Clonal Dynamics in Childhood ALL Reveals a Key Role for Transcriptional Intratumor Heterogeneity in Driving Resistance to Chemotherapy. Blood, 2016, 128, 606-606. | 1.4 | 0 |
| 57 | Genome-wide comparative analysis reveals human-mouse regulatory landscape and evolution. BMC Genomics, 2015, 16, 87. | 2.8 | 62 |
| 58 | Extending reference assembly models. Genome Biology, 2015, 16, 13. | 8.8 | 139 |
| 59 | A global reference for human genetic variation. Nature, 2015, 526, 68-74. | 27.8 | 13,998 |
| 60 | Current Methods for Automated Filtering of Multiple Sequence Alignments Frequently Worsen Single-Gene Phylogenetic Inference. Systematic Biology, 2015, 64, 778-791. | 5.6 | 200 |
| 61 | Ensembl 2014. Nucleic Acids Research, 2014, 42, D749-D755. | 14.5 | 1,211 |
| 62 | Alignathon: a competitive assessment of whole-genome alignment methods. Genome Research, 2014, 24, 2077-2089. | 5.5 | 102 |
| 63 | Principles of regulatory information conservation between mouse and human. Nature, 2014, 515, 371-375. | 27.8 | 259 |
| 64 | A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364. | 27.8 | 1,444 |
| 65 | The common marmoset genome provides insight into primate biology and evolution. Nature Genetics, 2014, 46, 850-857. | 21.4 | 225 |
| 66 | Gibbon genome and the fast karyotype evolution of small apes. Nature, 2014, 513, 195-201. | 27.8 | 320 |
| 67 | Integrating sequence and array data to create an improved 1000 Genomes Project haplotype reference panel. Nature Communications, 2014, 5, 3934. | 12.8 | 364 |
| 68 | Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235587. | 12.6 | 341 |
| 69 | The zebrafish reference genome sequence and its relationship to the human genome. Nature, 2013, 496, 498-503. | 27.8 | 3,708 |
| 70 | The draft genomes of soft-shell turtle and green sea turtle yield insights into the development and evolution of the turtle-specific body plan. Nature Genetics, 2013, 45, 701-706. | 21.4 | 409 |
| 71 | Sequencing of the sea lamprey (Petromyzon marinus) genome provides insights into vertebrate evolution. Nature Genetics, 2013, 45, 415-421. | 21.4 | 588 |
| 72 | The duck genome and transcriptome provide insight into an avian influenza virus reservoir species. Nature Genetics, 2013, 45, 776-783. | 21.4 | 327 |

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|----|--|------|-----------|
| 73 | Analysis of variation at transcription factor binding sites in Drosophila and humans. <i>Genome Biology</i> , 2012, 13, R49. | 9.6 | 83 |
| 74 | An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012, 489, 57-74. | 27.8 | 15,516 |
| 75 | Ensembl 2012. <i>Nucleic Acids Research</i> , 2012, 40, D84-D90. | 14.5 | 840 |
| 76 | The 1000 Genomes Project: data management and community access. <i>Nature Methods</i> , 2012, 9, 459-462. | 19.0 | 308 |
| 77 | Ensembl 2013. <i>Nucleic Acids Research</i> , 2012, 41, D48-D55. | 14.5 | 856 |
| 78 | An integrated map of genetic variation from 1,092 human genomes. <i>Nature</i> , 2012, 491, 56-65. | 27.8 | 7,199 |
| 79 | Insights into hominid evolution from the gorilla genome sequence. <i>Nature</i> , 2012, 483, 169-175. | 27.8 | 663 |
| 80 | The variant call format and VCFtools. <i>Bioinformatics</i> , 2011, 27, 2156-2158. | 4.1 | 11,326 |
| 81 | Genome sequence of an Australian kangaroo, <i>Macropus eugenii</i> , provides insight into the evolution of mammalian reproduction and development. <i>Genome Biology</i> , 2011, 12, 414. | 9.6 | 22 |
| 82 | Genome sequence of an Australian kangaroo, <i>Macropus eugenii</i> , provides insight into the evolution of mammalian reproduction and development. <i>Genome Biology</i> , 2011, 12, R81. | 9.6 | 167 |
| 83 | Considerations for the inclusion of 2x mammalian genomes in phylogenetic analyses. <i>Genome Biology</i> , 2011, 12, 401. | 9.6 | 7 |
| 84 | A User's Guide to the Encyclopedia of DNA Elements (ENCODE). <i>PLoS Biology</i> , 2011, 9, e1001046. | 5.6 | 1,257 |
| 85 | Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , 2011, 469, 529-533. | 27.8 | 541 |
| 86 | A high-resolution map of human evolutionary constraint using 29 mammals. <i>Nature</i> , 2011, 478, 476-482. | 27.8 | 1,016 |
| 87 | Variation in genome-wide mutation rates within and between human families. <i>Nature Genetics</i> , 2011, 43, 712-714. | 21.4 | 525 |
| 88 | Ensembl 2011. <i>Nucleic Acids Research</i> , 2011, 39, D800-D806. | 14.5 | 630 |
| 89 | RNAcentral: A vision for an international database of RNA sequences. <i>Rna</i> , 2011, 17, 1941-1946. | 3.5 | 67 |
| 90 | eHive: An Artificial Intelligence workflow system for genomic analysis. <i>BMC Bioinformatics</i> , 2010, 11, 240. | 2.6 | 37 |

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|-----|--|------|-----------|
| 91 | A map of human genome variation from population-scale sequencing. <i>Nature</i> , 2010, 467, 1061-1073. | 27.8 | 7,209 |
| 92 | Ensembl Genomes: Extending Ensembl across the taxonomic space. <i>Nucleic Acids Research</i> , 2010, 38, D563-D569. | 14.5 | 138 |
| 93 | Ensembl's 10th year. <i>Nucleic Acids Research</i> , 2010, 38, D557-D562. | 14.5 | 251 |
| 94 | Multi-Platform Next-Generation Sequencing of the Domestic Turkey (<i>Meleagris gallopavo</i>): Genome Assembly and Analysis. <i>PLoS Biology</i> , 2010, 8, e1000475. | 5.6 | 348 |
| 95 | Ensembl 2009. <i>Nucleic Acids Research</i> , 2009, 37, D690-D697. | 14.5 | 721 |
| 96 | Sequence progressive alignment, a framework for practical large-scale probabilistic consistency alignment. <i>Bioinformatics</i> , 2009, 25, 295-301. | 4.1 | 47 |
| 97 | A Bayesian deconvolution strategy for immunoprecipitation-based DNA methylome analysis. <i>Nature Biotechnology</i> , 2008, 26, 779-785. | 17.5 | 619 |
| 98 | Genome-wide nucleotide-level mammalian ancestor reconstruction. <i>Genome Research</i> , 2008, 18, 1829-1843. | 5.5 | 164 |
| 99 | Enredo and Pecan: Genome-wide mammalian consistency-based multiple alignment with paralogs. <i>Genome Research</i> , 2008, 18, 1814-1828. | 5.5 | 249 |
| 100 | Ensembl 2007. <i>Nucleic Acids Research</i> , 2007, 35, D610-D617. | 14.5 | 699 |
| 101 | Ensembl 2008. <i>Nucleic Acids Research</i> , 2007, 36, D707-D714. | 14.5 | 440 |
| 102 | TranscriptSNPView: a genome-wide catalog of mouse coding variation. <i>Nature Genetics</i> , 2006, 38, 853-853. | 21.4 | 14 |
| 103 | Next station in microarray data analysis: GEPAS. <i>Nucleic Acids Research</i> , 2006, 34, W486-W491. | 14.5 | 107 |
| 104 | GEPAS, an experiment-oriented pipeline for the analysis of microarray gene expression data. <i>Nucleic Acids Research</i> , 2005, 33, W616-W620. | 14.5 | 86 |
| 105 | New challenges in gene expression data analysis and the extended GEPAS. <i>Nucleic Acids Research</i> , 2004, 32, W485-W491. | 14.5 | 47 |
| 106 | Ensembl 2005. <i>Nucleic Acids Research</i> , 2004, 33, D447-D453. | 14.5 | 368 |
| 107 | Improved Class Prediction in DNA Microarray Gene Expression Data by Unsupervised Reduction of the Dimensionality followed by Supervised Learning with a Perceptron. <i>Journal of Signal Processing Systems</i> , 2003, 35, 245-253. | 1.0 | 9 |
| 108 | Title is missing!. <i>Artificial Intelligence Review</i> , 2003, 20, 39-51. | 15.7 | 32 |

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|-----|---|------|-----------|
| 109 | An Approach to Inferring Transcriptional Regulation Among Genes From Large-Scale Expression Data. Comparative and Functional Genomics, 2003, 4, 148-154. | 2.0 | 10 |
| 110 | Comparing Bacterial Genomes Through Conservation Profiles. Genome Research, 2003, 13, 991-998. | 5.5 | 26 |
| 111 | Gene expression data preprocessing. Bioinformatics, 2003, 19, 655-656. | 4.1 | 84 |
| 112 | GEPAS: a web-based resource for microarray gene expression data analysis. Nucleic Acids Research, 2003, 31, 3461-3467. | 14.5 | 161 |
| 113 | Supervised Neural Networks for Clustering Conditions in DNA Array Data After Reducing Noise by Clustering Gene Expression Profiles. , 2002, , 91-103. | | 20 |
| 114 | Combining Hierarchical Clustering and Self-Organizing Maps for Exploratory Analysis of Gene Expression Patterns. Journal of Proteome Research, 2002, 1, 467-470. | 3.7 | 49 |
| 115 | Identification of Genes Involved in Resistance to Interferon- α in Cutaneous T-Cell Lymphoma. American Journal of Pathology, 2002, 161, 1825-1837. | 3.8 | 106 |
| 116 | Bioinformatics methods for the analysis of expression arrays: data clustering and information extraction. Journal of Biotechnology, 2002, 98, 269-283. | 3.8 | 48 |
| 117 | Using Perceptrons for Supervised Classification of DNA Microarray Samples: Obtaining the Optimal Level of Information and Finding Differentially Expressed Genes. Lecture Notes in Computer Science, 2002, , 577-582. | 1.3 | 1 |
| 118 | A hierarchical unsupervised growing neural network for clustering gene expression patterns. Bioinformatics, 2001, 17, 126-136. | 4.1 | 562 |
| 119 | Annotated Draft Genomic Sequence from a <i>Streptococcus pneumoniae</i> Type 19F Clinical Isolate. Microbial Drug Resistance, 2001, 7, 99-125. | 2.0 | 98 |
| 120 | Using gene ontology on genome-scale studies to find significant associations of biologically relevant terms to groups of genes. , 0, , . | | 1 |