

# Javier Herrero

## List of Publications by Year in descending order

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120  
papers

87,460  
citations

14614

66  
h-index

18075

120  
g-index

139  
all docs

139  
docs citations

139  
times ranked

117772  
citing authors

#	ARTICLE	IF	CITATIONS
1	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012, 489, 57-74.	13.7	15,516
2	A global reference for human genetic variation. <i>Nature</i> , 2015, 526, 68-74.	13.7	13,998
3	The variant call format and VCFtools. <i>Bioinformatics</i> , 2011, 27, 2156-2158.	1.8	11,326
4	A map of human genome variation from population-scale sequencing. <i>Nature</i> , 2010, 467, 1061-1073.	13.7	7,209
5	An integrated map of genetic variation from 1,092 human genomes. <i>Nature</i> , 2012, 491, 56-65.	13.7	7,199
6	The zebrafish reference genome sequence and its relationship to the human genome. <i>Nature</i> , 2013, 496, 498-503.	13.7	3,708
7	Tracking the Evolution of Non-Small-Cell Lung Cancer. <i>New England Journal of Medicine</i> , 2017, 376, 2109-2121.	13.9	1,786
8	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014, 515, 355-364.	13.7	1,444
9	Phylogenetic ctDNA analysis depicts early-stage lung cancer evolution. <i>Nature</i> , 2017, 545, 446-451.	13.7	1,287
10	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). <i>PLoS Biology</i> , 2011, 9, e1001046.	2.6	1,257
11	Ensembl 2014. <i>Nucleic Acids Research</i> , 2014, 42, D749-D755.	6.5	1,211
12	A high-resolution map of human evolutionary constraint using 29 mammals. <i>Nature</i> , 2011, 478, 476-482.	13.7	1,016
13	Allele-Specific HLA Loss and Immune Escape in Lung Cancer Evolution. <i>Cell</i> , 2017, 171, 1259-1271.e11.	13.5	968
14	deconstructSigs: delineating mutational processes in single tumors distinguishes DNA repair deficiencies and patterns of carcinoma evolution. <i>Genome Biology</i> , 2016, 17, 31.	3.8	917
15	Ensembl 2013. <i>Nucleic Acids Research</i> , 2012, 41, D48-D55.	6.5	856
16	Ensembl 2012. <i>Nucleic Acids Research</i> , 2012, 40, D84-D90.	6.5	840
17	Ensembl 2009. <i>Nucleic Acids Research</i> , 2009, 37, D690-D697.	6.5	721
18	Ensembl 2007. <i>Nucleic Acids Research</i> , 2007, 35, D610-D617.	6.5	699

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19	Insights into hominid evolution from the gorilla genome sequence. <i>Nature</i> , 2012, 483, 169-175.	13.7	663
20	Neoantigen-directed immune escape in lung cancer evolution. <i>Nature</i> , 2019, 567, 479-485.	13.7	639
21	Ensembl 2011. <i>Nucleic Acids Research</i> , 2011, 39, D800-D806.	6.5	630
22	A Bayesian deconvolution strategy for immunoprecipitation-based DNA methylome analysis. <i>Nature Biotechnology</i> , 2008, 26, 779-785.	9.4	619
23	Sequencing of the sea lamprey ( <i>Petromyzon marinus</i> ) genome provides insights into vertebrate evolution. <i>Nature Genetics</i> , 2013, 45, 415-421.	9.4	588
24	A hierarchical unsupervised growing neural network for clustering gene expression patterns. <i>Bioinformatics</i> , 2001, 17, 126-136.	1.8	562
25	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , 2011, 469, 529-533.	13.7	541
26	Variation in genome-wide mutation rates within and between human families. <i>Nature Genetics</i> , 2011, 43, 712-714.	9.4	525
27	Meta-analysis of tumor- and T cell-intrinsic mechanisms of sensitization to checkpoint inhibition. <i>Cell</i> , 2021, 184, 596-614.e14.	13.5	485
28	Deterministic Evolutionary Trajectories Influence Primary Tumor Growth: TRACERx Renal. <i>Cell</i> , 2018, 173, 595-610.e11.	13.5	472
29	Fc Effector Function Contributes to the Activity of Human Anti-CTLA-4 Antibodies. <i>Cancer Cell</i> , 2018, 33, 649-663.e4.	7.7	448
30	Ensembl 2008. <i>Nucleic Acids Research</i> , 2007, 36, D707-D714.	6.5	440
31	The draft genomes of soft-shell turtle and green sea turtle yield insights into the development and evolution of the turtle-specific body plan. <i>Nature Genetics</i> , 2013, 45, 701-706.	9.4	409
32	Ensembl 2005. <i>Nucleic Acids Research</i> , 2004, 33, D447-D453.	6.5	368
33	Integrating sequence and array data to create an improved 1000 Genomes Project haplotype reference panel. <i>Nature Communications</i> , 2014, 5, 3934.	5.8	364
34	Multi-Platform Next-Generation Sequencing of the Domestic Turkey ( <i>Meleagris gallopavo</i> ): Genome Assembly and Analysis. <i>PLoS Biology</i> , 2010, 8, e1000475.	2.6	348
35	Ensembl comparative genomics resources. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, bav096.	1.4	344
36	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. <i>Science</i> , 2013, 342, 1235587.	6.0	341

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37	The duck genome and transcriptome provide insight into an avian influenza virus reservoir species. <i>Nature Genetics</i> , 2013, 45, 776-783.	9.4	327
38	Fc-Optimized Anti-CD25 Depletes Tumor-Infiltrating Regulatory T Cells and Synergizes with PD-1 Blockade to Eradicate Established Tumors. <i>Immunity</i> , 2017, 46, 577-586.	6.6	323
39	Gibbon genome and the fast karyotype evolution of small apes. <i>Nature</i> , 2014, 513, 195-201.	13.7	320
40	The 1000 Genomes Project: data management and community access. <i>Nature Methods</i> , 2012, 9, 459-462.	9.0	308
41	Principles of regulatory information conservation between mouse and human. <i>Nature</i> , 2014, 515, 371-375.	13.7	259
42	Ensembl's 10th year. <i>Nucleic Acids Research</i> , 2010, 38, D557-D562.	6.5	251
43	Enredo and Pecan: Genome-wide mammalian consistency-based multiple alignment with paralogs. <i>Genome Research</i> , 2008, 18, 1814-1828.	2.4	249
44	The common marmoset genome provides insight into primate biology and evolution. <i>Nature Genetics</i> , 2014, 46, 850-857.	9.4	225
45	Current Methods for Automated Filtering of Multiple Sequence Alignments Frequently Worsen Single-Gene Phylogenetic Inference. <i>Systematic Biology</i> , 2015, 64, 778-791.	2.7	200
46	H3.3K27M Cooperates with Trp53 Loss and PDGFRA Gain in Mouse Embryonic Neural Progenitor Cells to Induce Invasive High-Grade Gliomas. <i>Cancer Cell</i> , 2017, 32, 684-700.e9.	7.7	192
47	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.	13.9	167
48	Glioblastomas acquire myeloid-affiliated transcriptional programs via epigenetic immunoeediting to elicit immune evasion. <i>Cell</i> , 2021, 184, 2454-2470.e26.	13.5	165
49	Genome-wide nucleotide-level mammalian ancestor reconstruction. <i>Genome Research</i> , 2008, 18, 1829-1843.	2.4	164
50	GEPAS: a web-based resource for microarray gene expression data analysis. <i>Nucleic Acids Research</i> , 2003, 31, 3461-3467.	6.5	161
51	Spatial heterogeneity of the T cell receptor repertoire reflects the mutational landscape in lung cancer. <i>Nature Medicine</i> , 2019, 25, 1549-1559.	15.2	147
52	The HUSH complex cooperates with TRIM28 to repress young retrotransposons and new genes. <i>Genome Research</i> , 2018, 28, 836-845.	2.4	141
53	Extending reference assembly models. <i>Genome Biology</i> , 2015, 16, 13.	3.8	139
54	Ensembl Genomes: Extending Ensembl across the taxonomic space. <i>Nucleic Acids Research</i> , 2010, 38, D563-D569.	6.5	138

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55	Next station in microarray data analysis: GEPAS. <i>Nucleic Acids Research</i> , 2006, 34, W486-W491.	6.5	107
56	Identification of Genes Involved in Resistance to Interferon- $\lambda$ in Cutaneous T-Cell Lymphoma. <i>American Journal of Pathology</i> , 2002, 161, 1825-1837.	1.9	106
57	Alignathon: a competitive assessment of whole-genome alignment methods. <i>Genome Research</i> , 2014, 24, 2077-2089.	2.4	102
58	eFORGE: A Tool for Identifying Cell Type-Specific Signal in Epigenomic Data. <i>Cell Reports</i> , 2016, 17, 2137-2150.	2.9	102
59	Annotated Draft Genomic Sequence from a <i>Streptococcus pneumoniae</i> Type 19F Clinical Isolate. <i>Microbial Drug Resistance</i> , 2001, 7, 99-125.	0.9	98
60	<scp>KAP</scp> 1 regulates endogenous retroviruses in adult human cells and contributes to innate immune control. <i>EMBO Reports</i> , 2018, 19, .	2.0	88
61	GEPAS, an experiment-oriented pipeline for the analysis of microarray gene expression data. <i>Nucleic Acids Research</i> , 2005, 33, W616-W620.	6.5	86
62	G-tract RNA removes Polycomb repressive complex 2 from genes. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 899-909.	3.6	86
63	Gene expression data preprocessing. <i>Bioinformatics</i> , 2003, 19, 655-656.	1.8	84
64	Analysis of variation at transcription factor binding sites in <i>Drosophila</i> and humans. <i>Genome Biology</i> , 2012, 13, R49.	13.9	83
65	Enhancer accessibility and CTCF occupancy underlie asymmetric TAD architecture and cell type specific genome topology. <i>Nature Communications</i> , 2019, 10, 2908.	5.8	81
66	A clonal expression biomarker associates with lung cancer mortality. <i>Nature Medicine</i> , 2019, 25, 1540-1548.	15.2	75
67	The T cell differentiation landscape is shaped by tumour mutations in lung cancer. <i>Nature Cancer</i> , 2020, 1, 546-561.	5.7	74
68	Herpesviruses shape tumour microenvironment through exosomal transfer of viral microRNAs. <i>PLoS Pathogens</i> , 2017, 13, e1006524.	2.1	73
69	The pig X and Y Chromosomes: structure, sequence, and evolution. <i>Genome Research</i> , 2016, 26, 130-139.	2.4	69
70	RNAcentral: A vision for an international database of RNA sequences. <i>Rna</i> , 2011, 17, 1941-1946.	1.6	67
71	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.	0.4	67
72	A Human IPS Model Implicates Embryonic B-Myeloid Fate Restriction as Developmental Susceptibility to Acute Lymphoblastic Leukemia-Associated ETV6-RUNX1. <i>Developmental Cell</i> , 2018, 44, 362-377.e7.	3.1	65

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73	Genome-wide comparative analysis reveals human-mouse regulatory landscape and evolution. BMC Genomics, 2015, 16, 87.	1.2	62
74	Escape from nonsense-mediated decay associates with anti-tumor immunogenicity. Nature Communications, 2020, 11, 3800.	5.8	61
75	Combining Hierarchical Clustering and Self-Organizing Maps for Exploratory Analysis of Gene Expression Patterns. Journal of Proteome Research, 2002, 1, 467-470.	1.8	49
76	Bioinformatics methods for the analysis of expression arrays: data clustering and information extraction. Journal of Biotechnology, 2002, 98, 269-283.	1.9	48
77	New challenges in gene expression data analysis and the extended GEPAS. Nucleic Acids Research, 2004, 32, W485-W491.	6.5	47
78	Sequence progressive alignment, a framework for practical large-scale probabilistic consistency alignment. Bioinformatics, 2009, 25, 295-301.	1.8	47
79	Intratumoural evolutionary landscape of high-risk prostate cancer: the PROGENY study of genomic and immune parameters. Annals of Oncology, 2017, 28, 2472-2480.	0.6	45
80	Genetic variants alter T-bet binding and gene expression in mucosal inflammatory disease. PLoS Genetics, 2017, 13, e1006587.	1.5	40
81	A local human V $\alpha$ 1 T cell population is associated with survival in nonsmall-cell lung cancer. Nature Cancer, 2022, 3, 696-709.	5.7	39
82	eHive: An Artificial Intelligence workflow system for genomic analysis. BMC Bioinformatics, 2010, 11, 240.	1.2	37
83	Using DNA sequencing data to quantify T cell fraction and therapy response. Nature, 2021, 597, 555-560.	13.7	36
84	Personal Genome Project UK (PGP-UK): a research and citizen science hybrid project in support of personalized medicine. BMC Medical Genomics, 2018, 11, 108.	0.7	34
85	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. Clinical Cancer Research, 2020, 26, 3443-3454.	3.2	33
86	Title is missing!. Artificial Intelligence Review, 2003, 20, 39-51.	9.7	32
87	EZH2-Deficient T-cell Acute Lymphoblastic Leukemia Is Sensitized to CHK1 Inhibition through Enhanced Replication Stress. Cancer Discovery, 2020, 10, 998-1017.	7.7	29
88	Clonal Evolutionary Analysis during HER2 Blockade in HER2-Positive Inflammatory Breast Cancer: A Phase II Open-Label Clinical Trial of Afatinib +/- Vinorelbine. PLoS Medicine, 2016, 13, e1002136.	3.9	28
89	Comparing Bacterial Genomes Through Conservation Profiles. Genome Research, 2003, 13, 991-998.	2.4	26
90	Saturation analysis for whole-genome bisulfite sequencing data. Nature Biotechnology, 2016, 34, 691-693.	9.4	26

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91	Chemotherapy induces canalization of cell state in childhood B-cell precursor acute lymphoblastic leukemia. <i>Nature Cancer</i> , 2021, 2, 835-852.	5.7	25
92	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.	13.9	22
93	Supervised Neural Networks for Clustering Conditions in DNA Array Data After Reducing Noise by Clustering Gene Expression Profiles. , 2002, , 91-103.		20
94	Deciphering Genetic Intratumor Heterogeneity and Its Impact on Cancer Evolution. <i>Annual Review of Cancer Biology</i> , 2017, 1, 223-240.	2.3	20
95	ncRNA orthologies in the vertebrate lineage. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, bav127.	1.4	19
96	The Personal Genome Project-UK, an open access resource of human multi-omics data. <i>Scientific Data</i> , 2019, 6, 257.	2.4	19
97	Nascent RNA antagonizes the interaction of a set of regulatory proteins with chromatin. <i>Molecular Cell</i> , 2021, 81, 2944-2959.e10.	4.5	19
98	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.	3.3	17
99	CORALINA: a universal method for the generation of gRNA libraries for CRISPR-based screening. <i>BMC Genomics</i> , 2016, 17, 917.	1.2	16
100	Quantification of tumour evolution and heterogeneity via Bayesian epiallele detection. <i>BMC Bioinformatics</i> , 2017, 18, 354.	1.2	15
101	TranscriptSNPView: a genome-wide catalog of mouse coding variation. <i>Nature Genetics</i> , 2006, 38, 853-853.	9.4	14
102	RNA-seq of newly diagnosed patients in the PADIMAC study leads to a bortezomib/lenalidomide decision signature. <i>Blood</i> , 2018, 132, 2154-2165.	0.6	14
103	An Approach to Inferring Transcriptional Regulation Among Genes From Large-Scale Expression Data. <i>Comparative and Functional Genomics</i> , 2003, 4, 148-154.	2.0	10
104	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
105	A novel requirement for DROSHA in maintenance of mammalian CG methylation. <i>Nucleic Acids Research</i> , 2017, 45, 9398-9412.	6.5	9
106	Considerations for the inclusion of 2x mammalian genomes in phylogenetic analyses. <i>Genome Biology</i> , 2011, 12, 401.	13.9	7
107	Incorporating alignment uncertainty into Felsenstein's phylogenetic bootstrap to improve its reliability. <i>Bioinformatics</i> , 2021, 37, 1506-1514.	1.8	7
108	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.	2.2	7

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109	GenomeChronicler: The Personal Genome Project UK Genomic Report Generator Pipeline. <i>Frontiers in Genetics</i> , 2020, 11, 518644.	1.1	4
110	Systematic Evaluation of the Immune Environment of Small Intestinal Neuroendocrine Tumors. <i>Clinical Cancer Research</i> , 2022, 28, 2657-2668.	3.2	4
111	Using gene ontology on genome-scale studies to find significant associations of biologically relevant terms to groups of genes. , 0, , .		1
112	Aequatus: an open-source homology browser. <i>GigaScience</i> , 2018, 7, .	3.3	1
113	The Th1 cell regulatory circuitry is largely conserved between human and mouse. <i>Life Science Alliance</i> , 2021, 4, e202101075.	1.3	1
114	Using Perceptrons for Supervised Classification of DNA Microarray Samples: Obtaining the Optimal Level of Information and Finding Differentially Expressed Genes. <i>Lecture Notes in Computer Science</i> , 2002, , 577-582.	1.0	1
115	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.	6.3	0
116	A human ips model implicates embryonic B-myeloid fate restriction as a developmental susceptibility to ETV6-RUNX1. <i>Experimental Hematology</i> , 2017, 53, S45.	0.2	0
117	Generation of a cancer testis antigen mCherry reporter HCT116 colorectal carcinoma cell line. <i>Heliyon</i> , 2018, 4, e00858.	1.4	0
118	Abstract 2692: ETV6-RUNX1 targets a developmentally restricted embryonic human B-myeloid progenitor. , 2016, , .		0
119	Single-Cell Analysis of Clonal Dynamics in Childhood ALL Reveals a Key Role for Transcriptional Intratumor Heterogeneity in Driving Resistance to Chemotherapy. <i>Blood</i> , 2016, 128, 606-606.	0.6	0
120	Abstract 2678: A clonal expression biomarker improves prognostic accuracy: TRACERx lung. , 2019, , .		0