

# Javier Herrero

## List of Publications by Citations

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116  
papers

62,381  
citations

62  
h-index

139  
g-index

139  
ext. papers

78,412  
ext. citations

20.9  
avg, IF

8.34  
L-index

#	Paper	IF	Citations
116	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , <b>2012</b> , 489, 57-74	50.4	11449
115	A global reference for human genetic variation. <i>Nature</i> , <b>2015</b> , 526, 68-74	50.4	8599
114	The variant call format and VCFtools. <i>Bioinformatics</i> , <b>2011</b> , 27, 2156-8	7.2	6200
113	A map of human genome variation from population-scale sequencing. <i>Nature</i> , <b>2010</b> , 467, 1061-73	50.4	6142
112	An integrated map of genetic variation from 1,092 human genomes. <i>Nature</i> , <b>2012</b> , 491, 56-65	50.4	6049
111	The zebrafish reference genome sequence and its relationship to the human genome. <i>Nature</i> , <b>2013</b> , 496, 498-503	50.4	2550
110	Tracking the Evolution of Non-Small-Cell Lung Cancer. <i>New England Journal of Medicine</i> , <b>2017</b> , 376, 2109-2121	50.4	1156
109	Ensembl 2014. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, D749-55	20.1	1087
108	A user's guide to the encyclopedia of DNA elements (ENCODE). <i>PLoS Biology</i> , <b>2011</b> , 9, e1001046	9.7	1060
107	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , <b>2014</b> , 515, 355-64	50.4	1026
106	A high-resolution map of human evolutionary constraint using 29 mammals. <i>Nature</i> , <b>2011</b> , 478, 476-82	50.4	802
105	Ensembl 2012. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D84-90	20.1	798
104	Ensembl 2013. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D48-55	20.1	797
103	Phylogenetic ctDNA analysis depicts early-stage lung cancer evolution. <i>Nature</i> , <b>2017</b> , 545, 446-451	50.4	796
102	Ensembl 2009. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, D690-7	20.1	692
101	Ensembl 2007. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, D610-7	20.1	669
100	Ensembl 2011. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D800-6	20.1	590

99	DeconstructSigs: delineating mutational processes in single tumors distinguishes DNA repair deficiencies and patterns of carcinoma evolution. <i>Genome Biology</i> , <b>2016</b> , 17, 31	18.3	571
98	Allele-Specific HLA Loss and Immune Escape in Lung Cancer Evolution. <i>Cell</i> , <b>2017</b> , 171, 1259-1271.e11	56.2	541
97	A Bayesian deconvolution strategy for immunoprecipitation-based DNA methylome analysis. <i>Nature Biotechnology</i> , <b>2008</b> , 26, 779-85	44.5	533
96	Insights into hominid evolution from the gorilla genome sequence. <i>Nature</i> , <b>2012</b> , 483, 169-75	50.4	517
95	Sequencing of the sea lamprey ( <i>Petromyzon marinus</i> ) genome provides insights into vertebrate evolution. <i>Nature Genetics</i> , <b>2013</b> , 45, 415-21, 421e1-2	36.3	465
94	A hierarchical unsupervised growing neural network for clustering gene expression patterns. <i>Bioinformatics</i> , <b>2001</b> , 17, 126-36	7.2	465
93	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , <b>2011</b> , 469, 529-33	50.4	431
92	Ensembl 2008. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, D707-14	20.1	408
91	Variation in genome-wide mutation rates within and between human families. <i>Nature Genetics</i> , <b>2011</b> , 43, 712-4	36.3	404
90	Ensembl 2005. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, D447-53	20.1	363
89	Neoantigen-directed immune escape in lung cancer evolution. <i>Nature</i> , <b>2019</b> , 567, 479-485	50.4	358
88	Multi-platform next-generation sequencing of the domestic turkey ( <i>Meleagris gallopavo</i> ): genome assembly and analysis. <i>PLoS Biology</i> , <b>2010</b> , 8, e1000475	9.7	311
87	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> , <b>2013</b> , 45, 701-706	36.3	299
86	Fc Effector Function Contributes to the Activity of Human Anti-CTLA-4 Antibodies. <i>Cancer Cell</i> , <b>2018</b> , 33, 649-663.e4	24.3	296
85	Integrative annotation of variants from 1092 humans: application to cancer genomics. <i>Science</i> , <b>2013</b> , 342, 1235-587	33.3	281
84	Deterministic Evolutionary Trajectories Influence Primary Tumor Growth: TRACERx Renal. <i>Cell</i> , <b>2018</b> , 173, 595-610.e11	56.2	268
83	Integrating sequence and array data to create an improved 1000 Genomes Project haplotype reference panel. <i>Nature Communications</i> , <b>2014</b> , 5, 3934	17.4	253
82	Gibbon genome and the fast karyotype evolution of small apes. <i>Nature</i> , <b>2014</b> , 513, 195-201	50.4	241

81	The duck genome and transcriptome provide insight into an avian influenza virus reservoir species. <i>Nature Genetics</i> , <b>2013</b> , 45, 776-783	36.3	240
80	Ensembl 10th year. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, D557-62	20.1	240
79	Fc-Optimized Anti-CD25 Depletes Tumor-Infiltrating Regulatory T Cells and Synergizes with PD-1 Blockade to Eradicate Established Tumors. <i>Immunity</i> , <b>2017</b> , 46, 577-586	32.3	225
78	Enredo and Pecan: genome-wide mammalian consistency-based multiple alignment with paralogs. <i>Genome Research</i> , <b>2008</b> , 18, 1814-28	9.7	218
77	The 1000 Genomes Project: data management and community access. <i>Nature Methods</i> , <b>2012</b> , 9, 459-62	21.6	202
76	Principles of regulatory information conservation between mouse and human. <i>Nature</i> , <b>2014</b> , 515, 371-375	5.4	190
75	Ensembl comparative genomics resources. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2016</b> , 2016,	5	186
74	The common marmoset genome provides insight into primate biology and evolution. <i>Nature Genetics</i> , <b>2014</b> , 46, 850-7	36.3	179
73	Meta-analysis of tumor- and T cell-intrinsic mechanisms of sensitization to checkpoint inhibition. <i>Cell</i> , <b>2021</b> , 184, 596-614.e14	56.2	144
72	Genome sequence of an Australian kangaroo, <i>Macropus eugenii</i> , provides insight into the evolution of mammalian reproduction and development. <i>Genome Biology</i> , <b>2011</b> , 12, R81	18.3	142
71	GEPAS: A web-based resource for microarray gene expression data analysis. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 3461-7	20.1	139
70	Genome-wide nucleotide-level mammalian ancestor reconstruction. <i>Genome Research</i> , <b>2008</b> , 18, 1829-43	7.7	136
69	Current Methods for Automated Filtering of Multiple Sequence Alignments Frequently Worsen Single-Genes Phylogenetic Inference. <i>Systematic Biology</i> , <b>2015</b> , 64, 778-91	8.4	129
68	Ensembl Genomes: extending Ensembl across the taxonomic space. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, D563-9	20.1	127
67	H3.3 Cooperates with Trp53 Loss and PDGFRA Gain in Mouse Embryonic Neural Progenitor Cells to Induce Invasive High-Grade Gliomas. <i>Cancer Cell</i> , <b>2017</b> , 32, 684-700.e9	24.3	121
66	Extending reference assembly models. <i>Genome Biology</i> , <b>2015</b> , 16, 13	18.3	107
65	Next station in microarray data analysis: GEPAS. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, W486-91	20.1	101
64	Annotated draft genomic sequence from a <i>Streptococcus pneumoniae</i> type 19F clinical isolate. <i>Microbial Drug Resistance</i> , <b>2001</b> , 7, 99-125	2.9	94

63	Identification of genes involved in resistance to interferon-alpha in cutaneous T-cell lymphoma. <i>American Journal of Pathology</i> , <b>2002</b> , 161, 1825-37	5.8	91
62	Gene expression data preprocessing. <i>Bioinformatics</i> , <b>2003</b> , 19, 655-6	7.2	79
61	GEPAS, an experiment-oriented pipeline for the analysis of microarray gene expression data. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, W616-20	20.1	79
60	Spatial heterogeneity of the T cell receptor repertoire reflects the mutational landscape in lung cancer. <i>Nature Medicine</i> , <b>2019</b> , 25, 1549-1559	50.5	78
59	Alignathon: a competitive assessment of whole-genome alignment methods. <i>Genome Research</i> , <b>2014</b> , 24, 2077-89	9.7	74
58	The HUSH complex cooperates with TRIM28 to repress young retrotransposons and new genes. <i>Genome Research</i> , <b>2018</b> , 28, 836-845	9.7	72
57	Analysis of variation at transcription factor binding sites in Drosophila and humans. <i>Genome Biology</i> , <b>2012</b> , 13, R49	18.3	71
56	eFORGE: A Tool for Identifying Cell Type-Specific Signal in Epigenomic Data. <i>Cell Reports</i> , <b>2016</b> , 17, 2137-2150	21.6	70
55	Herpesviruses shape tumour microenvironment through exosomal transfer of viral microRNAs. <i>PLoS Pathogens</i> , <b>2017</b> , 13, e1006524	7.6	56
54	TALEN-Mediated Inactivation of PD-1 in Tumor-Reactive Lymphocytes Promotes Intratumoral T-cell Persistence and Rejection of Established Tumors. <i>Cancer Research</i> , <b>2016</b> , 76, 2087-93	10.1	55
53	RNAcentral: A vision for an international database of RNA sequences. <i>Rna</i> , <b>2011</b> , 17, 1941-6	5.8	54
52	The pig X and Y Chromosomes: structure, sequence, and evolution. <i>Genome Research</i> , <b>2016</b> , 26, 130-9	9.7	53
51	G-tract RNA removes Polycomb repressive complex 2 from genes. <i>Nature Structural and Molecular Biology</i> , <b>2019</b> , 26, 899-909	17.6	49
50	KAP1 regulates endogenous retroviruses in adult human cells and contributes to innate immune control. <i>EMBO Reports</i> , <b>2018</b> , 19,	6.5	49
49	Genome-wide comparative analysis reveals human-mouse regulatory landscape and evolution. <i>BMC Genomics</i> , <b>2015</b> , 16, 87	4.5	46
48	A Human IPS Model Implicates Embryonic B-Myeloid Fate Restriction as Developmental Susceptibility to B-Cell Acute Lymphoblastic Leukemia-Associated ETV6-RUNX1. <i>Developmental Cell</i> , <b>2018</b> , 44, 362-377.e7	10.2	46
47	New challenges in gene expression data analysis and the extended GEPAS. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, W485-91	20.1	44
46	Bioinformatics methods for the analysis of expression arrays: data clustering and information extraction. <i>Journal of Biotechnology</i> , <b>2002</b> , 98, 269-83	3.7	44

45	Sequence progressive alignment, a framework for practical large-scale probabilistic consistency alignment. <i>Bioinformatics</i> , <b>2009</b> , 25, 295-301	7.2	42
44	Combining hierarchical clustering and self-organizing maps for exploratory analysis of gene expression patterns. <i>Journal of Proteome Research</i> , <b>2002</b> , 1, 467-70	5.6	40
43	The T cell differentiation landscape is shaped by tumour mutations in lung cancer. <i>Nature Cancer</i> , <b>2020</b> , 1, 546-561	15.4	37
42	Enhancer accessibility and CTCF occupancy underlie asymmetric TAD architecture and cell type specific genome topology. <i>Nature Communications</i> , <b>2019</b> , 10, 2908	17.4	36
41	eHive: an artificial intelligence workflow system for genomic analysis. <i>BMC Bioinformatics</i> , <b>2010</b> , 11, 2403-6	3.6	36
40	Intratumoural evolutionary landscape of high-risk prostate cancer: the PROGENY study of genomic and immune parameters. <i>Annals of Oncology</i> , <b>2017</b> , 28, 2472-2480	10.3	35
39	Glioblastomas acquire myeloid-affiliated transcriptional programs via epigenetic immunoediting to elicit immune evasion. <i>Cell</i> , <b>2021</b> , 184, 2454-2470.e26	56.2	35
38	A clonal expression biomarker associates with lung cancer mortality. <i>Nature Medicine</i> , <b>2019</b> , 25, 1540-1548	48.5	34
37	Using a Genetic Algorithm and a Perceptron for Feature Selection and Supervised Class Learning in DNA Microarray Data. <i>Artificial Intelligence Review</i> , <b>2003</b> , 20, 39-51	9.7	28
36	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> , <b>2016</b> , 13, e1002136	11.6	25
35	Genetic variants alter T-bet binding and gene expression in mucosal inflammatory disease. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1006587	6	24
34	Saturation analysis for whole-genome bisulfite sequencing data. <i>Nature Biotechnology</i> , <b>2016</b> , 34, 691-693	14.5	23
33	Escape from nonsense-mediated decay associates with anti-tumor immunogenicity. <i>Nature Communications</i> , <b>2020</b> , 11, 3800	17.4	21
32	Comparing bacterial genomes through conservation profiles. <i>Genome Research</i> , <b>2003</b> , 13, 991-8	9.7	20
31	Personal Genome Project UK (PGP-UK): a research and citizen science hybrid project in support of personalized medicine. <i>BMC Medical Genomics</i> , <b>2018</b> , 11, 108	3.7	20
30	Genome sequence of an Australian kangaroo, <i>Macropus eugenii</i> , provides insight into the evolution of mammalian reproduction and development <b>2011</b> , 12, 414		18
29	Deciphering Genetic Intratumor Heterogeneity and Its Impact on Cancer Evolution. <i>Annual Review of Cancer Biology</i> , <b>2017</b> , 1, 223-240	13.3	16
28	A 3-way hybrid approach to generate a new high-quality chimpanzee reference genome (Pan_tro_3.0). <i>GigaScience</i> , <b>2017</b> , 6, 1-6	7.6	16

27	ncRNA orthologies in the vertebrate lineage. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2016</b> , 2016,	5	14
26	TranscriptSNPView: a genome-wide catalog of mouse coding variation. <i>Nature Genetics</i> , <b>2006</b> , 38, 853	36.3	14
25	Supervised Neural Networks for Clustering Conditions in DNA Array Data After Reducing Noise by Clustering Gene Expression Profiles <b>2002</b> , 91-103		14
24	Marrow-Infiltrating Regulatory T Cells Correlate with the Presence of Dysfunctional CD4PD-1 Cells and Inferior Survival in Patients with Newly Diagnosed Multiple Myeloma. <i>Clinical Cancer Research</i> , <b>2020</b> , 26, 3443-3454	12.9	12
23	-Deficient T-cell Acute Lymphoblastic Leukemia Is Sensitized to CHK1 Inhibition through Enhanced Replication Stress. <i>Cancer Discovery</i> , <b>2020</b> , 10, 998-1017	24.4	10
22	CORALINA: a universal method for the generation of gRNA libraries for CRISPR-based screening. <i>BMC Genomics</i> , <b>2016</b> , 17, 917	4.5	10
21	RNA-seq of newly diagnosed patients in the PADIMAC study leads to a bortezomib/lenalidomide decision signature. <i>Blood</i> , <b>2018</b> , 132, 2154-2165	2.2	10
20	Quantification of tumour evolution and heterogeneity via Bayesian epiallele detection. <i>BMC Bioinformatics</i> , <b>2017</b> , 18, 354	3.6	9
19	An approach to inferring transcriptional regulation among genes from large-scale expression data. <i>Comparative and Functional Genomics</i> , <b>2003</b> , 4, 148-54		9
18	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> , <b>2003</b> , 35, 245-253		8
17	Considerations for the inclusion of 2x mammalian genomes in phylogenetic analyses. <i>Genome Biology</i> , <b>2011</b> , 12, 401	18.3	7
16	Phylogenetic Identification and Functional Characterization of Orthologs and Paralogs across Human, Mouse, Fly, and Worm		7
15	The Personal Genome Project-UK, an open access resource of human multi-omics data. <i>Scientific Data</i> , <b>2019</b> , 6, 257	8.2	6
14	A novel requirement for DROSHA in maintenance of mammalian CG methylation. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, 9398-9412	20.1	5
13	Chemotherapy induces canalization of cell state in childhood B-cell precursor acute lymphoblastic leukemia. <i>Nature Cancer</i> , <b>2021</b> , 2, 835-852	15.4	5
12	Nascent RNA antagonizes the interaction of a set of regulatory proteins with chromatin. <i>Molecular Cell</i> , <b>2021</b> , 81, 2944-2959.e10	17.6	5
11	Using DNA sequencing data to quantify T cell fraction and therapy response. <i>Nature</i> , <b>2021</b> , 597, 555-560	50.4	5
10	Genome-wide comparative analysis reveals human- mouse regulatory landscape and evolution		3

9	Incorporating alignment uncertainty into Felsenstein's phylogenetic bootstrap to improve its reliability. <i>Bioinformatics</i> , <b>2019</b> ,	7.2	2
8	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> , <b>2021</b> , 12, 618610	8.4	2
7	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> , <b>2002</b> , 577-582	0.9	1
6	Escape from nonsense mediated decay associates with anti-tumor immunogenicity		1
5	PGP-UK: a research and citizen science hybrid project in support of personalized medicine		1
4	Aequatus: an open-source homology browser. <i>GigaScience</i> , <b>2018</b> , 7,	7.6	1
3	GenomeChronicler: The Personal Genome Project UK Genomic Report Generator Pipeline. <i>Frontiers in Genetics</i> , <b>2020</b> , 11, 518644	4.5	0
2	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> , <b>2016</b> , 128, 606-606	2.2	
1	Generation of a cancer testis antigen mCherry reporter HCT116 colorectal carcinoma cell line. <i>Heliyon</i> , <b>2018</b> , 4, e00858	3.6	