Javier Herrero

List of Publications by Year in Descending Order

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	Glioblastomas acquire myeloid-affiliated transcriptional programs via epigenetic immunoediting to elicit immune evasion. *Cell*, **2021**, 184, 2454-2470.e26	56.2	35
115	Chemotherapy induces canalization of cell state in childhood B-cell precursor acute lymphoblastic leukemia. *Nature Cancer*, **2021**, 2, 835-852	15.4	5
114	Increased Immune-Regulatory Receptor Expression on Effector T Cells as Early Indicators of Relapse Following Autologous Stem Cell Transplantation for Multiple Myeloma. *Frontiers in Immunology*, **2021**, 12, 618610	8.4	2
113	Meta-analysis of tumor- and T cell-intrinsic mechanisms of sensitization to checkpoint inhibition. *Cell*, **2021**, 184, 596-614.e14	56.2	144
112	Nascent RNA antagonizes the interaction of a set of regulatory proteins with chromatin. *Molecular Cell*, **2021**, 81, 2944-2959.e10	17.6	5
111	Using DNA sequencing data to quantify T cell fraction and therapy response. *Nature*, **2021**, 597, 555-560	50.4	5
110	-Deficient T-cell Acute Lymphoblastic Leukemia Is Sensitized to CHK1 Inhibition through Enhanced Replication Stress. *Cancer Discovery*, **2020**, 10, 998-1017	24.4	10
109	The T cell differentiation landscape is shaped by tumour mutations in lung cancer. *Nature Cancer*, **2020**, 1, 546-561	15.4	37
108	GenomeChronicler: The Personal Genome Project UK Genomic Report Generator Pipeline. *Frontiers in Genetics*, **2020**, 11, 518644	4.5	0
107	Escape from nonsense-mediated decay associates with anti-tumor immunogenicity. *Nature Communications*, **2020**, 11, 3800	17.4	21
106	Marrow-Infiltrating Regulatory T Cells Correlate with the Presence of Dysfunctional CD4PD-1 Cells and Inferior Survival in Patients with Newly Diagnosed Multiple Myeloma. *Clinical Cancer Research*, **2020**, 26, 3443-3454	12.9	12
105	Spatial heterogeneity of the T cell receptor repertoire reflects the mutational landscape in lung cancer. *Nature Medicine*, **2019**, 25, 1549-1559	50.5	78
104	A clonal expression biomarker associates with lung cancer mortality. *Nature Medicine*, **2019**, 25, 1540-1548	50.5	34
103	G-tract RNA removes Polycomb repressive complex 2 from genes. *Nature Structural and Molecular Biology*, **2019**, 26, 899-909	17.6	49
102	Neoantigen-directed immune escape in lung cancer evolution. *Nature*, **2019**, 567, 479-485	50.4	358
101	Incorporating alignment uncertainty into Felsenstein's phylogenetic bootstrap to improve its reliability. *Bioinformatics*, **2019**,	7.2	2
100	Enhancer accessibility and CTCF occupancy underlie asymmetric TAD architecture and cell type specific genome topology. *Nature Communications*, **2019**, 10, 2908	17.4	36

99	The Personal Genome Project-UK, an open access resource of human multi-omics data. *Scientific Data*, **2019**, 6, 257	8.2	6
98	Deterministic Evolutionary Trajectories Influence Primary Tumor Growth: TRACERx Renal. *Cell*, **2018**, 173, 595-610.e11	56.2	268
97	A Human IPS Model Implicates Embryonic B-Myeloid Fate Restriction as Developmental Susceptibility to B☐Acute Lymphoblastic Leukemia-Associated ETV6-RUNX1. *Developmental Cell*, **2018**, 44, 362-377.e7	10.2	46
96	Fc Effector Function Contributes to the Activity of Human Anti-CTLA-4 Antibodies. *Cancer Cell*, **2018**, 33, 649-663.e4	24.3	296
95	KAP1 regulates endogenous retroviruses in adult human cells and contributes to innate immune control. *EMBO Reports*, **2018**, 19,	6.5	49
94	The HUSH complex cooperates with TRIM28 to repress young retrotransposons and new genes. *Genome Research*, **2018**, 28, 836-845	9.7	72
93	Aequatus: an open-source homology browser. *GigaScience*, **2018**, 7,	7.6	1
92	Personal Genome Project UK (PGP-UK): a research and citizen science hybrid project in support of personalized medicine. *BMC Medical Genomics*, **2018**, 11, 108	3.7	20
91	Generation of a cancer testis antigen mCherry reporter HCT116 colorectal carcinoma cell line. *Heliyon*, **2018**, 4, e00858	3.6	
90	RNA-seq of newly diagnosed patients in the PADIMAC study leads to a bortezomib/lenalidomide decision signature. *Blood*, **2018**, 132, 2154-2165	2.2	10
89	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	32.3	225
88	Phylogenetic ctDNA analysis depicts early-stage lung cancer evolution. *Nature*, **2017**, 545, 446-451	50.4	796
87	Tracking the Evolution of Non-Small-Cell Lung Cancer. *New England Journal of Medicine*, **2017**, 376, 2109-2121	59.2	1156
86	Allele-Specific HLA Loss and Immune Escape in Lung Cancer Evolution. *Cell*, **2017**, 171, 1259-1271.e11	56.2	541
85	H3.3 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	24.3	121
84	A novel requirement for DROSHA in maintenance of mammalian CG methylation. *Nucleic Acids Research*, **2017**, 45, 9398-9412	20.1	5
83	Herpesviruses shape tumour microenvironment through exosomal transfer of viral microRNAs. *PLoS Pathogens*, **2017**, 13, e1006524	7.6	56
82	Genetic variants alter T-bet binding and gene expression in mucosal inflammatory disease. *PLoS Genetics*, **2017**, 13, e1006587	6	24

81	Quantification of tumour evolution and heterogeneity via Bayesian epiallele detection. *BMC Bioinformatics*, **2017**, 18, 354	3.6	9
80	Intratumoural evolutionary landscape of high-risk prostate cancer: the PROGENY study of genomic and immune parameters. *Annals of Oncology*, **2017**, 28, 2472-2480	10.3	35
79	Deciphering Genetic Intratumor Heterogeneity and Its Impact on Cancer Evolution. *Annual Review of Cancer Biology*, **2017**, 1, 223-240	13.3	16
78	A 3-way hybrid approach to generate a new high-quality chimpanzee reference genome (Pan_tro_3.0). *GigaScience*, **2017**, 6, 1-6	7.6	16
77	eFORGE: A Tool for Identifying Cell Type-Specific Signal in Epigenomic Data. *Cell Reports*, **2016**, 17, 2137-2150	10.6	70
76	CORALINA: a universal method for the generation of gRNA libraries for CRISPR-based screening. *BMC Genomics*, **2016**, 17, 917	4.5	10
75	Saturation analysis for whole-genome bisulfite sequencing data. *Nature Biotechnology*, **2016**, 34, 691-693	14.5	23
74	DeconstructSigs: delineating mutational processes in single tumors distinguishes DNA repair deficiencies and patterns of carcinoma evolution. *Genome Biology*, **2016**, 17, 31	18.3	571
73	ncRNA orthologies in the vertebrate lineage. *Database: the Journal of Biological Databases and Curation*, **2016**, 2016,	5	14
72	The pig X and Y Chromosomes: structure, sequence, and evolution. *Genome Research*, **2016**, 26, 130-9	9.7	53
71	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	2.2	
70	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	11.6	25
69	Ensembl comparative genomics resources. *Database: the Journal of Biological Databases and Curation*, **2016**, 2016,	5	186
68	TALEN-Mediated Inactivation of PD-1 in Tumor-Reactive Lymphocytes Promotes Intratumoral T-cell Persistence and Rejection of Established Tumors. *Cancer Research*, **2016**, 76, 2087-93	10.1	55
67	Genome-wide comparative analysis reveals human-mouse regulatory landscape and evolution. *BMC Genomics*, **2015**, 16, 87	4.5	46
66	Extending reference assembly models. *Genome Biology*, **2015**, 16, 13	18.3	107
65	A global reference for human genetic variation. *Nature*, **2015**, 526, 68-74	50.4	8599
64	Current Methods for Automated Filtering of Multiple Sequence Alignments Frequently Worsen Single-Gene Phylogenetic Inference. *Systematic Biology*, **2015**, 64, 778-91	8.4	129

63	Principles of regulatory information conservation between mouse and human. *Nature*, **2014**, 515, 371-375	50.4	190
62	A comparative encyclopedia of DNA elements in the mouse genome. *Nature*, **2014**, 515, 355-64	50.4	1026
61	The common marmoset genome provides insight into primate biology and evolution. *Nature Genetics*, **2014**, 46, 850-7	36.3	179
60	Gibbon genome and the fast karyotype evolution of small apes. *Nature*, **2014**, 513, 195-201	50.4	241
59	Integrating sequence and array data to create an improved 1000 Genomes Project haplotype reference panel. *Nature Communications*, **2014**, 5, 3934	17.4	253
58	Ensembl 2014. *Nucleic Acids Research*, **2014**, 42, D749-55	20.1	1087
57	Alignathon: a competitive assessment of whole-genome alignment methods. *Genome Research*, **2014**, 24, 2077-89	9.7	74
56	Integrative annotation of variants from 1092 humans: application to cancer genomics. *Science*, **2013**, 342, 1235587	33.3	281
55	Ensembl 2013. *Nucleic Acids Research*, **2013**, 41, D48-55	20.1	797
54	The zebrafish reference genome sequence and its relationship to the human genome. *Nature*, **2013**, 496, 498-503	50.4	2550
53	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	36.3	299
52	Sequencing of the sea lamprey (Petromyzon marinus) genome provides insights into vertebrate evolution. *Nature Genetics*, **2013**, 45, 415-21, 421e1-2	36.3	465
51	The duck genome and transcriptome provide insight into an avian influenza virus reservoir species. *Nature Genetics*, **2013**, 45, 776-783	36.3	240
50	Analysis of variation at transcription factor binding sites in Drosophila and humans. *Genome Biology*, **2012**, 13, R49	18.3	71
49	An integrated encyclopedia of DNA elements in the human genome. *Nature*, **2012**, 489, 57-74	50.4	11449
48	Ensembl 2012. *Nucleic Acids Research*, **2012**, 40, D84-90	20.1	798
47	The 1000 Genomes Project: data management and community access. *Nature Methods*, **2012**, 9, 459-62	21.6	202
46	An integrated map of genetic variation from 1,092 human genomes. *Nature*, **2012**, 491, 56-65	50.4	6049

45	Insights into hominid evolution from the gorilla genome sequence. *Nature*, **2012**, 483, 169-75	50.4	517
44	Genome sequence of an Australian kangaroo, Macropus eugenii, provides insight into the evolution of mammalian reproduction and development **2011**, 12, 414		18
43	Genome sequence of an Australian kangaroo, Macropus eugenii, provides insight into the evolution of mammalian reproduction and development. *Genome Biology*, **2011**, 12, R81	18.3	142
42	Considerations for the inclusion of 2x mammalian genomes in phylogenetic analyses. *Genome Biology*, **2011**, 12, 401	18.3	7
41	A user's guide to the encyclopedia of DNA elements (ENCODE). *PLoS Biology*, **2011**, 9, e1001046	9.7	1060
40	Comparative and demographic analysis of orang-utan genomes. *Nature*, **2011**, 469, 529-33	50.4	431
39	A high-resolution map of human evolutionary constraint using 29 mammals. *Nature*, **2011**, 478, 476-82	50.4	802
38	Variation in genome-wide mutation rates within and between human families. *Nature Genetics*, **2011**, 43, 712-4	36.3	404
37	The variant call format and VCFtools. *Bioinformatics*, **2011**, 27, 2156-8	7.2	6200
36	Ensembl 2011. *Nucleic Acids Research*, **2011**, 39, D800-6	20.1	590
35	RNAcentral: A vision for an international database of RNA sequences. *Rna*, **2011**, 17, 1941-6	5.8	54
34	A map of human genome variation from population-scale sequencing. *Nature*, **2010**, 467, 1061-73	50.4	6142
33	Ensembl Genomes: extending Ensembl across the taxonomic space. *Nucleic Acids Research*, **2010**, 38, D563-9	20.1	127
32	Ensembl's 10th year. *Nucleic Acids Research*, **2010**, 38, D557-62	20.1	240
31	Multi-platform next-generation sequencing of the domestic turkey (Meleagris gallopavo): genome assembly and analysis. *PLoS Biology*, **2010**, 8, e1000475	9.7	311
30	eHive: an artificial intelligence workflow system for genomic analysis. *BMC Bioinformatics*, **2010**, 11, 240	3.6	36
29	Ensembl 2009. *Nucleic Acids Research*, **2009**, 37, D690-7	20.1	692
28	Sequence progressive alignment, a framework for practical large-scale probabilistic consistency alignment. *Bioinformatics*, **2009**, 25, 295-301	7.2	42

27	A Bayesian deconvolution strategy for immunoprecipitation-based DNA methylome analysis. *Nature Biotechnology*, **2008**, 26, 779-85	44.5	533
26	Genome-wide nucleotide-level mammalian ancestor reconstruction. *Genome Research*, **2008**, 18, 1829-43	9.7	136
25	Enredo and Pecan: genome-wide mammalian consistency-based multiple alignment with paralogs. *Genome Research*, **2008**, 18, 1814-28	9.7	218
24	Ensembl 2008. *Nucleic Acids Research*, **2008**, 36, D707-14	20.1	408
23	Ensembl 2007. *Nucleic Acids Research*, **2007**, 35, D610-7	20.1	669
22	Next station in microarray data analysis: GEPAS. *Nucleic Acids Research*, **2006**, 34, W486-91	20.1	101
21	TranscriptSNPView: a genome-wide catalog of mouse coding variation. *Nature Genetics*, **2006**, 38, 853	36.3	14
20	Ensembl 2005. *Nucleic Acids Research*, **2005**, 33, D447-53	20.1	363
19	GEPAS, an experiment-oriented pipeline for the analysis of microarray gene expression data. *Nucleic Acids Research*, **2005**, 33, W616-20	20.1	79
18	New challenges in gene expression data analysis and the extended GEPAS. *Nucleic Acids Research*, **2004**, 32, W485-91	20.1	44
17	GEPAS: A web-based resource for microarray gene expression data analysis. *Nucleic Acids Research*, **2003**, 31, 3461-7	20.1	139
16	Improved Class Prediction in DNA Microarray Gene Expression Data by Unsupervised Reduction of the Dimensionality followed by Supervised Learning with a Perceptron. *Journal of Signal Processing Systems*, **2003**, 35, 245-253		8
15	Using a Genetic Algorithm and a Perceptron for Feature Selection and Supervised Class Learning in DNA Microarray Data. *Artificial Intelligence Review*, **2003**, 20, 39-51	9.7	28
14	An approach to inferring transcriptional regulation among genes from large-scale expression data. *Comparative and Functional Genomics*, **2003**, 4, 148-54		9
13	Comparing bacterial genomes through conservation profiles. *Genome Research*, **2003**, 13, 991-8	9.7	20
12	Gene expression data preprocessing. *Bioinformatics*, **2003**, 19, 655-6	7.2	79
11	Supervised Neural Networks for Clustering Conditions in DNA Array Data After Reducing Noise by Clustering Gene Expression Profiles **2002**, 91-103		14
10	Combining hierarchical clustering and self-organizing maps for exploratory analysis of gene expression patterns. *Journal of Proteome Research*, **2002**, 1, 467-70	5.6	40

9	Identification of genes involved in resistance to interferon-alpha in cutaneous T-cell lymphoma. *American Journal of Pathology*, **2002**, 161, 1825-37	5.8	91
8	Bioinformatics methods for the analysis of expression arrays: data clustering and information extraction. *Journal of Biotechnology*, **2002**, 98, 269-83	3.7	44
7	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	0.9	1
6	Annotated draft genomic sequence from a Streptococcus pneumoniae type 19F clinical isolate. *Microbial Drug Resistance*, **2001**, 7, 99-125	2.9	94
5	A hierarchical unsupervised growing neural network for clustering gene expression patterns. *Bioinformatics*, **2001**, 17, 126-36	7.2	465
4	Escape from nonsense mediated decay associates with anti-tumor immunogenicity		1
3	Phylogenetic Identification and Functional Characterization of Orthologs and Paralogs across Human, Mouse, Fly, and Worm		7
2	Genome-wide comparative analysis reveals human- mouse regulatory landscape and evolution		3
1	PGP-UK: a research and citizen science hybrid project in support of personalized medicine		1