

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	An integrated encyclopedia of DNA elements in the human genome. Nature, 2012, 489, 57-74.	27.8	15,516
2	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	27.8	13,998
3	The variant call format and VCFtools. Bioinformatics, 2011, 27, 2156-2158.	4.1	11,326
4	A map of human genome variation from population-scale sequencing. Nature, 2010, 467, 1061-1073.	27.8	7,209
5	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	27.8	7,199
6	The zebrafish reference genome sequence and its relationship to the human genome. Nature, 2013, 496, 498-503.	27.8	3,708
7	Tracking the Evolution of Nonâ€“Small-Cell Lung Cancer. New England Journal of Medicine, 2017, 376, 2109-2121.	27.0	1,786
8	A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364.	27.8	1,444
9	Phylogenetic ctDNA analysis depicts early-stage lung cancer evolution. Nature, 2017, 545, 446-451.	27.8	1,287
10	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). PLoS Biology, 2011, 9, e1001046.	5.6	1,257
11	Ensembl 2014. Nucleic Acids Research, 2014, 42, D749-D755.	14.5	1,211
12	A high-resolution map of human evolutionary constraint using 29 mammals. Nature, 2011, 478, 476-482.	27.8	1,016
13	Allele-Specific HLA Loss and Immune Escape in Lung Cancer Evolution. Cell, 2017, 171, 1259-1271.e11.	28.9	968
14	deconstructSigs: delineating mutational processes in single tumors distinguishes DNA repair deficiencies and patterns of carcinoma evolution. Genome Biology, 2016, 17, 31.	8.8	917
15	Ensembl 2013. Nucleic Acids Research, 2012, 41, D48-D55.	14.5	856
16	Ensembl 2012. Nucleic Acids Research, 2012, 40, D84-D90.	14.5	840
17	Ensembl 2009. Nucleic Acids Research, 2009, 37, D690-D697.	14.5	721
18	Ensembl 2007. Nucleic Acids Research, 2007, 35, D610-D617.	14.5	699

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19	Insights into hominid evolution from the gorilla genome sequence. <i>Nature</i> , 2012, 483, 169-175.	27.8	663
20	Neoantigen-directed immune escape in lung cancer evolution. <i>Nature</i> , 2019, 567, 479-485.	27.8	639
21	Ensembl 2011. <i>Nucleic Acids Research</i> , 2011, 39, D800-D806.	14.5	630
22	A Bayesian deconvolution strategy for immunoprecipitation-based DNA methylome analysis. <i>Nature Biotechnology</i> , 2008, 26, 779-785.	17.5	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.	21.4	588
24	A hierarchical unsupervised growing neural network for clustering gene expression patterns. <i>Bioinformatics</i> , 2001, 17, 126-136.	4.1	562
25	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , 2011, 469, 529-533.	27.8	541
26	Variation in genome-wide mutation rates within and between human families. <i>Nature Genetics</i> , 2011, 43, 712-714.	21.4	525
27	Meta-analysis of tumor- and T cell-intrinsic mechanisms of sensitization to checkpoint inhibition. <i>Cell</i> , 2021, 184, 596-614.e14.	28.9	485
28	Deterministic Evolutionary Trajectories Influence Primary Tumor Growth: TRACERx Renal. <i>Cell</i> , 2018, 173, 595-610.e11.	28.9	472
29	Fc Effector Function Contributes to the Activity of Human Anti-CTLA-4 Antibodies. <i>Cancer Cell</i> , 2018, 33, 649-663.e4.	16.8	448
30	Ensembl 2008. <i>Nucleic Acids Research</i> , 2007, 36, D707-D714.	14.5	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.	21.4	409
32	Ensembl 2005. <i>Nucleic Acids Research</i> , 2004, 33, D447-D453.	14.5	368
33	Integrating sequence and array data to create an improved 1000 Genomes Project haplotype reference panel. <i>Nature Communications</i> , 2014, 5, 3934.	12.8	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.	5.6	348
35	Ensembl comparative genomics resources. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, bav096.	3.0	344
36	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. <i>Science</i> , 2013, 342, 1235587.	12.6	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.	21.4	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.	14.3	323
39	Gibbon genome and the fast karyotype evolution of small apes. <i>Nature</i> , 2014, 513, 195-201.	27.8	320
40	The 1000 Genomes Project: data management and community access. <i>Nature Methods</i> , 2012, 9, 459-462.	19.0	308
41	Principles of regulatory information conservation between mouse and human. <i>Nature</i> , 2014, 515, 371-375.	27.8	259
42	Ensembl's 10th year. <i>Nucleic Acids Research</i> , 2010, 38, D557-D562.	14.5	251
43	Enredo and Pecan: Genome-wide mammalian consistency-based multiple alignment with paralogs. <i>Genome Research</i> , 2008, 18, 1814-1828.	5.5	249
44	The common marmoset genome provides insight into primate biology and evolution. <i>Nature Genetics</i> , 2014, 46, 850-857.	21.4	225
45	Current Methods for Automated Filtering of Multiple Sequence Alignments Frequently Worsen Single-Genes Phylogenetic Inference. <i>Systematic Biology</i> , 2015, 64, 778-791.	5.6	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.	16.8	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.	9.6	167
48	Glioblastomas acquire myeloid-affiliated transcriptional programs via epigenetic immunoediting to elicit immune evasion. <i>Cell</i> , 2021, 184, 2454-2470.e26.	28.9	165
49	Genome-wide nucleotide-level mammalian ancestor reconstruction. <i>Genome Research</i> , 2008, 18, 1829-1843.	5.5	164
50	GEPAS: a web-based resource for microarray gene expression data analysis. <i>Nucleic Acids Research</i> , 2003, 31, 3461-3467.	14.5	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.	30.7	147
52	The HUSH complex cooperates with TRIM28 to repress young retrotransposons and new genes. <i>Genome Research</i> , 2018, 28, 836-845.	5.5	141
53	Extending reference assembly models. <i>Genome Biology</i> , 2015, 16, 13.	8.8	139
54	Ensembl Genomes: Extending Ensembl across the taxonomic space. <i>Nucleic Acids Research</i> , 2010, 38, D563-D569.	14.5	138

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55	Next station in microarray data analysis: GEPAS. Nucleic Acids Research, 2006, 34, W486-W491.	14.5	107
56	Identification of Genes Involved in Resistance to Interferon- γ in Cutaneous T-Cell Lymphoma. American Journal of Pathology, 2002, 161, 1825-1837.	3.8	106
57	Alignathon: a competitive assessment of whole-genome alignment methods. Genome Research, 2014, 24, 2077-2089.	5.5	102
58	eFORGE: A Tool for Identifying Cell Type-Specific Signal in Epigenomic Data. Cell Reports, 2016, 17, 2137-2150.	6.4	102
59	Annotated Draft Genomic Sequence from a <i>Streptococcus pneumoniae</i> Type 19F Clinical Isolate. Microbial Drug Resistance, 2001, 7, 99-125.	2.0	98
60	<scp>KAP</scp> 1 regulates endogenous retroviruses in adult human cells and contributes to innate immune control. EMBO Reports, 2018, 19, .	4.5	88
61	GEPAS, an experiment-oriented pipeline for the analysis of microarray gene expression data. Nucleic Acids Research, 2005, 33, W616-W620.	14.5	86
62	G-tract RNA removes Polycomb repressive complex 2 from genes. Nature Structural and Molecular Biology, 2019, 26, 899-909.	8.2	86
63	Gene expression data preprocessing. Bioinformatics, 2003, 19, 655-656.	4.1	84
64	Analysis of variation at transcription factor binding sites in <i>Drosophila</i> and humans. Genome Biology, 2012, 13, R49.	9.6	83
65	Enhancer accessibility and CTCF occupancy underlie asymmetric TAD architecture and cell type specific genome topology. Nature Communications, 2019, 10, 2908.	12.8	81
66	A clonal expression biomarker associates with lung cancer mortality. Nature Medicine, 2019, 25, 1540-1548.	30.7	75
67	The T cell differentiation landscape is shaped by tumour mutations in lung cancer. Nature Cancer, 2020, 1, 546-561.	13.2	74
68	Herpesviruses shape tumour microenvironment through exosomal transfer of viral microRNAs. PLoS Pathogens, 2017, 13, e1006524.	4.7	73
69	The pig X and Y Chromosomes: structure, sequence, and evolution. Genome Research, 2016, 26, 130-139.	5.5	69
70	RNAcentral: A vision for an international database of RNA sequences. Rna, 2011, 17, 1941-1946.	3.5	67
71	TALEN-Mediated Inactivation of PD-1 in Tumor-Reactive Lymphocytes Promotes Intratumoral T-cell Persistence and Rejection of Established Tumors. Cancer Research, 2016, 76, 2087-2093.	0.9	67
72	A Human IPS Model Implicates Embryonic B-Myeloid Fate Restriction as Developmental Susceptibility to B- γ Acute Lymphoblastic Leukemia-Associated ETV6-RUNX1. Developmental Cell, 2018, 44, 362-377.e7.	7.0	65

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73	Genome-wide comparative analysis reveals human-mouse regulatory landscape and evolution. BMC Genomics, 2015, 16, 87.	2.8	62
74	Escape from nonsense-mediated decay associates with anti-tumor immunogenicity. Nature Communications, 2020, 11, 3800.	12.8	61
75	Combining Hierarchical Clustering and Self-Organizing Maps for Exploratory Analysis of Gene Expression Patterns. Journal of Proteome Research, 2002, 1, 467-470.	3.7	49
76	Bioinformatics methods for the analysis of expression arrays: data clustering and information extraction. Journal of Biotechnology, 2002, 98, 269-283.	3.8	48
77	New challenges in gene expression data analysis and the extended GEPAS. Nucleic Acids Research, 2004, 32, W485-W491.	14.5	47
78	Sequence progressive alignment, a framework for practical large-scale probabilistic consistency alignment. Bioinformatics, 2009, 25, 295-301.	4.1	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.	1.2	45
80	Genetic variants alter T-bet binding and gene expression in mucosal inflammatory disease. PLoS Genetics, 2017, 13, e1006587.	3.5	40
81	A local human V α 1 T cell population is associated with survival in nonsmall-cell lung cancer. Nature Cancer, 2022, 3, 696-709.	13.2	39
82	eHive: An Artificial Intelligence workflow system for genomic analysis. BMC Bioinformatics, 2010, 11, 240.	2.6	37
83	Using DNA sequencing data to quantify T cell fraction and therapy response. Nature, 2021, 597, 555-560.	27.8	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.	1.5	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.	7.0	33
86	Title is missing!. Artificial Intelligence Review, 2003, 20, 39-51.	15.7	32
87	EZH2-Deficient T-cell Acute Lymphoblastic Leukemia Is Sensitized to CHK1 Inhibition through Enhanced Replication Stress. Cancer Discovery, 2020, 10, 998-1017.	9.4	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.	8.4	28
89	Comparing Bacterial Genomes Through Conservation Profiles. Genome Research, 2003, 13, 991-998.	5.5	26
90	Saturation analysis for whole-genome bisulfite sequencing data. Nature Biotechnology, 2016, 34, 691-693.	17.5	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.	13.2	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.	9.6	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.	4.5	20
95	ncRNA orthologies in the vertebrate lineage. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, bav127.	3.0	19
96	The Personal Genome Project-UK, an open access resource of human multi-omics data. <i>Scientific Data</i> , 2019, 6, 257.	5.3	19
97	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
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.	6.4	17
99	CORALINA: a universal method for the generation of gRNA libraries for CRISPR-based screening. <i>BMC Genomics</i> , 2016, 17, 917.	2.8	16
100	Quantification of tumour evolution and heterogeneity via Bayesian epiallele detection. <i>BMC Bioinformatics</i> , 2017, 18, 354.	2.6	15
101	TranscriptSNPView: a genome-wide catalog of mouse coding variation. <i>Nature Genetics</i> , 2006, 38, 853-853.	21.4	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.	1.4	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.	14.5	9
106	Considerations for the inclusion of 2x mammalian genomes in phylogenetic analyses. <i>Genome Biology</i> , 2011, 12, 401.	9.6	7
107	Incorporating alignment uncertainty into Felsenstein's phylogenetic bootstrap to improve its reliability. <i>Bioinformatics</i> , 2021, 37, 1506-1514.	4.1	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.	4.8	7

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109	GenomeChronicle: The Personal Genome Project UK Genomic Report Generator Pipeline. <i>Frontiers in Genetics</i> , 2020, 11, 518644.	2.3	4
110	Systematic Evaluation of the Immune Environment of Small Intestinal Neuroendocrine Tumors. <i>Clinical Cancer Research</i> , 2022, 28, 2657-2668.	7.0	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, .	6.4	1
113	The Th1 cell regulatory circuitry is largely conserved between human and mouse. <i>Life Science Alliance</i> , 2021, 4, e202101075.	2.8	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.	1.3	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.	13.7	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.	0.4	0
117	Generation of a cancer testis antigen mCherry reporter HCT116 colorectal carcinoma cell line. <i>Heliyon</i> , 2018, 4, e00858.	3.2	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.	1.4	0
120	Abstract 2678: A clonal expression biomarker improves prognostic accuracy: TRACERx lung. , 2019, , .		0