

Javier Herrero

List of Publications by Year in descending order

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Version: 2024-02-01

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	Systematic Evaluation of the Immune Environment of Small Intestinal Neuroendocrine Tumors. <i>Clinical Cancer Research</i> , 2022, 28, 2657-2668.	3.2	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.	5.7	39
3	Incorporating alignment uncertainty into Felsenstein's phylogenetic bootstrap to improve its reliability. <i>Bioinformatics</i> , 2021, 37, 1506-1514.	1.8	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.	2.2	7
5	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
6	Glioblastomas acquire myeloid-affiliated transcriptional programs via epigenetic immunoeediting to elicit immune evasion. <i>Cell</i> , 2021, 184, 2454-2470.e26.	13.5	165
7	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
8	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
9	The Th1 cell regulatory circuitry is largely conserved between human and mouse. <i>Life Science Alliance</i> , 2021, 4, e202101075.	1.3	1
10	Using DNA sequencing data to quantify T cell fraction and therapy response. <i>Nature</i> , 2021, 597, 555-560.	13.7	36
11	GenomeChronicle: The Personal Genome Project UK Genomic Report Generator Pipeline. <i>Frontiers in Genetics</i> , 2020, 11, 518644.	1.1	4
12	Escape from nonsense-mediated decay associates with anti-tumor immunogenicity. <i>Nature Communications</i> , 2020, 11, 3800.	5.8	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.	7.7	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.	3.2	33
15	The T cell differentiation landscape is shaped by tumour mutations in lung cancer. <i>Nature Cancer</i> , 2020, 1, 546-561.	5.7	74
16	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
17	The Personal Genome Project-UK, an open access resource of human multi-omics data. <i>Scientific Data</i> , 2019, 6, 257.	2.4	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.	15.2	147

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19	A clonal expression biomarker associates with lung cancer mortality. <i>Nature Medicine</i> , 2019, 25, 1540-1548.	15.2	75
20	G-tract RNA removes Polycomb repressive complex 2 from genes. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 899-909.	3.6	86
21	Neoantigen-directed immune escape in lung cancer evolution. <i>Nature</i> , 2019, 567, 479-485.	13.7	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. <i>Cell</i> , 2018, 173, 595-610.e11.	13.5	472
24	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> , 2018, 44, 362-377.e7.	3.1	65
25	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
26	Aequatus: an open-source homology browser. <i>GigaScience</i> , 2018, 7, .	3.3	1
27	Personal Genome Project UK (PGP-UK): a research and citizen science hybrid project in support of personalized medicine. <i>BMC Medical Genomics</i> , 2018, 11, 108.	0.7	34
28	Generation of a cancer testis antigen mCherry reporter HCT116 colorectal carcinoma cell line. <i>Heliyon</i> , 2018, 4, e00858.	1.4	0
29	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
30	KAP1 regulates endogenous retroviruses in adult human cells and contributes to innate immune control. <i>EMBO Reports</i> , 2018, 19, .	2.0	88
31	The HUSH complex cooperates with TRIM28 to repress young retrotransposons and new genes. <i>Genome Research</i> , 2018, 28, 836-845.	2.4	141
32	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
33	Phylogenetic ctDNA analysis depicts early-stage lung cancer evolution. <i>Nature</i> , 2017, 545, 446-451.	13.7	1,287
34	Tracking the Evolution of Non-Small-Cell Lung Cancer. <i>New England Journal of Medicine</i> , 2017, 376, 2109-2121.	13.9	1,786
35	Allele-Specific HLA Loss and Immune Escape in Lung Cancer Evolution. <i>Cell</i> , 2017, 171, 1259-1271.e11.	13.5	968
36	H3K27M 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

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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.	0.2	0
38	A novel requirement for DROSHA in maintenance of mammalian CG methylation. <i>Nucleic Acids Research</i> , 2017, 45, 9398-9412.	6.5	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.	0.6	45
40	Deciphering Genetic Intratumor Heterogeneity and Its Impact on Cancer Evolution. <i>Annual Review of Cancer Biology</i> , 2017, 1, 223-240.	2.3	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.	3.3	17
42	Herpesviruses shape tumour microenvironment through exosomal transfer of viral microRNAs. <i>PLoS Pathogens</i> , 2017, 13, e1006524.	2.1	73
43	Genetic variants alter T-bet binding and gene expression in mucosal inflammatory disease. <i>PLoS Genetics</i> , 2017, 13, e1006587.	1.5	40
44	Quantification of tumour evolution and heterogeneity via Bayesian epiallele detection. <i>BMC Bioinformatics</i> , 2017, 18, 354.	1.2	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.	3.9	28
46	Ensembl comparative genomics resources. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, bav096.	1.4	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.	0.4	67
48	eFORGE: A Tool for Identifying Cell Type-Specific Signal in Epigenomic Data. <i>Cell Reports</i> , 2016, 17, 2137-2150.	2.9	102
49	CORALINA: a universal method for the generation of gRNA libraries for CRISPR-based screening. <i>BMC Genomics</i> , 2016, 17, 917.	1.2	16
50	Saturation analysis for whole-genome bisulfite sequencing data. <i>Nature Biotechnology</i> , 2016, 34, 691-693.	9.4	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.	6.3	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.	3.8	917
53	ncRNA orthologies in the vertebrate lineage. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, bav127.	1.4	19
54	The pig X and Y Chromosomes: structure, sequence, and evolution. <i>Genome Research</i> , 2016, 26, 130-139.	2.4	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.	0.6	0
57	Genome-wide comparative analysis reveals human-mouse regulatory landscape and evolution. BMC Genomics, 2015, 16, 87.	1.2	62
58	Extending reference assembly models. Genome Biology, 2015, 16, 13.	3.8	139
59	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
60	Current Methods for Automated Filtering of Multiple Sequence Alignments Frequently Worsen Single-Gene Phylogenetic Inference. Systematic Biology, 2015, 64, 778-791.	2.7	200
61	Ensembl 2014. Nucleic Acids Research, 2014, 42, D749-D755.	6.5	1,211
62	Alignathon: a competitive assessment of whole-genome alignment methods. Genome Research, 2014, 24, 2077-2089.	2.4	102
63	Principles of regulatory information conservation between mouse and human. Nature, 2014, 515, 371-375.	13.7	259
64	A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364.	13.7	1,444
65	The common marmoset genome provides insight into primate biology and evolution. Nature Genetics, 2014, 46, 850-857.	9.4	225
66	Gibbon genome and the fast karyotype evolution of small apes. Nature, 2014, 513, 195-201.	13.7	320
67	Integrating sequence and array data to create an improved 1000 Genomes Project haplotype reference panel. Nature Communications, 2014, 5, 3934.	5.8	364
68	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235-1238.	6.0	341
69	The zebrafish reference genome sequence and its relationship to the human genome. Nature, 2013, 496, 498-503.	13.7	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.	9.4	409
71	Sequencing of the sea lamprey (Petromyzon marinus) genome provides insights into vertebrate evolution. Nature Genetics, 2013, 45, 415-421.	9.4	588
72	The duck genome and transcriptome provide insight into an avian influenza virus reservoir species. Nature Genetics, 2013, 45, 776-783.	9.4	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.	13.9	83
74	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012, 489, 57-74.	13.7	15,516
75	Ensembl 2012. <i>Nucleic Acids Research</i> , 2012, 40, D84-D90.	6.5	840
76	The 1000 Genomes Project: data management and community access. <i>Nature Methods</i> , 2012, 9, 459-462.	9.0	308
77	Ensembl 2013. <i>Nucleic Acids Research</i> , 2012, 41, D48-D55.	6.5	856
78	An integrated map of genetic variation from 1,092 human genomes. <i>Nature</i> , 2012, 491, 56-65.	13.7	7,199
79	Insights into hominid evolution from the gorilla genome sequence. <i>Nature</i> , 2012, 483, 169-175.	13.7	663
80	The variant call format and VCFtools. <i>Bioinformatics</i> , 2011, 27, 2156-2158.	1.8	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.	13.9	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.	13.9	167
83	Considerations for the inclusion of 2x mammalian genomes in phylogenetic analyses. <i>Genome Biology</i> , 2011, 12, 401.	13.9	7
84	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). <i>PLoS Biology</i> , 2011, 9, e1001046.	2.6	1,257
85	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , 2011, 469, 529-533.	13.7	541
86	A high-resolution map of human evolutionary constraint using 29 mammals. <i>Nature</i> , 2011, 478, 476-482.	13.7	1,016
87	Variation in genome-wide mutation rates within and between human families. <i>Nature Genetics</i> , 2011, 43, 712-714.	9.4	525
88	Ensembl 2011. <i>Nucleic Acids Research</i> , 2011, 39, D800-D806.	6.5	630
89	RNAcentral: A vision for an international database of RNA sequences. <i>Rna</i> , 2011, 17, 1941-1946.	1.6	67
90	eHive: An Artificial Intelligence workflow system for genomic analysis. <i>BMC Bioinformatics</i> , 2010, 11, 240.	1.2	37

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91	A map of human genome variation from population-scale sequencing. <i>Nature</i> , 2010, 467, 1061-1073.	13.7	7,209
92	Ensembl Genomes: Extending Ensembl across the taxonomic space. <i>Nucleic Acids Research</i> , 2010, 38, D563-D569.	6.5	138
93	Ensembl's 10th year. <i>Nucleic Acids Research</i> , 2010, 38, D557-D562.	6.5	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.	2.6	348
95	Ensembl 2009. <i>Nucleic Acids Research</i> , 2009, 37, D690-D697.	6.5	721
96	Sequence progressive alignment, a framework for practical large-scale probabilistic consistency alignment. <i>Bioinformatics</i> , 2009, 25, 295-301.	1.8	47
97	A Bayesian deconvolution strategy for immunoprecipitation-based DNA methylome analysis. <i>Nature Biotechnology</i> , 2008, 26, 779-785.	9.4	619
98	Genome-wide nucleotide-level mammalian ancestor reconstruction. <i>Genome Research</i> , 2008, 18, 1829-1843.	2.4	164
99	Enredo and Pecan: Genome-wide mammalian consistency-based multiple alignment with paralogs. <i>Genome Research</i> , 2008, 18, 1814-1828.	2.4	249
100	Ensembl 2007. <i>Nucleic Acids Research</i> , 2007, 35, D610-D617.	6.5	699
101	Ensembl 2008. <i>Nucleic Acids Research</i> , 2007, 36, D707-D714.	6.5	440
102	TranscriptSNPView: a genome-wide catalog of mouse coding variation. <i>Nature Genetics</i> , 2006, 38, 853-853.	9.4	14
103	Next station in microarray data analysis: GEPAS. <i>Nucleic Acids Research</i> , 2006, 34, W486-W491.	6.5	107
104	GEPAS, an experiment-oriented pipeline for the analysis of microarray gene expression data. <i>Nucleic Acids Research</i> , 2005, 33, W616-W620.	6.5	86
105	New challenges in gene expression data analysis and the extended GEPAS. <i>Nucleic Acids Research</i> , 2004, 32, W485-W491.	6.5	47
106	Ensembl 2005. <i>Nucleic Acids Research</i> , 2004, 33, D447-D453.	6.5	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.	9.7	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.	2.4	26
111	Gene expression data preprocessing. Bioinformatics, 2003, 19, 655-656.	1.8	84
112	GEPAS: a web-based resource for microarray gene expression data analysis. Nucleic Acids Research, 2003, 31, 3461-3467.	6.5	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.	1.8	49
115	Identification of Genes Involved in Resistance to Interferon- γ in Cutaneous T-Cell Lymphoma. American Journal of Pathology, 2002, 161, 1825-1837.	1.9	106
116	Bioinformatics methods for the analysis of expression arrays: data clustering and information extraction. Journal of Biotechnology, 2002, 98, 269-283.	1.9	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.	1.0	1
118	A hierarchical unsupervised growing neural network for clustering gene expression patterns. Bioinformatics, 2001, 17, 126-136.	1.8	562
119	Annotated Draft Genomic Sequence from a Streptococcus pneumoniae Type 19F Clinical Isolate. Microbial Drug Resistance, 2001, 7, 99-125.	0.9	98
120	Using gene ontology on genome-scale studies to find significant associations of biologically relevant terms to groups of genes. , 0, , .		1