Sara Garcia

List of Publications by Year
in descending order

47 papers	4,141 citations	361296 20 h-index	276775 41 g-index
51 all docs	51 docs citations	51 times ranked	6098 citing authors

#	Article	IF	Citations
1	BCL11A enhancer dissection by Cas9-mediated in situ saturating mutagenesis. Nature, 2015, 527, 192-197.	13.7	726
2	Transcriptome-wide off-target RNA editing induced by CRISPR-guided DNA base editors. Nature, 2019, 569, 433-437.	13.7	434
3	In vivo CRISPR base editing of PCSK9 durably lowers cholesterol in primates. Nature, 2021, 593, 429-434.	13.7	408
4	CRISPR C-to-G base editors for inducing targeted DNA transversions in human cells. Nature Biotechnology, 2021, 39, 41-46.	9.4	328
5	In vivo CRISPR editing with no detectable genome-wide off-target mutations. Nature, 2018, 561, 416-419.	13.7	274
6	High levels of AAV vector integration into CRISPR-induced DNA breaks. Nature Communications, 2019, 10, 4439.	5.8	257
7	Transcriptional diversity during lineage commitment of human blood progenitors. Science, 2014, 345, 1251033.	6.0	253
8	CRISPR DNA base editors with reduced RNA off-target and self-editing activities. Nature Biotechnology, 2019, 37, 1041-1048.	9.4	236
9	Assessment of computational methods for the analysis of single-cell ATAC-seq data. Genome Biology, 2019, 20, 241.	3.8	225
10	A dual-deaminase CRISPR base editor enables concurrent adenine and cytosine editing. Nature Biotechnology, 2020, 38, 861-864.	9.4	168
11	Allele-specific gene editing prevents deafness in a model of dominant progressive hearing loss. Nature Medicine, 2019, 25, 1123-1130.	15.2	149
12	GReEn: a tool for efficient compression of genome resequencing data. Nucleic Acids Research, 2012, 40, e27-e27.	6.5	76
13	Genome analysis with inter-nucleotide distances. Bioinformatics, 2009, 25, 3064-3070.	1.8	75
14	Vangl2/RhoA Signaling Pathway Regulates Stem Cell Self-Renewal Programs and Growth in Rhabdomyosarcoma. Cell Stem Cell, 2018, 22, 414-427.e6.	5.2	61
15	tp53 deficiency causes a wide tumor spectrum and increases embryonal rhabdomyosarcoma metastasis in zebrafish. ELife, 2018, 7, .	2.8	51
16	Multivariate phase space reconstruction by nearest neighbor embedding with different time delays. Physical Review E, 2005, 72, 027205.	0.8	49
17	On finding minimal absent words. BMC Bioinformatics, 2009, 10, 137.	1.2	37
18	The breakdown of the word symmetry in the human genome. Journal of Theoretical Biology, 2013, 335, 153-159.	0.8	37

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19	Robust lineage reconstruction from high-dimensional single-cell data. Nucleic Acids Research, 2016, 44, e122-e122.	6.5	30
20	Nearest neighbor embedding with different time delays. Physical Review E, 2005, 71, 037204.	0.8	28
21	Cell of origin dictates aggression and stem cell number in acute lymphoblastic leukemia. Leukemia, 2018, 32, 1860-1865.	3.3	23
22	Minimal Absent Words in Prokaryotic and Eukaryotic Genomes. PLoS ONE, 2011, 6, e16065.	1.1	20
23	Therapeutic targeting of LCK tyrosine kinase and mTOR signaling in T-cell acute lymphoblastic leukemia. Blood, 2022, 140, 1891-1906.	0.6	19
24	Molecularly distinct models of zebrafish Myc-induced B cell leukemia. Leukemia, 2019, 33, 559-562.	3.3	14
25	DNA Sequences at a Glance. PLoS ONE, 2013, 8, e79922.	1.1	14
26	Ecoforecasting in real time for commercial fisheries: the Atlantic white shrimp as a case study. Marine Biology, 2007, 152, 15-24.	0.7	13
27	A dynamic and integrated epigenetic program at distal regions orchestrates transcriptional responses to VEGFA. Genome Research, 2019, 29, 193-207.	2.4	13
28	Minimal Absent Words in Four Human Genome Assemblies. PLoS ONE, 2011, 6, e29344.	1.1	11
29	PRL3 enhances T-cell acute lymphoblastic leukemia growth through suppressing T-cell signaling pathways and apoptosis. Leukemia, 2021, 35, 679-690.	3.3	11
30	Genome analysis with distance to the nearest dissimilar nucleotide. Journal of Theoretical Biology, 2011, 275, 52-58.	0.8	10
31	Phase behaviour of the catalyst dicarbonyl(î·5-cyclopentadienyl)-cobalt in carbon dioxide. Journal of Supercritical Fluids, 2004, 31, 1-8.	1.6	9
32	Transmission of information and synchronization in a pair of coupled chaotic circuits: An experimental overview. European Physical Journal: Special Topics, 2008, 165, 119-128.	1.2	8
33	Inter-dinucleotide distances in the human genome: an analysis of the whole-genome and protein-coding distributions. Journal of Integrative Bioinformatics, 2011, 8, 31-42.	1.0	8
34	A Genomic Distance for Assembly Comparison Based on Compressed Maximal Exact Matches. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 793-798.	1.9	8
35	Mutant Allele-Specific CRISPR Disruption in DYT1 Dystonia Fibroblasts Restores Cell Function. Molecular Therapy - Nucleic Acids, 2020, 21, 1-12.	2.3	8
36	Inter-dinucleotide distances in the human genome: an analysis of the whole-genome and protein-coding distributions. Journal of Integrative Bioinformatics, 2011, 8, 172.	1.0	8

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37	Potency of Human Cardiosphere-Derived Cells from Patients with Ischemic Heart Disease Is Associated with Robust Vascular Supportive Ability. Stem Cells Translational Medicine, 2017, 6, 1399-1411.	1.6	7
38	Inter-STOP symbol distances for the identification of coding regions. Journal of Integrative Bioinformatics, 2013, 10, 31-39.	1.0	2
39	The Breakdown of Symmetry in Word Pairs in 1,092 Human Genomes. Jurnal Teknologi (Sciences and) Tj ETQq1 1 0.784314 rgBT /Ov	0.3	2
40	Exploring Homology Using the Concept of Three-State Entropy Vector. Lecture Notes in Computer Science, 2010, , 161-170.	1.0	1
41	Analysis of Word Symmetries in Human Genomes Using Next-Generation Sequencing Data. Advances in Intelligent Systems and Computing, 2013, , 7-13.	0.5	0
42	Complexity Profiles of DNA Sequences Using Finite-Context Models. Lecture Notes in Computer Science, 2011, , 75-82.	1.0	0
43	Exon: A Web-Based Software Toolkit for DNA Sequence Analysis. Advances in Intelligent and Soft Computing, 2012, , 217-224.	0.2	0
44	Segmentation of DNA into Coding and Noncoding Regions Based on Inter-STOP Symbols Distances. Advances in Intelligent Systems and Computing, 2013, , 23-28.	0.5	0
45	Compressing Resequencing Data with GReEn. Methods in Molecular Biology, 2013, 1038, 27-37.	0.4	0
46	RUNX1 Is a Candidate Transcriptional Effector in Juvenile Myelomonocytic Leukemia. Blood, 2016, 128, 2699-2699.	0.6	0
47	Inter-STOP symbol distances for the identification of coding regions. Journal of Integrative Bioinformatics, 2013, 10, 230.	1.0	0