Sara Garcia

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8766457/publications.pdf

Version: 2024-02-01

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

| # | Article | IF | Citations |
|----|---|------|-----------|
| 1 | Therapeutic targeting of LCK tyrosine kinase and mTOR signaling in T-cell acute lymphoblastic leukemia. Blood, 2022, 140, 1891-1906. | 0.6 | 19 |
| 2 | PRL3 enhances T-cell acute lymphoblastic leukemia growth through suppressing T-cell signaling pathways and apoptosis. Leukemia, 2021, 35, 679-690. | 3.3 | 11 |
| 3 | CRISPR C-to-G base editors for inducing targeted DNA transversions in human cells. Nature Biotechnology, 2021, 39, 41-46. | 9.4 | 328 |
| 4 | In vivo CRISPR base editing of PCSK9 durably lowers cholesterol in primates. Nature, 2021, 593, 429-434. | 13.7 | 408 |
| 5 | Mutant Allele-Specific CRISPR Disruption in DYT1 Dystonia Fibroblasts Restores Cell Function. Molecular Therapy - Nucleic Acids, 2020, 21, 1-12. | 2.3 | 8 |
| 6 | A dual-deaminase CRISPR base editor enables concurrent adenine and cytosine editing. Nature Biotechnology, 2020, 38, 861-864. | 9.4 | 168 |
| 7 | Allele-specific gene editing prevents deafness in a model of dominant progressive hearing loss. Nature Medicine, 2019, 25, 1123-1130. | 15.2 | 149 |
| 8 | CRISPR DNA base editors with reduced RNA off-target and self-editing activities. Nature Biotechnology, 2019, 37, 1041-1048. | 9.4 | 236 |
| 9 | High levels of AAV vector integration into CRISPR-induced DNA breaks. Nature Communications, 2019, 10, 4439. | 5.8 | 257 |
| 10 | A dynamic and integrated epigenetic program at distal regions orchestrates transcriptional responses to VEGFA. Genome Research, 2019, 29, 193-207. | 2.4 | 13 |
| 11 | Transcriptome-wide off-target RNA editing induced by CRISPR-guided DNA base editors. Nature, 2019, 569, 433-437. | 13.7 | 434 |
| 12 | Assessment of computational methods for the analysis of single-cell ATAC-seq data. Genome Biology, 2019, 20, 241. | 3.8 | 225 |
| 13 | Molecularly distinct models of zebrafish Myc-induced B cell leukemia. Leukemia, 2019, 33, 559-562. | 3.3 | 14 |
| 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 | In vivo CRISPR editing with no detectable genome-wide off-target mutations. Nature, 2018, 561, 416-419. | 13.7 | 274 |
| 17 | Cell of origin dictates aggression and stem cell number in acute lymphoblastic leukemia. Leukemia, 2018, 32, 1860-1865. | 3.3 | 23 |
| 18 | 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 |

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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 | RUNX1 Is a Candidate Transcriptional Effector in Juvenile Myelomonocytic Leukemia. Blood, 2016, 128, 2699-2699. | 0.6 | 0 |
| 21 | BCL11A enhancer dissection by Cas9-mediated in situ saturating mutagenesis. Nature, 2015, 527, 192-197. | 13.7 | 726 |
| 22 | Transcriptional diversity during lineage commitment of human blood progenitors. Science, 2014, 345, 1251033. | 6.0 | 253 |
| 23 | The breakdown of the word symmetry in the human genome. Journal of Theoretical Biology, 2013, 335, 153-159. | 0.8 | 37 |
| 24 | Analysis of Word Symmetries in Human Genomes Using Next-Generation Sequencing Data. Advances in Intelligent Systems and Computing, 2013, , 7-13. | 0.5 | 0 |
| 25 | 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 |
| 26 | Inter-STOP symbol distances for the identification of coding regions. Journal of Integrative Bioinformatics, 2013, 10, 31-39. | 1.0 | 2 |
| 27 | DNA Sequences at a Glance. PLoS ONE, 2013, 8, e79922. | 1.1 | 14 |
| 28 | 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 |
| 29 | Compressing Resequencing Data with GReEn. Methods in Molecular Biology, 2013, 1038, 27-37. | 0.4 | 0 |
| 30 | The Breakdown of Symmetry in Word Pairs in 1,092 Human Genomes. Jurnal Teknologi (Sciences and) Tj ETQq0 | 0 O.rgBT /0 | Ovgrlock 10 T |
| 31 | Inter-STOP symbol distances for the identification of coding regions. Journal of Integrative Bioinformatics, 2013, 10, 230. | 1.0 | 0 |
| 32 | GReEn: a tool for efficient compression of genome resequencing data. Nucleic Acids Research, 2012, 40, e27-e27. | 6.5 | 76 |
| 33 | Exon: A Web-Based Software Toolkit for DNA Sequence Analysis. Advances in Intelligent and Soft Computing, 2012, , 217-224. | 0.2 | 0 |
| 34 | Minimal Absent Words in Four Human Genome Assemblies. PLoS ONE, 2011, 6, e29344. | 1.1 | 11 |
| 35 | 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 |
| 36 | Genome analysis with distance to the nearest dissimilar nucleotide. Journal of Theoretical Biology, 2011, 275, 52-58. | 0.8 | 10 |

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|----|---|-----|-----------|
| 37 | Minimal Absent Words in Prokaryotic and Eukaryotic Genomes. PLoS ONE, 2011, 6, e16065. | 1.1 | 20 |
| 38 | Complexity Profiles of DNA Sequences Using Finite-Context Models. Lecture Notes in Computer Science, 2011, , 75-82. | 1.0 | O |
| 39 | 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 |
| 40 | Exploring Homology Using the Concept of Three-State Entropy Vector. Lecture Notes in Computer Science, 2010, , 161-170. | 1.0 | 1 |
| 41 | Genome analysis with inter-nucleotide distances. Bioinformatics, 2009, 25, 3064-3070. | 1.8 | 75 |
| 42 | On finding minimal absent words. BMC Bioinformatics, 2009, 10, 137. | 1.2 | 37 |
| 43 | 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 |
| 44 | Ecoforecasting in real time for commercial fisheries: the Atlantic white shrimp as a case study. Marine Biology, 2007, 152, 15-24. | 0.7 | 13 |
| 45 | Multivariate phase space reconstruction by nearest neighbor embedding with different time delays. Physical Review E, 2005, 72, 027205. | 0.8 | 49 |
| 46 | Nearest neighbor embedding with different time delays. Physical Review E, 2005, 71, 037204. | 0.8 | 28 |
| 47 | Phase behaviour of the catalyst dicarbonyl(î·5-cyclopentadienyl)-cobalt in carbon dioxide. Journal of Supercritical Fluids, 2004, 31, 1-8. | 1.6 | 9 |