

Reporte de citas de las publicaciones del Dr. Alejandro Reyes Quiroz

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Los datos de las citas fueron colectados el día 5 de Febrero del 2020 de la base de datos de Web of Science.

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1	A practical guide to methods controlling false discoveries in computational biology. GENOME BIOLOGY, 2019.	0	4
2	Reproducible and replicable comparisons using Summarized Benchmark. BIOINFORMATICS, 2019.	1	1
3	Alternative start and termination sites of transcription drive most transcript isoform differences across human tissues. NUCLEIC ACIDS RESEARCH, 2018.	1	28
4	CTCF-Mediated Chromatin Loops between Promoter and Gene Body Regulate Alternative Splicing across Individuals. CELL SYSTEMS, 2017.	0	11
5	RNA sequencing identifies novel non-coding RNA and exon-specific effects associated with cigarette smoking. BMC MEDICAL GENOMICS, 2017.	10	4
6	Myc Depletion Induces a Pluripotent Dormant State Mimicking Diapause. CELL, 2016.	5	75
7	Orchestrating high-throughput genomic analysis with Bioconductor. NATURE METHODS, 2015.	47	820
8	Single-cell transcriptome analysis reveals coordinated ectopic gene-expression patterns in medullary thymic epithelial cells. NATURE IMMUNOLOGY, 2015.	2	50
9	Identification of Regulatory Networks in HSCs and Their Immediate Progeny via Integrated Proteome, Transcriptome, and DNA Methylation Analysis. CELL STEM CELL, 2014.	25	170
10	Transcriptome-wide Profiling and Posttranscriptional Analysis of Hematopoietic Stem/Progenitor Cell Differentiation toward Myeloid Commitment. STEM CELL REPORTS, 2014.	3	11
11	Direct Competition between hnRNP C and U2AF65 Protects the Transcriptome from the Exonization of Alu Elements. CELL, 2013.	27	157
12	Drift and conservation of differential exon usage across tissues in primate species. PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, 2013.	1	36
13	Detecting differential usage of exons from RNA-seq data. GENOME RESEARCH, 2012.	10	511
14	Personal receptor repertoires: olfaction as a model. BMC GENOMICS, 2012.	2	42

Citas de la publicación: A practical guide to methods controlling false discoveries in computational biology. GENOME BIOLOGY, 2019.

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3. Wilkins, Lamont J. et al. Defining Dysbiosis for a Cluster of Chronic Diseases. SCIENTIFIC REPORTS, 2019. doi: 10.1038/s41598-019-49452-y
4. Weber, Lukas M. et al. Essential guidelines for computational method benchmarking. GENOME BIOLOGY, 2019. doi: 10.1186/s13059-019-1738-8

Citas tipo B (Web of Science)

Citas de la publicación: Reproducible and replicable comparisons using Summarized Benchmark. BIOINFORMATICS, 2019.

Citas tipo A (Web of Science)

1. Weber, Lukas M. et al. Essential guidelines for computational method benchmarking. GENOME BIOLOGY, 2019. doi: 10.1186/s13059-019-1738-8

Citas tipo B (Web of Science)

1. Korthauer, Keegan et al. A practical guide to methods controlling false discoveries in computational biology. GENOME BIOLOGY, 2019. doi: 10.1186/s13059-019-1716-1

Citas de la publicación: Alternative start and termination sites of transcription drive most transcript isoform differences across human tissues. NUCLEIC ACIDS RESEARCH, 2018.

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1. Hekselman, Idan et al. Mechanisms of tissue and cell-type specificity in heritable traits and diseases. NATURE REVIEWS GENETICS, 2020. doi: 10.1038/s41576-019-0200-9
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1. Korthauer, Keegan et al. A practical guide to methods controlling false discoveries in computational biology. *GENOME BIOLOGY*, 2019. doi: 10.1186/s13059-019-1716-1

Citas de la publicación: CTCF-Mediated Chromatin Loops between Promoter and Gene Body Regulate Alternative Splicing across Individuals. CELL SYSTEMS, 2017.

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Citas tipo B (Web of Science)

Citas de la publicación: RNA sequencing identifies novel non-coding RNA and exon-specific effects associated with cigarette smoking. BMC MEDICAL GENOMICS, 2017.

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Citas de la publicación: Myc Depletion Induces a Pluripotent Dormant State Mimicking Diapause. CELL, 2016.

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