## Ricardo A Verdugo

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	The Association between Fasting Glucose and Sugar Sweetened Beverages Intake Is Greater in Latin Americans with a High Polygenic Risk Score for Type 2 Diabetes Mellitus. Nutrients, 2022, 14, 69.	4.1	9
2	Inflammatory profiles in Chilean Mapuche and non-Mapuche women with gallstones at risk of developing gallbladder cancer. Scientific Reports, 2021, 11, 3686.	3.3	6
3	The Chilean socio-ethno-genomic cline. Biodemography and Social Biology, 2021, 66, 156-171.	1.0	8
4	Validation of an NGS Panel Designed for Detection of Actionable Mutations in Tumors Common in Latin America. Journal of Personalized Medicine, 2021, 11, 899.	2.5	3
5	Paths and timings of the peopling of Polynesia inferred from genomic networks. Nature, 2021, 597, 522-526.	27.8	31
6	HLA-DRB1*07:01 and *08:02 Alleles Confer a Protective Effect Against ACPA-Positive Rheumatoid Arthritis in a Latin American Admixed Population. Biology, 2020, 9, 467.	2.8	5
7	Polymorphisms PSCA rs2294008, IL-4 rs2243250 and MUC1 rs4072037 are associated with gastric cancer in a high risk population. Molecular Biology Reports, 2020, 47, 9239-9243.	2.3	7
8	Association analysis in a Latin American population revealed ethnic differences in rheumatoid arthritis-associated SNPs in Caucasian and Asian populations. Scientific Reports, 2020, 10, 7879.	3.3	6
9	Native American gene flow into Polynesia predating Easter Island settlement. Nature, 2020, 583, 572-577.	27.8	64
10	Development of a small panel of SNPs to infer ancestry in Chileans that distinguishes Aymara and Mapuche components. Biological Research, 2020, 53, 15.	3.4	18
11	<i>HIST1H1E</i> heterozygous proteinâ€truncating variants cause a recognizable syndrome with intellectual disability and distinctive facial gestalt: A study to clarify the HIST1H1E syndrome phenotype in 30 individuals. American Journal of Medical Genetics, Part A, 2019, 179, 2049-2055.	1.2	16
12	Draft genome sequence data of maqui (Aristotelia chilensis) and identification of SSR markers. Data in Brief, 2019, 27, 104545.	1.0	1
13	Regulation of Tolerogenic Features on Dexamethasone-Modulated MPLA-Activated Dendritic Cells by MYC. Frontiers in Immunology, 2019, 10, 1171.	4.8	10
14	Genomic insights into the origin and diversification of late maritime hunter-gatherers from the Chilean Patagonia. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E4006-E4012.	7.1	50
15	The genetic prehistory of the Andean highlands 7000 years BP though European contact. Science Advances, 2018, 4, eaau4921.	10.3	115
16	ADAR1-mediated RNA-editing of 3′UTRs in breast cancer. Biological Research, 2018, 51, 36.	3.4	39
17	Killer cell immunoglobulin-like receptor genotypes in a Chilean population from Talca. Human Immunology, 2018, 79, 651-652.	2.4	1
18	Visualization of Results from Systems Genetics Studies in Chromosomal Context. Methods in Molecular Biology, 2017, 1488, 283-297.	0.9	0

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19	Dexamethasone and Monophosphoryl Lipid A Induce a Distinctive Profile on Monocyte-Derived Dendritic Cells through Transcriptional Modulation of Genes Associated With Essential Processes of the Immune Response. Frontiers in Immunology, 2017, 8, 1350.	4.8	31
20	Treatment with Dexamethasone and Monophosphoryl Lipid A Removes Disease-Associated Transcriptional Signatures in Monocyte-Derived Dendritic Cells from Rheumatoid Arthritis Patients and Confers Tolerogenic Features. Frontiers in Immunology, 2016, 7, 458.	4.8	12
21	chromPlot: visualization of genomic data in chromosomal context. Bioinformatics, 2016, 32, 2366-2368.	4.1	45
22	Overlapping mouse subcongenic strains successfully separate two linked body fat QTL on distal MMU 2. BMC Genomics, 2015, 16, 16.	2.8	16
23	SASH1, a new potential link between smoking and atherosclerosis. Atherosclerosis, 2015, 242, 571-579.	0.8	24
24	Graphical Modeling of Gene Expression in Monocytes Suggests Molecular Mechanisms Explaining Increased Atherosclerosis in Smokers. PLoS ONE, 2013, 8, e50888.	2.5	36
25	Using bioinformatics and systems genetics to dissect HDL-cholesterol genetics in an MRL/MpJ × SM/J intercross. Journal of Lipid Research, 2012, 53, 1163-1175.	4.2	13
26	Integration of QTL and bioinformatic tools to identify candidate genes for triglycerides in mice. Journal of Lipid Research, 2011, 52, 1672-1682.	4.2	26
27	Genetic analysis of complex traits in the emerging Collaborative Cross. Genome Research, 2011, 21, 1213-1222.	5.5	327
28	A survey of airway responsiveness in 36 inbred mouse strains facilitates gene mapping studies and identification of quantitative trait loci. Molecular Genetics and Genomics, 2010, 283, 317-326.	2.1	29
29	Serious limitations of the QTL/Microarray approach for QTL gene discovery. BMC Biology, 2010, 8, 96.	3.8	29
30	Identification of genetic determinants of IGFâ€1 levels and longevity among mouse inbred strains. Aging Cell, 2010, 9, 823-836.	6.7	32
31	Segregation Analysis of a Sex Ratio Distortion Locus in Congenic Mice. Journal of Heredity, 2010, 101, 351-359.	2.4	3
32	Importance of randomization in microarray experimental designs with Illumina platforms. Nucleic Acids Research, 2009, 37, 5610-5618.	14.5	29
33	Chromosome Y variants from different inbred mouse strains are linked to differences in the morphologic and molecular responses of cardiac cells to postpubertal testosterone. BMC Genomics, 2009, 10, 150.	2.8	15
34	Overexpression of Scg5 increases enzymatic activity of PCSK2 and is inversely correlated with body weight in congenic mice. BMC Genetics, 2008, 9, 34.	2.7	14
35	Comparison of gene coverage of mouse oligonucleotide microarray platforms. BMC Genomics, 2006, 7, 58.	2.8	24
36	Selection response of US Holstein AI bulls for milk production in Chile and Argentina. Livestock Science, 2004, 88, 9-16.	1.2	8