

# Leonardo A Meza-Zepeda

## List of Publications by Year in descending order

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Version: 2024-02-01

77  
papers

4,285  
citations

109311

35  
h-index

114455

63  
g-index

82  
all docs

82  
docs citations

82  
times ranked

8908  
citing authors

#	ARTICLE	IF	CITATIONS
1	Depletion of Murine Intestinal Microbiota: Effects on Gut Mucosa and Epithelial Gene Expression. PLoS ONE, 2011, 6, e17996.	2.5	421
2	Modulation of the Osteosarcoma Expression Phenotype by MicroRNAs. PLoS ONE, 2012, 7, e48086.	2.5	253
3	Multi-omics of 34 colorectal cancer cell lines - a resource for biomedical studies. Molecular Cancer, 2017, 16, 116.	19.2	232
4	The Architecture and Evolution of Cancer Neochromosomes. Cancer Cell, 2014, 26, 653-667.	16.8	161
5	Performance comparison of four exome capture systems for deep sequencing. BMC Genomics, 2014, 15, 449.	2.8	152
6	High-resolution analysis of genetic stability of human adipose tissue stem cells cultured to senescence. Journal of Cellular and Molecular Medicine, 2008, 12, 553-563.	3.6	148
7	Molecular characterization of commonly used cell lines for bone tumor research: A trans-European EuroBoNet effort. Genes Chromosomes and Cancer, 2010, 49, 40-51.	2.8	141
8	Deep Sequencing the MicroRNA Transcriptome in Colorectal Cancer. PLoS ONE, 2013, 8, e66165.	2.5	132
9	Identification of osteosarcoma driver genes by integrative analysis of copy number and gene expression data. Genes Chromosomes and Cancer, 2012, 51, 696-706.	2.8	108
10	Multifocal Primary Prostate Cancer Exhibits High Degree of Genomic Heterogeneity. European Urology, 2019, 75, 498-505.	1.9	108
11	Remodeling of secretory lysosomes during education tunes functional potential in NK cells. Nature Communications, 2019, 10, 514.	12.8	103
12	Epithelial-microbial crosstalk in polymeric Ig receptor deficient mice. European Journal of Immunology, 2012, 42, 2959-2970.	2.9	102
13	Array Comparative Genomic Hybridization Reveals Distinct DNA Copy Number Differences between Gastrointestinal Stromal Tumors and Leiomyosarcomas. Cancer Research, 2006, 66, 8984-8993.	0.9	97
14	Genomic landscape of liposarcoma. Oncotarget, 2015, 6, 42429-42444.	1.8	94
15	HMGIC, the gene for an architectural transcription factor, is amplified and rearranged in a subset of human sarcomas. Oncogene, 1997, 14, 2935-2941.	5.9	89
16	Adipocyte Differentiation of Human Bone Marrow-Derived Stromal Cells Is Modulated by MicroRNA-155, MicroRNA-221, and MicroRNA-222. Stem Cells and Development, 2012, 21, 873-883.	2.1	87
17	Integrative Analysis Reveals Relationships of Genetic and Epigenetic Alterations in Osteosarcoma. PLoS ONE, 2012, 7, e48262.	2.5	87
18	The Regulatory Landscape of Osteogenic Differentiation. Stem Cells, 2014, 32, 2780-2793.	3.2	85

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19	<i>LSAMP</i> , a novel candidate tumor suppressor gene in human osteosarcomas, identified by array comparative genomic hybridization. <i>Genes Chromosomes and Cancer</i> , 2009, 48, 679-693.	2.8	84
20	Rapid Gene Expression Changes in Peripheral Blood Lymphocytes upon Practice of a Comprehensive Yoga Program. <i>PLoS ONE</i> , 2013, 8, e61910.	2.5	82
21	TP53 Mutation Spectrum in Smokers and Never Smoking Lung Cancer Patients. <i>Frontiers in Genetics</i> , 2016, 07, 85.	2.3	76
22	Multilevel genomics of colorectal cancers with microsatellite instability—clinical impact of JAK1 mutations and consensus molecular subtype 1. <i>Genome Medicine</i> , 2017, 9, 46.	8.2	71
23	Metabolic reprogramming of metastatic breast cancer and melanoma by let-7a microRNA. <i>Oncotarget</i> , 2015, 6, 2451-2465.	1.8	68
24	Noninvasive Detection of ctDNA Reveals Intratumor Heterogeneity and Is Associated with Tumor Burden in Gastrointestinal Stromal Tumor. <i>Molecular Cancer Therapeutics</i> , 2018, 17, 2473-2480.	4.1	61
25	Unscrambling the genomic chaos of osteosarcoma reveals extensive transcript fusion, recurrent rearrangements and frequent novel TP53 aberrations. <i>Oncotarget</i> , 2016, 7, 5273-5288.	1.8	60
26	Analyses of single-copy Arabidopsis T-DNA-transformed lines show that the presence of vector backbone sequences, short inverted repeats and DNA methylation is not sufficient or necessary for the induction of transgene silencing. <i>Nucleic Acids Research</i> , 2002, 30, 4556-4566.	14.5	59
27	Amplification of chromosome 1 sequences in lipomatous tumors and other sarcomas. <i>International Journal of Cancer</i> , 2004, 109, 363-369.	5.1	55
28	Dedifferentiation of a well-differentiated liposarcoma to a highly malignant metastatic osteosarcoma. <i>Cancer Genetics and Cytogenetics</i> , 2001, 125, 100-111.	1.0	54
29	Amplification and overexpression of PRUNE in human sarcomas and breast carcinomas—a possible mechanism for altering the nm23-H1 activity. <i>Oncogene</i> , 2001, 20, 6881-6890.	5.9	52
30	Positional cloning identifies a novel cyclophilin as a candidate amplified oncogene in 1q21. <i>Oncogene</i> , 2002, 21, 2261-2269.	5.9	52
31	Sumoylation of Rap1 mediates the recruitment of TFIID to promote transcription of ribosomal protein genes. <i>Genome Research</i> , 2015, 25, 897-906.	5.5	49
32	Evaluation of commercial DNA and RNA extraction methods for high-throughput sequencing of FFPE samples. <i>PLoS ONE</i> , 2018, 13, e0197456.	2.5	46
33	Pembrolizumab in advanced osteosarcoma: results of a single-arm, open-label, phase 2 trial. <i>Cancer Immunology, Immunotherapy</i> , 2021, 70, 2617-2624.	4.2	45
34	Lymphomas can develop from B cells chronically helped by idiotype-specific T cells. <i>Journal of Experimental Medicine</i> , 2007, 204, 1181-1191.	8.5	41
35	Preclinical xenograft models of human sarcoma show nonrandom loss of aberrations. <i>Cancer</i> , 2012, 118, 558-570.	4.1	40
36	Ectopic sequences from truncated HMGIC in liposarcomas are derived from various amplified chromosomal regions. <i>Genes Chromosomes and Cancer</i> , 2001, 31, 264-273.	2.8	37

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37	Early-Onset Lymphoma and Extensive Embryonic Apoptosis in Two Domain-Specific <i>Fen1</i> Mice Mutants. <i>Cancer Research</i> , 2008, 68, 4571-4579.	0.9	37
38	<i>Cdc28</i> kinase activity regulates the basal transcription machinery at a subset of genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 10450-10455.	7.1	37
39	Correlation of <i>TP53</i> and <i>MDM2</i> genotypes with response to therapy in sarcoma. <i>Cancer</i> , 2013, 119, 1013-1022.	4.1	36
40	mRNA expression profiles of primary high-grade central osteosarcoma are preserved in cell lines and xenografts. <i>BMC Medical Genomics</i> , 2011, 4, 66.	1.5	30
41	Common Fusion Transcripts Identified in Colorectal Cancer Cell Lines by High-Throughput RNA Sequencing. <i>Translational Oncology</i> , 2013, 6, 546-IN5.	3.7	29
42	Clinical and molecular implications of NAB2-STAT6 fusion variants in solitary fibrous tumour. <i>Pathology</i> , 2021, 53, 713-719.	0.6	29
43	Human ALKBH4 Interacts with Proteins Associated with Transcription. <i>PLoS ONE</i> , 2012, 7, e49045.	2.5	27
44	A well-differentiated liposarcoma with a new type of chromosome 12-derived markers. <i>Cancer Genetics and Cytogenetics</i> , 2001, 131, 13-18.	1.0	26
45	ctDNA detected by ddPCR reveals changes in tumour load in metastatic malignant melanoma treated with bevacizumab. <i>Scientific Reports</i> , 2019, 9, 17471.	3.3	26
46	Reexpression of LSAMP inhibits tumor growth in a preclinical osteosarcoma model. <i>Molecular Cancer</i> , 2014, 13, 93.	19.2	25
47	Induction of homologous low temperature and ABA-responsive genes in frost resistant ( <i>Solanum</i> ) Tj ETQq1 1 0.784314 rgBT /Overload. <i>Biology</i> , 1996, 30, 331-336.	3.9	24
48	Upregulation of stem cell genes in multidrug resistant K562 leukemia cells. <i>Leukemia Research</i> , 2009, 33, 1379-1385.	0.8	23
49	Preclinical evaluation of potential therapeutic targets in dedifferentiated liposarcoma. <i>Oncotarget</i> , 2016, 7, 54583-54595.	1.8	23
50	Clonal evolution after treatment pressure in multiple myeloma: heterogenous genomic aberrations and transcriptomic convergence. <i>Leukemia</i> , 2022, 36, 1887-1897.	7.2	23
51	Use of liquid biopsies to monitor disease progression in a sarcoma patient: a case report. <i>BMC Cancer</i> , 2017, 17, 29.	2.6	21
52	Sample-Index Misassignment Impacts Tumour Exome Sequencing. <i>Scientific Reports</i> , 2018, 8, 5307.	3.3	17
53	OH-2, a hyperdiploid myeloma cell line without an IGH translocation, has a complex translocation juxtaposing MYC near MAFB and the IGK locus. <i>Leukemia Research</i> , 2009, 33, 1670-1677.	0.8	16
54	Chromosomal aberrations in head and neck squamous cell carcinomas in Norwegian and Sudanese populations by array comparative genomic hybridization. <i>Oncology Reports</i> , 2008, 20, 825-43.	2.6	14

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73	Accurate 3-gene-signature for early diagnosis of liposarcoma progression. <i>Clinical Sarcoma Research</i> , 2020, 10, 4.	2.3	4
74	The expressed mutational landscape of microsatellite stable colorectal cancers. <i>Genome Medicine</i> , 2021, 13, 142.	8.2	4
75	Discovery of Recurrent Mutations Associated with Chemo-Immunotherapy Relapse in Diffuse Large B-Cell Lymphoma. <i>Blood</i> , 2015, 126, 110-110.	1.4	1
76	Mutational Dynamics and Evolutionary Divergence in DLBCL: A Call for Relapse Sampling. <i>Blood</i> , 2019, 134, 1497-1497.	1.4	0
77	A comprehensive characterization of anatomical and molecular risk factors in gastric gastrointestinal stromal tumor.. <i>Journal of Clinical Oncology</i> , 2020, 38, e23522-e23522.	1.6	0