

Gonzalo GÃ³mez LÃ³pez

List of Publications by Year in descending order

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Version: 2024-02-01

132
papers

7,736
citations

50276

46
h-index

56724

83
g-index

140
all docs

140
docs citations

140
times ranked

15767
citing authors

#	ARTICLE	IF	CITATIONS
1	bolito: a flexible pipeline for comprehensive single-cell RNA-seq analyses. <i>Bioinformatics</i> , 2022, 38, 1155-1156.	4.1	6
2	An in silico analysis identifies drugs potentially modulating the cytokine storm triggered by SARS-CoV-2 infection. <i>Scientific Reports</i> , 2022, 12, 1626.	3.3	4
3	Endothelial Cell RNA-Seq Data: Differential Expression and Functional Enrichment Analyses to Study Phenotypic Switching. <i>Methods in Molecular Biology</i> , 2022, 2441, 369-426.	0.9	1
4	DREIMT: a drug repositioning database and prioritization tool for immunomodulation. <i>Bioinformatics</i> , 2021, 37, 578-579.	4.1	9
5	Spleen plays a major role in DLL4-driven acute T-cell lymphoblastic leukemia. <i>Theranostics</i> , 2021, 11, 1594-1608.	10.0	3
6	RANK links senescence to stemness in the mammary epithelia, delaying tumor onset but increasing tumor aggressiveness. <i>Developmental Cell</i> , 2021, 56, 1727-1741.e7.	7.0	21
7	A comprehensive database for integrated analysis of omics data in autoimmune diseases. <i>BMC Bioinformatics</i> , 2021, 22, 343.	2.6	12
8	Beyondcell: targeting cancer therapeutic heterogeneity in single-cell RNA-seq data. <i>Genome Medicine</i> , 2021, 13, 187.	8.2	25
9	Midkine rewires the melanoma microenvironment toward a tolerogenic and immune-resistant state. <i>Nature Medicine</i> , 2020, 26, 1865-1877.	30.7	62
10	How can bioinformatics contribute to the routine application of personalized precision medicine?. <i>Expert Review of Precision Medicine and Drug Development</i> , 2020, 5, 115-117.	0.7	3
11	TGF β -induced IGFBP3 is a key paracrine factor from activated pericytes that promotes colorectal cancer cell migration and invasion. <i>Molecular Oncology</i> , 2020, 14, 2609-2628.	4.6	18
12	Tumor regression and resistance mechanisms upon CDK4 and RAF1 inactivation in KRAS/P53 mutant lung adenocarcinomas. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 24415-24426.	7.1	15
13	The Hippo Pathway Transducers YAP1/TEAD Induce Acquired Resistance to Trastuzumab in HER2-Positive Breast Cancer. <i>Cancers</i> , 2020, 12, 1108.	3.7	13
14	Autocrine CCL5 Effect Mediates Trastuzumab Resistance by ERK Pathway Activation in HER2-Positive Breast Cancer. <i>Molecular Cancer Therapeutics</i> , 2020, 19, 1696-1707.	4.1	24
15	Global hyperactivation of enhancers stabilizes human and mouse naive pluripotency through inhibition of CDK8/19 Mediator kinases. <i>Nature Cell Biology</i> , 2020, 22, 1223-1238.	10.3	35
16	The correlation between immune subtypes and consensus molecular subtypes in colorectal cancer identifies novel tumour microenvironment profiles, with prognostic and therapeutic implications. <i>European Journal of Cancer</i> , 2019, 123, 118-129.	2.8	50
17	In Silico Drug Prescription for Targeting Cancer Patient Heterogeneity and Prediction of Clinical Outcome. <i>Cancers</i> , 2019, 11, 1361.	3.7	6
18	Specific Contributions of Cohesin-SA1 and Cohesin-SA2 to TADs and Polycomb Domains in Embryonic Stem Cells. <i>Cell Reports</i> , 2019, 27, 3500-3510.e4.	6.4	60

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19	vulcanSpot: a tool to prioritize therapeutic vulnerabilities in cancer. <i>Bioinformatics</i> , 2019, 35, 4846-4848.	4.1	10
20	MEK inhibition enhances the response to tyrosine kinase inhibitors in acute myeloid leukemia. <i>Scientific Reports</i> , 2019, 9, 18630.	3.3	24
21	p62/SQSTM1 Fuels Melanoma Progression by Opposing mRNA Decay of a Selective Set of Pro-metastatic Factors. <i>Cancer Cell</i> , 2019, 35, 46-63.e10.	16.8	50
22	Precision medicine needs pioneering clinical bioinformaticians. <i>Briefings in Bioinformatics</i> , 2019, 20, 752-766.	6.5	40
23	Abstract PD2-09: High-throughput phosphoproteomics (HTPS) in neoadjuvant (NEO) breast cancer (BC) reveals clusters of extreme sensitivity to paclitaxel (T). , 2019, , .		0
24	The RNA Polymerase II Factor RPAP1 Is Critical for Mediator-Driven Transcription and Cell Identity. <i>Cell Reports</i> , 2018, 22, 396-410.	6.4	30
25	In vivo phosphoproteomics reveals kinase activity profiles that predict treatment outcome in triple-negative breast cancer. <i>Nature Communications</i> , 2018, 9, 3501.	12.8	45
26	Therapeutic effects of telomerase in mice with pulmonary fibrosis induced by damage to the lungs and short telomeres. <i>ELife</i> , 2018, 7, .	6.0	88
27	PanDrugs: a novel method to prioritize anticancer drug treatments according to individual genomic data. <i>Genome Medicine</i> , 2018, 10, 41.	8.2	63
28	Distinct roles of cohesin-SA1 and cohesin-SA2 in 3D chromosome organization. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 496-504.	8.2	128
29	TWEAK increases CD74 expression and sensitizes to DDT proinflammatory actions in tubular cells. <i>PLoS ONE</i> , 2018, 13, e0199391.	2.5	11
30	Pax8 controls thyroid follicular polarity through Cadherin-16. <i>Journal of Cell Science</i> , 2017, 130, 219-231.	2.0	46
31	Vitamin D receptor expression and associated gene signature in tumour stromal fibroblasts predict clinical outcome in colorectal cancer. <i>Gut</i> , 2017, 66, 1449-1462.	12.1	131
32	Genomic and Molecular Screenings Identify Different Mechanisms for Acquired Resistance to MET Inhibitors in Lung Cancer Cells. <i>Molecular Cancer Therapeutics</i> , 2017, 16, 1366-1376.	4.1	23
33	Prediction of miRNA-mRNA Interactions Using miRGate. <i>Methods in Molecular Biology</i> , 2017, 1580, 225-237.	0.9	17
34	Genomic Profiling of Patient-Derived Xenografts for Lung Cancer Identifies B2M Inactivation Impairing Immunorecognition. <i>Clinical Cancer Research</i> , 2017, 23, 3203-3213.	7.0	66
35	Genomic Profiling of Patient-Derived Xenografts for Lung Cancer Identifies B2M Inactivation Impairing Immunorecognition. <i>Clinical Cancer Research</i> , 2017, 23, 3203-3213.	7.0	66
36	Pancreas Cancer Precision Treatment Using Avatar Mice from a Bioinformatics Perspective. <i>Public Health Genomics</i> , 2017, 20, 81-91.	1.0	10

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37	A Braf kinase-inactive mutant induces lung adenocarcinoma. <i>Nature</i> , 2017, 548, 239-243.	27.8	85
38	The molecular pathogenesis of the NUP98-HOXA9 fusion protein in acute myeloid leukemia. <i>Leukemia</i> , 2017, 31, 2000-2005.	7.2	28
39	RUBioSeq+: A multiplatform application that executes parallelized pipelines to analyse next-generation sequencing data. <i>Computer Methods and Programs in Biomedicine</i> , 2017, 138, 73-81.	4.7	11
40	Systems analysis identifies melanoma-enriched pro-oncogenic networks controlled by the RNA binding protein CELF1. <i>Nature Communications</i> , 2017, 8, 2249.	12.8	22
41	Abstract 1221: Triple-negative breast cancer (TNBC) phosphoproteomics. , 2017, , .		0
42	A genetic interaction between RAP1 and telomerase reveals an unanticipated role for RAP1 in telomere maintenance. <i>Aging Cell</i> , 2016, 15, 1113-1125.	6.7	39
43	Metastatic risk and resistance to BRAF inhibitors in melanoma defined by selective allelic loss of <i>ATG5</i> . <i>Autophagy</i> , 2016, 12, 1776-1790.	9.1	31
44	Lineage-specific roles of the cytoplasmic polyadenylation factor CPEB4 in the regulation of melanoma drivers. <i>Nature Communications</i> , 2016, 7, 13418.	12.8	46
45	Tissue damage and senescence provide critical signals for cellular reprogramming in vivo. <i>Science</i> , 2016, 354, .	12.6	466
46	KRAS-driven lung adenocarcinoma: combined DDR1/Notch inhibition as an effective therapy. <i>ESMO Open</i> , 2016, 1, e000076.	4.5	19
47	p21 ^{Cip1} plays a critical role in the physiological adaptation to fasting through activation of PPAR α . <i>Scientific Reports</i> , 2016, 6, 34542.	3.3	12
48	RUBioSeq+: An Application that Executes Parallelized Pipelines to Analyse Next-Generation Sequencing Data. <i>Advances in Intelligent Systems and Computing</i> , 2016, , 141-149.	0.6	0
49	Targeting Tumor Mitochondrial Metabolism Overcomes Resistance to Antiangiogenics. <i>Cell Reports</i> , 2016, 15, 2705-2718.	6.4	78
50	Combined inhibition of DDR1 and Notch signaling is a therapeutic strategy for KRAS-driven lung adenocarcinoma. <i>Nature Medicine</i> , 2016, 22, 270-277.	30.7	150
51	Analysis of Paired Primary-Metastatic Hormone-Receptor Positive Breast Tumors (HRPBC) Uncovers Potential Novel Drivers of Hormonal Resistance. <i>PLoS ONE</i> , 2016, 11, e0155840.	2.5	20
52	Proteomic Profiling of Ewing Sarcoma Reveals a Role for TRAF6 in Proliferation and Ribonucleoproteins/RNA Processing. <i>Journal of Proteomics and Bioinformatics</i> , 2016, 09, .	0.4	1
53	HDAC Inhibitors As Novel Targeted Therapies for NUP98-HOXA9 AML Patients. <i>Blood</i> , 2016, 128, 2685-2685.	1.4	2
54	MicroRNA expression signatures for the prediction of BRCA1/2 mutation-associated hereditary breast cancer in paraffin-embedded formalin-fixed breast tumors. <i>International Journal of Cancer</i> , 2015, 136, 593-602.	5.1	43

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55	Profiling of Sox4-dependent transcriptome in skin links tumour suppression and adult stem cell activation. <i>Genomics Data</i> , 2015, 6, 21-24.	1.3	3
56	Partial Loss of Rpl11 in Adult Mice Recapitulates Diamond-Blackfan Anemia and Promotes Lymphomagenesis. <i>Cell Reports</i> , 2015, 13, 712-722.	6.4	64
57	miRGate: a curated database of human, mouse and rat miRNA-mRNA targets. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav035.	3.0	87
58	The pluripotency factor NANOG promotes the formation of squamous cell carcinomas. <i>Scientific Reports</i> , 2015, 5, 10205.	3.3	32
59	Tumor MicroRNA Expression Profiling Identifies Circulating MicroRNAs for Early Breast Cancer Detection. <i>Clinical Chemistry</i> , 2015, 61, 1098-1106.	3.2	183
60	DNA repair capacity is impaired in healthy BRCA1 heterozygous mutation carriers. <i>Breast Cancer Research and Treatment</i> , 2015, 152, 271-282.	2.5	26
61	miRNA expression profiling of formalin-fixed paraffin-embedded (FFPE) hereditary breast tumors. <i>Genomics Data</i> , 2015, 3, 75-79.	1.3	12
62	Microenvironmental hCAP-18/LL-37 promotes pancreatic ductal adenocarcinoma by activating its cancer stem cell compartment. <i>Gut</i> , 2015, 64, 1921-1935.	12.1	112
63	The UBC-40 Urothelial Bladder Cancer cell line index: a genomic resource for functional studies. <i>BMC Genomics</i> , 2015, 16, 403.	2.8	86
64	Abstract B9: A phosphoproteomic portrait of triple - negative breast cancer: functional taxonomy. , 2015, , .		0
65	Exome sequencing reveals novel and recurrent mutations with clinical impact in blastic plasmacytoid dendritic cell neoplasm. <i>Leukemia</i> , 2014, 28, 823-829.	7.2	148
66	Transcriptome characterization by RNA sequencing identifies a major molecular and clinical subdivision in chronic lymphocytic leukemia. <i>Genome Research</i> , 2014, 24, 212-226.	5.5	175
67	Sox4 Links Tumor Suppression to Accelerated Aging in Mice by Modulating Stem Cell Activation. <i>Cell Reports</i> , 2014, 8, 487-500.	6.4	51
68	RAB7 Controls Melanoma Progression by Exploiting a Lineage-Specific Wiring of the Endolysosomal Pathway. <i>Cancer Cell</i> , 2014, 26, 61-76.	16.8	86
69	Lineage-restricted function of the pluripotency factor NANOG in stratified epithelia. <i>Nature Communications</i> , 2014, 5, 4226.	12.8	45
70	The Epstein Barr-encoded BART-6-3p microRNA affects regulation of cell growth and immuno response in Burkitt lymphoma. <i>Infectious Agents and Cancer</i> , 2014, 9, 12.	2.6	55
71	PLCG1 mutations in cutaneous T-cell lymphomas. <i>Blood</i> , 2014, 123, 2034-2043.	1.4	193
72	Differential Gene Expression of Medullary Thyroid Carcinoma Reveals Specific Markers Associated with Genetic Conditions. <i>American Journal of Pathology</i> , 2013, 182, 350-362.	3.8	35

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73	RAP1 Protects from Obesity through Its Extratelomeric Role Regulating Gene Expression. Cell Reports, 2013, 3, 2059-2074.	6.4	102
74	Programmed Cell Senescence during Mammalian Embryonic Development. Cell, 2013, 155, 1104-1118.	28.9	1,081
75	ARF triggers senescence in Brca2-deficient cells by altering the spectrum of p53 transcriptional targets. Nature Communications, 2013, 4, 2697.	12.8	37
76	RAP1 Protects from Obesity through Its Extratelomeric Role Regulating Gene Expression. Cell Reports, 2013, 4, 229.	6.4	0
77	Downregulation of specific miRNAs in hyperdiploid multiple myeloma mimics the oncogenic effect of IgH translocations occurring in the non-hyperdiploid subtype. Leukemia, 2013, 27, 925-931.	7.2	31
78	RUbioSeq: a suite of parallelized pipelines to automate exome variation and bisulfite-seq analyses. Bioinformatics, 2013, 29, 1687-1689.	4.1	37
79	ASXL1, TP53 and IKZF3 mutations are present in the chronic phase and blast crisis of chronic myeloid leukemia. Blood Cancer Journal, 2013, 3, e157-e157.	6.2	32
80	SIRT1 promotes thyroid carcinogenesis driven by PTEN deficiency. Oncogene, 2013, 32, 4052-4056.	5.9	70
81	CSF3R T618I co-occurs with mutations of splicing and epigenetic genes and with a new PIM3 truncated fusion gene in chronic neutrophilic leukemia. Blood Cancer Journal, 2013, 3, e158-e158.	6.2	15
82	INK4a/ARF limits the expansion of cells suffering from replication stress. Cell Cycle, 2013, 12, 1948-1954.	2.6	16
83	ARID1A Alterations Are Associated with FGFR3-Wild Type, Poor-Prognosis, Urothelial Bladder Tumors. PLoS ONE, 2013, 8, e62483.	2.5	52
84	New Insights into FoxE1 Functions: Identification of Direct FoxE1 Targets in Thyroid Cells. PLoS ONE, 2013, 8, e62849.	2.5	55
85	Abstract 51: Activating PLCG1 mutations in cutaneous T-cell lymphomas.., 2013, , .		1
86	The specific contributions of cohesin-SA1 to cohesion and gene expression. Cell Cycle, 2012, 11, 2233-2238.	2.6	22
87	Genetic inactivation of Cdk7 leads to cell cycle arrest and induces premature aging due to adult stem cell exhaustion. EMBO Journal, 2012, 31, 2498-2510.	7.8	85
88	Therapeutic Effect of $\hat{1}^3$ -Secretase Inhibition in KrasG12V-Driven Non-Small Cell Lung Carcinoma by Derepression of DUSP1 and Inhibition of ERK. Cancer Cell, 2012, 22, 222-234.	16.8	108
89	Chromatin modifications induced by the AML1-ETO fusion protein reversibly silence its genomic targets through AML1 and Sp1 binding motifs. Leukemia, 2012, 26, 1329-1337.	7.2	30
90	Pten Positively Regulates Brown Adipose Function, Energy Expenditure, and Longevity. Cell Metabolism, 2012, 15, 382-394.	16.2	308

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91	Genome-wide analysis of Pax8 binding provides new insights into thyroid functions. BMC Genomics, 2012, 13, 147.	2.8	38
92	A unique role of cohesin-SA1 in gene regulation and development. EMBO Journal, 2012, 31, 2090-2102.	7.8	134
93	MicroRNA signatures in B-cell lymphomas. Blood Cancer Journal, 2012, 2, e57-e57.	6.2	79
94	The tumour suppressor and chromatin remodelling factor BRG1 antagonizes Myc activity and promotes cell differentiation in human cancer. EMBO Molecular Medicine, 2012, 4, 603-616.	6.9	70
95	Integration of BRCA1-mediated miRNA and mRNA profiles reveals microRNA regulation of TRAF2 and NF- κ B pathway. Breast Cancer Research and Treatment, 2012, 134, 41-51.	2.5	34
96	Src kinases catalytic activity regulates proliferation, migration and invasiveness of MDA-MB-231 breast cancer cells. Cellular Signalling, 2012, 24, 1276-1286.	3.6	63
97	New Mutations in Chronic Lymphocytic Leukemia Identified by Target Enrichment and Deep Sequencing. PLoS ONE, 2012, 7, e38158.	2.5	38
98	Applying AIBench Framework to Develop Rich User Interfaces in NGS Studies. Advances in Intelligent and Soft Computing, 2012, , 189-196.	0.2	0
99	Mutations in PLCC1 Is a Frequent Event in Cutaneous T-Cell Lymphomas. Blood, 2012, 120, 300-300.	1.4	0
100	Combinatorial effects of microRNAs to suppress the Myc oncogenic pathway. Blood, 2011, 117, 6255-6266.	1.4	60
101	miRNA expression in diffuse large B-cell lymphoma treated with chemoimmunotherapy. Blood, 2011, 118, 1034-1040.	1.4	90
102	Expression and functional validation of new p38 transcriptional targets in tumorigenesis. Biochemical Journal, 2011, 434, 549-558.	3.7	2
103	Cdc14b regulates mammalian RNA polymerase II and represses cell cycle transcription. Scientific Reports, 2011, 1, 189.	3.3	35
104	PileLine: a toolbox to handle genome position information in next-generation sequencing studies. BMC Bioinformatics, 2011, 12, 31.	2.6	10
105	Transcriptional characteristics of familial non-BRCA1/BRCA2 breast tumors. International Journal of Cancer, 2011, 128, 2635-2644.	5.1	11
106	Epigenetic regulation of Nanog expression by Ezh2 in pluripotent stem cells. Cell Cycle, 2011, 10, 1488-1498.	2.6	52
107	PileLineGUI: a desktop environment for handling genome position files in next-generation sequencing studies. Nucleic Acids Research, 2011, 39, W562-W566.	14.5	6
108	Abstract 1190: Integration of mRNA and miRNA signatures induced by BRCA1 gene. , 2011, , .		0

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109	Whole genome analysis of p38 SAPK-mediated gene expression upon stress. BMC Genomics, 2010, 11, 144.	2.8	55
110	Molecular signature of response and potential pathways related to resistance to the HSP90 inhibitor, 17AAG, in breast cancer. BMC Medical Genomics, 2010, 3, 44.	1.5	25
111	Mantle cell lymphoma: transcriptional regulation by microRNAs. Leukemia, 2010, 24, 1335-1342.	7.2	72
112	Mammalian Rap1 controls telomere function and gene expression through binding to telomeric and extratelomeric sites. Nature Cell Biology, 2010, 12, 768-780.	10.3	220
113	PathJam: a new service for integrating biological pathway information. Journal of Integrative Bioinformatics, 2010, 7, .	1.5	3
114	Research Resource: Transcriptional Profiling Reveals Different Pseudohypoxic Signatures in SDHB and VHL-Related Pheochromocytomas. Molecular Endocrinology, 2010, 24, 2382-2391.	3.7	179
115	37 Integration analysis between differentially expressed mRNA and miRNA induced by BRCA1 gene. European Journal of Cancer, Supplement, 2010, 8, 10.	2.2	0
116	PathAgent: Multi-agent System for Updated Pathway Information Integration. Advances in Intelligent and Soft Computing, 2010, , 77-85.	0.2	0
117	PathJam: a new service for integrating biological pathway information. Journal of Integrative Bioinformatics, 2010, 7, .	1.5	4
118	The dynamic DNA methylomes of double-stranded DNA viruses associated with human cancer. Genome Research, 2009, 19, 438-451.	5.5	218
119	WhichGenes: a web-based tool for gathering, building, storing and exporting gene sets with application in gene set enrichment analysis. Nucleic Acids Research, 2009, 37, W329-W334.	14.5	30
120	Telomere shortening relaxes X chromosome inactivation and forces global transcriptome alterations. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 19393-19398.	7.1	46
121	Functional characterization of E- and P-cadherin in invasive breast cancer cells. BMC Cancer, 2009, 9, 74.	2.6	61
122	Functional signatures identified in B-cell non-Hodgkin lymphoma profiles. Leukemia and Lymphoma, 2009, 50, 1699-1708.	1.3	10
123	Translational disease interpretation with molecular networks. Genome Biology, 2009, 10, 221.	9.6	22
124	TCL1A expression delineates biological and clinical variability in B-cell lymphoma. Modern Pathology, 2009, 22, 206-215.	5.5	46
125	Current Efforts to Integrate Biological Pathway Information. Lecture Notes in Computer Science, 2009, , 1092-1096.	1.3	0
126	Bioinformatics and cancer research: building bridges for translational research. Clinical and Translational Oncology, 2008, 10, 85-95.	2.4	15

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127	Array CGH and gene-expression profiling reveals distinct genomic instability patterns associated with DNA repair and cell-cycle checkpoint pathways in Ewing's sarcoma. <i>Oncogene</i> , 2008, 27, 2084-2090.	5.9	62
128	DAX1, a direct target of EWS/FLI1 oncoprotein, is a principal regulator of cell-cycle progression in Ewing's tumor cells. <i>Oncogene</i> , 2008, 27, 6034-6043.	5.9	100
129	DAX1 is a direct target of EWS/FLI1 oncoprotein and a principal regulator of cell cycle progression in Ewing tumor cells. <i>European Journal of Cancer, Supplement</i> , 2008, 6, 34.	2.2	0
130	CARGO: a web portal to integrate customized biological information. <i>Nucleic Acids Research</i> , 2007, 35, W16-W20.	14.5	16
131	Nestin, a neuroectodermal stem cell marker molecule, is expressed in Leydig cells of the human testis and in some specific cell types from human testicular tumours. <i>Cell and Tissue Research</i> , 2004, 316, 369-376.	2.9	81
132	Beds and Bits: The Challenge of Translational Bioinformatics. <i>Advances in Soft Computing</i> , 0, , 128-136.	0.4	0