

# Gonzalo GÃ³mez LÃ³pez

## List of Publications by Year in descending order

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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	Programmed Cell Senescence during Mammalian Embryonic Development. <i>Cell</i> , 2013, 155, 1104-1118.	28.9	1,081
2	Tissue damage and senescence provide critical signals for cellular reprogramming in vivo. <i>Science</i> , 2016, 354, .	12.6	466
3	Pten Positively Regulates Brown Adipose Function, Energy Expenditure, and Longevity. <i>Cell Metabolism</i> , 2012, 15, 382-394.	16.2	308
4	Mammalian Rap1 controls telomere function and gene expression through binding to telomeric and extratelomeric sites. <i>Nature Cell Biology</i> , 2010, 12, 768-780.	10.3	220
5	The dynamic DNA methylomes of double-stranded DNA viruses associated with human cancer. <i>Genome Research</i> , 2009, 19, 438-451.	5.5	218
6	PLCG1 mutations in cutaneous T-cell lymphomas. <i>Blood</i> , 2014, 123, 2034-2043.	1.4	193
7	Tumor MicroRNA Expression Profiling Identifies Circulating MicroRNAs for Early Breast Cancer Detection. <i>Clinical Chemistry</i> , 2015, 61, 1098-1106.	3.2	183
8	Research Resource: Transcriptional Profiling Reveals Different Pseudohypoxic Signatures in SDHB and VHL-Related Pheochromocytomas. <i>Molecular Endocrinology</i> , 2010, 24, 2382-2391.	3.7	179
9	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
10	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
11	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
12	A unique role of cohesin-SA1 in gene regulation and development. <i>EMBO Journal</i> , 2012, 31, 2090-2102.	7.8	134
13	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
14	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
15	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
16	Therapeutic Effect of $\hat{3}$ -Secretase Inhibition in KrasG12V-Driven Non-Small Cell Lung Carcinoma by Derepression of DUSP1 and Inhibition of ERK. <i>Cancer Cell</i> , 2012, 22, 222-234.	16.8	108
17	RAP1 Protects from Obesity through Its Extratelomeric Role Regulating Gene Expression. <i>Cell Reports</i> , 2013, 3, 2059-2074.	6.4	102
18	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

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19	miRNA expression in diffuse large B-cell lymphoma treated with chemoimmunotherapy. <i>Blood</i> , 2011, 118, 1034-1040.	1.4	90
20	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
21	miRGate: a curated database of human, mouse and rat miRNAâ€™mRNA targets. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav035.	3.0	87
22	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
23	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
24	Genetic inactivation of Cdk7 leads to cell cycle arrest and induces premature aging due to adult stem cell exhaustion. <i>EMBO Journal</i> , 2012, 31, 2498-2510.	7.8	85
25	A Braf kinase-inactive mutant induces lung adenocarcinoma. <i>Nature</i> , 2017, 548, 239-243.	27.8	85
26	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
27	MicroRNA signatures in B-cell lymphomas. <i>Blood Cancer Journal</i> , 2012, 2, e57-e57.	6.2	79
28	Targeting Tumor Mitochondrial Metabolism Overcomes Resistance to Antiangiogenics. <i>Cell Reports</i> , 2016, 15, 2705-2718.	6.4	78
29	Mantle cell lymphoma: transcriptional regulation by microRNAs. <i>Leukemia</i> , 2010, 24, 1335-1342.	7.2	72
30	The tumour suppressor and chromatinâ€™remodelling factor BRG1 antagonizes Myc activity and promotes cell differentiation in human cancer. <i>EMBO Molecular Medicine</i> , 2012, 4, 603-616.	6.9	70
31	SIRT1 promotes thyroid carcinogenesis driven by PTEN deficiency. <i>Oncogene</i> , 2013, 32, 4052-4056.	5.9	70
32	Genomic Profiling of Patient-Derived Xenografts for Lung Cancer Identifies <i>B2M</i> Inactivation Impairing Immunorecognition. <i>Clinical Cancer Research</i> , 2017, 23, 3203-3213.	7.0	66
33	Genomic Profiling of Patient-Derived Xenografts for Lung Cancer Identifies <i>B2M</i> Inactivation Impairing Immunorecognition. <i>Clinical Cancer Research</i> , 2017, 23, 3203-3213.	7.0	66
34	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
35	Src kinases catalytic activity regulates proliferation, migration and invasiveness of MDA-MB-231 breast cancer cells. <i>Cellular Signalling</i> , 2012, 24, 1276-1286.	3.6	63
36	PanDrugs: a novel method to prioritize anticancer drug treatments according to individual genomic data. <i>Genome Medicine</i> , 2018, 10, 41.	8.2	63

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37	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
38	Midkine rewires the melanoma microenvironment toward a tolerogenic and immune-resistant state. <i>Nature Medicine</i> , 2020, 26, 1865-1877.	30.7	62
39	Functional characterization of E- and P-cadherin in invasive breast cancer cells. <i>BMC Cancer</i> , 2009, 9, 74.	2.6	61
40	Combinatorial effects of microRNAs to suppress the Myc oncogenic pathway. <i>Blood</i> , 2011, 117, 6255-6266.	1.4	60
41	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
42	Whole genome analysis of p38 SAPK-mediated gene expression upon stress. <i>BMC Genomics</i> , 2010, 11, 144.	2.8	55
43	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
44	New Insights into FoxE1 Functions: Identification of Direct FoxE1 Targets in Thyroid Cells. <i>PLoS ONE</i> , 2013, 8, e62849.	2.5	55
45	Epigenetic regulation of <i>Nanog</i> expression by Ezh2 in pluripotent stem cells. <i>Cell Cycle</i> , 2011, 10, 1488-1498.	2.6	52
46	ARID1A Alterations Are Associated with FGFR3-Wild Type, Poor-Prognosis, Urothelial Bladder Tumors. <i>PLoS ONE</i> , 2013, 8, e62483.	2.5	52
47	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
48	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
49	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
50	Telomere shortening relaxes X chromosome inactivation and forces global transcriptome alterations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 19393-19398.	7.1	46
51	TCL1A expression delineates biological and clinical variability in B-cell lymphoma. <i>Modern Pathology</i> , 2009, 22, 206-215.	5.5	46
52	Pax8 controls thyroid follicular polarity through Cadherin-16. <i>Journal of Cell Science</i> , 2017, 130, 219-231.	2.0	46
53	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
54	Lineage-restricted function of the pluripotency factor NANOG in stratified epithelia. <i>Nature Communications</i> , 2014, 5, 4226.	12.8	45

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55	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
56	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
57	Precision medicine needs pioneering clinical bioinformaticians. <i>Briefings in Bioinformatics</i> , 2019, 20, 752-766.	6.5	40
58	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
59	Genome-wide analysis of Pax8 binding provides new insights into thyroid functions. <i>BMC Genomics</i> , 2012, 13, 147.	2.8	38
60	New Mutations in Chronic Lymphocytic Leukemia Identified by Target Enrichment and Deep Sequencing. <i>PLoS ONE</i> , 2012, 7, e38158.	2.5	38
61	ARF triggers senescence in Brca2-deficient cells by altering the spectrum of p53 transcriptional targets. <i>Nature Communications</i> , 2013, 4, 2697.	12.8	37
62	RUBioSeq: a suite of parallelized pipelines to automate exome variation and bisulfite-seq analyses. <i>Bioinformatics</i> , 2013, 29, 1687-1689.	4.1	37
63	Cdc14b regulates mammalian RNA polymerase II and represses cell cycle transcription. <i>Scientific Reports</i> , 2011, 1, 189.	3.3	35
64	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
65	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
66	Integration of BRCA1-mediated miRNA and mRNA profiles reveals microRNA regulation of TRAF2 and NF- $\kappa$ B pathway. <i>Breast Cancer Research and Treatment</i> , 2012, 134, 41-51.	2.5	34
67	ASXL1, TP53 and IKZF3 mutations are present in the chronic phase and blast crisis of chronic myeloid leukemia. <i>Blood Cancer Journal</i> , 2013, 3, e157-e157.	6.2	32
68	The pluripotency factor NANOG promotes the formation of squamous cell carcinomas. <i>Scientific Reports</i> , 2015, 5, 10205.	3.3	32
69	Downregulation of specific miRNAs in hyperdiploid multiple myeloma mimics the oncogenic effect of IgH translocations occurring in the non-hyperdiploid subtype. <i>Leukemia</i> , 2013, 27, 925-931.	7.2	31
70	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
71	WhichGenes: a web-based tool for gathering, building, storing and exporting gene sets with application in gene set enrichment analysis. <i>Nucleic Acids Research</i> , 2009, 37, W329-W334.	14.5	30
72	Chromatin modifications induced by the AML1-ETO fusion protein reversibly silence its genomic targets through AML1 and Sp1 binding motifs. <i>Leukemia</i> , 2012, 26, 1329-1337.	7.2	30

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73	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
74	The molecular pathogenesis of the NUP98-HOXA9 fusion protein in acute myeloid leukemia. <i>Leukemia</i> , 2017, 31, 2000-2005.	7.2	28
75	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
76	Molecular signature of response and potential pathways related to resistance to the HSP90 inhibitor, 17AAG, in breast cancer. <i>BMC Medical Genomics</i> , 2010, 3, 44.	1.5	25
77	Beyondcell: targeting cancer therapeutic heterogeneity in single-cell RNA-seq data. <i>Genome Medicine</i> , 2021, 13, 187.	8.2	25
78	MEK inhibition enhances the response to tyrosine kinase inhibitors in acute myeloid leukemia. <i>Scientific Reports</i> , 2019, 9, 18630.	3.3	24
79	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
80	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
81	Translational disease interpretation with molecular networks. <i>Genome Biology</i> , 2009, 10, 221.	9.6	22
82	The specific contributions of cohesin-SA1 to cohesion and gene expression. <i>Cell Cycle</i> , 2012, 11, 2233-2238.	2.6	22
83	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
84	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
85	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
86	KRAS-driven lung adenocarcinoma: combined DDR1/Notch inhibition as an effective therapy. <i>ESMO Open</i> , 2016, 1, e000076.	4.5	19
87	TGFâ€²â€²-induced IGFBPâ€³ 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
88	Prediction of miRNAâ€²mRNA Interactions Using miRGate. <i>Methods in Molecular Biology</i> , 2017, 1580, 225-237.	0.9	17
89	CARGO: a web portal to integrate customized biological information. <i>Nucleic Acids Research</i> , 2007, 35, W16-W20.	14.5	16
90	INK4a/ARF limits the expansion of cells suffering from replication stress. <i>Cell Cycle</i> , 2013, 12, 1948-1954.	2.6	16

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91	Bioinformatics and cancer research: building bridges for translational research. <i>Clinical and Translational Oncology</i> , 2008, 10, 85-95.	2.4	15
92	CSF3R T618I co-occurs with mutations of splicing and epigenetic genes and with a new PIM3 truncated fusion gene in chronic neutrophilic leukemia. <i>Blood Cancer Journal</i> , 2013, 3, e158-e158.	6.2	15
93	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
94	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
95	miRNA expression profiling of formalin-fixed paraffin-embedded (FFPE) hereditary breast tumors. <i>Genomics Data</i> , 2015, 3, 75-79.	1.3	12
96	p21Cip1 plays a critical role in the physiological adaptation to fasting through activation of PPAR $\alpha$ . <i>Scientific Reports</i> , 2016, 6, 34542.	3.3	12
97	A comprehensive database for integrated analysis of omics data in autoimmune diseases. <i>BMC Bioinformatics</i> , 2021, 22, 343.	2.6	12
98	Transcriptional characteristics of familial non- $\epsilon$ -BRCA1/BRCA2 breast tumors. <i>International Journal of Cancer</i> , 2011, 128, 2635-2644.	5.1	11
99	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
100	TWEAK increases CD74 expression and sensitizes to DDT proinflammatory actions in tubular cells. <i>PLoS ONE</i> , 2018, 13, e0199391.	2.5	11
101	Functional signatures identified in B-cell non-Hodgkin lymphoma profiles. <i>Leukemia and Lymphoma</i> , 2009, 50, 1699-1708.	1.3	10
102	PileLine: a toolbox to handle genome position information in next-generation sequencing studies. <i>BMC Bioinformatics</i> , 2011, 12, 31.	2.6	10
103	Pancreas Cancer Precision Treatment Using Avatar Mice from a Bioinformatics Perspective. <i>Public Health Genomics</i> , 2017, 20, 81-91.	1.0	10
104	vulcanSpot: a tool to prioritize therapeutic vulnerabilities in cancer. <i>Bioinformatics</i> , 2019, 35, 4846-4848.	4.1	10
105	DREIMT: a drug repositioning database and prioritization tool for immunomodulation. <i>Bioinformatics</i> , 2021, 37, 578-579.	4.1	9
106	PileLineGUI: a desktop environment for handling genome position files in next-generation sequencing studies. <i>Nucleic Acids Research</i> , 2011, 39, W562-W566.	14.5	6
107	In Silico Drug Prescription for Targeting Cancer Patient Heterogeneity and Prediction of Clinical Outcome. <i>Cancers</i> , 2019, 11, 1361.	3.7	6
108	bollito: a flexible pipeline for comprehensive single-cell RNA-seq analyses. <i>Bioinformatics</i> , 2022, 38, 1155-1156.	4.1	6

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109	An in silico analysis identifies drugs potentially modulating the cytokine storm triggered by SARS-CoV-2 infection. Scientific Reports, 2022, 12, 1626.	3.3	4
110	PathJam: a new service for integrating biological pathway information. Journal of Integrative Bioinformatics, 2010, 7, .	1.5	4
111	PathJam: a new service for integrating biological pathway information. Journal of Integrative Bioinformatics, 2010, 7, .	1.5	3
112	Profiling of Sox4-dependent transcriptome in skin links tumour suppression and adult stem cell activation. Genomics Data, 2015, 6, 21-24.	1.3	3
113	How can bioinformatics contribute to the routine application of personalized precision medicine?. Expert Review of Precision Medicine and Drug Development, 2020, 5, 115-117.	0.7	3
114	Spleen plays a major role in DLL4-driven acute T-cell lymphoblastic leukemia. Theranostics, 2021, 11, 1594-1608.	10.0	3
115	Expression and functional validation of new p38 $\hat{\pm}$ transcriptional targets in tumorigenesis. Biochemical Journal, 2011, 434, 549-558.	3.7	2
116	HDAC Inhibitors As Novel Targeted Therapies for NUP98-HOXA9 AML Patients. Blood, 2016, 128, 2685-2685.	1.4	2
117	Proteomic Profiling of Ewing Sarcoma Reveals a Role for TRAF6 in Proliferation and Ribonucleoproteins/RNA Processing. Journal of Proteomics and Bioinformatics, 2016, 09, .	0.4	1
118	Abstract 51: Activating PLCG1 mutations in cutaneous T-cell lymphomas.. , 2013, , .		1
119	Endothelial Cell RNA-Seq Data: Differential Expression and Functional Enrichment Analyses to Study Phenotypic Switching. Methods in Molecular Biology, 2022, 2441, 369-426.	0.9	1
120	DAX1 is a direct target of EWS/FLI1 oncoprotein and a principal regulator of cell cycle progression in Ewing tumor cells. European Journal of Cancer, Supplement, 2008, 6, 34.	2.2	0
121	37 Integration analysis between differentially expressed mRNA and miRNA induced by BRCA1 gene. European Journal of Cancer, Supplement, 2010, 8, 10.	2.2	0
122	RAP1 Protects from Obesity through Its Extratelomeric Role Regulating Gene Expression. Cell Reports, 2013, 4, 229.	6.4	0
123	RUBioSeq+: An Application that Executes Parallelized Pipelines to Analyse Next-Generation Sequencing Data. Advances in Intelligent Systems and Computing, 2016, , 141-149.	0.6	0
124	Current Efforts to Integrate Biological Pathway Information. Lecture Notes in Computer Science, 2009, , 1092-1096.	1.3	0
125	PathAgent: Multi-agent System for Updated Pathway Information Integration. Advances in Intelligent and Soft Computing, 2010, , 77-85.	0.2	0
126	Abstract 1190: Integration of mRNA and miRNA signatures induced by BRCA1 gene. , 2011, , .		0

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127	Applying AlBench Framework to Develop Rich User Interfaces in NGS Studies. Advances in Intelligent and Soft Computing, 2012, , 189-196.	0.2	0
128	Mutations in PLCC1 Is a Frequent Event in Cutaneous T-Cell Lymphomas. Blood, 2012, 120, 300-300.	1.4	0
129	Abstract B9: A phosphoproteomic portrait of triple - negative breast cancer: functional taxonomy. , 2015, , .		0
130	Abstract 1221: Triple-negative breast cancer (TNBC) phosphoproteomics. , 2017, , .		0
131	Abstract PD2-09: High-throughput phosphoproteomics (HTPS) in neoadjuvant (NEO) breast cancer (BC) reveals clusters of extreme sensitivity to paclitaxel (T). , 2019, , .		0
132	Beds and Bits: The Challenge of Translational Bioinformatics. Advances in Soft Computing, 0, , 128-136.	0.4	0