

Ivan G Costa

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

106
papers

3,307
citations

32
h-index

55
g-index

128
ext. papers

4,819
ext. citations

9.1
avg, IF

5.42
L-index

#	Paper	IF	Citations
106	Clustering cancer gene expression data: a comparative study. <i>BMC Bioinformatics</i> , 2008 , 9, 497	3.6	248
105	Therapeutic inhibition of inflammatory monocyte recruitment reduces steatohepatitis and liver fibrosis. <i>Hepatology</i> , 2018 , 67, 1270-1283	11.2	225
104	SARS-CoV-2 infects and replicates in cells of the human endocrine and exocrine pancreas. <i>Nature Metabolism</i> , 2021 , 3, 149-165	14.6	176
103	Identification of transcription factor binding sites using ATAC-seq. <i>Genome Biology</i> , 2019 , 20, 45	18.3	139
102	Human pluripotent stem cell-derived acinar/ductal organoids generate human pancreas upon orthotopic transplantation and allow disease modelling. <i>Gut</i> , 2017 , 66, 473-486	19.2	120
101	A multiple kernel learning algorithm for drug-target interaction prediction. <i>BMC Bioinformatics</i> , 2016 , 17, 46	3.6	111
100	DNA methylation levels at individual age-associated CpG sites can be indicative for life expectancy. <i>Aging</i> , 2016 , 8, 394-401	5.6	99
99	Surface Topography Guides Morphology and Spatial Patterning of Induced Pluripotent Stem Cell Colonies. <i>Stem Cell Reports</i> , 2017 , 9, 654-666	8	95
98	The lncRNA HOTAIR impacts on mesenchymal stem cells via triple helix formation. <i>Nucleic Acids Research</i> , 2016 , 44, 10631-10643	20.1	94
97	HMGB2 Loss upon Senescence Entry Disrupts Genomic Organization and Induces CTCF Clustering across Cell Types. <i>Molecular Cell</i> , 2018 , 70, 730-744.e6	17.6	83
96	Analysis of computational footprinting methods for DNase sequencing experiments. <i>Nature Methods</i> , 2016 , 13, 303-9	21.6	82
95	CLEVER: clique-enumerating variant finder. <i>Bioinformatics</i> , 2012 , 28, 2875-82	7.2	79
94	Myeloid cells in liver and bone marrow acquire a functionally distinct inflammatory phenotype during obesity-related steatohepatitis. <i>Gut</i> , 2020 , 69, 551-563	19.2	71
93	Detection of RNA-DNA binding sites in long noncoding RNAs. <i>Nucleic Acids Research</i> , 2019 , 47, e32	20.1	70
92	On the selection of appropriate distances for gene expression data clustering. <i>BMC Bioinformatics</i> , 2014 , 15 Suppl 2, S2	3.6	68
91	Epigenetic age predictions based on buccal swabs are more precise in combination with cell type-specific DNA methylation signatures. <i>Aging</i> , 2016 , 8, 1034-48	5.6	68
90	Analyzing gene expression time-courses. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2005 , 2, 179-93	3	58

89	Detection of active transcription factor binding sites with the combination of DNase hypersensitivity and histone modifications. <i>Bioinformatics</i> , 2014 , 30, 3143-51	7.2	56
88	Detection of Hot-Spot Mutations in Circulating Cell-Free DNA From Patients With Intraductal Papillary Mucinous Neoplasms of the Pancreas. <i>Gastroenterology</i> , 2016 , 151, 267-70	13.3	53
87	Impact of missing data imputation methods on gene expression clustering and classification. <i>BMC Bioinformatics</i> , 2015 , 16, 64	3.6	47
86	Differential peak calling of ChIP-seq signals with replicates with THOR. <i>Nucleic Acids Research</i> , 2016 , 44, e153	20.1	46
85	Discovering motifs that induce sequencing errors. <i>BMC Bioinformatics</i> , 2013 , 14 Suppl 5, S1	3.6	44
84	Replicative senescence is associated with nuclear reorganization and with DNA methylation at specific transcription factor binding sites. <i>Clinical Epigenetics</i> , 2015 , 7, 19	7.7	42
83	Deep learning-based clustering approaches for bioinformatics. <i>Briefings in Bioinformatics</i> , 2021 , 22, 393-414	13.4	42
82	Cyclin E1 and cyclin-dependent kinase 2 are critical for initiation, but not for progression of hepatocellular carcinoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 9282-9287	11.5	41
81	Comparative analysis of clustering methods for gene expression time course data. <i>Genetics and Molecular Biology</i> , 2004 , 27, 623-631	2	41
80	Epigenetic Classification of Human Mesenchymal Stromal Cells. <i>Stem Cell Reports</i> , 2016 , 6, 168-75	8	40
79	Isolation and genome-wide characterization of cellular DNA:RNA triplex structures. <i>Nucleic Acids Research</i> , 2019 , 47, 2306-2321	20.1	40
78	Analysis of complexity indices for classification problems: Cancer gene expression data. <i>Neurocomputing</i> , 2012 , 75, 33-42	5.4	37
77	Epigenetic program and transcription factor circuitry of dendritic cell development. <i>Nucleic Acids Research</i> , 2015 , 43, 9680-93	20.1	34
76	Ranking and selecting clustering algorithms using a meta-learning approach 2008 ,		33
75	The interaction of MYC with the trithorax protein ASH2L promotes gene transcription by regulating H3K27 modification. <i>Nucleic Acids Research</i> , 2014 , 42, 6901-20	20.1	32
74	JAK2V617F but not CALR mutations confer increased molecular responses to interferon- γ via JAK1/STAT1 activation. <i>Leukemia</i> , 2019 , 33, 995-1010	10.7	29
73	Heterogeneous bone-marrow stromal progenitors drive myelofibrosis via a druggable alarmin axis. <i>Cell Stem Cell</i> , 2021 , 28, 637-652.e8	18	29
72	Impaired cellular energy metabolism in cord blood macrophages contributes to abortive response toward inflammatory threats. <i>Nature Communications</i> , 2019 , 10, 1685	17.4	28

71	Aging-regulated anti-apoptotic long non-coding RNA Sarrah augments recovery from acute myocardial infarction. <i>Nature Communications</i> , 2020 , 11, 2039	17.4	28
70	Nrf2 Is a Central Regulator of Metabolic Reprogramming of Myeloid-Derived Suppressor Cells in Steady State and Sepsis. <i>Frontiers in Immunology</i> , 2018 , 9, 1552	8.4	28
69	Binding of nuclear factor B to noncanonical consensus sites reveals its multimodal role during the early inflammatory response. <i>Genome Research</i> , 2016 , 26, 1478-1489	9.7	27
68	yyIncT Defines a Class of Divergently Transcribed lncRNAs and Safeguards the T-mediated Mesodermal Commitment of Human PSCs. <i>Cell Stem Cell</i> , 2019 , 24, 318-327.e8	18	27
67	Proximity measures for clustering gene expression microarray data: a validation methodology and a comparative analysis. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013 , 10, 845-857	3.7	26
66	Predicting gene expression in T cell differentiation from histone modifications and transcription factor binding affinities by linear mixture models. <i>BMC Bioinformatics</i> , 2011 , 12 Suppl 1, S29	3.6	26
65	Detecting differential peaks in CHIP-seq signals with ODIN. <i>Bioinformatics</i> , 2014 , 30, 3467-75	7.2	24
64	Constrained mixture estimation for analysis and robust classification of clinical time series. <i>Bioinformatics</i> , 2009 , 25, i6-14	7.2	24
63	Detection and interpretation of metabolite-transcript coresponses using combined profiling data. <i>Bioinformatics</i> , 2011 , 27, i357-65	7.2	24
62	SARS-CoV-2 infects the human kidney and drives fibrosis in kidney organoids.. <i>Cell Stem Cell</i> , 2021 ,	18	24
61	Hypoxia-inducible factor 1 (HIF-1) is a new therapeutic target in JAK2V617F-positive myeloproliferative neoplasms. <i>Leukemia</i> , 2020 , 34, 1062-1074	10.7	23
60	Data complexity meta-features for regression problems. <i>Machine Learning</i> , 2018 , 107, 209-246	4	21
59	The Graphical Query Language: a tool for analysis of gene expression time-courses. <i>Bioinformatics</i> , 2005 , 21, 2544-5	7.2	21
58	Comparative study on normalization procedures for cluster analysis of gene expression datasets 2008 ,		20
57	Tbx3 fosters pancreatic cancer growth by increased angiogenesis and activin/nodal-dependent induction of stemness. <i>Stem Cell Research</i> , 2016 , 17, 367-378	1.6	19
56	Unique and assay specific features of NOME-, ATAC- and DNase I-seq data. <i>Nucleic Acids Research</i> , 2019 , 47, 10580-10596	20.1	17
55	Stem cell persistence in CML is mediated by extrinsically activated JAK1-STAT3 signaling. <i>Leukemia</i> , 2019 , 33, 1964-1977	10.7	17
54	DNA Methylation-Mediated Modulation of Endocytosis as Potential Mechanism for Synaptic Function Regulation in Murine Inhibitory Cortical Interneurons. <i>Cerebral Cortex</i> , 2020 , 30, 3921-3937	5.1	16

53	Post-weaning epiphyseolysis causes distal femur dysplasia and foreshortened hindlimbs in fetuin-A-deficient mice. <i>PLoS ONE</i> , 2017 , 12, e0187030	3.7	14
52	Inferring differentiation pathways from gene expression. <i>Bioinformatics</i> , 2008 , 24, i156-64	7.2	14
51	Semi-supervised learning for the identification of syn-expressed genes from fused microarray and in situ image data. <i>BMC Bioinformatics</i> , 2007 , 8 Suppl 10, S3	3.6	14
50	Differential roles of STAT1 and STAT2 in the sensitivity of JAK2V617F- vs. BCR-ABL-positive cells to interferon alpha. <i>Journal of Hematology and Oncology</i> , 2019 , 12, 36	22.4	13
49	Thrombin stimulates insulin secretion via protease-activated receptor-3. <i>Islets</i> , 2015 , 7, e1118195	2	13
48	Prognostically Relevant Subtypes and Survival Prediction for Breast Cancer Based on Multimodal Genomics Data. <i>IEEE Access</i> , 2019 , 7, 133850-133864	3.5	12
47	A Comparison of External Clustering Evaluation Indices in the Context of Imbalanced Data Sets 2012 ,		12
46	Spatial multi-omic map of human myocardial infarction		12
45	Variants of cause transcript-specific DNA methylation patterns and affect hematopoiesis. <i>Life Science Alliance</i> , 2018 , 1, e201800153	5.8	11
44	Classifying short gene expression time-courses with Bayesian estimation of piecewise constant functions. <i>Bioinformatics</i> , 2011 , 27, 946-52	7.2	10
43	Mining Rules for the Automatic Selection Process of Clustering Methods Applied to Cancer Gene Expression Data. <i>Lecture Notes in Computer Science</i> , 2009 , 20-29	0.9	10
42	Clustering of RNA-Seq samples: Comparison study on cancer data. <i>Methods</i> , 2018 , 132, 42-49	4.6	10
41	Complexity measures of supervised classifications tasks: A case study for cancer gene expression data 2010 ,		9
40	Transcription factor motif enrichment in whole transcriptome analysis identifies STAT4 and BCL6 as the most prominent binding motif in systemic juvenile idiopathic arthritis. <i>Arthritis Research and Therapy</i> , 2018 , 20, 98	5.7	8
39	Inferring epigenetic and transcriptional regulation during blood cell development with a mixture of sparse linear models. <i>Bioinformatics</i> , 2012 , 28, 2297-303	7.2	8
38	Endothelium-derived stromal cells contribute to hematopoietic bone marrow niche formation. <i>Cell Stem Cell</i> , 2021 , 28, 653-670.e11	18	8
37	Comparison of Resources and Methods to infer Cell-Cell Communication from Single-cell RNA Data		8
36	A Drug-Target Network-Based Supervised Machine Learning Repurposing Method Allowing the Use of Multiple Heterogeneous Information Sources. <i>Methods in Molecular Biology</i> , 2019 , 1903, 281-289	1.4	8

35	A time frame permissive for Protein Kinase D2 activity to direct angiogenesis in mouse embryonic stem cells. <i>Scientific Reports</i> , 2015 , 5, 11742	4.9	7
34	CXCR6 protects from inflammation and fibrosis in NEMO mice. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2019 , 1865, 391-402	6.9	7
33	Hematopoietic stem and progenitor cell proliferation and differentiation requires the trithorax protein Ash2l. <i>Scientific Reports</i> , 2019 , 9, 8262	4.9	6
32	On the Complexity of Gene Expression Classification Data Sets 2008 ,		6
31	Gene expression trees in lymphoid development. <i>BMC Immunology</i> , 2007 , 8, 25	3.7	6
30	Mutations and variants of ONECUT1 in diabetes. <i>Nature Medicine</i> , 2021 , 27, 1928-1940	50.5	6
29	Deconvolution of cellular subsets in human tissue based on targeted DNA methylation analysis at individual CpG sites. <i>BMC Biology</i> , 2020 , 18, 178	7.3	6
28	Chromatin-accessibility estimation from single-cell ATAC data with scOpen		5
27	Infliximab therapy together with tyrosine kinase inhibition targets leukemic stem cells in chronic myeloid leukemia. <i>BMC Cancer</i> , 2019 , 19, 658	4.8	4
26	CrossTalker: Analysis and Visualisation of Ligand Receptor Networks. <i>Bioinformatics</i> , 2021 ,	7.2	4
25	Evaluating Correlation Coefficients for Clustering Gene Expression Profiles of Cancer. <i>Lecture Notes in Computer Science</i> , 2012 , 120-131	0.9	3
24	Using Supervised Complexity Measures in the Analysis of Cancer Gene Expression Data Sets. <i>Lecture Notes in Computer Science</i> , 2009 , 48-59	0.9	3
23	Triplex Domain Finder: Detection of Triple Helix Binding Domains in Long Non-Coding RNAs		3
22	Identification of Transcription Factor Binding Sites using ATAC-seq		3
21	Therapeutic inhibition of FcγRIIb signaling targets leukemic stem cells in chronic myeloid leukemia. <i>Leukemia</i> , 2020 , 34, 2635-2647	10.7	3
20	Dissecting CD8+ T cell pathology of severe SARS-CoV-2 infection by single-cell epitope mapping		3
19	Measuring the complexity of regression problems 2016 ,		2
18	pGQL: A probabilistic graphical query language for gene expression time courses. <i>BioData Mining</i> , 2011 , 4, 9	4.3	2

17	On the Complexity of Gene Marker Selection 2010 ,		2
16	Transcriptional changes and the role of ONECUT1 in hPSC pancreatic differentiation. <i>Communications Biology</i> , 2021 , 4, 1298	6.7	2
15	CrossTalker: Analysis and Visualisation of Ligand Receptor Networks		2
14	The spatial self-organization within pluripotent stem cell colonies is continued in detaching aggregates.. <i>Biomaterials</i> , 2022 , 282, 121389	15.6	1
13	CALR frameshift mutations in MPN patient-derived iPSCs accelerate maturation of megakaryocytes. <i>Stem Cell Reports</i> , 2021 , 16, 2768-2783	8	1
12	Chromatin-accessibility estimation from single-cell ATAC-seq data with scOpen. <i>Nature Communications</i> , 2021 , 12, 6386	17.4	1
11	Prediction of Transcription Factor Binding Sites by Integrating DNase Digestion and Histone Modification. <i>Lecture Notes in Computer Science</i> , 2012 , 109-119	0.9	1
10	The Expression of the Cancer-Associated lncRNA Is Modulated by EphrinA5-Induced Signaling. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	1
9	Early and late stage MPN patients show distinct gene expression profiles in CD34 cells. <i>Annals of Hematology</i> , 2021 , 100, 2943-2956	3	1
8	Cognate recognition of microbial antigens defines constricted CD4 T _H cell receptor repertoires in the inflamed colon. <i>Immunity</i> , 2021 , 54, 2565-2577.e6	32.3	1
7	Transcriptional Landscape of the Microenvironment in Bone Marrow Fibrosis at Single Cell Level. <i>Blood</i> , 2019 , 134, 1675-1675	2.2	0
6	Semi-supervised Approach for Finding Cancer Sub-classes on Gene Expression Data. <i>Lecture Notes in Computer Science</i> , 2010 , 25-34	0.9	0
5	Random Forest and Gene Networks for Association of SNPs to Alzheimer's Disease. <i>Lecture Notes in Computer Science</i> , 2013 , 104-115	0.9	
4	On External Indices for Mixtures: Validating Mixtures of Genes 2006 , 662-669		
3	Validating Gene Clusterings by Selecting Informative Gene Ontology Terms with Mutual Information. <i>Lecture Notes in Computer Science</i> , 2007 , 81-92	0.9	
2	Deconstructing the Clonal Advantage and Clonal Stability of 5q- Candidate Genes in Del(5q) MDS on a Single Cell Level. <i>Blood</i> , 2019 , 134, 559-559	2.2	
1	From cell to cell: Identification of actionable targets in bone marrow fibrosis using single-cell technologies. <i>Experimental Hematology</i> , 2021 , 104, 48-54	3.1	