Ivan G Costa

List of Publications by Year
in descending order

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111 papers	6,011 citations	81743 39 h-index	91712 69 g-index
128 all docs	128 docs citations	128 times ranked	10015 citing authors

#	Article	IF	Citations
1	Genetic barcoding systematically compares genes in del(5q) MDS and reveals a central role for CSNK1A1 in clonal expansion. Blood Advances, 2022, 6, 1780-1796.	2.5	7
2	The spatial self-organization within pluripotent stem cell colonies is continued in detaching aggregates. Biomaterials, 2022, 282, 121389.	5.7	15
3	SARS-CoV-2 infects the human kidney and drives fibrosis in kidney organoids. Cell Stem Cell, 2022, 29, 217-231.e8.	5.2	146
4	MOJITOO: a fast and universal method for integration of multimodal single-cell data. Bioinformatics, 2022, 38, i282-i289.	1.8	6
5	Human pluripotent stem cell-derived kidney organoids for personalized congenital and idiopathic nephrotic syndrome modeling. Development (Cambridge), 2022, 149, .	1.2	16
6	The area under the ROC curve as a measure of clustering quality. Data Mining and Knowledge Discovery, 2022, 36, 1219-1245.	2.4	14
7	LINC00152 Drives a Competing Endogenous RNA Network in Human Hepatocellular Carcinoma. Cells, 2022, 11, 1528.	1.8	6
8	Mapping the cardiac vascular niche in heart failure. Nature Communications, 2022, 13, .	5.8	31
9	Comparison of methods and resources for cell-cell communication inference from single-cell RNA-Seq data. Nature Communications, 2022, 13, .	5.8	143
10	Detection of cell markers from single cell RNA-seq with sc2marker. BMC Bioinformatics, 2022, 23, .	1.2	7
11	Induction of senescence upon loss of the Ash2l core subunit of H3K4 methyltransferase complexes. Nucleic Acids Research, 2022, 50, 7889-7905.	6.5	6
12	Heterogeneous bone-marrow stromal progenitors drive myelofibrosis via a druggable alarmin axis. Cell Stem Cell, 2021, 28, 637-652.e8.	5.2	92
13	The Expression of the Cancer-Associated lncRNA Snhg15 Is Modulated by EphrinA5-Induced Signaling. International Journal of Molecular Sciences, 2021, 22, 1332.	1.8	6
14	SARS-CoV-2 infects and replicates in cells of the human endocrine and exocrine pancreas. Nature Metabolism, 2021, 3, 149-165.	5.1	378
15	Endothelium-derived stromal cells contribute to hematopoietic bone marrow niche formation. Cell Stem Cell, 2021, 28, 653-670.e11.	5.2	31
16	CrossTalkeR: analysis and visualization of ligandâ€“receptorne tworks. Bioinformatics, 2021, 37, 4263-4265.	1.8	28
17	MO331LINEAGE TRACING OF REGENERATING PROXIMAL TUBULE CELLS (STC) BY SINGLE CELL PROFILING IN ACUTE KIDNEY INJURY. Nephrology Dialysis Transplantation, 2021, 36, .	0.4	0
18	Early and late stage MPN patients show distinct gene expression profiles in CD34+ cells. Annals of Hematology, 2021, 100, 2943-2956.	0.8	9

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19	Cognate recognition of microbial antigens defines constricted CD4+ TÂcell receptor repertoires in the inflamed colon. Immunity, 2021, 54, 2565-2577.e6.	6.6	8
20	From cell to cell - identification of actionable targets in bone marrow fibrosis using single cell technologies. Experimental Hematology, 2021, 104, 48-54.	0.2	1
21	Deep learning-based clustering approaches for bioinformatics. Briefings in Bioinformatics, 2021, 22, 393-415.	3.2	135
22	Mutations and variants of ONECUT1 in diabetes. Nature Medicine, 2021, 27, 1928-1940.	15.2	24
23	CALR frameshift mutations in MPN patient-derived iPSCs accelerate maturation of megakaryocytes. Stem Cell Reports, 2021, 16, 2768-2783.	2.3	8
24	Chromatin-accessibility estimation from single-cell ATAC-seq data with scOpen. Nature Communications, 2021, 12, 6386.	5.8	57
25	Cyclin E1 in Murine and Human Liver Cancer: A Promising Target for Therapeutic Intervention during Tumour Progression. Cancers, 2021, 13, 5680.	1.7	5
26	Transcriptional changes and the role of ONECUT1 in hPSC pancreatic differentiation. Communications Biology, 2021, 4, 1298.	2.0	16
27	Myeloid cells in liver and bone marrow acquire a functionally distinct inflammatory phenotype during obesity-related steatohepatitis. Gut, 2020, 69, 551-563.	6.1	142
28	Hypoxia-inducible factor 1 (HIF-1) is a new therapeutic target in JAK2V617F-positive myeloproliferative neoplasms. Leukemia, 2020, 34, 1062-1074.	3.3	42
29	Therapeutic inhibition of FcÎ³RIIb signaling targets leukemic stem cells in chronic myeloid leukemia. Leukemia, 2020, 34, 2635-2647.	3.3	8
30	Deconvolution of cellular subsets in human tissue based on targeted DNA methylation analysis at individual CpG sites. BMC Biology, 2020, 18, 178.	1.7	28
31	DNA Methylation-Mediated Modulation of Endocytosis as Potential Mechanism for Synaptic Function Regulation in Murine Inhibitory Cortical Interneurons. Cerebral Cortex, 2020, 30, 3921-3937.	1.6	42
32	Aging-regulated anti-apoptotic long non-coding RNA Sarrah augments recovery from acute myocardial infarction. Nature Communications, 2020, 11, 2039.	5.8	63
33	Infliximab therapy together with tyrosine kinase inhibition targets leukemic stem cells in chronic myeloid leukemia. BMC Cancer, 2019, 19, 658.	1.1	12
34	Unique and assay specific features of NOMe-, ATAC- and DNase I-seq data. Nucleic Acids Research, 2019, 47, 10580-10596.	6.5	31
35	Prognostically Relevant Subtypes and Survival Prediction for Breast Cancer Based on Multimodal Genomics Data. IEEE Access, 2019, 7, 133850-133864.	2.6	18
36	Detection of RNAâ€“DNA binding sites in long noncoding RNAs. Nucleic Acids Research, 2019, 47, e32-e32.	6.5	128

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37	Hematopoietic stem and progenitor cell proliferation and differentiation requires the trithorax protein Ash2l. Scientific Reports, 2019, 9, 8262.	1.6	24
38	Stem cell persistence in CML is mediated by extrinsically activated JAK1-STAT3 signaling. Leukemia, 2019, 33, 1964-1977.	3.3	35
39	Identification of transcription factor binding sites using ATAC-seq. Genome Biology, 2019, 20, 45.	3.8	346
40	Impaired cellular energy metabolism in cord blood macrophages contributes to abortive response toward inflammatory threats. Nature Communications, 2019, 10, 1685.	5.8	41
41	Differential roles of STAT1 and STAT2 in the sensitivity of JAK2V617F- vs. BCR-ABL-positive cells to interferon alpha. Journal of Hematology and Oncology, 2019, 12, 36.	6.9	19
42	Isolation and genome-wide characterization of cellular DNA:RNA triplex structures. Nucleic Acids Research, 2019, 47, 2306-2321.	6.5	78
43	A Drug-Target Network-Based Supervised Machine Learning Repurposing Method Allowing the Use of Multiple Heterogeneous Information Sources. Methods in Molecular Biology, 2019, 1903, 281-289.	0.4	15
44	CXCR6 protects from inflammation and fibrosis in NEMOLPC-KO mice. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2019, 1865, 391-402.	1.8	14
45	JAK2V617F but not CALR mutations confer increased molecular responses to interferon-Î± via JAK1/STAT1 activation. Leukemia, 2019, 33, 995-1010.	3.3	43
46	yylncT Defines a Class of Divergently Transcribed lncRNAs and Safeguards the T-mediated Mesodermal Commitment of Human PSCs. Cell Stem Cell, 2019, 24, 318-327.e8.	5.2	44
47	Transcriptional Landscape of the Microenvironment in Bone Marrow Fibrosis at Single Cell Level. Blood, 2019, 134, 1675-1675.	0.6	2
48	Deconstructing the Clonal Advantage and Clonal Stability of 5q- Candidate Genes in Del(5q) MDS on a Single Cell Level. Blood, 2019, 134, 559-559.	0.6	0
49	Data complexity meta-features for regression problems. Machine Learning, 2018, 107, 209-246.	3.4	41
50	HMGB2 Loss upon Senescence Entry Disrupts Genomic Organization and Induces CTCF Clustering across Cell Types. Molecular Cell, 2018, 70, 730-744.e6.	4.5	164
51	Therapeutic inhibition of inflammatory monocyte recruitment reduces steatohepatitis and liver fibrosis. Hepatology, 2018, 67, 1270-1283.	3.6	388
52	Clustering of RNA-Seq samples: Comparison study on cancer data. Methods, 2018, 132, 42-49.	1.9	22
53	Transcription factor motif enrichment in whole transcriptome analysis identifies STAT4 and BCL6 as the most prominent binding motif in systemic juvenile idiopathic arthritis. Arthritis Research and Therapy, 2018, 20, 98.	1.6	12
54	Nrf2 Is a Central Regulator of Metabolic Reprogramming of Myeloid-Derived Suppressor Cells in Steady State and Sepsis. Frontiers in Immunology, 2018, 9, 1552.	2.2	44

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55	Cyclin E1 and cyclin-dependent kinase 2 are critical for initiation, but not for progression of hepatocellular carcinoma. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 9282-9287.	3.3	68
56	Variants ofDNMT3Acause transcript-specific DNA methylation patterns and affect hematopoiesis. Life Science Alliance, 2018, 1, e201800153.	1.3	16
57	Human pluripotent stem cell-derived acinar/ductal organoids generate human pancreas upon orthotopic transplantation and allow disease modelling. Gut, 2017, 66, 473-486.	6.1	174
58	Surface Topography Guides Morphology and Spatial Patterning of Induced Pluripotent Stem Cell Colonies. Stem Cell Reports, 2017, 9, 654-666.	2.3	120
59	Post-weaning epiphysiolysis causes distal femur dysplasia and foreshortened hindlimbs in fetuin-A-deficient mice. PLoS ONE, 2017, 12, e0187030.	1.1	20
60	A multiple kernel learning algorithm for drug-target interaction prediction. BMC Bioinformatics, 2016, 17, 46.	1.2	154
61	Tbx3 fosters pancreatic cancer growth by increased angiogenesis and activin/nodal-dependent induction of stemness. Stem Cell Research, 2016, 17, 367-378.	0.3	27
62	Measuring the complexity of regression problems. , 2016, , .		4
63	Binding of nuclear factor ÎºB to noncanonical consensus sites reveals its multimodal role during the early inflammatory response. Genome Research, 2016, 26, 1478-1489.	2.4	43
64	The lncRNA HOTAIR impacts on mesenchymal stem cellsviatriple helix formation. Nucleic Acids Research, 2016, 44, 10631-10643.	6.5	141
65	Differential peak calling of ChIP-seq signals with replicates with THOR. Nucleic Acids Research, 2016, 44, gkw680.	6.5	66
66	Detection of Hot-Spot Mutations in Circulating Cell-Free DNA From Patients With Intraductal Papillary Mucinous Neoplasms ofÂthe Pancreas. Gastroenterology, 2016, 151, 267-270.	0.6	76
67	Analysis of computational footprinting methods for DNase sequencing experiments. Nature Methods, 2016, 13, 303-309.	9.0	141
68	Epigenetic Classification of Human Mesenchymal Stromal Cells. Stem Cell Reports, 2016, 6, 168-175.	2.3	47
69	DNA methylation levels at individual age-associated CpG sites can be indicative for life expectancy. Aging, 2016, 8, 394-401.	1.4	150
70	Epigenetic age predictions based on buccal swabs are more precise in combination with cell type-specific DNA methylation signatures. Aging, 2016, 8, 1034-1048.	1.4	90
71	Thrombin stimulates insulin secretion via protease-activated receptor-3. Islets, 2015, 7, e1118195.	0.9	20
72	A time frame permissive for Protein Kinase D2 activity to direct angiogenesis in mouse embryonic stem cells. Scientific Reports, 2015, 5, 11742.	1.6	7

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73	Impact of missing data imputation methods on gene expression clustering and classification. BMC Bioinformatics, 2015, 16, 64.	1.2	70
74	Replicative senescence is associated with nuclear reorganization and with DNA methylation at specific transcription factor binding sites. Clinical Epigenetics, 2015, 7, 19.	1.8	51
75	Epigenetic program and transcription factor circuitry of dendritic cell development. Nucleic Acids Research, 2015, 43, gkv1056.	6.5	62
76	The interaction of MYC with the trithorax protein ASH2L promotes gene transcription by regulating H3K27 modification. Nucleic Acids Research, 2014, 42, 6901-6920.	6.5	47
77	On the selection of appropriate distances for gene expression data clustering. BMC Bioinformatics, 2014, 15, S2.	1.2	113
78	Detecting differential peaks in ChIP-seq signals with ODIN. Bioinformatics, 2014, 30, 3467-3475.	1.8	36
79	Detection of active transcription factor binding sites with the combination of DNase hypersensitivity and histone modifications. Bioinformatics, 2014, 30, 3143-3151.	1.8	109
80	Proximity Measures for Clustering Gene Expression Microarray Data: A Validation Methodology and a Comparative Analysis. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 845-857.	1.9	42
81	Discovering motifs that induce sequencing errors. BMC Bioinformatics, 2013, 14, S1.	1.2	47
82	Random Forest and Gene Networks for Association of SNPs to Alzheimerâ€™s Disease. Lecture Notes in Computer Science, 2013, , 104-115.	1.0	3
83	Evaluating Correlation Coefficients for Clustering Gene Expression Profiles of Cancer. Lecture Notes in Computer Science, 2012, , 120-131.	1.0	7
84	CLEVER: clique-enumerating variant finder. Bioinformatics, 2012, 28, 2875-2882.	1.8	101
85	Inferring epigenetic and transcriptional regulation during blood cell development with a mixture of sparse linear models. Bioinformatics, 2012, 28, 2297-2303.	1.8	13
86	Predicting Gene Functions Using Semi-supervised Clustering Algorithms with Objective Function Optimization. , 2012, , .		0
87	A Comparison of External Clustering Evaluation Indices in the Context of Imbalanced Data Sets. , 2012, , .		25
88	Analysis of complexity indices for classification problems: Cancer gene expression data. Neurocomputing, 2012, 75, 33-42.	3.5	48
89	Prediction of Transcription Factor Binding Sites by Integrating DNase Digestion and Histone Modification. Lecture Notes in Computer Science, 2012, , 109-119.	1.0	1
90	pGQL: A probabilistic graphical query language for gene expression time courses. BioData Mining, 2011, 4, 9.	2.2	2

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91	Predicting gene expression in T cell differentiation from histone modifications and transcription factor binding affinities by linear mixture models. BMC Bioinformatics, 2011, 12, S29.	1.2	30
92	Classifying short gene expression time-courses with Bayesian estimation of piecewise constant functions. Bioinformatics, 2011, 27, 946-952.	1.8	14
93	Detection and interpretation of metaboliteâ€“transcript coresponses using combined profiling data. Bioinformatics, 2011, 27, i357-i365.	1.8	38
94	Complexity measures of supervised classifications tasks: A case study for cancer gene expression data. , 2010, , .		11
95	On the Complexity of Gene Marker Selection. , 2010, , .		2
96	Semi-supervised Approach for Finding Cancer Sub-classes on Gene Expression Data. Lecture Notes in Computer Science, 2010, , 25-34.	1.0	1
97	Constrained mixture estimation for analysis and robust classification of clinical time series. Bioinformatics, 2009, 25, i6-i14.	1.8	30
98	Using Supervised Complexity Measures in the Analysis of Cancer Gene Expression Data Sets. Lecture Notes in Computer Science, 2009, , 48-59.	1.0	5
99	Mining Rules for the Automatic Selection Process of Clustering Methods Applied to Cancer Gene Expression Data. Lecture Notes in Computer Science, 2009, , 20-29.	1.0	15
100	Ranking and selecting clustering algorithms using a meta-learning approach. , 2008, , .		53
101	Clustering cancer gene expression data: a comparative study. BMC Bioinformatics, 2008, 9, 497.	1.2	334
102	Inferring differentiation pathways from gene expression. Bioinformatics, 2008, 24, i156-i164.	1.8	16
103	On the Complexity of Gene Expression Classification Data Sets. , 2008, , .		13
104	Comparative study on normalization procedures for cluster analysis of gene expression datasets. , 2008, , .		25
105	Semi-supervised learning for the identification of syn-expressed genes from fused microarray and in situ image data. BMC Bioinformatics, 2007, 8, S3.	1.2	15
106	Gene expression trees in lymphoid development. BMC Immunology, 2007, 8, 25.	0.9	6
107	Validating Gene Clusterings by Selecting Informative Gene Ontology Terms with Mutual Information. Lecture Notes in Computer Science, 2007, , 81-92.	1.0	0
108	On External Indices for Mixtures: Validating Mixtures of Genes. , 2006, , 662-669.		0

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109	The Graphical Query Language: a tool for analysis of gene expression time-courses. Bioinformatics, 2005, 21, 2544-2545.	1.8	23
110	Analyzing Gene Expression Time-Courses. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2005, 2, 179-193.	1.9	65
111	Comparative analysis of clustering methods for gene expression time course data. Genetics and Molecular Biology, 2004, 27, 623-631.	0.6	52