Ivan G Costa

List of Publications by Year in Descending Order

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	The spatial self-organization within pluripotent stem cell colonies is continued in detaching aggregates.. *Biomaterials*, **2022**, 282, 121389	15.6	1
105	SARS-CoV-2 infects the human kidney and drives fibrosis in kidney organoids.. *Cell Stem Cell*, **2021**,	18	24
104	CALR frameshift mutations in MPN patient-derived iPSCs accelerate maturation of megakaryocytes. *Stem Cell Reports*, **2021**, 16, 2768-2783	8	1
103	Chromatin-accessibility estimation from single-cell ATAC-seq data with scOpen. *Nature Communications*, **2021**, 12, 6386	17.4	1
102	Transcriptional changes and the role of ONECUT1 in hPSC pancreatic differentiation. *Communications Biology*, **2021**, 4, 1298	6.7	2
101	Mutations and variants of ONECUT1 in diabetes. *Nature Medicine*, **2021**, 27, 1928-1940	50.5	6
100	Deep learning-based clustering approaches for bioinformatics. *Briefings in Bioinformatics*, **2021**, 22, 393-415	13.4	42
99	Endothelium-derived stromal cells contribute to hematopoietic bone marrow niche formation. *Cell Stem Cell*, **2021**, 28, 653-670.e11	18	8
98	CrossTalkeR: Analysis and Visualisation of Ligand Receptor Networks. *Bioinformatics*, **2021**,	7.2	4
97	Heterogeneous bone-marrow stromal progenitors drive myelofibrosis via a druggable alarmin axis. *Cell Stem Cell*, **2021**, 28, 637-652.e8	18	29
96	The Expression of the Cancer-Associated lncRNA Is Modulated by EphrinA5-Induced Signaling. *International Journal of Molecular Sciences*, **2021**, 22,	6.3	1
95	SARS-CoV-2 infects and replicates in cells of the human endocrine and exocrine pancreas. *Nature Metabolism*, **2021**, 3, 149-165	14.6	176
94	Early and late stage MPN patients show distinct gene expression profiles in CD34 cells. *Annals of Hematology*, **2021**, 100, 2943-2956	3	1
93	Cognate recognition of microbial antigens defines constricted CD4 T cell receptor repertoires in the inflamed colon. *Immunity*, **2021**, 54, 2565-2577.e6	32.3	1
92	From cell to cell: Identification of actionable targets in bone marrow fibrosis using single-cell technologies. *Experimental Hematology*, **2021**, 104, 48-54	3.1	
91	DNA Methylation-Mediated Modulation of Endocytosis as Potential Mechanism for Synaptic Function Regulation in Murine Inhibitory Cortical Interneurons. *Cerebral Cortex*, **2020**, 30, 3921-3937	5.1	16
90	Aging-regulated anti-apoptotic long non-coding RNA Sarrah augments recovery from acute myocardial infarction. *Nature Communications*, **2020**, 11, 2039	17.4	28

89	Hypoxia-inducible factor 1 (HIF-1) is a new therapeutic target in JAK2V617F-positive myeloproliferative neoplasms. *Leukemia*, **2020**, 34, 1062-1074	10.7	23
88	Therapeutic inhibition of FcɣRIIb signaling targets leukemic stem cells in chronic myeloid leukemia. *Leukemia*, **2020**, 34, 2635-2647	10.7	3
87	Deconvolution of cellular subsets in human tissue based on targeted DNA methylation analysis at individual CpG sites. *BMC Biology*, **2020**, 18, 178	7.3	6
86	Myeloid cells in liver and bone marrow acquire a functionally distinct inflammatory phenotype during obesity-related steatohepatitis. *Gut*, **2020**, 69, 551-563	19.2	71
85	Unique and assay specific features of NOMe-, ATAC- and DNase I-seq data. *Nucleic Acids Research*, **2019**, 47, 10580-10596	20.1	17
84	Prognostically Relevant Subtypes and Survival Prediction for Breast Cancer Based on Multimodal Genomics Data. *IEEE Access*, **2019**, 7, 133850-133864	3.5	12
83	Detection of RNA-DNA binding sites in long noncoding RNAs. *Nucleic Acids Research*, **2019**, 47, e32	20.1	70
82	Hematopoietic stem and progenitor cell proliferation and differentiation requires the trithorax protein Ash2l. *Scientific Reports*, **2019**, 9, 8262	4.9	6
81	Stem cell persistence in CML is mediated by extrinsically activated JAK1-STAT3 signaling. *Leukemia*, **2019**, 33, 1964-1977	10.7	17
80	Identification of transcription factor binding sites using ATAC-seq. *Genome Biology*, **2019**, 20, 45	18.3	139
79	Impaired cellular energy metabolism in cord blood macrophages contributes to abortive response toward inflammatory threats. *Nature Communications*, **2019**, 10, 1685	17.4	28
78	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	22.4	13
77	Infliximab therapy together with tyrosine kinase inhibition targets leukemic stem cells in chronic myeloid leukemia. *BMC Cancer*, **2019**, 19, 658	4.8	4
76	Transcriptional Landscape of the Microenvironment in Bone Marrow Fibrosis at Single Cell Level. *Blood*, **2019**, 134, 1675-1675	2.2	0
75	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	2.2	
74	Isolation and genome-wide characterization of cellular DNA:RNA triplex structures. *Nucleic Acids Research*, **2019**, 47, 2306-2321	20.1	40
73	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	1.4	8
72	CXCR6 protects from inflammation and fibrosis in NEMO mice. *Biochimica Et Biophysica Acta - Molecular Basis of Disease*, **2019**, 1865, 391-402	6.9	7

71	JAK2V617F but not CALR mutations confer increased molecular responses to interferon-α via JAK1/STAT1 activation. *Leukemia*, **2019**, 33, 995-1010	10.7	29
70	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	18	27
69	Data complexity meta-features for regression problems. *Machine Learning*, **2018**, 107, 209-246	4	21
68	HMGB2 Loss upon Senescence Entry Disrupts Genomic Organization and Induces CTCF Clustering across Cell Types. *Molecular Cell*, **2018**, 70, 730-744.e6	17.6	83
67	Therapeutic inhibition of inflammatory monocyte recruitment reduces steatohepatitis and liver fibrosis. *Hepatology*, **2018**, 67, 1270-1283	11.2	225
66	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	5.7	8
65	Nrf2 Is a Central Regulator of Metabolic Reprogramming of Myeloid-Derived Suppressor Cells in Steady State and Sepsis. *Frontiers in Immunology*, **2018**, 9, 1552	8.4	28
64	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	11.5	41
63	Variants of cause transcript-specific DNA methylation patterns and affect hematopoiesis. *Life Science Alliance*, **2018**, 1, e201800153	5.8	11
62	Clustering of RNA-Seq samples: Comparison study on cancer data. *Methods*, **2018**, 132, 42-49	4.6	10
61	Human pluripotent stem cell-derived acinar/ductal organoids generate human pancreas upon orthotopic transplantation and allow disease modelling. *Gut*, **2017**, 66, 473-486	19.2	120
60	Post-weaning epiphysiolysis causes distal femur dysplasia and foreshortened hindlimbs in fetuin-A-deficient mice. *PLoS ONE*, **2017**, 12, e0187030	3.7	14
59	Surface Topography Guides Morphology and Spatial Patterning of Induced Pluripotent Stem Cell Colonies. *Stem Cell Reports*, **2017**, 9, 654-666	8	95
58	Tbx3 fosters pancreatic cancer growth by increased angiogenesis and activin/nodal-dependent induction of stemness. *Stem Cell Research*, **2016**, 17, 367-378	1.6	19
57	Measuring the complexity of regression problems **2016**,		2
56	Binding of nuclear factor κB to noncanonical consensus sites reveals its multimodal role during the early inflammatory response. *Genome Research*, **2016**, 26, 1478-1489	9.7	27
55	The lncRNA HOTAIR impacts on mesenchymal stem cells via triple helix formation. *Nucleic Acids Research*, **2016**, 44, 10631-10643	20.1	94
54	Differential peak calling of ChIP-seq signals with replicates with THOR. *Nucleic Acids Research*, **2016**, 44, e153	20.1	46

53	Detection of Hot-Spot Mutations in Circulating Cell-Free DNA From Patients With Intraductal Papillary Mucinous Neoplasms of the Pancreas. *Gastroenterology*, **2016**, 151, 267-70	13.3	53
52	Analysis of computational footprinting methods for DNase sequencing experiments. *Nature Methods*, **2016**, 13, 303-9	21.6	82
51	Epigenetic Classification of Human Mesenchymal Stromal Cells. *Stem Cell Reports*, **2016**, 6, 168-75	8	40
50	DNA methylation levels at individual age-associated CpG sites can be indicative for life expectancy. *Aging*, **2016**, 8, 394-401	5.6	99
49	Epigenetic age predictions based on buccal swabs are more precise in combination with cell type-specific DNA methylation signatures. *Aging*, **2016**, 8, 1034-48	5.6	68
48	A multiple kernel learning algorithm for drug-target interaction prediction. *BMC Bioinformatics*, **2016**, 17, 46	3.6	111
47	A time frame permissive for Protein Kinase D2 activity to direct angiogenesis in mouse embryonic stem cells. *Scientific Reports*, **2015**, 5, 11742	4.9	7
46	Impact of missing data imputation methods on gene expression clustering and classification. *BMC Bioinformatics*, **2015**, 16, 64	3.6	47
45	Replicative senescence is associated with nuclear reorganization and with DNA methylation at specific transcription factor binding sites. *Clinical Epigenetics*, **2015**, 7, 19	7.7	42
44	Epigenetic program and transcription factor circuitry of dendritic cell development. *Nucleic Acids Research*, **2015**, 43, 9680-93	20.1	34
43	Thrombin stimulates insulin secretion via protease-activated receptor-3. *Islets*, **2015**, 7, e1118195	2	13
42	On the selection of appropriate distances for gene expression data clustering. *BMC Bioinformatics*, **2014**, 15 Suppl 2, S2	3.6	68
41	Detecting differential peaks in ChIP-seq signals with ODIN. *Bioinformatics*, **2014**, 30, 3467-75	7.2	24
40	Detection of active transcription factor binding sites with the combination of DNase hypersensitivity and histone modifications. *Bioinformatics*, **2014**, 30, 3143-51	7.2	56
39	The interaction of MYC with the trithorax protein ASH2L promotes gene transcription by regulating H3K27 modification. *Nucleic Acids Research*, **2014**, 42, 6901-20	20.1	32
38	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, 845-57	3	26
37	Discovering motifs that induce sequencing errors. *BMC Bioinformatics*, **2013**, 14 Suppl 5, S1	3.6	44
36	Random Forest and Gene Networks for Association of SNPs to Alzheimer's Disease. *Lecture Notes in Computer Science*, **2013**, 104-115	0.9	

35	Analysis of complexity indices for classification problems: Cancer gene expression data. *Neurocomputing*, **2012**, 75, 33-42	5.4	37
34	Inferring epigenetic and transcriptional regulation during blood cell development with a mixture of sparse linear models. *Bioinformatics*, **2012**, 28, 2297-303	7.2	8
33	A Comparison of External Clustering Evaluation Indices in the Context of Imbalanced Data Sets **2012**,		12
32	Evaluating Correlation Coefficients for Clustering Gene Expression Profiles of Cancer. *Lecture Notes in Computer Science*, **2012**, 120-131	0.9	3
31	CLEVER: clique-enumerating variant finder. *Bioinformatics*, **2012**, 28, 2875-82	7.2	79
30	Prediction of Transcription Factor Binding Sites by Integrating DNase Digestion and Histone Modification. *Lecture Notes in Computer Science*, **2012**, 109-119	0.9	1
29	pGQL: A probabilistic graphical query language for gene expression time courses. *BioData Mining*, **2011**, 4, 9	4.3	2
28	Predicting gene expression in T cell differentiation from histone modifications and transcription factor binding affinities by linear mixture models. *BMC Bioinformatics*, **2011**, 12 Suppl 1, S29	3.6	26
27	Classifying short gene expression time-courses with Bayesian estimation of piecewise constant functions. *Bioinformatics*, **2011**, 27, 946-52	7.2	10
26	Detection and interpretation of metabolite-transcript coresponses using combined profiling data. *Bioinformatics*, **2011**, 27, i357-65	7.2	24
25	Complexity measures of supervised classifications tasks: A case study for cancer gene expression data **2010**,		9
24	On the Complexity of Gene Marker Selection **2010**,		2
23	Semi-supervised Approach for Finding Cancer Sub-classes on Gene Expression Data. *Lecture Notes in Computer Science*, **2010**, 25-34	0.9	0
22	Constrained mixture estimation for analysis and robust classification of clinical time series. *Bioinformatics*, **2009**, 25, i6-14	7.2	24
21	Using Supervised Complexity Measures in the Analysis of Cancer Gene Expression Data Sets. *Lecture Notes in Computer Science*, **2009**, 48-59	0.9	3
20	Mining Rules for the Automatic Selection Process of Clustering Methods Applied to Cancer Gene Expression Data. *Lecture Notes in Computer Science*, **2009**, 20-29	0.9	10
19	Ranking and selecting clustering algorithms using a meta-learning approach **2008**,		33
18	Clustering cancer gene expression data: a comparative study. *BMC Bioinformatics*, **2008**, 9, 497	3.6	248

List of Publications

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17	Inferring differentiation pathways from gene expression. *Bioinformatics*, **2008**, 24, i156-64	7.2	14
16	On the Complexity of Gene Expression Classification Data Sets **2008**,		6
15	Comparative study on normalization procedures for cluster analysis of gene expression datasets **2008**,		20
14	Semi-supervised learning for the identification of syn-expressed genes from fused microarray and in situ image data. *BMC Bioinformatics*, **2007**, 8 Suppl 10, S3	3.6	14
13	Gene expression trees in lymphoid development. *BMC Immunology*, **2007**, 8, 25	3.7	6
12	Validating Gene Clusterings by Selecting Informative Gene Ontology Terms with Mutual Information. *Lecture Notes in Computer Science*, **2007**, 81-92	0.9	
11	On External Indices for Mixtures: Validating Mixtures of Genes **2006**, 662-669		
10	Analyzing gene expression time-courses. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2005**, 2, 179-93	3	58
9	The Graphical Query Language: a tool for analysis of gene expression time-courses. *Bioinformatics*, **2005**, 21, 2544-5	7.2	21
8	Comparative analysis of clustering methods for gene expression time course data. *Genetics and Molecular Biology*, **2004**, 27, 623-631	2	41
7	Triplex Domain Finder: Detection of Triple Helix Binding Domains in Long Non-Coding RNAs		3
6	Spatial multi-omic map of human myocardial infarction		12
5	Identification of Transcription Factor Binding Sites using ATAC-seq		3
4	Chromatin-accessibility estimation from single-cell ATAC data with scOpen		5
3	Comparison of Resources and Methods to infer Cell-Cell Communication from Single-cell RNA Data		8
2	CrossTalkeR: Analysis and Visualisation of Ligand Receptor Networks		2
1	Dissecting CD8+ T cell pathology of severe SARS-CoV-2 infection by single-cell epitope mapping		3