

Ivan G Costa

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8565342/publications.pdf>

Version: 2024-02-01

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	Therapeutic inhibition of inflammatory monocyte recruitment reduces steatohepatitis and liver fibrosis. <i>Hepatology</i> , 2018, 67, 1270-1283.	3.6	388
2	SARS-CoV-2 infects and replicates in cells of the human endocrine and exocrine pancreas. <i>Nature Metabolism</i> , 2021, 3, 149-165.	5.1	378
3	Identification of transcription factor binding sites using ATAC-seq. <i>Genome Biology</i> , 2019, 20, 45.	3.8	346
4	Clustering cancer gene expression data: a comparative study. <i>BMC Bioinformatics</i> , 2008, 9, 497.	1.2	334
5	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.	6.1	174
6	HMGB2 Loss upon Senescence Entry Disrupts Genomic Organization and Induces CTCF Clustering across Cell Types. <i>Molecular Cell</i> , 2018, 70, 730-744.e6.	4.5	164
7	A multiple kernel learning algorithm for drug-target interaction prediction. <i>BMC Bioinformatics</i> , 2016, 17, 46.	1.2	154
8	DNA methylation levels at individual age-associated CpG sites can be indicative for life expectancy. <i>Aging</i> , 2016, 8, 394-401.	1.4	150
9	SARS-CoV-2 infects the human kidney and drives fibrosis in kidney organoids. <i>Cell Stem Cell</i> , 2022, 29, 217-231.e8.	5.2	146
10	Comparison of methods and resources for cell-cell communication inference from single-cell RNA-Seq data. <i>Nature Communications</i> , 2022, 13, .	5.8	143
11	Myeloid cells in liver and bone marrow acquire a functionally distinct inflammatory phenotype during obesity-related steatohepatitis. <i>Gut</i> , 2020, 69, 551-563.	6.1	142
12	The lncRNA HOTAIR impacts on mesenchymal stem cells via triple helix formation. <i>Nucleic Acids Research</i> , 2016, 44, 10631-10643.	6.5	141
13	Analysis of computational footprinting methods for DNase sequencing experiments. <i>Nature Methods</i> , 2016, 13, 303-309.	9.0	141
14	Deep learning-based clustering approaches for bioinformatics. <i>Briefings in Bioinformatics</i> , 2021, 22, 393-415.	3.2	135
15	Detection of RNA-DNA binding sites in long noncoding RNAs. <i>Nucleic Acids Research</i> , 2019, 47, e32-e32.	6.5	128
16	Surface Topography Guides Morphology and Spatial Patterning of Induced Pluripotent Stem Cell Colonies. <i>Stem Cell Reports</i> , 2017, 9, 654-666.	2.3	120
17	On the selection of appropriate distances for gene expression data clustering. <i>BMC Bioinformatics</i> , 2014, 15, S2.	1.2	113
18	Detection of active transcription factor binding sites with the combination of DNase hypersensitivity and histone modifications. <i>Bioinformatics</i> , 2014, 30, 3143-3151.	1.8	109

#	ARTICLE	IF	CITATIONS
19	CLEVER: clique-enumerating variant finder. <i>Bioinformatics</i> , 2012, 28, 2875-2882.	1.8	101
20	Heterogeneous bone-marrow stromal progenitors drive myelofibrosis via a druggable alarmin axis. <i>Cell Stem Cell</i> , 2021, 28, 637-652.e8.	5.2	92
21	Epigenetic age predictions based on buccal swabs are more precise in combination with cell type-specific DNA methylation signatures. <i>Aging</i> , 2016, 8, 1034-1048.	1.4	90
22	Isolation and genome-wide characterization of cellular DNA:RNA triplex structures. <i>Nucleic Acids Research</i> , 2019, 47, 2306-2321.	6.5	78
23	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, 267-270.	0.6	76
24	Impact of missing data imputation methods on gene expression clustering and classification. <i>BMC Bioinformatics</i> , 2015, 16, 64.	1.2	70
25	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.	3.3	68
26	Differential peak calling of ChIP-seq signals with replicates with THOR. <i>Nucleic Acids Research</i> , 2016, 44, gkw680.	6.5	66
27	Analyzing Gene Expression Time-Courses. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2005, 2, 179-193.	1.9	65
28	Aging-regulated anti-apoptotic long non-coding RNA Sarrah augments recovery from acute myocardial infarction. <i>Nature Communications</i> , 2020, 11, 2039.	5.8	63
29	Epigenetic program and transcription factor circuitry of dendritic cell development. <i>Nucleic Acids Research</i> , 2015, 43, gkv1056.	6.5	62
30	Chromatin-accessibility estimation from single-cell ATAC-seq data with scOpen. <i>Nature Communications</i> , 2021, 12, 6386.	5.8	57
31	Ranking and selecting clustering algorithms using a meta-learning approach. , 2008, , .		53
32	Comparative analysis of clustering methods for gene expression time course data. <i>Genetics and Molecular Biology</i> , 2004, 27, 623-631.	0.6	52
33	Replicative senescence is associated with nuclear reorganization and with DNA methylation at specific transcription factor binding sites. <i>Clinical Epigenetics</i> , 2015, 7, 19.	1.8	51
34	Analysis of complexity indices for classification problems: Cancer gene expression data. <i>Neurocomputing</i> , 2012, 75, 33-42.	3.5	48
35	Discovering motifs that induce sequencing errors. <i>BMC Bioinformatics</i> , 2013, 14, S1.	1.2	47
36	The interaction of MYC with the trithorax protein ASH2L promotes gene transcription by regulating H3K27 modification. <i>Nucleic Acids Research</i> , 2014, 42, 6901-6920.	6.5	47

#	ARTICLE	IF	CITATIONS
37	Epigenetic Classification of Human Mesenchymal Stromal Cells. <i>Stem Cell Reports</i> , 2016, 6, 168-175.	2.3	47
38	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.	2.2	44
39	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.	5.2	44
40	Binding of nuclear factor $\hat{\text{I}}^{\text{B}}$ to noncanonical consensus sites reveals its multimodal role during the early inflammatory response. <i>Genome Research</i> , 2016, 26, 1478-1489.	2.4	43
41	JAK2V617F but not CALR mutations confer increased molecular responses to interferon- $\hat{\text{I}}^{\text{I}}$ via JAK1/STAT1 activation. <i>Leukemia</i> , 2019, 33, 995-1010.	3.3	43
42	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.	1.9	42
43	Hypoxia-inducible factor 1 (HIF-1) is a new therapeutic target in JAK2V617F-positive myeloproliferative neoplasms. <i>Leukemia</i> , 2020, 34, 1062-1074.	3.3	42
44	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.	1.6	42
45	Data complexity meta-features for regression problems. <i>Machine Learning</i> , 2018, 107, 209-246.	3.4	41
46	Impaired cellular energy metabolism in cord blood macrophages contributes to abortive response toward inflammatory threats. <i>Nature Communications</i> , 2019, 10, 1685.	5.8	41
47	Detection and interpretation of metabolite- $\hat{\text{I}}$ transcript coresponses using combined profiling data. <i>Bioinformatics</i> , 2011, 27, i357-i365.	1.8	38
48	Detecting differential peaks in ChIP-seq signals with ODIN. <i>Bioinformatics</i> , 2014, 30, 3467-3475.	1.8	36
49	Stem cell persistence in CML is mediated by extrinsically activated JAK1-STAT3 signaling. <i>Leukemia</i> , 2019, 33, 1964-1977.	3.3	35
50	Unique and assay specific features of NOME-, ATAC- and DNase I-seq data. <i>Nucleic Acids Research</i> , 2019, 47, 10580-10596.	6.5	31
51	Endothelium-derived stromal cells contribute to hematopoietic bone marrow niche formation. <i>Cell Stem Cell</i> , 2021, 28, 653-670.e11.	5.2	31
52	Mapping the cardiac vascular niche in heart failure. <i>Nature Communications</i> , 2022, 13, .	5.8	31
53	Constrained mixture estimation for analysis and robust classification of clinical time series. <i>Bioinformatics</i> , 2009, 25, i6-i14.	1.8	30
54	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, S29.	1.2	30

#	ARTICLE	IF	CITATIONS
55	Deconvolution of cellular subsets in human tissue based on targeted DNA methylation analysis at individual CpG sites. <i>BMC Biology</i> , 2020, 18, 178.	1.7	28
56	CrossTalker: analysis and visualization of ligand-receptor networks. <i>Bioinformatics</i> , 2021, 37, 4263-4265.	1.8	28
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.	0.3	27
58	Comparative study on normalization procedures for cluster analysis of gene expression datasets. , 2008, , .		25
59	A Comparison of External Clustering Evaluation Indices in the Context of Imbalanced Data Sets. , 2012, , .		25
60	Hematopoietic stem and progenitor cell proliferation and differentiation requires the trithorax protein Ash2l. <i>Scientific Reports</i> , 2019, 9, 8262.	1.6	24
61	Mutations and variants of ONECUT1 in diabetes. <i>Nature Medicine</i> , 2021, 27, 1928-1940.	15.2	24
62	The Graphical Query Language: a tool for analysis of gene expression time-courses. <i>Bioinformatics</i> , 2005, 21, 2544-2545.	1.8	23
63	Clustering of RNA-Seq samples: Comparison study on cancer data. <i>Methods</i> , 2018, 132, 42-49.	1.9	22
64	Thrombin stimulates insulin secretion via protease-activated receptor-3. <i>Islets</i> , 2015, 7, e1118195.	0.9	20
65	Post-weaning epiphyseolysis causes distal femur dysplasia and foreshortened hindlimbs in fetuin-A-deficient mice. <i>PLoS ONE</i> , 2017, 12, e0187030.	1.1	20
66	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.	6.9	19
67	Prognostically Relevant Subtypes and Survival Prediction for Breast Cancer Based on Multimodal Genomics Data. <i>IEEE Access</i> , 2019, 7, 133850-133864.	2.6	18
68	Inferring differentiation pathways from gene expression. <i>Bioinformatics</i> , 2008, 24, i156-i164.	1.8	16
69	Variants of <i>DNMT3A</i> cause transcript-specific DNA methylation patterns and affect hematopoiesis. <i>Life Science Alliance</i> , 2018, 1, e201800153.	1.3	16
70	Transcriptional changes and the role of ONECUT1 in hPSC pancreatic differentiation. <i>Communications Biology</i> , 2021, 4, 1298.	2.0	16
71	Human pluripotent stem cell-derived kidney organoids for personalized congenital and idiopathic nephrotic syndrome modeling. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	16
72	Semi-supervised learning for the identification of syn-expressed genes from fused microarray and in situ image data. <i>BMC Bioinformatics</i> , 2007, 8, S3.	1.2	15

#	ARTICLE	IF	CITATIONS
73	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.	0.4	15
74	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.	1.0	15
75	The spatial self-organization within pluripotent stem cell colonies is continued in detaching aggregates. <i>Biomaterials</i> , 2022, 282, 121389.	5.7	15
76	Classifying short gene expression time-courses with Bayesian estimation of piecewise constant functions. <i>Bioinformatics</i> , 2011, 27, 946-952.	1.8	14
77	CXCR6 protects from inflammation and fibrosis in NEMOLPC-KO mice. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2019, 1865, 391-402.	1.8	14
78	The area under the ROC curve as a measure of clustering quality. <i>Data Mining and Knowledge Discovery</i> , 2022, 36, 1219-1245.	2.4	14
79	On the Complexity of Gene Expression Classification Data Sets. , 2008, , .		13
80	Inferring epigenetic and transcriptional regulation during blood cell development with a mixture of sparse linear models. <i>Bioinformatics</i> , 2012, 28, 2297-2303.	1.8	13
81	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.	1.6	12
82	Infliximab therapy together with tyrosine kinase inhibition targets leukemic stem cells in chronic myeloid leukemia. <i>BMC Cancer</i> , 2019, 19, 658.	1.1	12
83	Complexity measures of supervised classifications tasks: A case study for cancer gene expression data. , 2010, , .		11
84	Early and late stage MPN patients show distinct gene expression profiles in CD34+ cells. <i>Annals of Hematology</i> , 2021, 100, 2943-2956.	0.8	9
85	Therapeutic inhibition of Fc γ RIIb signaling targets leukemic stem cells in chronic myeloid leukemia. <i>Leukemia</i> , 2020, 34, 2635-2647.	3.3	8
86	Cognate recognition of microbial antigens defines constricted CD4+ T \hat{A} cell receptor repertoires in the inflamed colon. <i>Immunity</i> , 2021, 54, 2565-2577.e6.	6.6	8
87	CALR frameshift mutations in MPN patient-derived iPSCs accelerate maturation of megakaryocytes. <i>Stem Cell Reports</i> , 2021, 16, 2768-2783.	2.3	8
88	Evaluating Correlation Coefficients for Clustering Gene Expression Profiles of Cancer. <i>Lecture Notes in Computer Science</i> , 2012, , 120-131.	1.0	7
89	A time frame permissive for Protein Kinase D2 activity to direct angiogenesis in mouse embryonic stem cells. <i>Scientific Reports</i> , 2015, 5, 11742.	1.6	7
90	Genetic barcoding systematically compares genes in del(5q) MDS and reveals a central role for <i>CSNK1A1</i> in clonal expansion. <i>Blood Advances</i> , 2022, 6, 1780-1796.	2.5	7

#	ARTICLE	IF	CITATIONS
91	Detection of cell markers from single cell RNA-seq with sc2marker. BMC Bioinformatics, 2022, 23, .	1.2	7
92	Gene expression trees in lymphoid development. BMC Immunology, 2007, 8, 25.	0.9	6
93	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
94	MOJITOO: a fast and universal method for integration of multimodal single-cell data. Bioinformatics, 2022, 38, i282-i289.	1.8	6
95	LINC00152 Drives a Competing Endogenous RNA Network in Human Hepatocellular Carcinoma. Cells, 2022, 11, 1528.	1.8	6
96	Induction of senescence upon loss of the Ash2l core subunit of H3K4 methyltransferase complexes. Nucleic Acids Research, 2022, 50, 7889-7905.	6.5	6
97	Using Supervised Complexity Measures in the Analysis of Cancer Gene Expression Data Sets. Lecture Notes in Computer Science, 2009, , 48-59.	1.0	5
98	Cyclin E1 in Murine and Human Liver Cancer: A Promising Target for Therapeutic Intervention during Tumour Progression. Cancers, 2021, 13, 5680.	1.7	5
99	Measuring the complexity of regression problems. , 2016, , .		4
100	Random Forest and Gene Networks for Association of SNPs to Alzheimer's Disease. Lecture Notes in Computer Science, 2013, , 104-115.	1.0	3
101	On the Complexity of Gene Marker Selection. , 2010, , .		2
102	pGQL: A probabilistic graphical query language for gene expression time courses. BioData Mining, 2011, 4, 9.	2.2	2
103	Transcriptional Landscape of the Microenvironment in Bone Marrow Fibrosis at Single Cell Level. Blood, 2019, 134, 1675-1675.	0.6	2
104	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
105	Prediction of Transcription Factor Binding Sites by Integrating DNase Digestion and Histone Modification. Lecture Notes in Computer Science, 2012, , 109-119.	1.0	1
106	Semi-supervised Approach for Finding Cancer Sub-classes on Gene Expression Data. Lecture Notes in Computer Science, 2010, , 25-34.	1.0	1
107	Predicting Gene Functions Using Semi-supervised Clustering Algorithms with Objective Function Optimization. , 2012, , .		0
108	MO331LINEAGE TRACING OF REGENERATING PROXIMAL TUBULE CELLS (STC) BY SINGLE CELL PROFILING IN ACUTE KIDNEY INJURY. Nephrology Dialysis Transplantation, 2021, 36, .	0.4	0

#	ARTICLE	IF	CITATIONS
109	Validating Gene Clusterings by Selecting Informative Gene Ontology Terms with Mutual Information. Lecture Notes in Computer Science, 2007, , 81-92.	1.0	0
110	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
111	On External Indices for Mixtures: Validating Mixtures of Genes. , 2006, , 662-669.		0