

Barbara Di Camillo

List of Publications by Year in descending order

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Version: 2024-02-01

117
papers

4,023
citations

185998

28
h-index

138251

58
g-index

121
all docs

121
docs citations

121
times ranked

8155
citing authors

#	ARTICLE	IF	CITATIONS
1	Identify, quantify and characterize cellular communication from single-cell RNA sequencing data with <i>scSeqComm</i> . <i>Bioinformatics</i> , 2022, 38, 1920-1929.	1.8	17
2	Guest Editorial: Deep Learning For Genomics. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 95-96.	1.9	0
3	Predicting functional impairment trajectories in amyotrophic lateral sclerosis: a probabilistic, multifactorial model of disease progression. <i>Journal of Neurology</i> , 2022, 269, 3858-3878.	1.8	7
4	Performance assessment across different care settings of a heart failure hospitalisation risk-score for type 2 diabetes using administrative claims. <i>Scientific Reports</i> , 2022, 12, 7762.	1.6	1
5	Time-series analysis of multidimensional clinical-laboratory data by dynamic Bayesian networks reveals trajectories of COVID-19 outcomes. <i>Computer Methods and Programs in Biomedicine</i> , 2022, 221, 106873.	2.6	3
6	Recurrent Neural Network to Predict Renal Function Impairment in Diabetic Patients via Longitudinal Routine Check-up Data. <i>Lecture Notes in Computer Science</i> , 2021, , 329-337.	1.0	0
7	FZD6 triggers Wnt signalling driven by WNT10B ^{IVS1} expression and highlights new targets in T cell acute lymphoblastic leukemia. <i>Hematological Oncology</i> , 2021, 39, 364-379.	0.8	8
8	Identification of a Candidate Gene Set Signature for the Risk of Progression in IgM MGUS to Smoldering/Symptomatic Waldenström Macroglobulinemia (WM) by a Comparative Transcriptome Analysis of B Cells and Plasma Cells. <i>Cancers</i> , 2021, 13, 1837.	1.7	7
9	Temporal Transcriptome Analysis Reveals Dynamic Gene Expression Patterns Driving T _H 2-Cell Maturation. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 648791.	1.8	9
10	Faecal Microbiome Transplantation as a Solution to Chronic Enteropathies in Dogs: A Case Study of Beneficial Microbial Evolution. <i>Animals</i> , 2021, 11, 1433.	1.0	12
11	A Dynamic Bayesian Network model for simulating the progression to diabetes onset in the ageing population. , 2021, , .		2
12	Nilotinib-induced bone marrow CD34 ⁺ /lin ⁻ Ph ⁺ cells early clearance in newly diagnosed CPaChronic Myeloid Leukemia: Final report of the PhilosoPhi34 study. <i>European Journal of Haematology</i> , 2021, 107, 436-448.	1.1	4
13	A Variable Ranking Method for Machine Learning Models with Correlated Features: In-Silico Validation and Application for Diabetes Prediction. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 7740.	1.3	4
14	A Deep Learning Approach to Predict Diabetes TM Cardiovascular Complications From Administrative Claims. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2021, 25, 3608-3617.	3.9	25
15	Outcomes of patients with type 2 diabetes treated with SGLT-2 inhibitors versus DPP-4 inhibitors. An Italian real-world study in the context of other observational studies. <i>Diabetes Research and Clinical Practice</i> , 2021, 179, 109024.	1.1	6
16	Cardiovascular effectiveness of human-based vs. exendin-based glucagon like peptide-1 receptor agonists: a retrospective study in patients with type 2 diabetes. <i>European Journal of Preventive Cardiology</i> , 2021, 28, 22-29.	0.8	12
17	Modeling Microbial Community Networks: Methods and Tools. <i>Current Genomics</i> , 2021, 22, 267-290.	0.7	2
18	Mathematical modelling of SigE regulatory network reveals new insights into bistability of mycobacterial stress response. <i>BMC Bioinformatics</i> , 2021, 22, 558.	1.2	7

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19	Common Gene Expression Signature of B-Cells of Waldenström's Macroglobulinemia (WM) and IgM Monoclonal Gammopathies of Undetermined Significance (IgM MGUS) Compared to Healthy Subjects. <i>Blood</i> , 2021, 138, 4317-4317.	0.6	0
20	Cardiovascular outcomes after initiating GLP-1 receptor agonist or basal insulin for the routine treatment of type 2 diabetes: a region-wide retrospective study. <i>Cardiovascular Diabetology</i> , 2021, 20, 222.	2.7	7
21	Beware to ignore the rare: how imputing zero-values can improve the quality of 16S rRNA gene studies results. <i>BMC Bioinformatics</i> , 2021, 22, 618.	1.2	3
22	Comparing the Predictive Power of Heart Failure Hospitalisation Risk Scores in the Diabetic Outpatient Clinic and Primary Care Settings. , 2021, , .		1
23	SPARSim single cell: a count data simulator for scRNA-seq data. <i>Bioinformatics</i> , 2020, 36, 1468-1475.	1.8	33
24	Diabetes diagnosis from administrative claims and estimation of the true prevalence of diabetes among 4.2 million individuals of the Veneto region (North East Italy). <i>Nutrition, Metabolism and Cardiovascular Diseases</i> , 2020, 30, 84-91.	1.1	33
25	Addressing practical issues of predictive models translation into everyday practice and public health management: a combined model to predict the risk of type 2 diabetes improves incidence prediction and reduces the prevalence of missing risk predictions. <i>BMJ Open Diabetes Research and Care</i> , 2020, 8, e001223.	1.2	3
26	Prediction of Cardiovascular Complications in Diabetes from Pharmacy Administrative Claims. , 2020, , .		2
27	Exploiting mutual information for the imputation of static and dynamic mixed-type clinical data with an adaptive k-nearest neighbours approach. <i>BMC Medical Informatics and Decision Making</i> , 2020, 20, 174.	1.5	12
28	Guest Editorial Data Science in Smart Healthcare: Challenges and Opportunities. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2020, 24, 3041-3043.	3.9	8
29	Genetic perturbation of IFN- γ transcriptional modulators in human endothelial cells uncovers pivotal regulators of angiogenesis. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3977-3986.	1.9	6
30	Exposure to dipeptidyl peptidase-4 inhibitors and COVID-19 among people with type 2 diabetes: A case-control study. <i>Diabetes, Obesity and Metabolism</i> , 2020, 22, 1946-1950.	2.2	91
31	Better cardiovascular outcomes of type 2 diabetic patients treated with GLP-1 receptor agonists versus DPP-4 inhibitors in clinical practice. <i>Cardiovascular Diabetology</i> , 2020, 19, 74.	2.7	26
32	A practical perspective on the concordance index for the evaluation and selection of prognostic time-to-event models. <i>Journal of Biomedical Informatics</i> , 2020, 108, 103496.	2.5	95
33	Cardiovascular outcomes of type 2 diabetic patients treated with SGLT-2 inhibitors versus GLP-1 receptor agonists in real-life. <i>BMJ Open Diabetes Research and Care</i> , 2020, 8, e001451.	1.2	48
34	A Combined Interpolation and Weighted K-Nearest Neighbours Approach for the Imputation of Longitudinal ICU Laboratory Data. <i>Journal of Healthcare Informatics Research</i> , 2020, 4, 174-188.	5.3	15
35	Cell Surface Proteins of B Cells and Plasmacells Are Differently Expressed in Waldenström's Macroglobulinemia (WM) Patients Vs. Subjects with Monoclonal Gammopathy of Uncertain Significance (IgMMGUS) Vs. Healthy Donors. <i>Blood</i> , 2020, 136, 41-41.	0.6	0
36	Nilotinib interferes with cell cycle, ABC transporters and JAK-STAT signaling pathway in CD34+/-cells of patients with chronic phase chronic myeloid leukemia after 12 months of treatment. <i>PLoS ONE</i> , 2019, 14, e0218444.	1.1	9

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37	Improved long-term cardiovascular outcomes after intensive versus standard screening of diabetic complications: an observational study. <i>Cardiovascular Diabetology</i> , 2019, 18, 117.	2.7	11
38	Stratification of amyotrophic lateral sclerosis patients: a crowdsourcing approach. <i>Scientific Reports</i> , 2019, 9, 690.	1.6	46
39	Identification of Novel Components of Target-of-Rapamycin Signaling Pathway by Network-Based Multi-Omics Integrative Analysis. <i>OMICS A Journal of Integrative Biology</i> , 2019, 23, 274-284.	1.0	1
40	A Dynamic Bayesian Network model for the simulation of Amyotrophic Lateral Sclerosis progression. <i>BMC Bioinformatics</i> , 2019, 20, 118.	1.2	20
41	Interpolation and K-Nearest Neighbours Combined Imputation for Longitudinal ICU Laboratory Data. , 2019, , .		1
42	metaSPARSim: a 16S rRNA gene sequencing count data simulator. <i>BMC Bioinformatics</i> , 2019, 20, 416.	1.2	16
43	Analysis of a Minimal Gene Regulatory Network for Cell Differentiation. , 2019, 3, 302-307.		1
44	How to design a single-cell RNA-sequencing experiment: pitfalls, challenges and perspectives. <i>Briefings in Bioinformatics</i> , 2019, 20, 1384-1394.	3.2	66
45	Progressive Down Regulation of JAK-STAT, Cell Cycle, and ABC Transporter Genes in CD34+/Lin- Cells of Chronic-Phase Chronic Myeloid Leukemia (CP-CML) Patients at Diagnosis Vs. 12 Months of Nilotinib Treatment Vs. Healthy Subjects. <i>Blood</i> , 2019, 134, 5034-5034.	0.6	2
46	Transmembrane Receptors, Cytoskeleton and Cell Cycle Genes Were Progressively Deregulated in the Bone Marrow CD19+ and CD138+ Cells of Patients with Waldenstrom's Macroglobulinemia (WM) Vs. Subjects with IgM Monoclonal Gammopathy of Undetermined Significance Igmmgus Vs. Healthy Subjects. <i>Blood</i> , 2019, 134, 5036-5036.	0.6	0
47	Measuring the diversity of the human microbiota with targeted next-generation sequencing. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw119.	3.2	58
48	Nilotinib induced bone marrow CD34+/lin- Ph+ cells early clearance in newly diagnosed CP-chronic myeloid leukemia. <i>American Journal of Hematology</i> , 2018, 93, E162-E164.	2.0	4
49	HAPT2D: high accuracy of prediction of T2D with a model combining basic and advanced data depending on availability. <i>European Journal of Endocrinology</i> , 2018, 178, 331-341.	1.9	12
50	HPV16 E6 and E7 upregulate the histone lysine demethylase KDM2B through the c-MYC/miR-146a-5p axis. <i>Oncogene</i> , 2018, 37, 1654-1668.	2.6	55
51	Importance of Recalibrating Models for Type 2 Diabetes Onset Prediction: Application of the Diabetes Population Risk Tool on the Health and Retirement Study. , 2018, 2018, 5358-5361.		3
52	Optimizing PCR primers targeting the bacterial 16S ribosomal RNA gene. <i>BMC Bioinformatics</i> , 2018, 19, 343.	1.2	39
53	Mycobacterium tuberculosis-induced miR-155 subverts autophagy by targeting ATG3 in human dendritic cells. <i>PLoS Pathogens</i> , 2018, 14, e1006790.	2.1	100
54	Jak-2 and Nfkb Gene Expression Play a Strategic Role in Chronic Myeloid Leukemia (CML) Molecular Response during Early Nilotinib Treatment: The PhilosoPhi34 Data. <i>Blood</i> , 2018, 132, 5118-5118.	0.6	2

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55	bnstruct: an R package for Bayesian Network structure learning in the presence of missing data. <i>Bioinformatics</i> , 2017, 33, 1250-1252.	1.8	65
56	Simulation-based comprehensive benchmarking of RNA-seq aligners. <i>Nature Methods</i> , 2017, 14, 135-139.	9.0	229
57	Wide-transcriptome analysis and cellularity of bone marrow CD34+/lin- cells of patients with chronic-phase chronic myeloid leukemia at diagnosis vs. 12 months of first-line nilotinib treatment. <i>Cancer Biomarkers</i> , 2017, 21, 41-53.	0.8	3
58	DNA methylation profiling reveals common signatures of tumorigenesis and defines epigenetic prognostic subtypes of canine Diffuse Large B-cell Lymphoma. <i>Scientific Reports</i> , 2017, 7, 11591.	1.6	29
59	Down-regulation of microRNA-146a is associated with high-risk human papillomavirus infection and epidermal growth factor receptor overexpression in penile squamous cell carcinoma. <i>Human Pathology</i> , 2017, 61, 33-40.	1.1	34
60	The Genetic Landscape of Renal Complications in Type 1 Diabetes. <i>Journal of the American Society of Nephrology: JASN</i> , 2017, 28, 557-574.	3.0	101
61	A rule-based model of insulin signalling pathway. <i>BMC Systems Biology</i> , 2016, 10, 38.	3.0	23
62	Reconstruction of gene regulatory modules from RNA silencing of IFN- λ modulators: experimental set-up and inference method. <i>BMC Genomics</i> , 2016, 17, 228.	1.2	3
63	Can ecological history influence response to pollutants? Transcriptomic analysis of Manila clam collected in different Venice lagoon areas and exposed to heavy metal. <i>Aquatic Toxicology</i> , 2016, 174, 123-133.	1.9	27
64	FunPat: function-based pattern analysis on RNA-seq time series data. <i>BMC Genomics</i> , 2015, 16, S2.	1.2	63
65	Changes in microRNA expression during disease progression in patients with chronic viral hepatitis. <i>Liver International</i> , 2015, 35, 1324-1333.	1.9	12
66	A Bayesian Network for Probabilistic Reasoning and Imputation of Missing Risk Factors in Type 2 Diabetes. <i>Lecture Notes in Computer Science</i> , 2015, , 172-176.	1.0	6
67	A Dynamic Bayesian Network model for long-term simulation of clinical complications in type 1 diabetes. <i>Journal of Biomedical Informatics</i> , 2015, 57, 369-376.	2.5	46
68	A Bayesian Network analysis of the probabilistic relations between risk factors in the predisposition to type 2 diabetes. , 2015, 2015, 2119-22.		13
69	Toxicogenomic markers for corticosteroid treatment in beef cattle: Integrated analysis of transcriptomic data. <i>Food and Chemical Toxicology</i> , 2015, 77, 1-11.	1.8	8
70	Measuring differential gene expression with RNA-seq: challenges and strategies for data analysis. <i>Briefings in Functional Genomics</i> , 2015, 14, 130-142.	1.3	186
71	GEP Analyses of Bone Marrow CD34+/Lin- Cells of Chronic Phase CML Patients at Diagnosis Identified Different Sets of Genes Associated to the Molecular Response after 3 and 6 Months of First-Line Nilotinib Treatment. <i>Blood</i> , 2015, 126, 3645-3645.	0.6	0
72	ABACUS: an entropy-based cumulative bivariate statistic robust to rare variants and different direction of genotype effect. <i>Bioinformatics</i> , 2014, 30, 384-391.	1.8	4

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73	Reducing bias in RNA sequencing data: a novel approach to compute counts. BMC Bioinformatics, 2014, 15, S7.	1.2	51
74	Early origins of adult disease: Low birth weight and vascular remodeling. Atherosclerosis, 2014, 237, 391-399.	0.4	153
75	Global genomic and transcriptomic analysis of human pancreatic islets reveals novel genes influencing glucose metabolism. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 13924-13929.	3.3	407
76	Compression and fast retrieval of SNP data. Bioinformatics, 2014, 30, 3078-3085.	1.8	5
77	Novel genetic susceptibility loci for diabetic end-stage renal disease identified through robust naive Bayes classification. Diabetologia, 2014, 57, 1611-1622.	2.9	19
78	Leucine modulates dynamic phosphorylation events in insulin signaling pathway and enhances insulin-dependent glycogen synthesis in human skeletal muscle cells. BMC Cell Biology, 2014, 15, 9.	3.0	22
79	Transcriptome-Wide Analysis of Bone Marrow CD19+ Cells As Well As Bone Marrow B Cell Clones of Waldenström's Macroglobulinemia (WM) Vs. IgM Monoclonal Gammopathy of Undetermined Significance (IgM-MGUS). Blood, 2014, 124, 5176-5176.	0.6	2
80	Gene Expression Profiling of IgM Monoclonal Gammopathy of Undetermined Significance (IgM-MGUS). Blood, 2014, 124, 5187-5187.	0.6	0
81	Gene Expression Profiling of CD34+/Lin- Cells of Patients with Chronic Myeloid Leukemia at Diagnosis and after 12 Months of Nilotinib. Blood, 2014, 124, 5177-5177.	0.6	0
82	Microarray of Bone Marrow CD34+/Lin- Cells from Patients with Chronic Myeloid Leukemia (CML). Blood, 2014, 124, 5178-5178.	0.6	0
83	Knowledge Driven Variable Selection (KDVS) – a new approach to enrichment analysis of gene signatures obtained from high-throughput data. Source Code for Biology and Medicine, 2013, 8, 2.	1.7	7
84	Microarray Demonstrates Different Gene Expression Profiling Signatures Between Waldenström Macroglobulinemia and IgM Monoclonal Gammopathy of Undetermined Significance. Clinical Lymphoma, Myeloma and Leukemia, 2013, 13, 208-210.	0.2	10
85	A large-scale evaluation of computational protein function prediction. Nature Methods, 2013, 10, 221-227.	9.0	789
86	Genomic comparative analysis and gene function prediction in infectious diseases: application to the investigation of a meningitis outbreak. BMC Infectious Diseases, 2013, 13, 554.	1.3	18
87	Integration of Genetic Variation as External Perturbation to Reverse Engineer Regulatory Networks from Gene Expression Data. , 2013, , 107-118.		0
88	Characterization Of Genes and Pathways From The Comparison Between Bone Marrow B Cells As Well As Plasma Cells Of Waldenström Macroglobulinemia (WM) Vs. IgM Monoclonal Gammopathy Of Undetermined Significance (IgM-MGUS) Vs. Healthy Subjects Using Gene Profiling. Blood, 2013, 122, 3772-3772.	0.6	0
89	Integrating literature-constrained and data-driven inference of signalling networks. Bioinformatics, 2012, 28, 2311-2317.	1.8	34
90	Gene expression profiling identifies ARSD as a new marker of disease progression and the sphingolipid metabolism as a potential novel metabolism in chronic lymphocytic leukemia. Cancer Biomarkers, 2012, 11, 15-28.	0.8	21

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91	Dynamic Modeling of miRNA-mediated Feed-Forward Loops. <i>Journal of Computational Biology</i> , 2012, 19, 188-199.	0.8	8
92	Qualitative Reasoning for Biological Network Inference from Systematic Perturbation Experiments. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 1482-1491.	1.9	5
93	MORE: Mixed Optimization for Reverse Engineering An Application to Modeling Biological Networks Response via Sparse Systems of Nonlinear Differential Equations. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 1459-1471.	1.9	6
94	Comparative analysis of algorithms for whole-genome assembly of pyrosequencing data. <i>Briefings in Bioinformatics</i> , 2012, 13, 269-280.	3.2	23
95	Argot2: a large scale function prediction tool relying on semantic similarity of weighted Gene Ontology terms. <i>BMC Bioinformatics</i> , 2012, 13, S14.	1.2	137
96	Improving biomarker list stability by integration of biological knowledge in the learning process. <i>BMC Bioinformatics</i> , 2012, 13, S22.	1.2	14
97	SimBioNeT: A Simulator of Biological Network Topology. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 592-600.	1.9	6
98	Bag of Naïve Bayes: biomarker selection and classification from genome-wide SNP data. <i>BMC Bioinformatics</i> , 2012, 13, S2.	1.2	25
99	Effect of Size and Heterogeneity of Samples on Biomarker Discovery: Synthetic and Real Data Assessment. <i>PLoS ONE</i> , 2012, 7, e32200.	1.1	23
100	Function-Based Discovery of Significant Transcriptional Temporal Patterns in Insulin Stimulated Muscle Cells. <i>PLoS ONE</i> , 2012, 7, e32391.	1.1	11
101	Confined 3D microenvironment regulates early differentiation in human pluripotent stem cells. <i>Biotechnology and Bioengineering</i> , 2012, 109, 3119-3132.	1.7	44
102	Quantitative modeling of the terminal differentiation of B cells and mechanisms of lymphomagenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 2672-2677.	3.3	37
103	Microarray Identifies Different Molecular Signatures of Waldenstrom Macroglobulinemia (WM) Compared to IgM Monoclonal Gammopathy of Undetermined Significance (IgMMGUS). <i>Blood</i> , 2012, 120, 3495-3495.	0.6	0
104	Sensitivity Analysis of Retrovirus HTLV-1 Transactivation. <i>Journal of Computational Biology</i> , 2011, 18, 183-193.	0.8	5
105	Hemodynamics assessed via approximate entropy analysis of impedance cardiography time series: effect of metabolic syndrome. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2011, 301, H592-H598.	1.5	11
106	Qualitative Reasoning on Systematic Gene Perturbation Experiments. <i>Lecture Notes in Computer Science</i> , 2011, , 135-146.	1.0	1
107	Microarray Gene Expression Signature Indicates ARSD As a New Marker Associated with Ighv Mutational Status, ZAP-70 and Disease Progression in CLL. <i>Blood</i> , 2011, 118, 3447-3447.	0.6	0
108	An optimized data structure for high-throughput 3D proteomics data: mzRTree. <i>Journal of Proteomics</i> , 2010, 73, 1176-1182.	1.2	5

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109	Reconstruction of gene association network reveals a transmembrane protein required for adipogenesis and targeted by PPAR α . Cellular and Molecular Life Sciences, 2010, 67, 4049-4064.	2.4	38
110	The Transcriptional Response in Human Umbilical Vein Endothelial Cells Exposed to Insulin: A Dynamic Gene Expression Approach. PLoS ONE, 2010, 5, e14390.	1.1	8
111	Draft Genome Sequences of Two Neisseria meningitidis Serogroup C Clinical Isolates. Journal of Bacteriology, 2010, 192, 5270-5271.	1.0	2
112	A Boolean Approach to Linear Prediction for Signaling Network Modeling. PLoS ONE, 2010, 5, e12789.	1.1	13
113	On the Difficulty of Inferring Gene Regulatory Networks: A Study of the Fitness Landscape Generated by Relative Squared Error. Lecture Notes in Computer Science, 2010, , 74-85.	1.0	1
114	A Gene Network Simulator to Assess Reverse Engineering Algorithms. Annals of the New York Academy of Sciences, 2009, 1158, 125-142.	1.8	39
115	Significance analysis of microarray transcript levels in time series experiments. BMC Bioinformatics, 2007, 8, S10.	1.2	28
116	A quantization method based on threshold optimization for microarray short time series. BMC Bioinformatics, 2005, 6, S11.	1.2	30
117	Use of a novel triple-tracer approach to assess postprandial glucose metabolism. American Journal of Physiology - Endocrinology and Metabolism, 2003, 284, E55-E69.	1.8	158