

# 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	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013, 10, 221-227.	9.0	789
2	Global genomic and transcriptomic analysis of human pancreatic islets reveals novel genes influencing glucose metabolism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 13924-13929.	3.3	407
3	Simulation-based comprehensive benchmarking of RNA-seq aligners. <i>Nature Methods</i> , 2017, 14, 135-139.	9.0	229
4	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
5	Use of a novel triple-tracer approach to assess postprandial glucose metabolism. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2003, 284, E55-E69.	1.8	158
6	Early origins of adult disease: Low birth weight and vascular remodeling. <i>Atherosclerosis</i> , 2014, 237, 391-399.	0.4	153
7	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
8	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
9	<i>Mycobacterium tuberculosis</i> -induced miR-155 subverts autophagy by targeting ATG3 in human dendritic cells. <i>PLoS Pathogens</i> , 2018, 14, e1006790.	2.1	100
10	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
11	Exposure to dipeptidylâ€peptidaseâ€4 inhibitors and COVIDâ€19 among people with type 2 diabetes: A caseâ€control study. <i>Diabetes, Obesity and Metabolism</i> , 2020, 22, 1946-1950.	2.2	91
12	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
13	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
14	FunPat: function-based pattern analysis on RNA-seq time series data. <i>BMC Genomics</i> , 2015, 16, S2.	1.2	63
15	Measuring the diversity of the human microbiota with targeted next-generation sequencing. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw119.	3.2	58
16	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
17	Reducing bias in RNA sequencing data: a novel approach to compute counts. <i>BMC Bioinformatics</i> , 2014, 15, S7.	1.2	51
18	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

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19	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
20	Stratification of amyotrophic lateral sclerosis patients: a crowdsourcing approach. <i>Scientific Reports</i> , 2019, 9, 690.	1.6	46
21	Confined 3D microenvironment regulates early differentiation in human pluripotent stem cells. <i>Biotechnology and Bioengineering</i> , 2012, 109, 3119-3132.	1.7	44
22	A Gene Network Simulator to Assess Reverse Engineering Algorithms. <i>Annals of the New York Academy of Sciences</i> , 2009, 1158, 125-142.	1.8	39
23	Optimizing PCR primers targeting the bacterial 16S ribosomal RNA gene. <i>BMC Bioinformatics</i> , 2018, 19, 343.	1.2	39
24	Reconstruction of gene association network reveals a transmembrane protein required for adipogenesis and targeted by PPAR $\beta$ . <i>Cellular and Molecular Life Sciences</i> , 2010, 67, 4049-4064.	2.4	38
25	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
26	Integrating literature-constrained and data-driven inference of signalling networks. <i>Bioinformatics</i> , 2012, 28, 2311-2317.	1.8	34
27	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
28	SPARSim single cell: a count data simulator for scRNA-seq data. <i>Bioinformatics</i> , 2020, 36, 1468-1475.	1.8	33
29	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
30	A quantization method based on threshold optimization for microarray short time series. <i>BMC Bioinformatics</i> , 2005, 6, S11.	1.2	30
31	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
32	Significance analysis of microarray transcript levels in time series experiments. <i>BMC Bioinformatics</i> , 2007, 8, S10.	1.2	28
33	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
34	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
35	Bag of Naïve Bayes: biomarker selection and classification from genome-wide SNP data. <i>BMC Bioinformatics</i> , 2012, 13, S2.	1.2	25
36	A Deep Learning Approach to Predict Diabetesâ€™ Cardiovascular Complications From Administrative Claims. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2021, 25, 3608-3617.	3.9	25

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37	Comparative analysis of algorithms for whole-genome assembly of pyrosequencing data. <i>Briefings in Bioinformatics</i> , 2012, 13, 269-280.	3.2	23
38	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
39	A rule-based model of insulin signalling pathway. <i>BMC Systems Biology</i> , 2016, 10, 38.	3.0	23
40	Leucine modulates dynamic phosphorylation events in insulin signaling pathway and enhances insulin-dependent glycogen synthesis in human skeletal muscle cells. <i>BMC Cell Biology</i> , 2014, 15, 9.	3.0	22
41	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. <i>Cancer Biomarkers</i> , 2012, 11, 15-28.	0.8	21
42	A Dynamic Bayesian Network model for the simulation of Amyotrophic Lateral Sclerosis progression. <i>BMC Bioinformatics</i> , 2019, 20, 118.	1.2	20
43	Novel genetic susceptibility loci for diabetic end-stage renal disease identified through robust naive Bayes classification. <i>Diabetologia</i> , 2014, 57, 1611-1622.	2.9	19
44	Genomic comparative analysis and gene function prediction in infectious diseases: application to the investigation of a meningitis outbreak. <i>BMC Infectious Diseases</i> , 2013, 13, 554.	1.3	18
45	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
46	metaSPARSim: a 16S rRNA gene sequencing count data simulator. <i>BMC Bioinformatics</i> , 2019, 20, 416.	1.2	16
47	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
48	Improving biomarker list stability by integration of biological knowledge in the learning process. <i>BMC Bioinformatics</i> , 2012, 13, S22.	1.2	14
49	A Bayesian Network analysis of the probabilistic relations between risk factors in the predisposition to type 2 diabetes. , 2015, 2015, 2119-22.		13
50	A Boolean Approach to Linear Prediction for Signaling Network Modeling. <i>PLoS ONE</i> , 2010, 5, e12789.	1.1	13
51	Changes in microRNA expression during disease progression in patients with chronic viral hepatitis. <i>Liver International</i> , 2015, 35, 1324-1333.	1.9	12
52	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
53	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
54	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

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55	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
56	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
57	Function-Based Discovery of Significant Transcriptional Temporal Patterns in Insulin Stimulated Muscle Cells. <i>PLoS ONE</i> , 2012, 7, e32391.	1.1	11
58	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
59	Microarray Demonstrates Different Gene Expression Profiling Signatures Between Waldenström Macroglobulinemia and IgM Monoclonal Gammopathy of Undetermined Significance. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2013, 13, 208-210.	0.2	10
60	Nilotinib interferes with cell cycle, ABC transporters and JAK-STAT signaling pathway in CD34+/lin- cells of patients with chronic phase chronic myeloid leukemia after 12 months of treatment. <i>PLoS ONE</i> , 2019, 14, e0218444.	1.1	9
61	Temporal Transcriptome Analysis Reveals Dynamic Gene Expression Patterns Driving $\beta^2$ -Cell Maturation. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 648791.	1.8	9
62	The Transcriptional Response in Human Umbilical Vein Endothelial Cells Exposed to Insulin: A Dynamic Gene Expression Approach. <i>PLoS ONE</i> , 2010, 5, e14390.	1.1	8
63	Dynamic Modeling of miRNA-mediated Feed-Forward Loops. <i>Journal of Computational Biology</i> , 2012, 19, 188-199.	0.8	8
64	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
65	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
66	FZD6 triggers Wnt signaling driven by WNT10B <sup>IVS1</sup> expression and highlights new targets in T cell acute lymphoblastic leukemia. <i>Hematological Oncology</i> , 2021, 39, 364-379.	0.8	8
67	Knowledge Driven Variable Selection (KDVS) – a new approach to enrichment analysis of gene signatures obtained from high-throughput data. <i>Source Code for Biology and Medicine</i> , 2013, 8, 2.	1.7	7
68	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
69	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
70	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
71	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
72	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

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73	SimBioNet: A Simulator of Biological Network Topology. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 592-600.	1.9	6
74	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
75	Genetic perturbation of IFN- $\gamma$ 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
76	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
77	An optimized data structure for high-throughput 3D proteomics data: mzRTree. <i>Journal of Proteomics</i> , 2010, 73, 1176-1182.	1.2	5
78	Sensitivity Analysis of Retrovirus HTLV-1 Transactivation. <i>Journal of Computational Biology</i> , 2011, 18, 183-193.	0.8	5
79	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
80	Compression and fast retrieval of SNP data. <i>Bioinformatics</i> , 2014, 30, 3078-3085.	1.8	5
81	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
82	Nilotinib induced bone marrow CD34+/lin <sup>-</sup> Ph <sup>+</sup> cells early clearance in newly diagnosed CP $\epsilon$ chronic myeloid leukemia. <i>American Journal of Hematology</i> , 2018, 93, E162-E164.	2.0	4
83	Nilotinib $\epsilon$ induced bone marrow CD34+/lin <sup>-</sup> Ph <sup>+</sup> cells early clearance in newly diagnosed CP $\epsilon$ Chronic Myeloid Leukemia: Final report of the PhilosoPhi34 study. <i>European Journal of Haematology</i> , 2021, 107, 436-448.	1.1	4
84	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
85	Reconstruction of gene regulatory modules from RNA silencing of IFN- $\gamma$ modulators: experimental set-up and inference method. <i>BMC Genomics</i> , 2016, 17, 228.	1.2	3
86	Wide-transcriptome analysis and cellularity of bone marrow CD34+/lin <sup>-</sup> 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
87	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
88	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
89	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
90	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

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91	Draft Genome Sequences of Two <i>Neisseria meningitidis</i> Serogroup C Clinical Isolates. <i>Journal of Bacteriology</i> , 2010, 192, 5270-5271.	1.0	2
92	Prediction of Cardiovascular Complications in Diabetes from Pharmacy Administrative Claims. , 2020, , .		2
93	A Dynamic Bayesian Network model for simulating the progression to diabetes onset in the ageing population. , 2021, , .		2
94	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). <i>Blood</i> , 2014, 124, 5176-5176.	0.6	2
95	Jak-2 and Nfkbia Gene Expression Play a Strategic Role in Chronic Myeloid Leukemia (CML) Molecular Response during Early Nilotinib Treatment: The PhiloPhi34 Data. <i>Blood</i> , 2018, 132, 5118-5118.	0.6	2
96	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
97	Modeling Microbial Community Networks: Methods and Tools. <i>Current Genomics</i> , 2021, 22, 267-290.	0.7	2
98	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
99	Interpolation and K-Nearest Neighbours Combined Imputation for Longitudinal ICU Laboratory Data. , 2019, , .		1
100	Analysis of a Minimal Gene Regulatory Network for Cell Differentiation. , 2019, 3, 302-307.		1
101	On the Difficulty of Inferring Gene Regulatory Networks: A Study of the Fitness Landscape Generated by Relative Squared Error. <i>Lecture Notes in Computer Science</i> , 2010, , 74-85.	1.0	1
102	Qualitative Reasoning on Systematic Gene Perturbation Experiments. <i>Lecture Notes in Computer Science</i> , 2011, , 135-146.	1.0	1
103	Comparing the Predictive Power of Heart Failure Hospitalisation Risk Scores in the Diabetic Outpatient Clinic and Primary Care Settings. , 2021, , .		1
104	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
105	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
106	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
107	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
108	Integration of Genetic Variation as External Perturbation to Reverse Engineer Regulatory Networks from Gene Expression Data. , 2013, , 107-118.		0

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109	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
110	Gene Expression Profiling of IgM Monoclonal Gammopathy of Undetermined Significance (IgM-MGUS). Blood, 2014, 124, 5187-5187.	0.6	0
111	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
112	Microarray of Bone Marrow CD34+/Lin- Cells from Patients with Chronic Myeloid Leukemia (CML). Blood, 2014, 124, 5178-5178.	0.6	0
113	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. Blood, 2015, 126, 3645-3645.	0.6	0
114	Transmembrane Receptors, Cytoskeleton and Cell Cycle Genes Were Progressively Deregulated in the Bone Marrow CD19+ and CD138+ Cells of Patients with Waldenström's Macroglobulinemia (WM) Vs. Subjects with IgM Monoclonal Gammopathy of Undetermined Significance Igmmgus Vs. Healthy Subjects. Blood, 2019, 134, 5036-5036.	0.6	0
115	Common Gene Expression Signature of B-Cells of Waldenström Macroglobulinemia (WM) and IgM Monoclonal Gammopathies of Undetermined Significance (IgM MGUS) Compared to Healthy Subjects. Blood, 2021, 138, 4317-4317.	0.6	0
116	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. Blood, 2020, 136, 41-41.	0.6	0
117	Guest Editorial: Deep Learning For Genomics. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 95-96.	1.9	0