

Panayiotis V Benos

List of Publications by Year in descending order

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Version: 2024-02-01

94
papers

5,832
citations

126907

33
h-index

79698

73
g-index

132
all docs

132
docs citations

132
times ranked

9771
citing authors

#	ARTICLE	IF	CITATIONS
1	Essential Regression: A generalizable framework for inferring causal latent factors from multi-omic datasets. <i>Patterns</i> , 2022, 3, 100473.	5.9	8
2	Editorial: Advances in Mathematical and Computational Oncology. <i>Frontiers in Physiology</i> , 2022, 13, 889198.	2.8	2
3	Topographic heterogeneity of lung microbiota in end-stage idiopathic pulmonary fibrosis: the Microbiome in Lung Explants-2 (MiLEs-2) study. <i>Thorax</i> , 2021, 76, 239-247.	5.6	11
4	A Pipeline for Integrated Theory and Data-Driven Modeling of Biomedical Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 811-822.	3.0	1
5	Neurological Complications Acquired During Pediatric Critical Illness. <i>Pediatric Critical Care Medicine</i> , 2021, Publish Ahead of Print, 906-914.	0.5	2
6	Transcriptomics of bronchoalveolar lavage cells identifies new molecular endotypes of sarcoidosis. <i>European Respiratory Journal</i> , 2021, 58, 2002950.	6.7	29
7	Plasma 1,3-β-d-glucan levels predict adverse clinical outcomes in critical illness. <i>JCI Insight</i> , 2021, 6, .	5.0	9
8	Compensatory hepatic adaptation accompanies permanent absence of intrahepatic biliary network due to YAP1 loss in liver progenitors. <i>Cell Reports</i> , 2021, 36, 109310.	6.4	17
9	Myofibroblast transcriptome indicates SFRP2hi fibroblast progenitors in systemic sclerosis skin. <i>Nature Communications</i> , 2021, 12, 4384.	12.8	101
10	Reduced Proportion and Activity of Natural Killer Cells in the Lung of Patients with Idiopathic Pulmonary Fibrosis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2021, 204, 608-610.	5.6	9
11	Human ex vivo lung perfusion: a novel model to study human lung diseases. <i>Scientific Reports</i> , 2021, 11, 490.	3.3	15
12	People critically ill with COVID-19 exhibit peripheral immune profiles predictive of mortality and reflective of SARS-CoV-2 lung viral burden. <i>Cell Reports Medicine</i> , 2021, 2, 100476.	6.5	11
13	Causal network perturbations for instance-specific analysis of single cell and disease samples. <i>Bioinformatics</i> , 2020, 36, 2515-2521.	4.1	14
14	Protecting the lungs but hurting the kidneys: causal inference study for the risk of ventilation-induced kidney injury in ARDS. <i>Annals of Translational Medicine</i> , 2020, 8, 985-985.	1.7	0
15	miR-1207-5p Can Contribute to Dysregulation of Inflammatory Response in COVID-19 via Targeting SARS-CoV-2 RNA. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 586592.	3.9	32
16	Respiratory Tract Dysbiosis Is Associated with Worse Outcomes in Mechanically Ventilated Patients. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020, 202, 1666-1677.	5.6	49
17	An improvement of ComiR algorithm for microRNA target prediction by exploiting coding region sequences of mRNAs. <i>BMC Bioinformatics</i> , 2020, 21, 201.	2.6	12
18	CausalMGM: an interactive web-based causal discovery tool. <i>Nucleic Acids Research</i> , 2020, 48, W597-W602.	14.5	10

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19	The evolution of radiographic edema in ARDS and its association with clinical outcomes: A prospective cohort study in adult patients. <i>Journal of Critical Care</i> , 2020, 56, 222-228.	2.2	34
20	Expression patterns of small numbers of transcripts from functionally-related pathways predict survival in multiple cancers. <i>BMC Cancer</i> , 2019, 19, 686.	2.6	8
21	Proliferating SPP1/MERTK-expressing macrophages in idiopathic pulmonary fibrosis. <i>European Respiratory Journal</i> , 2019, 54, 1802441.	6.7	400
22	PARP1 rs1805407 Increases Sensitivity to PARP1 Inhibitors in Cancer Cells Suggesting an Improved Therapeutic Strategy. <i>Scientific Reports</i> , 2019, 9, 3309.	3.3	25
23	Feasibility of lung cancer prediction from low-dose CT scan and smoking factors using causal models. <i>Thorax</i> , 2019, 74, 643-649.	5.6	49
24	Host-Response Subphenotypes Offer Prognostic Enrichment in Patients With or at Risk for Acute Respiratory Distress Syndrome*. <i>Critical Care Medicine</i> , 2019, 47, 1724-1734.	0.9	62
25	Mixed graphical models for integrative causal analysis with application to chronic lung disease diagnosis and prognosis. <i>Bioinformatics</i> , 2019, 35, 1204-1212.	4.1	63
26	Regional Molecular Signature of the Symptomatic Atherosclerotic Carotid Plaque. <i>Neurosurgery</i> , 2019, 85, E284-E293.	1.1	14
27	Transcriptional regulatory model of fibrosis progression in the human lung. <i>JCI Insight</i> , 2019, 4, .	5.0	113
28	COPDGeneÂ® 2019: Redefining the Diagnosis of Chronic Obstructive Pulmonary Disease. <i>Chronic Obstructive Pulmonary Diseases (Miami, Fla)</i> , 2019, 6, 384-399.	0.7	112
29	Biomarker identification for statin sensitivity of cancer cell lines. <i>Biochemical and Biophysical Research Communications</i> , 2018, 495, 659-665.	2.1	38
30	An Insulin-Responsive Sensor in the SIRT1 Disordered Region Binds DBC1 and PACS-2 to Control Enzyme Activity. <i>Molecular Cell</i> , 2018, 72, 985-998.e7.	9.7	33
31	piMGM: incorporating multi-source priors in mixed graphical models for learning disease networks. <i>Bioinformatics</i> , 2018, 34, i848-i856.	4.1	19
32	ECCB 2018: The 17th European Conference on Computational Biology. <i>Bioinformatics</i> , 2018, 34, i595-i598.	4.1	1
33	Respiratory Microbiome Profiling for Etiologic Diagnosis of Pneumonia in Mechanically Ventilated Patients. <i>Frontiers in Microbiology</i> , 2018, 9, 1413.	3.5	61
34	Comparison of strategies for scalable causal discovery of latent variable models from mixed data. <i>International Journal of Data Science and Analytics</i> , 2018, 6, 33-45.	4.1	32
35	Surveillance for melanoma (MEL): Results of a database study of stage I-III MEL.. <i>Journal of Clinical Oncology</i> , 2018, 36, 9586-9586.	1.6	1
36	Evaluation of Causal Structure Learning Methods on Mixed Data Types. <i>Proceedings of Machine Learning Research</i> , 2018, 92, 48-65.	0.3	20

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37	Epigenetic and Transcriptomic Regulation of Lung Repair during Recovery from Influenza Infection. American Journal of Pathology, 2017, 187, 851-863.	3.8	47
38	Integrated Theory-and Data-Driven Feature Selection in Gene Expression Data Analysis. , 2017, 2017, 1525-1532.		20
39	Ribosomopathy-like properties of murine and human cancers. PLoS ONE, 2017, 12, e0182705.	2.5	29
40	Abstract 479: Modeling miRNA induced silencing in breast cancer with PARADIGM. , 2017, , .		0
41	Regulation of alveolar septation by microRNA-489. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2016, 310, L476-L487.	2.9	63
42	Non-coding single nucleotide variants affecting estrogen receptor binding and activity. Genome Medicine, 2016, 8, 128.	8.2	5
43	Learning mixed graphical models with separate sparsity parameters and stability-based model selection. BMC Bioinformatics, 2016, 17, 175.	2.6	53
44	Abstract 473: A tumor and immune related miRNA signature predicts progression-free survival of melanoma patients treated with ipilimumab. , 2016, , .		1
45	MicroRNA expression profiling predicts clinical outcome of carboplatin/paclitaxel-based therapy in metastatic melanoma treated on the ECOG-ACRIN trial E2603. Clinical Epigenetics, 2015, 7, 58.	4.1	19
46	Gene expression profiling distinguishes proneural glioma stem cells from mesenchymal glioma stem cells. Genomics Data, 2015, 5, 333-336.	1.3	29
47	The center for causal discovery of biomedical knowledge from big data. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 1132-1136.	4.4	30
48	Abstract A1-14: Discovery of a functional SNP in an estrogen receptor binding site in the IGF1R gene. , 2015, , .		0
49	Aldosterone Regulates MicroRNAs in the Cortical Collecting Duct to Alter Sodium Transport. Journal of the American Society of Nephrology: JASN, 2014, 25, 2445-2457.	6.1	42
50	T-RECS: STABLE SELECTION OF DYNAMICALLY FORMED GROUPS OF FEATURES WITH APPLICATION TO PREDICTION OF CLINICAL OUTCOMES. , 2014, , .		7
51	microRNA (miRNA) expression profiling predicts clinical outcome of carboplatin/paclitaxel-based therapy (CP) in metastatic melanoma (MM) treated on the intergroup trial E2603.. Journal of Clinical Oncology, 2014, 32, 9048-9048.	1.6	0
52	Overexpression of microRNA-1 promotes cardiomyocyte commitment from human cardiovascular progenitors via suppressing WNT and FGF signaling pathways. Journal of Molecular and Cellular Cardiology, 2013, 63, 146-154.	1.9	62
53	Estrogen represses gene expression through reconfiguring chromatin structures. Nucleic Acids Research, 2013, 41, 8061-8071.	14.5	17
54	ComiR: combinatorial microRNA target prediction tool. Nucleic Acids Research, 2013, 41, W159-W164.	14.5	174

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55	Expression of Regulatory Platelet MicroRNAs in Patients with Sickle Cell Disease. PLoS ONE, 2013, 8, e60932.	2.5	21
56	Novel Modeling of Combinatorial miRNA Targeting Identifies SNP with Potential Role in Bone Density. PLoS Computational Biology, 2012, 8, e1002830.	3.2	38
57	SPECTRAL CLUSTERING STRATEGIES FOR HETEROGENEOUS DISEASE EXPRESSION DATA. , 2012, , .		4
58	To bind or not to bind - FoxA1 determines estrogen receptor action in breast cancer progression. Breast Cancer Research, 2012, 14, 312.	5.0	9
59	Profibrotic Role of miR-154 in Pulmonary Fibrosis. American Journal of Respiratory Cell and Molecular Biology, 2012, 47, 879-887.	2.9	162
60	High Throughput Determination of TGF β 1/SMAD3 Targets in A549 Lung Epithelial Cells. PLoS ONE, 2011, 6, e20319.	2.5	57
61	Large Scale Comparison of Innate Responses to Viral and Bacterial Pathogens in Mouse and Macaque. PLoS ONE, 2011, 6, e22401.	2.5	24
62	RNA Deep Sequencing Reveals Differential MicroRNA Expression during Development of Sea Urchin and Sea Star. PLoS ONE, 2011, 6, e29217.	2.5	22
63	Finding subtypes of transcription factor motif pairs with distinct regulatory roles. Nucleic Acids Research, 2011, 39, e76-e76.	14.5	16
64	mirConnX: condition-specific mRNA-microRNA network integrator. Nucleic Acids Research, 2011, 39, W416-W423.	14.5	109
65	Electrostatic hot spot on DNA-binding domains mediates phosphate desolvation and the pre-organization of specificity determinant side chains. Nucleic Acids Research, 2010, 38, 2134-2144.	14.5	9
66	Inhibition and Role of let-7d in Idiopathic Pulmonary Fibrosis. American Journal of Respiratory and Critical Care Medicine, 2010, 182, 220-229.	5.6	454
67	Extracting biologically significant patterns from short time series gene expression data. BMC Bioinformatics, 2009, 10, 255.	2.6	16
68	HHMMiR: efficient de novo prediction of microRNAs using hierarchical hidden Markov models. BMC Bioinformatics, 2009, 10, S35.	2.6	87
69	In Silico Discovery of DNA Regulatory Sites and Modules. , 2009, , 353-366.		0
70	The role of RNA folding free energy in the evolution of the polymerase genes of the influenza A virus. Genome Biology, 2009, 10, R18.	9.6	24
71	Features of Mammalian microRNA Promoters Emerge from Polymerase II Chromatin Immunoprecipitation Data. PLoS ONE, 2009, 4, e5279.	2.5	240
72	Web-Based Primer Design Software for Genome-Scale Genotyping by Pyrosequencing [®] . , 2007, 373, 25-38.		1

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73	Human Transcriptome Subtraction by Using Short Sequence Tags To Search for Tumor Viruses in Conjunctival Carcinoma. <i>Journal of Virology</i> , 2007, 81, 11332-11340.	3.4	105
74	DNA Familial Binding Profiles Made Easy: Comparison of Various Motif Alignment and Clustering Strategies. <i>PLoS Computational Biology</i> , 2007, 3, e61.	3.2	113
75	Inferring protein-DNA dependencies using motif alignments and mutual information. <i>Bioinformatics</i> , 2007, 23, i297-i304.	4.1	31
76	Combined analysis reveals a core set of cycling genes. <i>Genome Biology</i> , 2007, 8, R146.	9.6	36
77	Regulatory conservation of protein coding and microRNA genes in vertebrates: lessons from the opossum genome. <i>Genome Biology</i> , 2007, 8, R84.	9.6	26
78	STAMP: a web tool for exploring DNA-binding motif similarities. <i>Nucleic Acids Research</i> , 2007, 35, W253-W258.	14.5	428
79	Genome of the marsupial <i>Monodelphis domestica</i> reveals innovation in non-coding sequences. <i>Nature</i> , 2007, 447, 167-177.	27.8	661
80	Web-Based Identification of Evolutionary Conserved DNA cis-Regulatory Elements. <i>Methods in Molecular Biology</i> , 2007, 395, 425-436.	0.9	2
81	Self-organizing neural networks to support the discovery of DNA-binding motifs. <i>Neural Networks</i> , 2006, 19, 950-962.	5.9	22
82	Reconstructing an Ancestral Mammalian Immune Supercomplex from a Marsupial Major Histocompatibility Complex. <i>PLoS Biology</i> , 2006, 4, e46.	5.6	150
83	Improved detection of DNA motifs using a self-organized clustering of familial binding profiles. <i>Bioinformatics</i> , 2005, 21, i283-i291.	4.1	34
84	Deregulation of common genes by c-Myc and its direct target, MT-MC1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 18968-18973.	7.1	26
85	Footer: A quantitative comparative genomics method for efficient recognition of cis-regulatory elements. <i>Genome Research</i> , 2005, 15, 840-847.	5.5	23
86	FOOTER: a web tool for finding mammalian DNA regulatory regions using phylogenetic footprinting. <i>Nucleic Acids Research</i> , 2005, 33, W442-W446.	14.5	27
87	enoLOGOS: a versatile web tool for energy normalized sequence logos. <i>Nucleic Acids Research</i> , 2005, 33, W389-W392.	14.5	199
88	A Sequence Alignment-Independent Method for Protein Classification. <i>Applied Bioinformatics</i> , 2004, 3, 137-148.	1.6	19
89	Probabilistic Code for DNA Recognition by Proteins of the EGR Family. <i>Journal of Molecular Biology</i> , 2002, 323, 701-727.	4.2	109
90	Additivity in protein-DNA interactions: how good an approximation is it?. <i>Nucleic Acids Research</i> , 2002, 30, 4442-4451.	14.5	284

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91	Is there a code for protein-DNA recognition? Probab(ilstical)ly?. BioEssays, 2002, 24, 466-475.	2.5	94
92	Mapping and identification of essential gene functions on the X chromosome of Drosophila. EMBO Reports, 2002, 3, 34-38.	4.5	105
93	The Drosophila Alcohol Dehydrogenase Gene May Have Evolved Independently of the Functionally Homologous Medfly, Olive Fly, and Flesh Fly Genes. Molecular Biology and Evolution, 2001, 18, 322-329.	8.9	18
94	MicroRNAs: Target Prediction and Involvement in Gene Regulatory Networks. , 0, , 291-309.		0