

Panayiotis V Benos

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8699560/publications.pdf>

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	Genome of the marsupial <i>Monodelphis domestica</i> reveals innovation in non-coding sequences. <i>Nature</i> , 2007, 447, 167-177.	27.8	661
2	Inhibition and Role of let-7d in Idiopathic Pulmonary Fibrosis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2010, 182, 220-229.	5.6	454
3	STAMP: a web tool for exploring DNA-binding motif similarities. <i>Nucleic Acids Research</i> , 2007, 35, W253-W258.	14.5	428
4	Proliferating SPP1/MERTK-expressing macrophages in idiopathic pulmonary fibrosis. <i>European Respiratory Journal</i> , 2019, 54, 1802441.	6.7	400
5	Additivity in protein-DNA interactions: how good an approximation is it?. <i>Nucleic Acids Research</i> , 2002, 30, 4442-4451.	14.5	284
6	Features of Mammalian microRNA Promoters Emerge from Polymerase II Chromatin Immunoprecipitation Data. <i>PLoS ONE</i> , 2009, 4, e5279.	2.5	240
7	enoLOGOS: a versatile web tool for energy normalized sequence logos. <i>Nucleic Acids Research</i> , 2005, 33, W389-W392.	14.5	199
8	ComiR: combinatorial microRNA target prediction tool. <i>Nucleic Acids Research</i> , 2013, 41, W159-W164.	14.5	174
9	Profibrotic Role of miR-154 in Pulmonary Fibrosis. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2012, 47, 879-887.	2.9	162
10	Reconstructing an Ancestral Mammalian Immune Supercomplex from a Marsupial Major Histocompatibility Complex. <i>PLoS Biology</i> , 2006, 4, e46.	5.6	150
11	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
12	Transcriptional regulatory model of fibrosis progression in the human lung. <i>JCI Insight</i> , 2019, 4, .	5.0	113
13	COPDGene® 2019: Redefining the Diagnosis of Chronic Obstructive Pulmonary Disease. <i>Chronic Obstructive Pulmonary Diseases (Miami, Fla)</i> , 2019, 6, 384-399.	0.7	112
14	Probabilistic Code for DNA Recognition by Proteins of the EGR Family. <i>Journal of Molecular Biology</i> , 2002, 323, 701-727.	4.2	109
15	mirConnX: condition-specific mRNA-microRNA network integrator. <i>Nucleic Acids Research</i> , 2011, 39, W416-W423.	14.5	109
16	Mapping and identification of essential gene functions on the X chromosome of <i>Drosophila</i> . <i>EMBO Reports</i> , 2002, 3, 34-38.	4.5	105
17	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
18	Myofibroblast transcriptome indicates SFRP2hi fibroblast progenitors in systemic sclerosis skin. <i>Nature Communications</i> , 2021, 12, 4384.	12.8	101

#	ARTICLE	IF	CITATIONS
19	Is there a code for protein-DNA recognition? Probab(ilstical)ly?. <i>BioEssays</i> , 2002, 24, 466-475.	2.5	94
20	HHMMiR: efficient de novo prediction of microRNAs using hierarchical hidden Markov models. <i>BMC Bioinformatics</i> , 2009, 10, S35.	2.6	87
21	Regulation of alveolar septation by microRNA-489. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2016, 310, L476-L487.	2.9	63
22	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
23	Overexpression of microRNA-1 promotes cardiomyocyte commitment from human cardiovascular progenitors via suppressing WNT and FGF signaling pathways. <i>Journal of Molecular and Cellular Cardiology</i> , 2013, 63, 146-154.	1.9	62
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	Respiratory Microbiome Profiling for Etiologic Diagnosis of Pneumonia in Mechanically Ventilated Patients. <i>Frontiers in Microbiology</i> , 2018, 9, 1413.	3.5	61
26	High Throughput Determination of TGF β 1/SMAD3 Targets in A549 Lung Epithelial Cells. <i>PLoS ONE</i> , 2011, 6, e20319.	2.5	57
27	Learning mixed graphical models with separate sparsity parameters and stability-based model selection. <i>BMC Bioinformatics</i> , 2016, 17, 175.	2.6	53
28	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
29	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
30	Epigenetic and Transcriptomic Regulation of Lung Repair during Recovery from Influenza Infection. <i>American Journal of Pathology</i> , 2017, 187, 851-863.	3.8	47
31	Aldosterone Regulates MicroRNAs in the Cortical Collecting Duct to Alter Sodium Transport. <i>Journal of the American Society of Nephrology: JASN</i> , 2014, 25, 2445-2457.	6.1	42
32	Novel Modeling of Combinatorial miRNA Targeting Identifies SNP with Potential Role in Bone Density. <i>PLoS Computational Biology</i> , 2012, 8, e1002830.	3.2	38
33	Biomarker identification for statin sensitivity of cancer cell lines. <i>Biochemical and Biophysical Research Communications</i> , 2018, 495, 659-665.	2.1	38
34	Combined analysis reveals a core set of cycling genes. <i>Genome Biology</i> , 2007, 8, R146.	9.6	36
35	Improved detection of DNA motifs using a self-organized clustering of familial binding profiles. <i>Bioinformatics</i> , 2005, 21, i283-i291.	4.1	34
36	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

#	ARTICLE	IF	CITATIONS
37	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
38	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
39	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
40	Inferring protein-DNA dependencies using motif alignments and mutual information. <i>Bioinformatics</i> , 2007, 23, i297-i304.	4.1	31
41	The center for causal discovery of biomedical knowledge from big data. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2015, 22, 1132-1136.	4.4	30
42	Gene expression profiling distinguishes proneural glioma stem cells from mesenchymal glioma stem cells. <i>Genomics Data</i> , 2015, 5, 333-336.	1.3	29
43	Transcriptomics of bronchoalveolar lavage cells identifies new molecular endotypes of sarcoidosis. <i>European Respiratory Journal</i> , 2021, 58, 2002950.	6.7	29
44	Ribosomopathy-like properties of murine and human cancers. <i>PLoS ONE</i> , 2017, 12, e0182705.	2.5	29
45	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
46	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
47	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
48	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
49	The role of RNA folding free energy in the evolution of the polymerase genes of the influenza A virus. <i>Genome Biology</i> , 2009, 10, R18.	9.6	24
50	Large Scale Comparison of Innate Responses to Viral and Bacterial Pathogens in Mouse and Macaque. <i>PLoS ONE</i> , 2011, 6, e22401.	2.5	24
51	Footer: A quantitative comparative genomics method for efficient recognition of cis-regulatory elements. <i>Genome Research</i> , 2005, 15, 840-847.	5.5	23
52	Self-organizing neural networks to support the discovery of DNA-binding motifs. <i>Neural Networks</i> , 2006, 19, 950-962.	5.9	22
53	RNA Deep Sequencing Reveals Differential MicroRNA Expression during Development of Sea Urchin and Sea Star. <i>PLoS ONE</i> , 2011, 6, e29217.	2.5	22
54	Expression of Regulatory Platelet MicroRNAs in Patients with Sickle Cell Disease. <i>PLoS ONE</i> , 2013, 8, e60932.	2.5	21

#	ARTICLE	IF	CITATIONS
55	Integrated Theory and Data-Driven Feature Selection in Gene Expression Data Analysis. , 2017, 2017, 1525-1532.		20
56	Evaluation of Causal Structure Learning Methods on Mixed Data Types. Proceedings of Machine Learning Research, 2018, 92, 48-65.	0.3	20
57	A Sequence Alignment-Independent Method for Protein Classification. Applied Bioinformatics, 2004, 3, 137-148.	1.6	19
58	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
59	piMGM: incorporating multi-source priors in mixed graphical models for learning disease networks. Bioinformatics, 2018, 34, i848-i856.	4.1	19
60	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
61	Estrogen represses gene expression through reconfiguring chromatin structures. Nucleic Acids Research, 2013, 41, 8061-8071.	14.5	17
62	Compensatory hepatic adaptation accompanies permanent absence of intrahepatic biliary network due to YAP1 loss in liver progenitors. Cell Reports, 2021, 36, 109310.	6.4	17
63	Extracting biologically significant patterns from short time series gene expression data. BMC Bioinformatics, 2009, 10, 255.	2.6	16
64	Finding subtypes of transcription factor motif pairs with distinct regulatory roles. Nucleic Acids Research, 2011, 39, e76-e76.	14.5	16
65	Human ex vivo lung perfusion: a novel model to study human lung diseases. Scientific Reports, 2021, 11, 490.	3.3	15
66	Regional Molecular Signature of the Symptomatic Atherosclerotic Carotid Plaque. Neurosurgery, 2019, 85, E284-E293.	1.1	14
67	Causal network perturbations for instance-specific analysis of single cell and disease samples. Bioinformatics, 2020, 36, 2515-2521.	4.1	14
68	An improvement of ComiR algorithm for microRNA target prediction by exploiting coding region sequences of mRNAs. BMC Bioinformatics, 2020, 21, 201.	2.6	12
69	Topographic heterogeneity of lung microbiota in end-stage idiopathic pulmonary fibrosis: the Microbiome in Lung Explants-2 (MiLEs-2) study. Thorax, 2021, 76, 239-247.	5.6	11
70	People critically ill with COVID-19 exhibit peripheral immune profiles predictive of mortality and reflective of SARS-CoV-2 lung viral burden. Cell Reports Medicine, 2021, 2, 100476.	6.5	11
71	CausalMGM: an interactive web-based causal discovery tool. Nucleic Acids Research, 2020, 48, W597-W602.	14.5	10
72	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

#	ARTICLE	IF	CITATIONS
73	To bind or not to bind - FoxA1 determines estrogen receptor action in breast cancer progression. Breast Cancer Research, 2012, 14, 312.	5.0	9
74	Plasma 1,3-β-d-glucan levels predict adverse clinical outcomes in critical illness. JCI Insight, 2021, 6, .	5.0	9
75	Reduced Proportion and Activity of Natural Killer Cells in the Lung of Patients with Idiopathic Pulmonary Fibrosis. American Journal of Respiratory and Critical Care Medicine, 2021, 204, 608-610.	5.6	9
76	Expression patterns of small numbers of transcripts from functionally-related pathways predict survival in multiple cancers. BMC Cancer, 2019, 19, 686.	2.6	8
77	Essential Regression: A generalizable framework for inferring causal latent factors from multi-omic datasets. Patterns, 2022, 3, 100473.	5.9	8
78	T-RECS: STABLE SELECTION OF DYNAMICALLY FORMED GROUPS OF FEATURES WITH APPLICATION TO PREDICTION OF CLINICAL OUTCOMES. , 2014, , .		7
79	Non-coding single nucleotide variants affecting estrogen receptor binding and activity. Genome Medicine, 2016, 8, 128.	8.2	5
80	SPECTRAL CLUSTERING STRATEGIES FOR HETEROGENEOUS DISEASE EXPRESSION DATA. , 2012, , .		4
81	Neurological Complications Acquired During Pediatric Critical Illness. Pediatric Critical Care Medicine, 2021, Publish Ahead of Print, 906-914.	0.5	2
82	Web-Based Identification of Evolutionary Conserved DNA cis-Regulatory Elements. Methods in Molecular Biology, 2007, 395, 425-436.	0.9	2
83	Editorial: Advances in Mathematical and Computational Oncology. Frontiers in Physiology, 2022, 13, 889198.	2.8	2
84	Web-Based Primer Design Software for Genome-Scale Genotyping by Pyrosequencing[®]. , 2007, 373, 25-38.		1
85	ECCB 2018: The 17th European Conference on Computational Biology. Bioinformatics, 2018, 34, i595-i598.	4.1	1
86	A Pipeline for Integrated Theory and Data-Driven Modeling of Biomedical Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 811-822.	3.0	1
87	Surveillance for melanoma (MEL): Results of a database study of stage I-III MEL.. Journal of Clinical Oncology, 2018, 36, 9586-9586.	1.6	1
88	Abstract 473: A tumor and immune related miRNA signature predicts progression-free survival of melanoma patients treated with ipilimumab. , 2016, , .		1
89	In Silico Discovery of DNA Regulatory Sites and Modules. , 2009, , 353-366.		0
90	MicroRNAs: Target Prediction and Involvement in Gene Regulatory Networks. , 0, , 291-309.		0

#	ARTICLE	IF	CITATIONS
91	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
92	microRNA (miRNA) expression profiling predicts clinical outcome of carboplatin/paclitaxel-based therapy (CP) in metastatic melanoma (MM) treated on the intergroup trial E2603.. <i>Journal of Clinical Oncology</i> , 2014, 32, 9048-9048.	1.6	0
93	Abstract A1-14: Discovery of a functional SNP in an estrogen receptor binding site in the IGF1R gene. , 2015, , .		0
94	Abstract 479: Modeling miRNA induced silencing in breast cancer with PARADIGM. , 2017, , .		0