Ilias Tagkopoulos

List of Publications by Year
in descending order

63 papers	2,834 citations	304743 22 h-index	189892 50 g-index
70 all docs	70 docs citations	70 times ranked	4798 citing authors

#	Article	IF	Citations
1	An Arabidopsis gene regulatory network for secondary cell wall synthesis. Nature, 2015, 517, 571-575.	27.8	636
2	Predictive Behavior Within Microbial Genetic Networks. Science, 2008, 320, 1313-1317.	12.6	414
3	Benzalkonium Chlorides: Uses, Regulatory Status, and Microbial Resistance. Applied and Environmental Microbiology, 2019, 85, .	3.1	178
4	From vital signs to clinical outcomes for patients with sepsis: a machine learning basis for a clinical decision support system. Journal of the American Medical Informatics Association: JAMIA, 2014, 21, 315-325.	4.4	139
5	Multi-omics integration accurately predicts cellular state in unexplored conditions for Escherichia coli. Nature Communications, 2016, 7, 13090.	12.8	123
6	Transcriptional Network Analysis Identifies BACH1 as a Master Regulator of Breast Cancer Bone Metastasis. Journal of Biological Chemistry, 2012, 287, 33533-33544.	3.4	118
7	Evolutionary potential, cross‐stress behavior and the genetic basis of acquired stress resistance in <i>Escherichia coli</i>. Molecular Systems Biology, 2013, 9, 643.	7.2	115
8	An integrative, multi‐scale, genome‐wide model reveals the phenotypic landscape of <i><scp>E</scp>scherichia coli</i>. Molecular Systems Biology, 2014, 10, 735.	7.2	73
9	Data integration and predictive modeling methods for multi-omics datasets. Molecular Omics, 2018, 14, 8-25.	2.8	73
10	From Data to Optimal Decision Making: A Data-Driven, Probabilistic Machine Learning Approach to Decision Support for Patients With Sepsis. JMIR Medical Informatics, 2015, 3, e11.	2.6	62
11	Application of machine learning in rheumatic disease research. Korean Journal of Internal Medicine, 2019, 34, 708-722.	1.7	48
12	Biocide-Induced Emergence of Antibiotic Resistance in Escherichia coli. Frontiers in Microbiology, 2021, 12, 640923.	3.5	43
13	SBROME: A Scalable Optimization and Module Matching Framework for Automated Biosystems Design. ACS Synthetic Biology, 2013, 2, 263-273.	3.8	42
14	Kinetic Characterization of 100 Glycoside Hydrolase Mutants Enables the Discovery of Structural Features Correlated with Kinetic Constants. PLoS ONE, 2016, 11, e0147596.	2.5	42
15	A synthetic biology approach to self-regulatory recombinant protein production in Escherichia coli. Journal of Biological Engineering, 2012, 6, 2.	4.7	39
16	Integrated omics analyses of retrograde signaling mutant delineate interrelated stress‐response strata. Plant Journal, 2017, 91, 70-84.	5.7	36
17	Predicting early risk of chronic kidney disease in cats using routine clinical laboratory tests and machine learning. Journal of Veterinary Internal Medicine, 2019, 33, 2644-2656.	1.6	36
18	The genetic and transcriptional basis of short and long term adaptation across multiple stresses in <i>Escherichia coli</i>. Molecular Biology and Evolution, 2017, 34, msw269.	8.9	35

#	Article	IF	Citations
19	Compendium of skin molecular signatures identifies key pathological features associated with fibrosis in systemic sclerosis. Annals of the Rheumatic Diseases, 2019, 78, 817-825.	0.9	32
20	The Computational Diet: A Review of Computational Methods Across Diet, Microbiome, and Health. Frontiers in Microbiology, 2020, 11, 393.	3.5	32
21	Horizontal gene transfer dynamics and distribution of fitness effects during microbial in silico evolution. BMC Bioinformatics, 2012, 13, S13.	2.6	31
22	Genetic Neural Networks: an artificial neural network architecture for capturing gene expression relationships. Bioinformatics, 2019, 35, 2226-2234.	4.1	27
23	Preliminary Techno-Economic Assessment of Animal Cell-Based Meat. Foods, 2021, 10, 3.	4.3	27
24	Microbial Forensics: Predicting Phenotypic Characteristics and Environmental Conditions from Large-Scale Gene Expression Profiles. PLoS Computational Biology, 2015, 11, e1004127.	3.2	26
25	Predicting the evolution of Escherichia coli by a data-driven approach. Nature Communications, 2018, 9, 3562.	12.8	26
26	Automatic Design of Synthetic Gene Circuits through Mixed Integer Non-linear Programming. PLoS ONE, 2012, 7, e35529.	2.5	22
27	Optimal Part and Module Selection for Synthetic Gene Circuit Design Automation. ACS Synthetic Biology, 2014, 3, 556-564.	3.8	22
28	Nutrient Estimation from 24-Hour Food Recalls Using Machine Learning and Database Mapping: A Case Study with Lactose. Nutrients, 2019, 11, 3045.	4.1	22
29	Methane and fatty acid metabolism pathways are predictive of Low-FODMAP diet efficacy for patients with irritable bowel syndrome. Clinical Nutrition, 2021, 40, 4414-4421.	5.0	22
30	DeepPep: Deep proteome inference from peptide profiles. PLoS Computational Biology, 2017, 13, e1005661.	3.2	22
31	Compendium of synovial signatures identifies pathologic characteristics for predicting treatment response in rheumatoid arthritis patients. Clinical Immunology, 2019, 202, 1-10.	3.2	21
32	Microbial evolution in vivo and in silico: methods and applications. Integrative Biology (United) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 222	1.3	18
33	Elucidating Substrate Promiscuity within the FabI Enzyme Family. ACS Chemical Biology, 2017, 12, 2465-2473.	3.4	17
34	Promoter Element Arising from the Fusion of Standard BioBrick Parts. ACS Synthetic Biology, 2013, 2, 111-120.	3.8	15
35	Accelerated knowledge discovery from omics data by optimal experimental design. Nature Communications, 2020, 11, 5026.	12.8	15
36	A systems biology analysis of brain microvascular endothelial cell lipotoxicity. BMC Systems Biology, 2014, 8, 80.	3.0	14

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37	A Parts Database with Consensus Parameter Estimation for Synthetic Circuit Design. ACS Synthetic Biology, 2016, 5, 1412-1420.	3.8	13
38	Short- and Long-Term Transcriptomic Responses of Escherichia coli to Biocides: a Systems Analysis. Applied and Environmental Microbiology, 2020, 86, .	3.1	13
39	Adaptive laboratory evolution for improved tolerance of isobutyl acetate in Escherichia coli. Metabolic Engineering, 2022, 69, 50-58.	7.0	13
40	Discovery, Design, and Structural Characterization of Alkane-Producing Enzymes across the Ferritin-like Superfamily. Biochemistry, 2020, 59, 3834-3843.	2.5	11
41	Guided evolution of in silico microbial populations in complex environments accelerates evolutionary rates through a step-wise adaptation. BMC Bioinformatics, 2012, 13, S10.	2.6	9
42	Population collapse and adaptive rescue during longâ€term chemostat fermentation. Biotechnology and Bioengineering, 2019, 116, 693-703.	3.3	9
43	Network-based modeling of drug effects on disease module in systemic sclerosis. Scientific Reports, 2020, 10, 13393.	3.3	9
44	Fast and Accurate Circuit Design Automation through Hierarchical Model Switching. ACS Synthetic Biology, 2015, 4, 890-897.	3.8	8
45	Using Word Embeddings to Learn a Better Food Ontology. Frontiers in Artificial Intelligence, 2020, 3, 584784.	3.4	8
46	Reduced Graphene Oxide-Metalloporphyrin Sensors for Human Breath Screening. Applied Sciences (Switzerland), 2021, 11, 11290.	2.5	8
47	SYMMETRIC AND ASYMMETRIC MULTI-MODALITY BICLUSTERING ANALYSIS FOR MICROARRAY DATA MATRIX. Journal of Bioinformatics and Computational Biology, 2006, 04, 275-298.	0.8	7
48	A Bayesian network for early diagnosis of sepsis patients: a basis for a clinical decision support system. , 2012, , .		7
49	RiboTALE: A modular, inducible system for accurate gene expression control. Scientific Reports, 2015, 5, 10658.	3.3	5
50	A dataâ€driven, machine learning framework for optimal pest management in cotton. Ecosphere, 2016, 7, e01263.	2.2	5
51	Tolerance to Glutaraldehyde in Escherichia coli Mediated by Overexpression of the Aldehyde Reductase YqhD by YqhC. Frontiers in Microbiology, 2021, 12, 680553.	3.5	5
52	Knowledge integration and decision support for accelerated discovery of antibiotic resistance genes. Nature Communications, 2022, 13, 2360.	12.8	5
53	A scalable multi-scale framework for parallel simulation and visualization of microbial evolution. , 2011, , .		4
54	Microbial factories under control. Bioengineered, 2013, 4, 5-8.	3.2	4

#	ARTICLE	IF	CITATIONS
55	BWCNN: Blink to Word, a Real-Time Convolutional Neural Network Approach. Lecture Notes in Computer Science, 2020, , 133-140.	1.3	4
56	Predictive Behavior within Microbial Genetic Networks. Topologica, 2009, 2, 018.	0.3	3
57	A flood-based information flow analysis and network minimization method for gene regulatory networks. BMC Bioinformatics, 2013, 14, 137.	2.6	3
58	Novel classification of axial spondyloarthritis to predict radiographic progression using machine learning. Clinical and Experimental Rheumatology, 2021, 39, 508-518.	0.8	3
59	Novel classification of axial spondyloarthritis to predict radiographic progression using machine learning. Clinical and Experimental Rheumatology, 2021, 39, 508-518.	0.8	2
60	Identification of Differential, Health-Related Compounds in Chardonnay Marc through Network-Based Meta-Analysis. Current Developments in Nutrition, 2020, 4, nzaa045_108.	0.3	1
61	Special report: AI Institute for next generation food systems (AIFS). Computers and Electronics in Agriculture, 2022, 196, 106819.	7.7	1
62	Understanding the Formation and Mechanism of Anticipatory Responses in Escherichia coli. International Journal of Molecular Sciences, 2022, 23, 5985.	4.1	1
63	A robust, library-based, optimization-driven method for automatic gene circuit design. , 2012, , .		0