

Ilias Tagkopoulos

List of Publications by Year in descending order

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Version: 2024-02-01

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 | Adaptive laboratory evolution for improved tolerance of isobutyl acetate in Escherichia coli. <i>Metabolic Engineering</i> , 2022, 69, 50-58. | 7.0 | 13 |
| 2 | Special report: AI Institute for next generation food systems (AIFS). <i>Computers and Electronics in Agriculture</i> , 2022, 196, 106819. | 7.7 | 1 |
| 3 | Knowledge integration and decision support for accelerated discovery of antibiotic resistance genes. <i>Nature Communications</i> , 2022, 13, 2360. | 12.8 | 5 |
| 4 | Understanding the Formation and Mechanism of Anticipatory Responses in Escherichia coli. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5985. | 4.1 | 1 |
| 5 | Biocide-Induced Emergence of Antibiotic Resistance in Escherichia coli. <i>Frontiers in Microbiology</i> , 2021, 12, 640923. | 3.5 | 43 |
| 6 | Methane and fatty acid metabolism pathways are predictive of Low-FODMAP diet efficacy for patients with irritable bowel syndrome. <i>Clinical Nutrition</i> , 2021, 40, 4414-4421. | 5.0 | 22 |
| 7 | Tolerance to Glutaraldehyde in Escherichia coli Mediated by Overexpression of the Aldehyde Reductase YqhD by YqhC. <i>Frontiers in Microbiology</i> , 2021, 12, 680553. | 3.5 | 5 |
| 8 | Preliminary Techno-Economic Assessment of Animal Cell-Based Meat. <i>Foods</i> , 2021, 10, 3. | 4.3 | 27 |
| 9 | Reduced Graphene Oxide-Metalloporphyrin Sensors for Human Breath Screening. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 11290. | 2.5 | 8 |
| 10 | Novel classification of axial spondyloarthritis to predict radiographic progression using machine learning. <i>Clinical and Experimental Rheumatology</i> , 2021, 39, 508-518. | 0.8 | 2 |
| 11 | Novel classification of axial spondyloarthritis to predict radiographic progression using machine learning. <i>Clinical and Experimental Rheumatology</i> , 2021, 39, 508-518. | 0.8 | 3 |
| 12 | Identification of Differential, Health-Related Compounds in Chardonnay Marc through Network-Based Meta-Analysis. <i>Current Developments in Nutrition</i> , 2020, 4, nzaa045_108. | 0.3 | 1 |
| 13 | Network-based modeling of drug effects on disease module in systemic sclerosis. <i>Scientific Reports</i> , 2020, 10, 13393. | 3.3 | 9 |
| 14 | Accelerated knowledge discovery from omics data by optimal experimental design. <i>Nature Communications</i> , 2020, 11, 5026. | 12.8 | 15 |
| 15 | Discovery, Design, and Structural Characterization of Alkane-Producing Enzymes across the Ferritin-like Superfamily. <i>Biochemistry</i> , 2020, 59, 3834-3843. | 2.5 | 11 |
| 16 | Short- and Long-Term Transcriptomic Responses of Escherichia coli to Biocides: a Systems Analysis. <i>Applied and Environmental Microbiology</i> , 2020, 86, . | 3.1 | 13 |
| 17 | The Computational Diet: A Review of Computational Methods Across Diet, Microbiome, and Health. <i>Frontiers in Microbiology</i> , 2020, 11, 393. | 3.5 | 32 |
| 18 | Using Word Embeddings to Learn a Better Food Ontology. <i>Frontiers in Artificial Intelligence</i> , 2020, 3, 584784. | 3.4 | 8 |

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|----|---|------|-----------|
| 19 | BWCNN: Blink to Word, a Real-Time Convolutional Neural Network Approach. Lecture Notes in Computer Science, 2020, , 133-140. | 1.3 | 4 |
| 20 | 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 |
| 21 | Benzalkonium Chlorides: Uses, Regulatory Status, and Microbial Resistance. Applied and Environmental Microbiology, 2019, 85, . | 3.1 | 178 |
| 22 | Compendium of synovial signatures identifies pathologic characteristics for predicting treatment response in rheumatoid arthritis patients. Clinical Immunology, 2019, 202, 1-10. | 3.2 | 21 |
| 23 | 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 |
| 24 | 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 |
| 25 | Genetic Neural Networks: an artificial neural network architecture for capturing gene expression relationships. Bioinformatics, 2019, 35, 2226-2234. | 4.1 | 27 |
| 26 | Population collapse and adaptive rescue during long-term chemostat fermentation. Biotechnology and Bioengineering, 2019, 116, 693-703. | 3.3 | 9 |
| 27 | Application of machine learning in rheumatic disease research. Korean Journal of Internal Medicine, 2019, 34, 708-722. | 1.7 | 48 |
| 28 | Data integration and predictive modeling methods for multi-omics datasets. Molecular Omics, 2018, 14, 8-25. | 2.8 | 73 |
| 29 | Predicting the evolution of Escherichia coli by a data-driven approach. Nature Communications, 2018, 9, 3562. | 12.8 | 26 |
| 30 | The genetic and transcriptional basis of short and long term adaptation across multiple stresses in Escherichia coli. Molecular Biology and Evolution, 2017, 34, msw269. | 8.9 | 35 |
| 31 | Integrated omics analyses of retrograde signaling mutant delineate interrelated stress-response strata. Plant Journal, 2017, 91, 70-84. | 5.7 | 36 |
| 32 | Elucidating Substrate Promiscuity within the FabI Enzyme Family. ACS Chemical Biology, 2017, 12, 2465-2473. | 3.4 | 17 |
| 33 | DeepPep: Deep proteome inference from peptide profiles. PLoS Computational Biology, 2017, 13, e1005661. | 3.2 | 22 |
| 34 | A Parts Database with Consensus Parameter Estimation for Synthetic Circuit Design. ACS Synthetic Biology, 2016, 5, 1412-1420. | 3.8 | 13 |
| 35 | Multi-omics integration accurately predicts cellular state in unexplored conditions for Escherichia coli. Nature Communications, 2016, 7, 13090. | 12.8 | 123 |
| 36 | A data-driven, machine learning framework for optimal pest management in cotton. Ecosphere, 2016, 7, e01263. | 2.2 | 5 |

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|----|---|------|-----------|
| 37 | 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 |
| 38 | Microbial Forensics: Predicting Phenotypic Characteristics and Environmental Conditions from Large-Scale Gene Expression Profiles. PLoS Computational Biology, 2015, 11, e1004127. | 3.2 | 26 |
| 39 | RiboTALE: A modular, inducible system for accurate gene expression control. Scientific Reports, 2015, 5, 10658. | 3.3 | 5 |
| 40 | Fast and Accurate Circuit Design Automation through Hierarchical Model Switching. ACS Synthetic Biology, 2015, 4, 890-897. | 3.8 | 8 |
| 41 | An Arabidopsis gene regulatory network for secondary cell wall synthesis. Nature, 2015, 517, 571-575. | 27.8 | 636 |
| 42 | 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 |
| 43 | A systems biology analysis of brain microvascular endothelial cell lipotoxicity. BMC Systems Biology, 2014, 8, 80. | 3.0 | 14 |
| 44 | An integrative, multi-scale, genome-wide model reveals the phenotypic landscape of <i>Escherichia coli</i> . Molecular Systems Biology, 2014, 10, 735. | 7.2 | 73 |
| 45 | Optimal Part and Module Selection for Synthetic Gene Circuit Design Automation. ACS Synthetic Biology, 2014, 3, 556-564. | 3.8 | 22 |
| 46 | 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 |
| 47 | A flood-based information flow analysis and network minimization method for gene regulatory networks. BMC Bioinformatics, 2013, 14, 137. | 2.6 | 3 |
| 48 | Promoter Element Arising from the Fusion of Standard BioBrick Parts. ACS Synthetic Biology, 2013, 2, 111-120. | 3.8 | 15 |
| 49 | SBROME: A Scalable Optimization and Module Matching Framework for Automated Biosystems Design. ACS Synthetic Biology, 2013, 2, 263-273. | 3.8 | 42 |
| 50 | Microbial evolution in vivo and in silico: methods and applications. Integrative Biology (United Kingdom), 2012, 4, 18-22. | 1.3 | 18 |
| 51 | 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 |
| 52 | Microbial factories under control. Bioengineered, 2013, 4, 5-8. | 3.2 | 4 |
| 53 | A Bayesian network for early diagnosis of sepsis patients: a basis for a clinical decision support system. , 2012, , . | | 7 |
| 54 | 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 |

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|----|---|------|-----------|
| 55 | A robust, library-based, optimization-driven method for automatic gene circuit design. , 2012, , . | | 0 |
| 56 | Automatic Design of Synthetic Gene Circuits through Mixed Integer Non-linear Programming. PLoS ONE, 2012, 7, e35529. | 2.5 | 22 |
| 57 | A synthetic biology approach to self-regulatory recombinant protein production in Escherichia coli. Journal of Biological Engineering, 2012, 6, 2. | 4.7 | 39 |
| 58 | 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 |
| 59 | Horizontal gene transfer dynamics and distribution of fitness effects during microbial in silico evolution. BMC Bioinformatics, 2012, 13, S13. | 2.6 | 31 |
| 60 | A scalable multi-scale framework for parallel simulation and visualization of microbial evolution. , 2011, , . | | 4 |
| 61 | Predictive Behavior within Microbial Genetic Networks. Topologica, 2009, 2, 018. | 0.3 | 3 |
| 62 | Predictive Behavior Within Microbial Genetic Networks. Science, 2008, 320, 1313-1317. | 12.6 | 414 |
| 63 | SYMMETRIC AND ASYMMETRIC MULTI-MODALITY BICLUSTERING ANALYSIS FOR MICROARRAY DATA MATRIX. Journal of Bioinformatics and Computational Biology, 2006, 04, 275-298. | 0.8 | 7 |