## **Athanasios Typas**

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2776785/publications.pdf

Version: 2024-02-01

70961 118652 11,321 62 41 62 citations h-index g-index papers 84 84 84 15762 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Extensive impact of non-antibiotic drugs on human gut bacteria. Nature, 2018, 555, 623-628.	13.7	1,339
2	From the regulation of peptidoglycan synthesis to bacterial growth and morphology. Nature Reviews Microbiology, 2012, 10, 123-136.	13.6	1,062
3	Salt-responsive gut commensal modulates TH17 axis and disease. Nature, 2017, 551, 585-589.	13.7	896
4	Phenotypic Landscape of a Bacterial Cell. Cell, 2011, 144, 143-156.	13.5	623
5	Recovery of gut microbiota of healthy adults following antibiotic exposure. Nature Microbiology, 2018, 3, 1255-1265.	5.9	483
6	Construction and Analysis of Two Genome-Scale Deletion Libraries for Bacillus subtilis. Cell Systems, 2017, 4, 291-305.e7.	2.9	457
7	A new antibiotic selectively kills Gram-negative pathogens. Nature, 2019, 576, 459-464.	13.7	456
8	Selective Ribosome Profiling Reveals the Cotranslational Chaperone Action of Trigger Factor InÂVivo. Cell, 2011, 147, 1295-1308.	13.5	419
9	Country-specific antibiotic use practices impact the human gut resistome. Genome Research, 2013, 23, 1163-1169.	2.4	356
10	Regulation of Peptidoglycan Synthesis by Outer-Membrane Proteins. Cell, 2010, 143, 1097-1109.	13.5	335
11	Species-specific activity of antibacterial drug combinations. Nature, 2018, 559, 259-263.	13.7	276
12	Yeast Creates a Niche for Symbiotic Lactic Acid Bacteria through Nitrogen Overflow. Cell Systems, 2017, 5, 345-357.e6.	2.9	247
13	Emerging and evolving concepts in gene essentiality. Nature Reviews Genetics, 2018, 19, 34-49.	7.7	230
14	High-throughput, quantitative analyses of genetic interactions in E. coli. Nature Methods, 2008, 5, 781-787.	9.0	214
15	A Dual-Mechanism Antibiotic Kills Gram-Negative Bacteria and Avoids Drug Resistance. Cell, 2020, 181, 1518-1532.e14.	13.5	202
16	Fe-S Cluster Biosynthesis Controls Uptake of Aminoglycosides in a ROS-Less Death Pathway. Science, 2013, 340, 1583-1587.	6.0	201
17	Host-Microbe Co-metabolism Dictates Cancer Drug Efficacy in C.Âelegans. Cell, 2017, 169, 442-456.e18.	13.5	198
18	Nutritional preferences of human gut bacteria reveal their metabolic idiosyncrasies. Nature Microbiology, 2018, 3, 514-522.	5.9	196

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19	Pervasive Protein Thermal Stability Variation during the Cell Cycle. Cell, 2018, 173, 1495-1507.e18.	13.5	183
20	Bioaccumulation of therapeutic drugs by human gut bacteria. Nature, 2021, 597, 533-538.	13.7	159
21	Unravelling the collateral damage of antibiotics on gut bacteria. Nature, 2021, 599, 120-124.	13.7	159
22	Detecting Envelope Stress by Monitoring β-Barrel Assembly. Cell, 2014, 159, 1652-1664.	13.5	154
23	Coordination of peptidoglycan synthesis and outer membrane constriction during Escherichia coli cell division. ELife, 2015, 4, .	2.8	154
24	Thermal proteome profiling for interrogating protein interactions. Molecular Systems Biology, 2020, 16, e9232.	3.2	150
25	The molecular basis of selective promoter activation by the ?Ssubunit of RNA polymerase. Molecular Microbiology, 2007, 63, 1296-1306.	1.2	147
26	Thermal proteome profiling in bacteria: probing protein state <i>inÂvivo</i> . Molecular Systems Biology, 2018, 14, e8242.	3.2	130
27	Stationary phase reorganisation of the Escherichia coli transcription machinery by Crl protein, a fine-tuner of ls activity and levels. EMBO Journal, 2007, 26, 1569-1578.	3.5	107
28	A Genome-Wide Screen for Bacterial Envelope Biogenesis Mutants Identifies a Novel Factor Involved in Cell Wall Precursor Metabolism. PLoS Genetics, 2014, 10, e1004056.	1.5	99
29	An atlas of human kinase regulation. Molecular Systems Biology, 2016, 12, 888.	3.2	98
30	Outer-membrane lipoprotein LpoB spans the periplasm to stimulate the peptidoglycan synthase PBP1B. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 8197-8202.	3.3	95
31	Escherichia coli limits Salmonella Typhimurium infections after diet shifts and fat-mediated microbiota perturbation in mice. Nature Microbiology, 2019, 4, 2164-2174.	5.9	88
32	Bacterial protein networks: properties and functions. Nature Reviews Microbiology, 2015, 13, 559-572.	13.6	86
33	A resource of variant effect predictions of single nucleotide variants in model organisms. Molecular Systems Biology, 2018, 14, e8430.	3.2	84
34	Role of the spacer between the -35 and -10 regions in sigmas promoter selectivity in Escherichia coli. Molecular Microbiology, 2006, 59, 1037-1051.	1.2	73
35	Outer membrane lipoprotein NlpI scaffolds peptidoglycan hydrolases within multiâ€enzyme complexes in <i>Escherichia coli</i> . EMBO Journal, 2020, 39, e102246.	3.5	69
36	A tool named Iris for versatile high-throughput phenotyping in microorganisms. Nature Microbiology, 2017, 2, 17014.	5.9	68

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37	The $\ddot{l}fS$ subunit of RNA polymerase as a signal integrator and network master regulator in the general stress response in Escherichia coli. Science Progress, 2007, 90, 103-127.	1.0	65
38	Systematically investigating the impact of medication on the gut microbiome. Current Opinion in Microbiology, 2017, 39, 128-135.	2.3	65
39	Towards a mechanistic understanding of reciprocal drug–microbiome interactions. Molecular Systems Biology, 2021, 17, e10116.	3.2	64
40	Escherichia coli $\sharp f$ 70 senses sequence and conformation of the promoter spacer region. Nucleic Acids Research, 2011, 39, 5109-5118.	6.5	58
41	The functional proteome landscape of Escherichia coli. Nature, 2020, 588, 473-478.	13.7	58
42	Impact of phosphorylation on thermal stability of proteins. Nature Methods, 2021, 18, 757-759.	9.0	58
43	Proton Motive Force Disruptors Block Bacterial Competence and Horizontal Gene Transfer. Cell Host and Microbe, 2020, 27, 544-555.e3.	5.1	53
44	High-throughput approaches to understanding gene function and mapping network architecture in bacteria. Current Opinion in Microbiology, 2013, 16, 199-206.	2.3	52
45	Bacterial retrons encode phage-defending tripartite toxin–antitoxin systems. Nature, 2022, 609, 144-150.	13.7	52
46	The impact of the genetic background on gene deletion phenotypes in <i>Saccharomyces cerevisiae</i> Molecular Systems Biology, 2019, 15, e8831.	3.2	44
47	Global mapping of Salmonella enterica-host protein-protein interactions during infection. Cell Host and Microbe, 2021, 29, 1316-1332.e12.	5.1	39
48	Phenotype inference in an Escherichia coli strain panel. ELife, 2017, 6, .	2.8	38
49	Differential ability of $\parallel f$ s and $\parallel f$ 70 of Escherichia coli to utilize promoters containing half or full UP-element sites. Molecular Microbiology, 2004, 55, 250-260.	1.2	37
50	A Chemical-Genomic Screen of Neglected Antibiotics Reveals Illicit Transport of Kasugamycin and Blasticidin S. PLoS Genetics, 2016, 12, e1006124.	1.5	36
51	Spatiotemporal proteomics uncovers cathepsin-dependent macrophage cell death during Salmonella infection. Nature Microbiology, 2020, 5, 1119-1133.	5.9	30
52	The ?35 sequence location and the Fis?sigma factor interface determine ?Sselectivity of the proP (P2) promoter in Escherichia coli. Molecular Microbiology, 2007, 63, 780-96.	1.2	28
53	Chemical genetics in drug discovery. Current Opinion in Systems Biology, 2017, 4, 35-42.	1.3	26
54	Systematic Localization of Escherichia coli Membrane Proteins. MSystems, 2020, 5, .	1.7	24

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55	High-throughput functional characterization of protein phosphorylation sites in yeast. Nature Biotechnology, 2022, 40, 382-390.	9.4	24
56	SARSâ€CoVâ€2 infection remodels the host protein thermal stability landscape. Molecular Systems Biology, 2021, 17, e10188.	3.2	17
57	Dynamic protein complexes for cell growth. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 4355-4356.	3.3	13
58	Bioactivity assessment of natural compounds using machine learning models trained on target similarity between drugs. PLoS Computational Biology, 2022, 18, e1010029.	1.5	10
59	Transcriptional and Post-Transcriptional Polar Effects in Bacterial Gene Deletion Libraries. MSystems, 2021, 6, e0081321.	1.7	9
60	Individuality and temporal stability of the human gut microbiome. Central Asian Journal of Global Health, 2013, 2, 120.	0.6	6
61	Early midcell localization of Escherichia coli PBP4 supports the function of peptidoglycan amidases. PLoS Genetics, 2022, 18, e1010222.	1.5	5
62	Editorial overview: Microbial systems biology. Current Opinion in Microbiology, 2015, 27, viii-ix.	2.3	0