Athanasios Typas

List of Publications by Year
in descending order

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

#	Article	IF	Citations
1	High-throughput functional characterization of protein phosphorylation sites in yeast. Nature Biotechnology, 2022, 40, 382-390.	9.4	24
2	Bioactivity assessment of natural compounds using machine learning models trained on target similarity between drugs. PLoS Computational Biology, 2022, 18, e1010029.	1.5	10
3	Early midcell localization of Escherichia coli PBP4 supports the function of peptidoglycan amidases. PLoS Genetics, 2022, 18, e1010222.	1.5	5
4	Bacterial retrons encode phage-defending tripartite toxinâ€“antitoxin systems. Nature, 2022, 609, 144-150.	13.7	52
5	SARSâ€CoVâ€2 infection remodels the host protein thermal stability landscape. Molecular Systems Biology, 2021, 17, e10188.	3.2	17
6	Towards a mechanistic understanding of reciprocal drugâ€“microbiome interactions. Molecular Systems Biology, 2021, 17, e10116.	3.2	64
7	Impact of phosphorylation on thermal stability of proteins. Nature Methods, 2021, 18, 757-759.	9.0	58
8	Global mapping of Salmonella enterica-host protein-protein interactions during infection. Cell Host and Microbe, 2021, 29, 1316-1332.e12.	5.1	39
9	Transcriptional and Post-Transcriptional Polar Effects in Bacterial Gene Deletion Libraries. MSystems, 2021, 6, e0081321.	1.7	9
10	Bioaccumulation of therapeutic drugs by human gut bacteria. Nature, 2021, 597, 533-538.	13.7	159
11	Unravelling the collateral damage of antibiotics on gut bacteria. Nature, 2021, 599, 120-124.	13.7	159
12	The functional proteome landscape of Escherichia coli. Nature, 2020, 588, 473-478.	13.7	58
13	Systematic Localization of Escherichia coli Membrane Proteins. MSystems, 2020, 5, .	1.7	24
14	A Dual-Mechanism Antibiotic Kills Gram-Negative Bacteria and Avoids Drug Resistance. Cell, 2020, 181, 1518-1532.e14.	13.5	202
15	Spatiotemporal proteomics uncovers cathepsin-dependent macrophage cell death during Salmonella infection. Nature Microbiology, 2020, 5, 1119-1133.	5.9	30
16	Proton Motive Force Disruptors Block Bacterial Competence and Horizontal Gene Transfer. Cell Host and Microbe, 2020, 27, 544-555.e3.	5.1	53
17	Thermal proteome profiling for interrogating protein interactions. Molecular Systems Biology, 2020, 16, e9232.	3.2	150
18	Outer membrane lipoprotein NlpI scaffolds peptidoglycan hydrolases within multiâ€enzyme complexes in <i>Escherichia coli</i>. EMBO Journal, 2020, 39, e102246.	3.5	69

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19	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
20	A new antibiotic selectively kills Gram-negative pathogens. Nature, 2019, 576, 459-464.	13.7	456
21	The impact of the genetic background on gene deletion phenotypes in <i>Saccharomyces cerevisiae</i>. Molecular Systems Biology, 2019, 15, e8831.	3.2	44
22	Pervasive Protein Thermal Stability Variation during the Cell Cycle. Cell, 2018, 173, 1495-1507.e18.	13.5	183
23	Extensive impact of non-antibiotic drugs on human gut bacteria. Nature, 2018, 555, 623-628.	13.7	1,339
24	Nutritional preferences of human gut bacteria reveal their metabolic idiosyncrasies. Nature Microbiology, 2018, 3, 514-522.	5.9	196
25	Emerging and evolving concepts in gene essentiality. Nature Reviews Genetics, 2018, 19, 34-49.	7.7	230
26	A resource of variant effect predictions of single nucleotide variants in model organisms. Molecular Systems Biology, 2018, 14, e8430.	3.2	84
27	Recovery of gut microbiota of healthy adults following antibiotic exposure. Nature Microbiology, 2018, 3, 1255-1265.	5.9	483
28	Species-specific activity of antibacterial drug combinations. Nature, 2018, 559, 259-263.	13.7	276
29	Thermal proteome profiling in bacteria: probing protein state <i>inÂvivo</i>. Molecular Systems Biology, 2018, 14, e8242.	3.2	130
30	A tool named Iris for versatile high-throughput phenotyping in microorganisms. Nature Microbiology, 2017, 2, 17014.	5.9	68
31	Construction and Analysis of Two Genome-Scale Deletion Libraries for Bacillus subtilis. Cell Systems, 2017, 4, 291-305.e7.	2.9	457
32	Host-Microbe Co-metabolism Dictates Cancer Drug Efficacy in C.Âelegans. Cell, 2017, 169, 442-456.e18.	13.5	198
33	Yeast Creates a Niche for Symbiotic Lactic Acid Bacteria through Nitrogen Overflow. Cell Systems, 2017, 5, 345-357.e6.	2.9	247
34	Chemical genetics in drug discovery. Current Opinion in Systems Biology, 2017, 4, 35-42.	1.3	26
35	Salt-responsive gut commensal modulates TH17 axis and disease. Nature, 2017, 551, 585-589.	13.7	896
36	Systematically investigating the impact of medication on the gut microbiome. Current Opinion in Microbiology, 2017, 39, 128-135.	2.3	65

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37	Phenotype inference in an Escherichia coli strain panel. ELife, 2017, 6, .	2.8	38
38	A Chemical-Genomic Screen of Neglected Antibiotics Reveals Illicit Transport of Kasugamycin and Blasticidin S. PLoS Genetics, 2016, 12, e1006124.	1.5	36
39	An atlas of human kinase regulation. Molecular Systems Biology, 2016, 12, 888.	3.2	98
40	Bacterial protein networks: properties and functions. Nature Reviews Microbiology, 2015, 13, 559-572.	13.6	86
41	Editorial overview: Microbial systems biology. Current Opinion in Microbiology, 2015, 27, viii-ix.	2.3	0
42	Coordination of peptidoglycan synthesis and outer membrane constriction during Escherichia coli cell division. ELife, 2015, 4, .	2.8	154
43	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
44	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
45	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
46	Detecting Envelope Stress by Monitoring Î²-Barrel Assembly. Cell, 2014, 159, 1652-1664.	13.5	154
47	High-throughput approaches to understanding gene function and mapping network architecture in bacteria. Current Opinion in Microbiology, 2013, 16, 199-206.	2.3	52
48	Country-specific antibiotic use practices impact the human gut resistome. Genome Research, 2013, 23, 1163-1169.	2.4	356
49	Fe-S Cluster Biosynthesis Controls Uptake of Aminoglycosides in a ROS-Less Death Pathway. Science, 2013, 340, 1583-1587.	6.0	201
50	Individuality and temporal stability of the human gut microbiome. Central Asian Journal of Global Health, 2013, 2, 120.	0.6	6
51	From the regulation of peptidoglycan synthesis to bacterial growth and morphology. Nature Reviews Microbiology, 2012, 10, 123-136.	13.6	1,062
52	Phenotypic Landscape of a Bacterial Cell. Cell, 2011, 144, 143-156.	13.5	623
53	Selective Ribosome Profiling Reveals the Cotranslational Chaperone Action of Trigger Factor InÂVivo. Cell, 2011, 147, 1295-1308.	13.5	419
54	Escherichia coli Ïƒ 70 senses sequence and conformation of the promoter spacer region. Nucleic Acids Research, 2011, 39, 5109-5118.	6.5	58

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55	Regulation of Peptidoglycan Synthesis by Outer-Membrane Proteins. Cell, 2010, 143, 1097-1109.	13.5	335
56	High-throughput, quantitative analyses of genetic interactions in E. coli. Nature Methods, 2008, 5, 781-787.	9.0	214
57	The ÏƒS 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
58	Stationary phase reorganisation of the Escherichia coli transcription machinery by Crl protein, a fine-tuner of Ïƒs activity and levels. EMBO Journal, 2007, 26, 1569-1578.	3.5	107
59	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
60	The molecular basis of selective promoter activation by the ?Ssubunit of RNA polymerase. Molecular Microbiology, 2007, 63, 1296-1306.	1.2	147
61	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
62	Differential ability of Ïƒs and Ïƒ70 of Escherichia coli to utilize promoters containing half or full UP-element sites. Molecular Microbiology, 2004, 55, 250-260.	1.2	37