

Chrystala Constantinidou

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11427334/publications.pdf>

Version: 2024-02-01

29
papers

4,166
citations

304602

22
h-index

501076

28
g-index

30
all docs

30
docs citations

30
times ranked

7092
citing authors

#	ARTICLE	IF	CITATIONS
1	Bridging the N-terminal and middle domains in FliG of the flagellar rotor. <i>Current Research in Structural Biology</i> , 2022, 4, 59-67.	1.1	2
2	P10 Rapid capture of uropathogenic bacteria and on-chip determination of antimicrobial resistance. <i>JAC-Antimicrobial Resistance</i> , 2022, 4, .	0.9	0
3	Posttranscriptional Regulation in Response to Different Environmental Stresses in <i>Campylobacter jejuni</i> . <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	1
4	Modification of Bacteriophages to Increase Their Association with Lung Epithelium Cells In Vitro. <i>Pharmaceuticals</i> , 2021, 14, 308.	1.7	5
5	Identification of an RNA sponge that controls the RoxS riboregulator of central metabolism in <i>Bacillus subtilis</i> . <i>Nucleic Acids Research</i> , 2021, 49, 6399-6419.	6.5	14
6	Comparison of CRISPR and Marker-Based Methods for the Engineering of Phage T7. <i>Viruses</i> , 2020, 12, 193.	1.5	23
7	The gut-adherent microbiota of PSC is distinct to that of IBD. <i>Gut</i> , 2017, 66, 386.1-388.	6.1	132
8	The Enigmatic Esx Proteins: Looking Beyond Mycobacteria. <i>Trends in Microbiology</i> , 2017, 25, 192-204.	3.5	109
9	Seeking the source of <i>Pseudomonas aeruginosa</i> infections in a recently opened hospital: an observational study using whole-genome sequencing. <i>BMJ Open</i> , 2014, 4, e006278.	0.8	104
10	Extensive Microbial and Functional Diversity within the Chicken Cecal Microbiome. <i>PLoS ONE</i> , 2014, 9, e91941.	1.1	359
11	A Culture-Independent Sequence-Based Metagenomics Approach to the Investigation of an Outbreak of Shiga-Toxigenic <i>Escherichia coli</i> O104:H4. <i>JAMA - Journal of the American Medical Association</i> , 2013, 309, 1502.	3.8	290
12	High-throughput bacterial genome sequencing: an embarrassment of choice, a world of opportunity. <i>Nature Reviews Microbiology</i> , 2012, 10, 599-606.	13.6	367
13	Genome sequencing in clinical microbiology. <i>Nature Biotechnology</i> , 2012, 30, 1068-1071.	9.4	37
14	High-Throughput Sequencing of 16S rRNA Gene Amplicons: Effects of Extraction Procedure, Primer Length and Annealing Temperature. <i>PLoS ONE</i> , 2012, 7, e38094.	1.1	65
15	Performance comparison of benchtop high-throughput sequencing platforms. <i>Nature Biotechnology</i> , 2012, 30, 434-439.	9.4	1,226
16	YieJ (CbrC) Mediates CreBC-Dependent Colicin E2 Tolerance in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2010, 192, 3329-3336.	1.0	17
17	Exposure of <i>Escherichia coli</i> and <i>Salmonella enterica</i> serovar Typhimurium to triclosan induces a species-specific response, including drug detoxification. <i>Journal of Antimicrobial Chemotherapy</i> , 2009, 64, 973-985.	1.3	65
18	Global responses of <i>Escherichia coli</i> to adverse conditions determined by microarrays and FT-IR spectroscopy. <i>Canadian Journal of Microbiology</i> , 2009, 55, 714-728.	0.8	44

#	ARTICLE	IF	CITATIONS
19	The NsrR Regulon of Escherichia coli K-12 Includes Genes Encoding the Hybrid Cluster Protein and the Periplasmic, Respiratory Nitrite Reductase. <i>Journal of Bacteriology</i> , 2007, 189, 4410-4417.	1.0	118
20	Deletion of a previously uncharacterized flagellar-hook-length control gene <i>fliK</i> modulates the σ^{54} -dependent regulon in <i>Campylobacter jejuni</i> . <i>Microbiology (United Kingdom)</i> , 2007, 153, 3099-3111.	0.7	26
21	Comparative Genomic Hybridization Detects Secondary Chromosomal Deletions in <i>Escherichia coli</i> K-12 MG1655 Mutants and Highlights Instability in the <i>flhDC</i> Region. <i>Journal of Bacteriology</i> , 2007, 189, 8786-8792.	1.0	15
22	The multicopper oxidase (CueO) and cell aggregation in <i>Escherichia coli</i> . <i>Environmental Microbiology</i> , 2007, 9, 2110-2116.	1.8	24
23	Analysis of fimbrial gene clusters and their expression in enterohaemorrhagic <i>Escherichia coli</i> O157:H7. <i>Environmental Microbiology</i> , 2006, 8, 1033-1047.	1.8	98
24	A Reassessment of the FNR Regulon and Transcriptomic Analysis of the Effects of Nitrate, Nitrite, NarXL, and NarQP as <i>Escherichia coli</i> K12 Adapts from Aerobic to Anaerobic Growth. <i>Journal of Biological Chemistry</i> , 2006, 281, 4802-4815.	1.6	234
25	The expression profile of <i>Escherichia coli</i> K-12 in response to minimal, optimal and excess copper concentrations. <i>Microbiology (United Kingdom)</i> , 2005, 151, 1187-1198.	0.7	131
26	Genomic Studies with <i>Escherichia coli</i> MelR Protein: Applications of Chromatin Immunoprecipitation and Microarrays. <i>Journal of Bacteriology</i> , 2004, 186, 6938-6943.	1.0	92
27	Regulators Encoded in the <i>Escherichia coli</i> Type III Secretion System 2 Gene Cluster Influence Expression of Genes within the Locus for Enterocyte Effacement in Enterohemorrhagic <i>E. coli</i> O157:H7. <i>Infection and Immunity</i> , 2004, 72, 7282-7293.	1.0	89
28	Identification of the CRP regulon using in vitro and in vivo transcriptional profiling. <i>Nucleic Acids Research</i> , 2004, 32, 5874-5893.	6.5	358
29	Roles of <i>rpoN</i> , <i>fliA</i> , and <i>flgR</i> in Expression of Flagella in <i>Campylobacter jejuni</i> . <i>Journal of Bacteriology</i> , 2001, 183, 2937-2942.	1.0	85