Julia Frunzke

List of Publications by Year
in descending order

65	3,225	136885 32	155592 55
papers	citations	h-index	g-index
77	77	77	2769
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The diversity of heme sensor systems â€“ heme-responsive transcriptional regulation mediated by transient heme protein interactions. FEMS Microbiology Reviews, 2022, 46, .	3.9	7
2	Aminoglycoside Antibiotics Inhibit Phage Infection by Blocking an Early Step of the Infection Cycle. MBio, 2022, 13, e0078322.	1.8	33
3	Isolation of Novel Xanthomonas Phages Infecting the Plant Pathogens X. translucens and X. campestris. Viruses, 2022, 14, 1449.	1.5	6
4	Automated Rational Strain Construction Based on High-Throughput Conjugation. ACS Synthetic Biology, 2021, 10, 589-599.	1.9	18
5	Genome Sequence of the Bacteriophage CL31 and Interaction with the Host Strain Corynebacterium glutamicum ATCC 13032. Viruses, 2021, 13, 495.	1.5	3
6	Identification of Gip as a novel phageâ€encoded gyrase inhibitor protein of <i>Corynebacterium glutamicum</i>. Molecular Microbiology, 2021, 116, 1268-1280.	1.2	3
7	Biosensor-based growth-coupling and spatial separation as an evolution strategy to improve small molecule production of Corynebacterium glutamicum. Metabolic Engineering, 2021, 68, 162-173.	3.6	11
8	Phylogenetic Distribution of WhiB- and Lsr2-Type Regulators in Actinobacteriophage Genomes. Microbiology Spectrum, 2021, 9, e0072721.	1.2	5
9	Biosensor-based isolation of amino acid-producing Vibrio natriegens strains. Metabolic Engineering Communications, 2021, 13, e00187.	1.9	5
10	Genome Sequence and Characterization of Five Bacteriophages Infecting Streptomyces coelicolor and Streptomyces venezuelae: Alderaan, Coruscant, Dagobah, Endor1 and Endor2. Viruses, 2020, 12, 1065.	1.5	17
11	Inducible Expression Systems Based on Xenogeneic Silencing and Counter-Silencing and Design of a Metabolic Toggle Switch. ACS Synthetic Biology, 2020, 9, 2023-2038.	1.9	8
12	Deciphering the Rules Underlying Xenogeneic Silencing and Counter-Silencing of Lsr2-like Proteins Using CgpS of Corynebacterium glutamicum as a Model. MBio, 2020, 11, .	1.8	15
13	HrrSA orchestrates a systemic response to heme and determines prioritization of terminal cytochrome oxidase expression. Nucleic Acids Research, 2020, 48, 6547-6562.	6.5	10
14	Impact of CO ₂ /HCO ₃ ^{â€“} Availability on Anaplerotic Flux in Pyruvate Dehydrogenase Complex-Deficient Corynebacterium glutamicum Strains. Journal of Bacteriology, 2019, 201, .	1.0	3
15	Generation of a Prophage-Free Variant of the Fast-Growing Bacterium Vibrio natriegens. Applied and Environmental Microbiology, 2019, 85, .	1.4	31
16	The MarR-Type Regulator MalR Is Involved in Stress-Responsive Cell Envelope Remodeling in Corynebacterium glutamicum. Frontiers in Microbiology, 2019, 10, 1039.	1.5	14
17	Evolutionary engineering of <i>Corynebacterium glutamicum</i>. Biotechnology Journal, 2019, 14, e1800444.	1.8	46
18	Impact of Xenogeneic Silencing on Phageâ€“Host Interactions. Journal of Molecular Biology, 2019, 431, 4670-4683.	2.0	34

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19	Toxic but tasty â€“ temporal dynamics and network architecture of hemeâ€responsive twoâ€component signaling in <i>Corynebacterium glutamicum</i>. Molecular Microbiology, 2019, 111, 1367-1381.	1.2	9
20	<i>Corynebacterium glutamicum</i> Chassis C1*: Building and Testing a Novel Platform Host for Synthetic Biology and Industrial Biotechnology. ACS Synthetic Biology, 2018, 7, 132-144.	1.9	63
21	Cytometry meets next-generation sequencing â€“ RNA-Seq of sorted subpopulations reveals regional replication and iron-triggered prophage induction in Corynebacterium glutamicum. Scientific Reports, 2018, 8, 14856.	1.6	14
22	Membrane Topology and Heme Binding of the Histidine Kinases HrrS and ChrS in Corynebacterium glutamicum. Frontiers in Microbiology, 2018, 9, 183.	1.5	14
23	Lichtblicke in der mikrobiellen Stammentwicklung. Nachrichten Aus Der Chemie, 2018, 66, 589-592.	0.0	0
24	Heterologous expression of the Halothiobacillus neapolitanus carboxysomal gene cluster in Corynebacterium glutamicum. Journal of Biotechnology, 2017, 258, 126-135.	1.9	40
25	Construction of Recombinant Pdu Metabolosome Shells for Small Molecule Production in <i>Corynebacterium glutamicum</i>. ACS Synthetic Biology, 2017, 6, 2145-2156.	1.9	41
26	Adaptive laboratory evolution of Corynebacterium glutamicum towards higher growth rates on glucose minimal medium. Scientific Reports, 2017, 7, 16780.	1.6	50
27	Chassis organism from Corynebacterium glutamicum â€“ Genome reduction as a tool toward improved strains for synthetic biology and industrial biotechnology. New Biotechnology, 2016, 33, S25.	2.4	1
28	Impact of LytR-CpsA-Psr Proteins on Cell Wall Biosynthesis in Corynebacterium glutamicum. Journal of Bacteriology, 2016, 198, 3045-3059.	1.0	30
29	Light-Controlled Cell Factories: Employing Photocaged Isopropyl-Î²- <scp>d</scp> -Thiogalactopyranoside for Light-Mediated Optimization of <i>lac</i> Promoter-Based Gene Expression and (+)-Valencene Biosynthesis in Corynebacterium glutamicum. Applied and Environmental Microbiology, 2016, 82, 6141-6149.	1.4	40
30	Establishment of synthetic microcompartments in Corynebacterium glutamicum. New Biotechnology, 2016, 33, S184.	2.4	0
31	Silencing of cryptic prophages inCorynebacterium glutamicum. Nucleic Acids Research, 2016, 44, gkw692.	6.5	35
32	Screening of an Escherichia coli promoter library for a phenylalanine biosensor. Applied Microbiology and Biotechnology, 2016, 100, 6739-6753.	1.7	42
33	Transcription factor-based biosensors in biotechnology: current state and future prospects. Applied Microbiology and Biotechnology, 2016, 100, 79-90.	1.7	178
34	Multiple ÏƒEcfG and NepR Proteins Are Involved in the General Stress Response in Methylobacterium extorquens. PLoS ONE, 2016, 11, e0152519.	1.1	12
35	Live cell imaging of <scp>SOS</scp> and prophage dynamics in isogenic bacterial populations. Molecular Microbiology, 2015, 98, 636-650.	1.2	41
36	Spatiotemporal microbial singleâ€cell analysis using a highâ€throughput microfluidics cultivation platform. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2015, 87, 1101-1115.	1.1	88

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37	Impact of Spontaneous Prophage Induction on the Fitness of Bacterial Populations and Host-Microbe Interactions. Journal of Bacteriology, 2015, 197, 410-419.	1.0	232
38	The general stress response in Alphaproteobacteria. Trends in Microbiology, 2015, 23, 164-171.	3.5	65
39	Chassis organism from <i>Corynebacterium glutamicum</i> â€" a topâ€down approach to identify and delete irrelevant gene clusters. Biotechnology Journal, 2015, 10, 290-301.	1.8	102
40	The manganese-responsive regulator MntR represses transcription of a predicted ZIP family metal ion transporter in Corynebacterium glutamicum. FEMS Microbiology Letters, 2015, 362, 1-10.	0.7	11
41	Biosensor-driven adaptive laboratory evolution of l-valine production in Corynebacterium glutamicum. Metabolic Engineering, 2015, 32, 184-194.	3.6	145
42	A prophage-encoded actin-like protein required for efficient viral DNA replication in bacteria. Nucleic Acids Research, 2015, 43, 5002-5016.	6.5	31
43	Genetically-encoded Biosensors for Strain Development and Single Cell Analysis of Corynebacterium glutamicum. , 2015, , 179-196.		2
44	Application of a Genetically Encoded Biosensor for Live Cell Imaging of L-Valine Production in Pyruvate Dehydrogenase Complex-Deficient Corynebacterium glutamicum Strains. PLoS ONE, 2014, 9, e85731.	1.1	100
45	Analysis of SOS-Induced Spontaneous Prophage Induction in Corynebacterium glutamicum at the Single-Cell Level. Journal of Bacteriology, 2014, 196, 180-188.	1.0	64
46	Looking for the pick of the bunch: high-throughput screening of producing microorganisms with biosensors. Current Opinion in Biotechnology, 2014, 26, 148-154.	3.3	125
47	Phosphatase activity of the histidine kinases ensures pathway specificity of the <scp>ChrSA</scp> and <scp>HrrSA</scp> twoâ€component systems in <scp><i>C</i></scp><i>orynebacterium glutamicum</i>. Molecular Microbiology, 2014, 92, 1326-1342.	1.2	20
48	Construction of a Prophage-Free Variant of Corynebacterium glutamicum ATCC 13032 for Use as a Platform Strain for Basic Research and Industrial Biotechnology. Applied and Environmental Microbiology, 2013, 79, 6006-6015.	1.4	142
49	Monitoring of population dynamics of <i><scp>C</scp>orynebacterium glutamicum</i> by multiparameter flow cytometry. Microbial Biotechnology, 2013, 6, 157-167.	2.0	41
50	Destabilized <scp>eYFP</scp> variants for dynamic gene expression studies in <i><scp>C</scp>orynebacterium glutamicum</i>. Microbial Biotechnology, 2013, 6, 196-201.	2.0	37
51	Microfluidic Picoliter Bioreactor for Microbial Single-cell Analysis: Fabrication, System Setup, and Operation. Journal of Visualized Experiments, 2013, , 50560.	0.2	49
52	IpsA, a novel LacI-type regulator, is required for inositol-derived lipid formation in Corynebacteria and Mycobacteria. BMC Biology, 2013, 11, 122.	1.7	38
53	The two-component system ChrSA is crucial for haem tolerance and interferes with HrrSA in haem-dependent gene regulation in Corynebacterium glutamicum. Microbiology (United Kingdom), 2012, 158, 3020-3031.	0.7	25
54	Deletion of manC in Corynebacterium glutamicum results in a phospho-myo-inositol mannoside- and lipoglycan-deficient mutant. Microbiology (United Kingdom), 2012, 158, 1908-1917.	0.7	25

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55	Lrp of Corynebacterium glutamicum controls expression of the brnFE operon encoding the export system for l-methionine and branched-chain amino acids. Journal of Biotechnology, 2012, 158, 231-241.	1.9	78
56	The development and application of a single-cell biosensor for the detection of l-methionine and branched-chain amino acids. Metabolic Engineering, 2012, 14, 449-457.	3.6	200
57	Control of Heme Homeostasis in <i>Corynebacterium glutamicum</i> by the Two-Component System HrrSA. Journal of Bacteriology, 2011, 193, 1212-1221.	1.0	47
58	The PhyRâ€Ïƒ^{EcfG} signalling cascade is involved in stress response and symbiotic efficiency in <i>Bradyrhizobium japonicum</i>. Molecular Microbiology, 2009, 73, 291-305.	1.2	103
59	Sigma factor mimicry involved in regulation of general stress response. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 3467-3472.	3.3	121
60	Coâ€ordinated regulation of gluconate catabolism and glucose uptake in <i>Corynebacterium glutamicum</i> by two functionally equivalent transcriptional regulators, GntR1 and GntR2. Molecular Microbiology, 2008, 67, 305-322.	1.2	145
61	Population Heterogeneity in<i>Corynebacterium glutamicum</i>ATCC 13032 Caused by Prophage CGP3. Journal of Bacteriology, 2008, 190, 5111-5119.	1.0	54
62	RamB, the Transcriptional Regulator of Acetate Metabolism in Corynebacterium glutamicum , Is Subject to Regulation by RamA and RamB. Journal of Bacteriology, 2007, 189, 1145-1149.	1.0	45
63	The DtxR Regulon of Corynebacterium glutamicum. Journal of Bacteriology, 2006, 188, 2907-2918.	1.0	104
64	The AraC-type Regulator RipA Represses Aconitase and Other Iron Proteins from Corynebacterium under Iron Limitation and Is Itself Repressed by DtxR. Journal of Biological Chemistry, 2005, 280, 40500-40508.	1.6	98
65	The General Stress Response in Alphaproteobacteria. , 0, , 291-300.		1