

JÃ¼rgen Lassak

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

1,923
citations

394421

19
h-index

330143

37
g-index

50
all docs

50
docs citations

50
times ranked

2068
citing authors

#	ARTICLE	IF	CITATIONS
1	Exceptionally versatile take II: post-translational modifications of lysine and their impact on bacterial physiology. <i>Biological Chemistry</i> , 2022, 403, 819-858.	2.5	7
2	Identification of <i>Pseudomonas asiatica</i> subsp. <i>bavariensis</i> str. JM1 as the first ϵ -carboxy(m)ethyllysine-degrading soil bacterium. <i>Environmental Microbiology</i> , 2022, 24, 3229-3241.	3.8	4
3	Synthetic post-translational modifications of elongation factor P using the ligase EpmA. <i>FEBS Journal</i> , 2021, 288, 663-677.	4.7	5
4	Transcriptional regulation of the ϵ -fructoselysine metabolism in <i>Escherichia coli</i> by global and substrate-specific cues. <i>Molecular Microbiology</i> , 2021, 115, 175-190.	2.5	10
5	Proline codon pair selection determines ribosome pausing strength and translation efficiency in bacteria. <i>Communications Biology</i> , 2021, 4, 589.	4.4	13
6	Two RmlC homologs catalyze dTDP-4-keto-6-deoxy-d-glucose epimerization in <i>Pseudomonas putida</i> KT2440. <i>Scientific Reports</i> , 2021, 11, 11991.	3.3	6
7	A β -hairpin epitope as novel structural requirement for protein arginine rhamnosylation. <i>Chemical Science</i> , 2021, 12, 1560-1567.	7.4	4
8	A set of rhamnosylation-specific antibodies enables detection of novel protein glycosylations in bacteria. <i>Organic and Biomolecular Chemistry</i> , 2020, 18, 6823-6828.	2.8	5
9	Molecular Design of a Signaling System Influences Noise in Protein Abundance under Acid Stress in Different Gammaproteobacteria. <i>Journal of Bacteriology</i> , 2020, 202, .	2.2	14
10	Highlight: young research groups in Germany – 3rd edition. <i>Biological Chemistry</i> , 2020, 402, 5-6.	2.5	1
11	Switching the Post-translational Modification of Translation Elongation Factor EF-P. <i>Frontiers in Microbiology</i> , 2019, 10, 1148.	3.5	16
12	Exceptionally versatile ϵ -arginine in bacterial post-translational protein modifications. <i>Biological Chemistry</i> , 2019, 400, 1397-1427.	2.5	15
13	Bacterial transmembrane signalling systems and their engineering for biosensing. <i>Open Biology</i> , 2018, 8, 180023.	3.6	43
14	Evolutionary analysis of polyproline motifs in <i>Escherichia coli</i> reveals their regulatory role in translation. <i>PLoS Computational Biology</i> , 2018, 14, e1005987.	3.2	31
15	Structure-function analysis of the DNA-binding domain of a transmembrane transcriptional activator. <i>Scientific Reports</i> , 2017, 7, 1051.	3.3	46
16	A Versatile Toolbox for the Control of Protein Levels Using ϵ -Acetyl-lysine Dependent Amber Suppression. <i>ACS Synthetic Biology</i> , 2017, 6, 1892-1902.	3.8	21
17	Structural Basis for EarP-Mediated Arginine Glycosylation of Translation Elongation Factor EF-P. <i>MBio</i> , 2017, 8, .	4.1	24
18	Identification and Initial Characterization of Prophages in <i>Vibrio campbellii</i> . <i>PLoS ONE</i> , 2016, 11, e0156010.	2.5	26

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19	Resolving the β -glycosidic linkage of arginine-rhamnosylated translation elongation factor P triggers generation of the first Arg^{Rha} specific antibody. <i>Chemical Science</i> , 2016, 7, 6995-7001.	7.4	30
20	Stall no more at polyproline stretches with the translation elongation factors EF-P and IF5A. <i>Molecular Microbiology</i> , 2016, 99, 219-235.	2.5	70
21	Structural and Functional Analysis of the Signal-Transducing Linker in the pH-Responsive One-Component System CadC of <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 2015, 427, 2548-2561.	4.2	35
22	Arginine-rhamnosylation as new strategy to activate translation elongation factor P. <i>Nature Chemical Biology</i> , 2015, 11, 266-270.	8.0	116
23	Deciphering the role of the type II glyoxalase isoenzyme YcbL (GlxII-2) in <i>Escherichia coli</i> . <i>FEMS Microbiology Letters</i> , 2015, 362, 1-7.	1.8	15
24	A Conserved Proline Triplet in Val-tRNA Synthetase and the Origin of Elongation Factor P. <i>Cell Reports</i> , 2014, 9, 476-483.	6.4	41
25	Translational stalling at polyproline stretches is modulated by the sequence context upstream of the stall site. <i>Nucleic Acids Research</i> , 2014, 42, 10711-10719.	14.5	88
26	The bacterial translation stress response. <i>FEMS Microbiology Reviews</i> , 2014, 38, 1172-1201.	8.6	165
27	Translation Elongation Factor EF-P Alleviates Ribosome Stalling at Polyproline Stretches. <i>Science</i> , 2013, 339, 82-85.	12.6	393
28	Distinct XPPX sequence motifs induce ribosome stalling, which is rescued by the translation elongation factor EF-P. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 15265-15270.	7.1	167
29	Domain Analysis of ArcS, the Hybrid Sensor Kinase of the <i>Shewanella oneidensis</i> MR-1 Arc Two-Component System, Reveals Functional Differentiation of Its Two Receiver Domains. <i>Journal of Bacteriology</i> , 2013, 195, 482-492.	2.2	19
30	A comprehensive toolbox for the rapid construction of lacZ fusion reporters. <i>Journal of Microbiological Methods</i> , 2012, 91, 537-543.	1.6	31
31	Analysis of the BarA/UvrY Two-Component System in <i>Shewanella oneidensis</i> MR-1. <i>PLoS ONE</i> , 2011, 6, e23440.	2.5	16
32	Phage-induced lysis enhances biofilm formation in <i>Shewanella oneidensis</i> MR-1. <i>ISME Journal</i> , 2011, 5, 613-626.	9.8	161
33	Cervimycin C resistance in <i>Bacillus subtilis</i> is due to a promoter up-mutation and increased mRNA stability of the constitutive ABC-transporter gene <i>bmrA</i> . <i>FEMS Microbiology Letters</i> , 2010, 313, 155-163.	1.8	22
34	ArcS, the Cognate Sensor Kinase in an Atypical Arc System of <i>Shewanella oneidensis</i> MR-1. <i>Applied and Environmental Microbiology</i> , 2010, 76, 3263-3274.	3.1	118
35	Two different stator systems drive a single polar flagellum in <i>Shewanella oneidensis</i> MR-1. <i>Molecular Microbiology</i> , 2009, 71, 836-850.	2.5	139
36	Switching the Post-Translational Modification of Elongation Factor P. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0