

Jörg Soppa

List of Publications by Year in descending order

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76
papers

3,526
citations

126907

33
h-index

149698

56
g-index

79
all docs

79
docs citations

79
times ranked

2631
citing authors

#	ARTICLE	IF	CITATIONS
1	Non-equivalent genomes in polyploid prokaryotes. <i>Nature Microbiology</i> , 2022, 7, 186-188.	13.3	14
2	Biological functions, genetic and biochemical characterization, and NMR structure determination of the small zinc finger protein HVO_2753 from <i>Haloferax volcanii</i> . <i>FEBS Journal</i> , 2021, 288, 2042-2062.	4.7	10
3	Characterization of Non-selected Intermolecular Gene Conversion in the Polyploid Haloarchaeon <i>Haloferax volcanii</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 680854.	3.5	3
4	Genome Copy Number Quantification Revealed That the Ethanologenic Alpha-Proteobacterium <i>Zymomonas mobilis</i> Is Polyploid. <i>Frontiers in Microbiology</i> , 2021, 12, 705895.	3.5	9
5	Elucidation of the Translation Initiation Factor Interaction Network of <i>Haloferax volcanii</i> Reveals Coupling of Transcription and Translation in Haloarchaea. <i>Frontiers in Microbiology</i> , 2021, 12, 742806.	3.5	2
6	Rapid Biophysical Characterization and NMR Spectroscopy Structural Analysis of Small Proteins from Bacteria and Archaea. <i>ChemBioChem</i> , 2020, 21, 1178-1187.	2.6	24
7	Regulated Iron Siderophore Production of the Halophilic Archaeon <i>Haloferax volcanii</i> . <i>Biomolecules</i> , 2020, 10, 1072.	4.0	11
8	A Haloarchaeal Small Regulatory RNA (sRNA) Is Essential for Rapid Adaptation to Phosphate Starvation Conditions. <i>Frontiers in Microbiology</i> , 2019, 10, 1219.	3.5	12
9	Translational coupling via termination-reinitiation in archaea and bacteria. <i>Nature Communications</i> , 2019, 10, 4006.	12.8	45
10	Polyploidy in halophilic archaea: regulation, evolutionary advantages, and gene conversion. <i>Biochemical Society Transactions</i> , 2019, 47, 933-944.	3.4	29
11	Characterization of the transcriptome of <i>Haloferax volcanii</i> , grown under four different conditions, with mixed RNA-Seq. <i>PLoS ONE</i> , 2019, 14, e0215986.	2.5	39
12	Several One-Domain Zinc Finger $\hat{\mu}$ -Proteins of <i>Haloferax Volcanii</i> Are Important for Stress Adaptation, Biofilm Formation, and Swarming. <i>Genes</i> , 2019, 10, 361.	2.4	18
13	Bioinformatic and genetic characterization of three genes localized adjacent to the major replication origin of <i>Haloferax volcanii</i> . <i>FEMS Microbiology Letters</i> , 2019, 366, .	1.8	8
14	Regulated ploidy of <i>Bacillus subtilis</i> and three new isolates of <i>Bacillus</i> and <i>Paenibacillus</i> . <i>FEMS Microbiology Letters</i> , 2018, 365, .	1.8	8
15	Characterization of Copy Number Control of Two <i>Haloferax volcanii</i> Replication Origins Using Deletion Mutants and Haloarchaeal Artificial Chromosomes. <i>Journal of Bacteriology</i> , 2018, 200, .	2.2	29
16	Influence of Origin Recognition Complex Proteins on the Copy Numbers of Three Chromosomes in <i>Haloferax volcanii</i> . <i>Journal of Bacteriology</i> , 2018, 200, .	2.2	8
17	Polyploidy and community structure. <i>Nature Microbiology</i> , 2017, 2, 16261.	13.3	25
18	Diverse Functions of Small RNAs (sRNAs) in Halophilic Archaea: From Non-coding Regulatory sRNAs to Microprotein-Encoding sRNAs. <i>Nucleic Acids and Molecular Biology</i> , 2017, , 225-242.	0.2	2

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19	Effects of Kasugamycin on the Translatome of Escherichia coli. PLoS ONE, 2017, 12, e0168143.	2.5	15
20	The glpD gene is a novel reporter gene for E. coli that is superior to established reporter genes like lacZ and gusA. Journal of Microbiological Methods, 2016, 131, 181-187.	1.6	9
21	Genome-wide identification of transcriptional start sites in the haloarchaeon Haloferax volcanii based on differential RNA-Seq (dRNA-Seq). BMC Genomics, 2016, 17, 629.	2.8	125
22	Key Enzymes of the Semiphosphorylative Entner-Doudoroff Pathway in the Haloarchaeon Haloferax volcanii: Characterization of Glucose Dehydrogenase, Gluconate Dehydratase, and 2-Keto-3-Deoxy-6-Phosphogluconate Aldolase. Journal of Bacteriology, 2016, 198, 2251-2262.	2.2	22
23	The ploidy level of Synechocystis sp. PCC 6803 is highly variable and is influenced by growth phase and by chemical and physical external parameters. Microbiology (United Kingdom), 2016, 162, 730-739.	1.8	88
24	Deletion of the Sm1 encoding motif in the lsm gene results in distinct changes in the transcriptome and enhanced swarming activity of Haloferax cells. Biochimie, 2015, 117, 129-137.	2.6	27
25	Generation and Phenotyping of a Collection of sRNA Gene Deletion Mutants of the Haloarchaeon Haloferax volcanii. PLoS ONE, 2014, 9, e90763.	2.5	34
26	DNA as a Phosphate Storage Polymer and the Alternative Advantages of Polyploidy for Growth or Survival. PLoS ONE, 2014, 9, e94819.	2.5	78
27	Haloferax volcanii, a Prokaryotic Species that Does Not Use the Shine Dalgarno Mechanism for Translation Initiation at 5' UTRs. PLoS ONE, 2014, 9, e94979.	2.5	30
28	Small regulatory RNAs in Archaea. RNA Biology, 2014, 11, 484-493.	3.1	99
29	Polyploidy in haloarchaea: advantages for growth and survival. Frontiers in Microbiology, 2014, 5, 274.	3.5	64
30	Polyploidy in Archaea and Bacteria: About Desiccation Resistance, Giant Cell Size, Long-Term Survival, Enforcement by a Eukaryotic Host and Additional Aspects. Journal of Molecular Microbiology and Biotechnology, 2014, 24, 409-419.	1.0	94
31	Halophilic Archaea Cultivated from Surface Sterilized Middle-Late Eocene Rock Salt Are Polyploid. PLoS ONE, 2014, 9, e110533.	2.5	34
32	Evolutionary advantages of polyploidy in halophilic archaea. Biochemical Society Transactions, 2013, 41, 339-343.	3.4	65
33	Nitrogen regulation of protein-protein interactions and transcript levels of GlnK^{sc}PIL</sup> regulator and AmtB ammonium transporter homologs in Archaea. MicrobiologyOpen, 2013, 2, 826-840.	3.0	18
34	A Comprehensive Analysis of the Importance of Translation Initiation Factors for Haloferax volcanii Applying Deletion and Conditional Depletion Mutants. PLoS ONE, 2013, 8, e77188.	2.5	17
35	High throughput sequencing reveals a plethora of small RNAs including tRNA derived fragments in Haloferax volcanii. RNA Biology, 2012, 9, 1011-1018.	3.1	71
36	Identification of the enzyme responsible for N1-methylation of pseudouridine 54 in archaeal tRNAs. Rna, 2012, 18, 412-420.	3.5	21

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37	Archaea Employ Small RNAs as Regulators. , 2012, , 131-145.		2
38	Regulatory RNAs in <i>Haloferax volcanii</i> . Biochemical Society Transactions, 2011, 39, 159-162.	3.4	20
39	Functional Genomic and Advanced Genetic Studies Reveal Novel Insights into the Metabolism, Regulation, and Biology of <i>Haloferax volcanii</i> . Archaea, 2011, 2011, 1-14.	2.3	14
40	Quantification of Ploidy in Proteobacteria Revealed the Existence of Monoploid, (Mero-)Oligoploid and Polyploid Species. PLoS ONE, 2011, 6, e16392.	2.5	88
41	Ploidy and gene conversion in Archaea. Biochemical Society Transactions, 2011, 39, 150-154.	3.4	49
42	Gene conversion results in the equalization of genome copies in the polyploid haloarchaeon <i>Haloferax volcanii</i> . Molecular Microbiology, 2011, 80, 666-677.	2.5	44
43	Phenotyping in the archaea: optimization of growth parameters and analysis of mutants of <i>Haloferax volcanii</i> . FEMS Microbiology Letters, 2011, 322, 123-130.	1.8	35
44	Ploidy in cyanobacteria. FEMS Microbiology Letters, 2011, 323, 124-131.	1.8	231
45	Bioinformatic prediction and experimental verification of sRNAs in the haloarchaeon <i>Haloferax volcanii</i> . RNA Biology, 2011, 8, 806-816.	3.1	37
46	Genome Copy Numbers and Gene Conversion in Methanogenic Archaea. Journal of Bacteriology, 2011, 193, 734-743.	2.2	109
47	Initiation and Regulation of Translation in Halophilic Archaea. , 2011, , 191-205.		0
48	Protein Acetylation in Archaea, Bacteria, and Eukaryotes. Archaea, 2010, 2010, 1-9.	2.3	101
49	The Archaeal Lsm Protein Binds to Small RNAs. Journal of Biological Chemistry, 2010, 285, 34429-34438.	3.4	63
50	A 2-oxoacid dehydrogenase complex of <i>Haloferax volcanii</i> is essential for growth on isoleucine but not on other branched-chain amino acids. Microbiology (United Kingdom), 2010, 156, 521-529.	1.8	16
51	Regulation of Translation in Haloarchaea: 5' and 3'-UTRs Are Essential and Have to Functionally Interact In Vivo. PLoS ONE, 2009, 4, e4484.	2.5	35
52	Small RNAs in Haloarchaea: Identification, differential expression and biological function. RNA Biology, 2009, 6, 281-292.	3.1	73
53	d-Xylose Degradation Pathway in the Halophilic Archaeon <i>Haloferax volcanii</i> . Journal of Biological Chemistry, 2009, 284, 27290-27303.	3.4	92
54	A novel mechanism for translation initiation operates in haloarchaea. Molecular Microbiology, 2009, 71, 1451-1463.	2.5	60

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55	Small RNAs of the halophilic archaeon <i>Haloferax volcanii</i> . <i>Biochemical Society Transactions</i> , 2009, 37, 133-136.	3.4	25
56	Characterization of a <i>Haloferax volcanii</i> member of the enolase superfamily: deletion mutant construction, expression analysis, and transcriptome comparison. <i>Archives of Microbiology</i> , 2008, 190, 341-353.	2.2	21
57	Gene regulation and genome function in Archaea: a progress survey. <i>Archives of Microbiology</i> , 2008, 190, 195-196.	2.2	1
58	Optimized generation of vectors for the construction of <i>Haloferax volcanii</i> deletion mutants. <i>Journal of Microbiological Methods</i> , 2008, 75, 201-204.	1.6	42
59	Experimental Characterization of Cis-Acting Elements Important for Translation and Transcription in Halophilic Archaea. <i>PLoS Genetics</i> , 2007, 3, e229.	3.5	132
60	Three 2-oxoacid dehydrogenase operons in <i>Haloferax volcanii</i> : expression, deletion mutants and evolution. <i>Microbiology (United Kingdom)</i> , 2007, 153, 3303-3313.	1.8	18
61	Global Analysis of mRNA Decay in <i>Halobacterium salinarum</i> NRC-1 at Single-Gene Resolution Using DNA Microarrays. <i>Journal of Bacteriology</i> , 2007, 189, 6936-6944.	2.2	32
62	Transcriptome changes and cAMP oscillations in an archaeal cell cycle. <i>BMC Cell Biology</i> , 2007, 8, 21.	3.0	35
63	Characterization of a tightly controlled promoter of the halophilic archaeon <i>Haloferax volcanii</i> and its use in the analysis of the essential <i>cct1</i> gene. <i>Molecular Microbiology</i> , 2007, 66, 1092-1106.	2.5	94
64	Genome-wide analysis of growth phase-dependent translational and transcriptional regulation in halophilic archaea. <i>BMC Genomics</i> , 2007, 8, 415.	2.8	39
65	From genomes to function: haloarchaea as model organisms. <i>Microbiology (United Kingdom)</i> , 2006, 152, 585-590.	1.8	118
66	Regulated Polyploidy in Halophilic Archaea. <i>PLoS ONE</i> , 2006, 1, e92.	2.5	169
67	From replication to cultivation: hot news from Haloarchaea. <i>Current Opinion in Microbiology</i> , 2005, 8, 737-744.	5.1	8
68	Construction and usage of a onefold-coverage shotgun DNA microarray to characterize the metabolism of the archaeon <i>Haloferax volcanii</i> . <i>Molecular Microbiology</i> , 2003, 48, 1089-1105.	2.5	78
69	Functional Role for a 2-Oxo Acid Dehydrogenase in the Halophilic Archaeon <i>Haloferax volcanii</i> . <i>Journal of Bacteriology</i> , 2002, 184, 3114-3121.	2.2	24
70	Cell cycle-dependent expression of an essential SMC-like protein and dynamic chromosome localization in the archaeon <i>Halobacterium salinarum</i> . <i>Molecular Microbiology</i> , 2002, 46, 395-409.	2.5	48
71	Basal and regulated transcription in Archaea. <i>Advances in Applied Microbiology</i> , 2001, 50, 171-217.	2.4	30
72	Transcription initiation in Archaea: facts, factors and future aspects. <i>Molecular Microbiology</i> , 1999, 31, 1295-1305.	2.5	133

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73	Normalized nucleotide frequencies allow the definition of archaeal promoter elements for different archaeal groups and reveal base-specific TFB contacts upstream of the TATA box. <i>Molecular Microbiology</i> , 1999, 31, 1589-1592.	2.5	62
74	Genetic Identification of Three ABC Transporters as Essential Elements for Nitrate Respiration in <i>Haloferax volcanii</i> . <i>Genetics</i> , 1999, 152, 1417-1428.	2.9	36
75	Optimization of the 5-bromo-2-deoxyuridine selection and its application for the isolation of nitrate respiration-deficient mutants of <i>Haloferax volcanii</i> . <i>Journal of Microbiological Methods</i> , 1998, 34, 41-48.	1.6	8
76	Characterization of the distal promoter element of halobacteria in vivo using saturation mutagenesis and selection. <i>Molecular Microbiology</i> , 1996, 19, 1265-1276.	2.5	81