

Alexei Sorokine

List of Publications by Year in descending order

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61
papers

11,058
citations

147566

31
h-index

143772

57
g-index

61
all docs

61
docs citations

61
times ranked

8941
citing authors

#	ARTICLE	IF	CITATIONS
1	The complete genome sequence of the Gram-positive bacterium <i>Bacillus subtilis</i> . <i>Nature</i> , 1997, 390, 249-256.	13.7	3,519
2	Clustered regularly interspaced short palindrome repeats (CRISPRs) have spacers of extrachromosomal origin. <i>Microbiology (United Kingdom)</i> , 2005, 151, 2551-2561.	0.7	1,396
3	The Complete Genome Sequence of the Lactic Acid Bacterium <i>Lactococcus lactis</i> ssp. <i>lactis</i> IL1403. <i>Genome Research</i> , 2001, 11, 731-753.	2.4	904
4	Genome sequence of <i>Bacillus cereus</i> and comparative analysis with <i>Bacillus anthracis</i> . <i>Nature</i> , 2003, 423, 87-91.	13.7	740
5	The Complete Genome Sequence of the Lactic Acid Bacterium <i>Lactococcus lactis</i> ssp. <i>lactis</i> IL1403. <i>Genome Research</i> , 2001, 11, 731-753.	2.4	582
6	Complete sequence and comparative genome analysis of the dairy bacterium <i>Streptococcus thermophilus</i> . <i>Nature Biotechnology</i> , 2004, 22, 1554-1558.	9.4	485
7	Ecological diversification in the <i>Bacillus cereus</i> Group. <i>Environmental Microbiology</i> , 2008, 10, 851-865.	1.8	413
8	Complete genome sequence of the industrial bacterium <i>Bacillus licheniformis</i> and comparisons with closely related <i>Bacillus</i> species. <i>Genome Biology</i> , 2004, 5, r77.	13.9	319
9	<i>Bacillus cytotoxicus</i> sp. nov. is a novel thermotolerant species of the <i>Bacillus cereus</i> Group occasionally associated with food poisoning. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 31-40.	0.8	303
10	Regulators of aerobic and anaerobic respiration in <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 1996, 178, 1374-1385.	1.0	169
11	Analysis of six prophages in <i>Lactococcus lactis</i> IL1403: different genetic structure of temperate and virulent phage populations. <i>Nucleic Acids Research</i> , 2001, 29, 644-651.	6.5	162
12	Low-redundancy sequencing of the entire <i>Lactococcus lactis</i> IL1403 genome. <i>Antonie Van Leeuwenhoek</i> , 1999, 76, 27-76.	0.7	153
13	Expression of a stress- and starvation-induced <i>dps/pexB</i> -homologous gene is controlled by the alternative sigma factor <i>sigmaB</i> in <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 1997, 179, 7251-7256.	1.0	142
14	Extending the <i>Bacillus cereus</i> group genomics to putative food-borne pathogens of different toxicity. <i>Chemico-Biological Interactions</i> , 2008, 171, 236-249.	1.7	140
15	<i>SecDF</i> of <i>Bacillus subtilis</i> , a Molecular Siamese Twin Required for the Efficient Secretion of Proteins. <i>Journal of Biological Chemistry</i> , 1998, 273, 21217-21224.	1.6	123
16	Multiple-Locus Sequence Typing Analysis of <i>Bacillus cereus</i> and <i>Bacillus thuringiensis</i> Reveals Separate Clustering and a Distinct Population Structure of Psychrotrophic Strains. <i>Applied and Environmental Microbiology</i> , 2006, 72, 1569-1578.	1.4	122
17	The <i>Bacillus subtilis</i> <i>sigma(X)</i> protein is an extracytoplasmic function sigma factor contributing to survival at high temperature. <i>Journal of Bacteriology</i> , 1997, 179, 2915-2921.	1.0	87
18	The organization of the <i>Bacillus subtilis</i> 168 chromosome region between the <i>spoVA</i> and <i>serA</i> genetic loci, based on sequence data. <i>Molecular Microbiology</i> , 1993, 10, 385-395.	1.2	84

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19	Adaptation of <i>Bacillus cereus</i> , an ubiquitous worldwide-distributed foodborne pathogen, to a changing environment. <i>Food Research International</i> , 2010, 43, 1885-1894.	2.9	76
20	Discovering lactic acid bacteria by genomics. , 2002, 82, 29-58.		74
21	Comparative genome analysis of <i>Bacillus cereus</i> group genomes with <i>Bacillus subtilis</i> . <i>FEMS Microbiology Letters</i> , 2005, 250, 175-184.	0.7	73
22	<i>Bacillus subtilis</i> can modulate its capacity and specificity for protein secretion through temporally controlled expression of the <i>sipS</i> gene for signal peptidase I. <i>Molecular Microbiology</i> , 1996, 22, 605-618.	1.2	59
23	Genetic Recombination in <i>Bacillus subtilis</i> 168: Effects of <i>recU</i> and <i>recS</i> Mutations on DNA Repair and Homologous Recombination. <i>Journal of Bacteriology</i> , 1998, 180, 3405-3409.	1.0	58
24	Cloning and characterization of the <i>Bacillus subtilis</i> <i>birA</i> gene encoding a repressor of the biotin operon. <i>Journal of Bacteriology</i> , 1995, 177, 2572-2575.	1.0	56
25	The <i>Bacillus subtilis</i> chromosome region encoding homologues of the <i>Escherichia coli</i> <i>mssA</i> and <i>rpsA</i> gene products. <i>Microbiology (United Kingdom)</i> , 1995, 141, 311-319.	0.7	46
26	Sequencing and functional annotation of the <i>Bacillus subtilis</i> genes in the 200 kb <i>rrnB-dnaB</i> region. <i>Microbiology (United Kingdom)</i> , 1997, 143, 3431-3441.	0.7	45
27	The Genetically Remote Pathogenic Strain NVH391-98 of the <i>Bacillus cereus</i> Group Is Representative of a Cluster of Thermophilic Strains. <i>Applied and Environmental Microbiology</i> , 2008, 74, 1276-1280.	1.4	41
28	Characterization of the <i>Bacillus subtilis</i> <i>YxdJ</i> response regulator as the inducer of expression for the cognate ABC transporter <i>YxdLM</i> . <i>Microbiology (United Kingdom)</i> , 2004, 150, 2609-2617.	0.7	36
29	Nucleotide sequence of the <i>Bacillus subtilis</i> <i>dnaD</i> gene. <i>Microbiology (United Kingdom)</i> , 1995, 141, 321-322.	0.7	35
30	Genome Sequence of <i>Candidatus</i> <i>Arthromitus</i> sp. Strain SFB-Mouse-NL, a Commensal Bacterium with a Key Role in Postnatal Maturation of Gut Immune Functions. <i>Genome Announcements</i> , 2014, 2, .	0.8	35
31	Nucleotide sequence analysis of the cloned salmon preproinsulin cDNA. <i>Gene</i> , 1982, 20, 367-376.	1.0	34
32	A new approach using multiplex long accurate PCR and yeast artificial chromosomes for bacterial chromosome mapping and sequencing.. <i>Genome Research</i> , 1996, 6, 448-453.	2.4	34
33	Two distinct types of rRNA operons in the <i>Bacillus cereus</i> group. <i>Microbiology (United Kingdom)</i> , 2004, 150, 601-611.	0.7	33
34	Role of plasmid plasticity and mobile genetic elements in the entomopathogen <i>Bacillus thuringiensis</i> serovar <i>israelensis</i> . <i>FEMS Microbiology Reviews</i> , 2018, 42, 829-856.	3.9	33
35	The transcriptional organization of the <i>Bacillus subtilis</i> 168 chromosome region between the <i>spoVAF</i> and <i>serA</i> genetic loci. <i>Molecular Microbiology</i> , 1993, 10, 397-405.	1.2	32
36	Sequence analysis of the <i>Bacillus subtilis</i> chromosome region between the <i>serA</i> and <i>kdg</i> loci cloned in a yeast artificial chromosome. <i>Microbiology (United Kingdom)</i> , 1996, 142, 2005-2016.	0.7	32

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37	The <i>kdgRKAT</i> operon of <i>Bacillus subtilis</i> : detection of the transcript and regulation by the <i>kdgR</i> and <i>ccpA</i> genes. <i>Microbiology (United Kingdom)</i> , 1998, 144, 3111-3118.	0.7	32
38	Temperature-inducible gene expression in <i>Bacillus subtilis</i> mediated by the <i>c1857</i> -encoded repressor of bacteriophage lambda. <i>Gene</i> , 1990, 93, 35-40.	1.0	31
39	Recent Genetic Transfer between <i>Lactococcus lactis</i> and Enterobacteria. <i>Journal of Bacteriology</i> , 2004, 186, 6671-6677.	1.0	28
40	Comparative genomics of extrachromosomal elements in <i>Bacillus thuringiensis</i> subsp. <i>israelensis</i> . <i>Research in Microbiology</i> , 2017, 168, 331-344.	1.0	28
41	Complete Genome Sequence of <i>Lactococcus lactis</i> subsp. <i>cremoris</i> A76. <i>Journal of Bacteriology</i> , 2012, 194, 1241-1242.	1.0	26
42	GenoFrag: software to design primers optimized for whole genome scanning by long-range PCR amplification. <i>Nucleic Acids Research</i> , 2004, 32, 17-24.	6.5	24
43	Co-linear scaffold of the <i>Bacillus licheniformis</i> and <i>Bacillus subtilis</i> genomes and its use to compare their competence genes. <i>FEMS Microbiology Letters</i> , 2002, 209, 23-30.	0.7	23
44	Sequence of the <i>Bacillus subtilis</i> genome region in the vicinity of the <i>lev</i> operon reveals two new extracytoplasmic function RNA polymerase sigma factors SigV and SigZ. <i>Microbiology (United Kingdom)</i> , 2007, 147, 107-114.	1.0	21
45	Genome Sequence of the Atypical Symbiotic <i>Frankia</i> R43 Strain, a Nitrogen-Fixing and Hydrogen-Producing Actinobacterium. <i>Genome Announcements</i> , 2015, 3, .	0.8	21
46	Detection of the cryptic prophage-like molecule pBtic235 in <i>Bacillus thuringiensis</i> subsp. <i>israelensis</i> . <i>Research in Microbiology</i> , 2017, 168, 319-330.	1.0	19
47	A 23 911 bp region of the <i>Bacillus subtilis</i> genome comprising genes located upstream and downstream of the <i>lev</i> operon. <i>Microbiology (United Kingdom)</i> , 1997, 143, 1321-1326.	0.7	18
48	Sequence Analysis of Inducible Prophage phiS3501 Integrated into the Haemolysin II Gene of <i>Bacillus thuringiensis</i> var <i>israelensis</i> ATCC35646. <i>Genetics Research International</i> , 2012, 2012, 1-9.	2.0	17
49	Molecular Mechanisms That Contribute to Horizontal Transfer of Plasmids by the Bacteriophage SPP1. <i>Frontiers in Microbiology</i> , 2017, 8, 1816.	1.5	17
50	Organization of the <i>Bacillus subtilis</i> 168 chromosome between <i>kdg</i> and the attachment site of the SPÂ prophage: use of Long Accurate PCR and yeast artificial chromosomes for sequencing. <i>Microbiology (United Kingdom)</i> , 1996, 142, 3005-3015.	0.7	15
51	Orientation specificity of the <i>Lactococcus lactis</i> Chi site. <i>Genes To Cells</i> , 2000, 5, 453-461.	0.5	11
52	Functional and Morphological Adaptation to Peptidoglycan Precursor Alteration in <i>Lactococcus lactis</i> . <i>Journal of Biological Chemistry</i> , 2010, 285, 24003-24013.	1.6	11
53	Studies of genomes of dairy bacteria <i>Lactococcus lactis</i> . <i>Sciences Des Aliments</i> , 2002, 22, 45-53.	0.2	9
54	Mapping of the 150 kb <i>spoIIIC-pheA</i> region of the <i>Bacillus subtilis</i> chromosome using Long Accurate PCR and three yeast artificial chromosomes. <i>Microbiology (United Kingdom)</i> , 1996, 142, 3017-3020.	0.7	8

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55	Low-redundancy sequencing of the entire <i>Lactococcus lactis</i> IL1403 genome. , 1999, , 27-76.		6
56	Complete Genome Sequence of the Highly Hemolytic Strain <i>Bacillus cereus</i> F837/76. <i>Journal of Bacteriology</i> , 2012, 194, 1630-1630.	1.0	5
57	The <i>Bacillus cereus</i> Group. , 2015, , 1041-1078.		5
58	Genomic Sequence of the Prophage-Free <i>Lactococcus lactis</i> Strain IL6288. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
59	ORFograph: search for novel insecticidal protein genes in genomic and metagenomic assembly graphs. <i>Microbiome</i> , 2021, 9, 149.	4.9	3
60	<i>Bacillus thuringiensis</i> Genetics and Phagesâ€™ From Transduction and Sequencing to Recombineering. , 2012, , 131-157.		1
61	Long inverted repeats around the chromosome replication terminus in the model strain <i>Bacillus thuringiensis</i> serovar israelensis BGSC 4Q7. <i>Microbial Genomics</i> , 2020, 6, .	1.0	1