

Frank-Jörg Vorhölter

List of Publications by Year in descending order

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29
papers

2,031
citations

516710

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477307

29
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29
all docs

29
docs citations

29
times ranked

2474
citing authors

#	ARTICLE	IF	CITATIONS
1	Pathogenomics of <i>Xanthomonas</i> : understanding bacterium-plant interactions. <i>Nature Reviews Microbiology</i> , 2011, 9, 344-355.	28.6	428
2	EDGAR: A software framework for the comparative analysis of prokaryotic genomes. <i>BMC Bioinformatics</i> , 2009, 10, 154.	2.6	401
3	Insights into Genome Plasticity and Pathogenicity of the Plant Pathogenic Bacterium <i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> Revealed by the Complete Genome Sequence. <i>Journal of Bacteriology</i> , 2005, 187, 7254-7266.	2.2	321
4	The genome of <i>Xanthomonas campestris</i> pv. <i>campestris</i> B100 and its use for the reconstruction of metabolic pathways involved in xanthan biosynthesis. <i>Journal of Biotechnology</i> , 2008, 134, 33-45.	3.8	238
5	Mechanistic insights into host adaptation, virulence and epidemiology of the phytopathogen <i>Xanthomonas</i> . <i>FEMS Microbiology Reviews</i> , 2020, 44, 1-32.	8.6	148
6	Analysis of outer membrane vesicle associated proteins isolated from the plant pathogenic bacterium <i>Xanthomonas campestris</i> pv. <i>campestris</i> . <i>BMC Microbiology</i> , 2008, 8, 87.	3.3	118
7	The noncanonical type III secretion system of <i>Xanthomonas translucens</i> pv. <i>graminis</i> is essential for forage grass infection. <i>Molecular Plant Pathology</i> , 2013, 14, 576-588.	4.2	48
8	Establishment, in silico analysis, and experimental verification of a large-scale metabolic network of the xanthan producing <i>Xanthomonas campestris</i> pv. <i>campestris</i> strain B100. <i>Journal of Biotechnology</i> , 2013, 167, 123-134.	3.8	43
9	Genome wide transcription start sites analysis of <i>Xanthomonas campestris</i> pv. <i>campestris</i> B100 with insights into the gum gene cluster directing the biosynthesis of the exopolysaccharide xanthan. <i>Journal of Biotechnology</i> , 2016, 225, 18-28.	3.8	38
10	Identification of <i>Xanthomonas campestris</i> pv. <i>campestris</i> galactose utilization genes from transcriptome data. <i>Journal of Biotechnology</i> , 2008, 135, 309-317.	3.8	36
11	Involvement of bacterial TonB-dependent signaling in the generation of an oligogalacturonide damage-associated molecular pattern from plant cell walls exposed to <i>Xanthomonas campestris</i> pv. <i>campestris</i> pectate lyases. <i>BMC Microbiology</i> , 2012, 12, 239.	3.3	33
12	Metabolic flux pattern of glucose utilization by <i>Xanthomonas campestris</i> pv. <i>campestris</i> : prevalent role of the Entner-Doudoroff pathway and minor fluxes through the pentose phosphate pathway and glycolysis. <i>Molecular BioSystems</i> , 2014, 10, 2663-2676.	2.9	28
13	Complete Genome Sequence of the Barley Pathogen <i>Xanthomonas translucens</i> pv. <i>translucens</i> DSM 18974 ^T (ATCC 19319 ^T). <i>Genome Announcements</i> , 2016, 4, .	0.8	24
14	Comparative genomics of host adaptive traits in <i>Xanthomonas translucens</i> pv. <i>graminis</i> . <i>BMC Genomics</i> , 2017, 18, 35.	2.8	24
15	Draft genome of the xanthan producer <i>Xanthomonas campestris</i> NRRL B-1459 (ATCC 13951). <i>Journal of Biotechnology</i> , 2015, 204, 45-46.	3.8	19
16	Dynamic protein phosphorylation during the growth of <i>Xanthomonas campestris</i> pv. <i>campestris</i> B100 revealed by a gel-based proteomics approach. <i>Journal of Biotechnology</i> , 2013, 167, 111-122.	3.8	16
17	Characterization of the pyrophosphate-dependent 6-phosphofructokinase from <i>Xanthomonas campestris</i> pv. <i>campestris</i> . <i>Archives of Biochemistry and Biophysics</i> , 2014, 546, 53-63.	3.0	14
18	The lipopolysaccharide of the crop pathogen <i>Xanthomonas translucens</i> pv. <i>translucens</i> : chemical characterization and determination of signaling events in plant cells. <i>Glycobiology</i> , 2017, 27, 264-274.	2.5	8

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19	Comparative transcription profiling of two fermentation cultures of <i>Xanthomonas campestris</i> pv. <i>campestris</i> B100 sampled in the growth and in the stationary phase. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 6613-6625.	3.6	8
20	Refined annotation of the complete genome of the phytopathogenic and xanthan producing <i>Xanthomonas campestris</i> pv. <i>campestris</i> strain B100 based on RNA sequence data. <i>Journal of Biotechnology</i> , 2017, 253, 55-61.	3.8	7
21	Systems and synthetic biology perspective of the versatile plant-pathogenic and polysaccharide-producing bacterium <i>Xanthomonas campestris</i> . <i>Microbiology (United Kingdom)</i> , 2017, 163, 1117-1144.	1.8	7
22	Draft genome sequences of three <i>Xanthomonas translucens</i> pathovar reference strains (pv.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 627 T Genomic Sciences, 2016, 11, 50.	1.5	6
23	Regulatory associations between the metabolism of sulfur-containing amino acids and xanthan biosynthesis in <i>Xanthomonas campestris</i> pv. <i>campestris</i> B100. <i>FEMS Microbiology Letters</i> , 2019, 366, .	1.8	4
24	Draft Genome Sequence of <i>Pseudomonas aeruginosa</i> Strain WS136, a Highly Cytotoxic ExoS-Positive Wound Isolate Recovered from <i>Pyoderma Gangrenosum</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	3
25	Applying DNA affinity chromatography to specifically screen for sucrose-related DNA-binding transcriptional regulators of <i>Xanthomonas campestris</i> . <i>Journal of Biotechnology</i> , 2016, 232, 89-98.	3.8	3
26	Two Flagellar mutants of <i>Xanthomonas campestris</i> are characterized by enhanced xanthan production and higher xanthan viscosity. <i>Journal of Biotechnology</i> , 2022, 347, 9-17.	3.8	3
27	Genome Sequence of the Urethral Isolate <i>Pseudomonas aeruginosa</i> RN21. <i>Genome Announcements</i> , 2015, 3, .	0.8	2
28	Genome Sequence of the Urethral Catheter Isolate <i>Pseudomonas aeruginosa</i> MH19. <i>Genome Announcements</i> , 2015, 3, .	0.8	2
29	Draft Genome Sequence of <i>Pseudomonas aeruginosa</i> Strain WS394, a Multidrug-Resistant and Highly Cytotoxic Wound Isolate from Chronic Ulcus Cruris. <i>Genome Announcements</i> , 2014, 2, .	0.8	1