

Sylvie Reverchon

List of Publications by Year in descending order

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papers

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71004

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docs citations

112
times ranked

3470
citing authors

#	ARTICLE	IF	CITATIONS
1	Carbon catabolite repression in pectin digestion by the phytopathogen <i>Dickeya dadantii</i> . <i>Journal of Biological Chemistry</i> , 2022, 298, 101446.	1.6	1
2	Specificity and genetic polymorphism in the Vfm quorum sensing system of plant pathogenic bacteria of the genus <i>Dickeya</i> . <i>Environmental Microbiology</i> , 2022, 24, 1467-1483.	1.8	8
3	Implications of carbon catabolite repression for plant-microbe interactions. <i>Plant Communications</i> , 2022, 3, 100272.	3.6	11
4	Relationship between the Chromosome Structural Dynamics and Gene Expression—A Chicken and Egg Dilemma?. <i>Microorganisms</i> , 2022, 10, 846.	1.6	7
5	Mapping the Complex Transcriptional Landscape of the Phytopathogenic Bacterium <i>Dickeya dadantii</i> . <i>MBio</i> , 2022, 13, e0052422.	1.8	4
6	Quantitative contribution of the spacer length in the supercoiling-sensitivity of bacterial promoters. <i>Nucleic Acids Research</i> , 2022, 50, 7287-7297.	6.5	1
7	Separation and quantification of 2-keto-3-deoxy-gluconate (KDG) a major metabolite in pectin and alginate degradation pathways. <i>Analytical Biochemistry</i> , 2021, 619, 114061.	1.1	6
8	Pattern and causes of the establishment of the invasive bacterial potato pathogen <i>Dickeya solani</i> and of the maintenance of the resident pathogen <i>D. adianthicola</i> . <i>Molecular Ecology</i> , 2021, 30, 608-624.	2.0	13
9	The nucleoid-associated protein IHF acts as a transcriptional domain protein coordinating the bacterial virulence traits with global transcription. <i>Nucleic Acids Research</i> , 2021, 49, 776-790.	6.5	21
10	Quorum Sensing Regulation in Phytopathogenic Bacteria. <i>Microorganisms</i> , 2021, 9, 239.	1.6	37
11	RNA Chaperones Hfq and ProQ Play a Key Role in the Virulence of the Plant Pathogenic Bacterium <i>Dickeya dadantii</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 687484.	1.5	5
12	Role of the Discriminator Sequence in the Supercoiling Sensitivity of Bacterial Promoters. <i>MSystems</i> , 2021, 6, e0097821.	1.7	13
13	Design and comparative characterization of RecA variants. <i>Scientific Reports</i> , 2021, 11, 21106.	1.6	0
14	Acetic acid bacteria (AAB) involved in cocoa fermentation from Ivory Coast: species diversity and performance in acetic acid production. <i>Journal of Food Science and Technology</i> , 2020, 57, 1904-1916.	1.4	24
15	<i>Dickeya poaceiphila</i> sp. nov., a plant-pathogenic bacterium isolated from sugar cane (<i>Saccharum</i>) Tj ETQq1 1 0.784314 rgBT /Overloc	0.8	30
16	DNA Supercoiling: an Ancestral Regulator of Gene Expression in Pathogenic Bacteria?. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 1047-1055.	1.9	33
17	Bacterial genome architecture shapes global transcriptional regulation by DNA supercoiling. <i>Nucleic Acids Research</i> , 2019, 47, 5648-5657.	6.5	60
18	APER0: a genome-wide approach for identifying bacterial small RNAs from RNA-Seq data. <i>Nucleic Acids Research</i> , 2019, 47, e88-e88.	6.5	21

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19	The phytopathogenic nature of <i>Dickeya aquatica</i> 174/2 and the dynamic early evolution of <i>Dickeya</i> pathogenicity. <i>Environmental Microbiology</i> , 2019, 21, 2809-2835.	1.8	32
20	Coherent Domains of Transcription Coordinate Gene Expression During Bacterial Growth and Adaptation. <i>Microorganisms</i> , 2019, 7, 694.	1.6	13
21	Modeling the bioconversion of polysaccharides in a continuous reactor: A case study of the production of oligogalacturonates by <i>Dickeya dadantii</i> . <i>Journal of Biological Chemistry</i> , 2019, 294, 1753-1762.	1.6	4
22	RecA and DNA recombination: a review of molecular mechanisms. <i>Biochemical Society Transactions</i> , 2019, 47, 1511-1531.	1.6	32
23	Chromosomal organization of transcription: in a nutshell. <i>Current Genetics</i> , 2018, 64, 555-565.	0.8	39
24	Lactic acid bacteria involved in cocoa beans fermentation from Ivory Coast: Species diversity and citrate lyase production. <i>International Journal of Food Microbiology</i> , 2017, 256, 11-19.	2.1	61
25	New nucleic acid testing devices to diagnose infectious diseases in resource-limited settings. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2017, 36, 1717-1731.	1.3	57
26	Regulation of the synthesis of pulp degrading enzymes in <i>Bacillus</i> isolated from cocoa fermentation. <i>Food Microbiology</i> , 2017, 63, 255-262.	2.1	20
27	Plant-phytopathogen interactions: bacterial responses to environmental and plant stimuli. <i>Environmental Microbiology</i> , 2017, 19, 1689-1716.	1.8	65
28	Global transcriptional response of <i>Dickeya dadantii</i> to environmental stimuli relevant to the plant infection. <i>Environmental Microbiology</i> , 2016, 18, 3651-3672.	1.8	53
29	From multiple pathogenicity islands to a unique organized pathogenicity archipelago. <i>Scientific Reports</i> , 2016, 6, 27978.	1.6	17
30	Regulation of <i>pel</i> genes, major virulence factors in the plant pathogen bacterium <i>Dickeya dadantii</i> , is mediated by cooperative binding of the nucleoid-associated protein H-NS. <i>Research in Microbiology</i> , 2016, 167, 247-253.	1.0	6
31	Virulence Program of a Bacterial Plant Pathogen: The <i>Dickeya</i> Model. <i>Progress in Molecular Biology and Translational Science</i> , 2016, 142, 51-92.	0.9	65
32	Temporal control of <i>Dickeya dadantii</i> main virulence gene expression by growth phase-dependent alteration of regulatory nucleoprotein complexes. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016, 1859, 1470-1480.	0.9	16
33	Transcriptional start site turnover in the evolution of bacterial paralogous genes: the <i>pelE</i> - <i>pelD</i> virulence genes in <i>Dickeya</i> . <i>FEBS Journal</i> , 2016, 283, 4192-4207.	2.2	15
34	IscR Regulates Synthesis of Colonization Factor Antigen I Fimbriae in Response to Iron Starvation in Enterotoxigenic <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2015, 197, 2896-2907.	1.0	35
35	Chromosomal "Stress-Response" Domains Govern the Spatiotemporal Expression of the Bacterial Virulence Program. <i>MBio</i> , 2015, 6, e00353-15.	1.8	49
36	Rethinking the Bacterial Genetic Regulation. <i>Biochemistry and Analytical Biochemistry: Current Research</i> , 2015, 04, .	0.4	4

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37	Bacterial virulence and Fis: adapting regulatory networks to the host environment. Trends in Microbiology, 2014, 22, 92-99.	3.5	46
38	Role of the <i>LysR</i> -type transcriptional regulator <i>PecT</i> and <i>DNA</i> supercoiling in the thermoregulation of <i>pel</i> genes, the major virulence factors in <i>Dickeya dadantii</i> . Environmental Microbiology, 2014, 16, 734-745.	1.8	30
39	<i>Dickeya</i> ecology, environment sensing and regulation of virulence programme. Environmental Microbiology Reports, 2013, 5, 622-636.	1.0	163
40	Vfm a new quorum sensing system controls the virulence of <i>Dickeya dadantii</i> . Environmental Microbiology, 2013, 15, 865-880.	1.8	95
41	The nucleoid-associated protein Fis directly modulates the synthesis of cellulose, an essential component of pellicle biofilms in the phytopathogenic bacterium <i>Dickeya dadantii</i> . Molecular Microbiology, 2012, 86, 172-186.	1.2	55
42	The nucleoid-associated proteins H-NS and FIS modulate the DNA supercoiling response of the <i>pel</i> genes, the major virulence factors in the plant pathogen bacterium <i>Dickeya dadantii</i> . Nucleic Acids Research, 2012, 40, 4306-4319.	6.5	80
43	Quorum Sensing Signaling Molecules Produced by Reference and Emerging Soft-Rot Bacteria (<i>Dickeya</i>) Tj ETQq1 1 0,784314,rgBT /Over	1.1	54
44	The Role of Secretion Systems and Small Molecules in Soft-Rot <i>Enterobacteriaceae</i> Pathogenicity. Annual Review of Phytopathology, 2012, 50, 425-449.	3.5	217
45	<i>PecS</i> is an important player in the regulatory network governing the coordinated expression of virulence genes during the interaction between <i>Dickeya dadantii</i> 3937 and plants. Environmental Microbiology, 2011, 13, 2901-2914.	1.8	32
46	Molecular identification and pectate lyase production by <i>Bacillus</i> strains involved in cocoa fermentation. Food Microbiology, 2011, 28, 1-8.	2.1	45
47	LuxR dependent quorum sensing inhibition by N,N ² -disubstituted imidazolium salts. Bioorganic and Medicinal Chemistry, 2011, 19, 4868-4875.	1.4	15
48	Genome Sequence of the Plant-Pathogenic Bacterium <i>Dickeya dadantii</i> 3937. Journal of Bacteriology, 2011, 193, 2076-2077.	1.0	113
49	<i>lpxC</i> and <i>yafS</i> are the Most Suitable Internal Controls to Normalize Real Time RT-qPCR Expression in the Phytopathogenic Bacteria <i>Dickeya dadantii</i> . PLoS ONE, 2011, 6, e20269.	1.1	41
50	Systematic targeted mutagenesis of the <i>MarR/SlyA</i> family members of <i>Dickeya dadantii</i> 3937 reveals a role for <i>MfbR</i> in the modulation of virulence gene expression in response to acidic pH. Molecular Microbiology, 2010, 78, 1018-1037.	1.2	37
51	Toward a Quantitative Modeling of the Synthesis of the Pectate Lyases, Essential Virulence Factors in <i>Dickeya dadantii</i> . Journal of Biological Chemistry, 2010, 285, 28565-28576.	1.6	38
52	Biochemical Properties of Pectate Lyases Produced by Three Different <i>Bacillus</i> Strains Isolated from Fermenting Cocoa Beans and Characterization of Their Cloned Genes. Applied and Environmental Microbiology, 2010, 76, 5214-5220.	1.4	34
53	Identification of <i>TogMNAB</i> , an ABC transporter which mediates the uptake of pectic oligomers in <i>Erwinia chrysanthemi</i> 3937. Molecular Microbiology, 2008, 41, 1113-1123.	1.2	47
54	Two transporters, <i>TogT</i> and <i>TogMNAB</i> , are responsible for oligogalacturonide uptake in <i>Erwinia chrysanthemi</i> 3937. Molecular Microbiology, 2008, 41, 1125-1132.	1.2	37

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55	Synthetic homoserine lactone-derived sulfonylureas as inhibitors of <i>Vibrio fischeri</i> quorum sensing regulator. <i>Bioorganic and Medicinal Chemistry</i> , 2008, 16, 3550-3556.	1.4	42
56	N-Acyl-3-amino-5H-furanone derivatives as new inhibitors of LuxR-dependent quorum sensing: Synthesis, biological evaluation and binding mode study. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2008, 18, 4321-4324.	1.0	45
57	The GacA global regulator is required for the appropriate expression of <i>Erwinia chrysanthemi</i> 3937 pathogenicity genes during plant infection. <i>Environmental Microbiology</i> , 2008, 10, 545-559.	1.8	81
58	PecS Is a Global Regulator of the Symptomatic Phase in the Phytopathogenic Bacterium <i>Erwinia chrysanthemi</i> 3937. <i>Journal of Bacteriology</i> , 2008, 190, 7508-7522.	1.0	94
59	Analysis of the Lacl Family Regulators of <i>Erwinia chrysanthemi</i> 3937, Involvement in the Bacterial Phytopathogenicity. <i>Molecular Plant-Microbe Interactions</i> , 2008, 21, 1471-1481.	1.4	28
60	Differential Role of Ferritins in Iron Metabolism and Virulence of the Plant-Pathogenic Bacterium <i>Erwinia chrysanthemi</i> 3937. <i>Journal of Bacteriology</i> , 2008, 190, 1518-1530.	1.0	40
61	Efflux Pump Gene Expression in <i>Erwinia chrysanthemi</i> Is Induced by Exposure to Phenolic Acids. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 313-320.	1.4	43
62	Modeling the onset of virulence in a pectinolytic bacterium. <i>Journal of Theoretical Biology</i> , 2007, 244, 239-257.	0.8	49
63	New insights into the regulatory mechanisms of the LuxR family of quorum sensing regulators. <i>Analytical and Bioanalytical Chemistry</i> , 2007, 387, 381-390.	1.9	102
64	The PecM protein is necessary for the DNA-binding capacity of the PecS repressor, one of the regulators of virulence-factor synthesis in <i>Erwinia chrysanthemi</i> . <i>FEMS Microbiology Letters</i> , 2006, 154, 265-270.	0.7	12
65	Synthesis and biological evaluation of homoserine lactone derived ureas as antagonists of bacterial quorum sensing. <i>Bioorganic and Medicinal Chemistry</i> , 2006, 14, 4781-4791.	1.4	76
66	Synthesis and Biological Evaluation of the Trifluoromethyl Analog of (4S)-4,5-Dihydroxy-2,3-pentanedione (DPD). <i>European Journal of Organic Chemistry</i> , 2006, 2006, 4731-4736.	1.2	40
67	Direct Evidence for the Modulation of the Activity of the <i>Erwinia chrysanthemi</i> Quorum-sensing Regulator ExpR by Acylhomoserine Lactone Pheromone. <i>Journal of Biological Chemistry</i> , 2006, 281, 29972-29987.	1.6	46
68	PecS and PecT Coregulate the Synthesis of HrpN and Pectate Lyases, Two Virulence Determinants in <i>Erwinia chrysanthemi</i> 3937. <i>Molecular Plant-Microbe Interactions</i> , 2005, 18, 1205-1214.	1.4	30
69	Definition of a Consensus DNA-binding Site for PecS, a Global Regulator of Virulence Gene Expression in <i>Erwinia chrysanthemi</i> and Identification of New Members of the PecS Regulon. <i>Journal of Biological Chemistry</i> , 2004, 279, 30158-30167.	1.6	51
70	N-Sulfonyl homoserine lactones as antagonists of bacterial quorum sensing. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2004, 14, 5145-5149.	1.0	109
71	Characterization of Indigoidine Biosynthetic Genes in <i>Erwinia chrysanthemi</i> and Role of This Blue Pigment in Pathogenicity. <i>Journal of Bacteriology</i> , 2002, 184, 654-665.	1.0	177
72	New synthetic analogues of N -acyl homoserine lactones as agonists or antagonists of transcriptional regulators involved in bacterial quorum sensing. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2002, 12, 1153-1157.	1.0	135

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73	H-NS-dependent activation of pectate lyases synthesis in the phytopathogenic bacterium <i>Erwinia chrysanthemi</i> mediated by the PecT repressor. <i>Molecular Microbiology</i> , 2002, 43, 733-748.	1.2	61
74	Role of the Nucleoid-Associated Protein H-NS in the Synthesis of Virulence Factors in the Phytopathogenic Bacterium <i>Erwinia chrysanthemi</i> . <i>Molecular Plant-Microbe Interactions</i> , 2001, 14, 10-20.	1.4	47
75	The PecT repressor interacts with regulatory regions of pectate lyase genes in <i>Erwinia chrysanthemi</i> . <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1998, 1442, 148-160.	2.4	15
76	Characterization of the <i>Erwinia chrysanthemi</i> <i>expR</i> locus directing the synthesis of two <i>N</i> -acetyl-homoserine lactone signal molecules. <i>Molecular Microbiology</i> , 1998, 29, 1391-1405.	1.2	173
77	Integration of the quorum-sensing system in the regulatory networks controlling virulence factor synthesis in <i>Erwinia chrysanthemi</i> . <i>Molecular Microbiology</i> , 1998, 29, 1407-1418.	1.2	99
78	Characterization of the <i>pecT</i> control region from <i>Erwinia chrysanthemi</i> 3937. <i>Journal of Bacteriology</i> , 1997, 179, 4909-4918.	1.0	32
79	The cyclic AMP receptor protein is the main activator of pectinolysis genes in <i>Erwinia chrysanthemi</i> . <i>Journal of Bacteriology</i> , 1997, 179, 3500-3508.	1.0	96
80	Mutual control of the PecS/PecM couple, two proteins regulating virulence factor synthesis in <i>Erwinia chrysanthemi</i> . <i>Molecular Microbiology</i> , 1997, 24, 803-814.	1.2	36
81	Antagonistic effect of CRP and KdgR in the transcription control of the <i>Erwinia chrysanthemi</i> pectinolysis genes. <i>Molecular Microbiology</i> , 1997, 26, 1071-1082.	1.2	60
82	Regulation of pectinase biosynthesis in <i>Erwinia chrysanthemi</i> . <i>Progress in Biotechnology</i> , 1996, , 311-330.	0.2	2
83	REGULATION OF PECTINOLYSIS IN <i>ERWINIA CHRYSANTHEMI</i> . <i>Annual Review of Microbiology</i> , 1996, 50, 213-257.	2.9	401
84	Purification and functional characterization of PecS, a regulator of virulence-factor synthesis in <i>Erwinia chrysanthemi</i> . <i>Molecular Microbiology</i> , 1996, 20, 391-402.	1.2	80
85	<i>pecS</i> : a locus controlling pectinase, cellulase and blue pigment production in <i>Erwinia chrysanthemi</i> . <i>Molecular Microbiology</i> , 1994, 11, 1127-1139.	1.2	151
86	Specific Interactions of <i>Erwinia chrysanthemi</i> KdgR Repressor with Different Operators of Genes Involved in Pectinolysis. <i>Journal of Molecular Biology</i> , 1994, 236, 427-440.	2.0	110
87	Pectate lyase from <i>Bacillus subtilis</i> : molecular characterization of the gene, and properties of the cloned enzyme. <i>FEBS Letters</i> , 1993, 335, 319-326.	1.3	60
88	Regulation of the expression of a <i>pelA::uidA</i> fusion in <i>Erwinia chrysanthemi</i> and demonstration of the synergistic action of plant extract with polygalacturonate on pectate lyase synthesis. <i>Journal of General Microbiology</i> , 1993, 139, 1-9.	2.3	45
89	Purification and functional characterization of the KdgR protein, a major repressor of pectinolysis genes of <i>Erwinia chrysanthemi</i> . <i>Molecular Microbiology</i> , 1992, 6, 257-265.	1.2	87
90	Characterization of <i>kdgR</i> , a gene of <i>Erwinia chrysanthemi</i> that regulates pectin degradation. <i>Molecular Microbiology</i> , 1991, 5, 2203-2216.	1.2	112

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91	Expanded linkage map of <i>Erwinia chrysanthemi</i> strain 3937. <i>Molecular Microbiology</i> , 1989, 3, 573-581.	1.2	47
92	Nucleotide sequences of the <i>Erwinia chrysanthemi</i> <i>ogl</i> and <i>pelE</i> genes negatively regulated by the <i>kdgR</i> gene product. <i>Gene</i> , 1989, 85, 125-134.	1.0	64
93	Nucleotide sequence of the <i>Erwinia chrysanthemi</i> gene encoding 2-keto-3-deoxygluconate permease. <i>Gene</i> , 1989, 83, 233-241.	1.0	14
94	Regulation of expression of pectate lyase genes <i>pelA</i> , <i>pelD</i> , and <i>pelE</i> in <i>Erwinia chrysanthemi</i> . <i>Journal of Bacteriology</i> , 1987, 169, 2417-2423.	1.0	27
95	Molecular cloning of an <i>Erwinia chrysanthemi</i> oligogalacturonate lyase gene involved in pectin degradation. <i>Gene</i> , 1987, 55, 125-133.	1.0	22
96	Organization of a pectate lyase gene family in <i>Erwinia chrysanthemi</i> . <i>Gene</i> , 1986, 49, 215-224.	1.0	58
97	Genetic transformation of the phytopathogenic bacteria, <i>Erwinia chrysanthemi</i> . <i>Biochimie</i> , 1985, 67, 253-257.	1.3	18
98	Cloning of genes encoding pectolytic enzymes from a genomic library of the phytopathogenic bacterium, <i>Erwinia chrysanthemi</i> . <i>Gene</i> , 1985, 35, 121-130.	1.0	57