Henri William Nasser

List of Publications by Year
in descending order

#	Article	IF	Citations
1	Carbon catabolite repression in pectin digestion by the phytopathogen Dickeya dadantii. Journal of Biological Chemistry, 2022, 298, 101446.	3.4	1
2	Implications of carbon catabolite repression for plantâ€“microbe interactions. Plant Communications, 2022, 3, 100272.	7.7	11
3	Relationship between the Chromosome Structural Dynamics and Gene Expressionâ€"A Chicken and Egg Dilemma?. Microorganisms, 2022, 10, 846.	3.6	7
4	Mapping the Complex Transcriptional Landscape of the Phytopathogenic Bacterium Dickeya dadantii. MBio, 2022, 13, e0052422.	4.1	4
5	Quantitative contribution of the spacer length in the supercoiling-sensitivity of bacterial promoters. Nucleic Acids Research, 2022, 50, 7287-7297.	14.5	1
6	Separation and quantification of 2-keto-3-deoxy-gluconate (KDG) a major metabolite in pectin and alginate degradation pathways. Analytical Biochemistry, 2021, 619, 114061.	2.4	6
7	The nucleoid-associated protein IHF acts as a â€˜transcriptional domaininâ€™ protein coordinating the bacterial virulence traits with global transcription. Nucleic Acids Research, 2021, 49, 776-790.	14.5	21
8	DNA sequence-directed cooperation between nucleoid-associated proteins. IScience, 2021, 24, 102408.	4.1	12
9	RNA Chaperones Hfq and ProQ Play a Key Role in the Virulence of the Plant Pathogenic Bacterium Dickeya dadantii. Frontiers in Microbiology, 2021, 12, 687484.	3.5	5
10	Role of the Discriminator Sequence in the Supercoiling Sensitivity of Bacterial Promoters. MSystems, 2021, 6, e0097821.	3.8	13
11	Design and comparative characterization of RecA variants. Scientific Reports, 2021, 11, 21106.	3.3	0
12	Acetic acid bacteria (AAB) involved in cocoa fermentation from Ivory Coast: species diversity and performance in acetic acid production. Journal of Food Science and Technology, 2020, 57, 1904-1916.	2.8	24
13	DNA Supercoiling: an Ancestral Regulator of Gene Expression in Pathogenic Bacteria?. Computational and Structural Biotechnology Journal, 2019, 17, 1047-1055.	4.1	33
14	Bacterial genome architecture shapes global transcriptional regulation by DNA supercoiling. Nucleic Acids Research, 2019, 47, 5648-5657.	14.5	60
15	APERO: a genome-wide approach for identifying bacterial small RNAs from RNA-Seq data. Nucleic Acids Research, 2019, 47, e88-e88.	14.5	21
16	The phytopathogenic nature of <i>Dickeya aquatica</i> 174/2 and the dynamic early evolution of <i>Dickeya</i> pathogenicity. Environmental Microbiology, 2019, 21, 2809-2835.	3.8	32
17	Coherent Domains of Transcription Coordinate Gene Expression During Bacterial Growth and Adaptation. Microorganisms, 2019, 7, 694.	3.6	13
18	Modeling the bioconversion of polysaccharides in a continuous reactor: A case study of the production of oligogalacturonates by Dickeya dadantii. Journal of Biological Chemistry, 2019, 294, 1753-1762.	3.4	4

#	Article	IF	Citations
19	Chromosomal organization of transcription: in a nutshell. Current Genetics, 2018, 64, 555-565.	1.7	39
20	Lactic acid bacteria involved in cocoa beans fermentation from Ivory Coast: Species diversity and citrate lyase production. International Journal of Food Microbiology, 2017, 256, 11-19.	4.7	61
21	Spatial organization of DNA sequences directs the assembly of bacterial chromatin by a nucleoid-associated protein. Journal of Biological Chemistry, 2017, 292, 7607-7618.	3.4	33
22	Regulation of the synthesis of pulp degrading enzymes in Bacillus isolated from cocoa fermentation. Food Microbiology, 2017, 63, 255-262.	4.2	20
23	Plantâ€“phytopathogen interactions: bacterial responses to environmental and plant stimuli. Environmental Microbiology, 2017, 19, 1689-1716.	3.8	65
24	Global transcriptional response of <i>Dickeya dadantii</i> to environmental stimuli relevant to the plant infection. Environmental Microbiology, 2016, 18, 3651-3672.	3.8	53
25	Regulation of pel genes, major virulence factors in the plant pathogen bacterium Dickeya dadantii , is mediated by cooperative binding of the nucleoid-associated protein H-NS. Research in Microbiology, 2016, 167, 247-253.	2.1	6
26	Temporal control of Dickeya dadantii main virulence gene expression by growth phase-dependent alteration of regulatory nucleoprotein complexes. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2016, 1859, 1470-1480.	1.9	16
27	Transcriptional start site turnover in the evolution of bacterial paralogous genes â€“ the <i>pelEâ€•pelD</i> virulence genes in <i>Dickeya</i>. FEBS Journal, 2016, 283, 4192-4207.	4.7	15
28	IscR Regulates Synthesis of Colonization Factor Antigen I Fimbriae in Response to Iron Starvation in Enterotoxigenic Escherichia coli. Journal of Bacteriology, 2015, 197, 2896-2907.	2.2	35
29	Upstream Binding of Idling RNA Polymerase Modulates Transcription Initiation from a Nearby Promoter. Journal of Biological Chemistry, 2015, 290, 8095-8109.	3.4	18
30	Chromosomal â€œStress-Responseâ€•Domains Govern the Spatiotemporal Expression of the Bacterial Virulence Program. MBio, 2015, 6, e00353-15.	4.1	49
31	Identification of Novel Components Influencing Colonization Factor Antigen I Expression in Enterotoxigenic Escherichia coli. PLoS ONE, 2015, 10, e0141469.	2.5	13
32	Rethinking the Bacterial Genetic Regulation. Biochemistry and Analytical Biochemistry: Current Research, 2015, 04, .	0.4	4
33	Bacterial virulence and Fis: adapting regulatory networks to the host environment. Trends in Microbiology, 2014, 22, 92-99.	7.7	46
34	Role of the <scp>LysR</scp>â€•type transcriptional regulator <scp>PecT</scp> and <scp>DNA</scp> supercoiling in the thermoregulation of <scp><i>pel</i></scp> genes, the major virulence factors in <i><scp>D</scp>ickeya dadantii</i>. Environmental Microbiology, 2014, 16, 734-745.	3.8	30
35	<i><scp>D</scp>ickeya</i> ecology, environment sensing and regulation of virulence programme. Environmental Microbiology Reports, 2013, 5, 622-636.	2.4	163
36	Vfm a new quorum sensing system controls the virulence of <i><scp>D</scp>ickeya dadantii</i>. Environmental Microbiology, 2013, 15, 865-880.	3.8	95

#	Article	IF	Citations
37	The nucleoidâ€associated protein Fis directly modulates the synthesis of cellulose, an essential component of pellicleâ€“biofilms in the phytopathogenic bacterium <i>Dickeya dadantii</i>. Molecular Microbiology, 2012, 86, 172-186.	2.5	55
38	The nucleoid-associated proteins H-NS and FIS modulate the DNA supercoiling response of the pel genes, the major virulence factors in the plant pathogen bacterium Dickeya dadantii. Nucleic Acids Research, 2012, 40, 4306-4319.	14.5	80
39	Quorum Sensing Signaling Molecules Produced by Reference and Emerging Soft-Rot Bacteria (Dickeya) Tj ETQq1 1 0.784314 rgBT /Ov	2.5	54
40	PecS 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.	3.8	32
41	Molecular identification and pectate lyase production by Bacillus strains involved in cocoa fermentation. Food Microbiology, 2011, 28, 1-8.	4.2	45
42	lpxC and yafS are the Most Suitable Internal Controls to Normalize Real Time RT-qPCR Expression in the Phytopathogenic Bacteria Dickeya dadantii. PLoS ONE, 2011, 6, e20269.	2.5	41
43	Systematic targeted mutagenesis of the MarR/SlyA family members of Dickeya dadantii 3937 reveals a role for MfbR in the modulation of virulence gene expression in response to acidic pH. Molecular Microbiology, 2010, 78, 1018-1037.	2.5	37
44	Toward a Quantitative Modeling of the Synthesis of the Pectate Lyases, Essential Virulence Factors in Dickeya dadantii. Journal of Biological Chemistry, 2010, 285, 28565-28576.	3.4	38
45	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.	3.1	34
46	The GacA global regulator is required for the appropriate expression of <i>Erwinia chrysanthemi</i> 3937 pathogenicity genes during plant infection. Environmental Microbiology, 2008, 10, 545-559.	3.8	81
47	PecS Is a Global Regulator of the Symptomatic Phase in the Phytopathogenic Bacterium <i>Erwinia chrysanthemi</i> 3937. Journal of Bacteriology, 2008, 190, 7508-7522.	2.2	94
48	Modeling the onset of virulence in a pectinolytic bacterium. Journal of Theoretical Biology, 2007, 244, 239-257.	1.7	49
49	Integration of two essential virulence modulating signals at the Erwinia chrysanthemi pel gene promoters: a role for Fis in the growth-phase regulation. Molecular Microbiology, 2007, 66, 071119190133005-???.	2.5	28
50	The DNA nucleoidâ€associated protein Fis coâ€ordinates the expression of the main virulence genes in the phytopathogenic bacterium <i>Erwinia chrysanthemi</i>. Molecular Microbiology, 2007, 66, 1474-1490.	2.5	43
51	New insights into the regulatory mechanisms of the LuxR family of quorum sensing regulators. Analytical and Bioanalytical Chemistry, 2007, 387, 381-390.	3.7	102
52	The PecM protein is necessary for the DNA-binding capacity of the PecS repressor, one of the regulators of virulence-factor synthesis in Erwinia chrysanthemi. FEMS Microbiology Letters, 2006, 154, 265-270.	1.8	12
53	Synthesis and biological evaluation of homoserine lactone derived ureas as antagonists of bacterial quorum sensing. Bioorganic and Medicinal Chemistry, 2006, 14, 4781-4791.	3.0	76
54	Direct Evidence for the Modulation of the Activity of the Erwinia chrysanthemi Quorum-sensing Regulator ExpR by Acylhomoserine Lactone Pheromone. Journal of Biological Chemistry, 2006, 281, 29972-29987.	3.4	46

#	Article	IF	Citations
55	PecS and PecT Coregulate the Synthesis of HrpN and Pectate Lyases, Two Virulence Determinants in Erwinia chrysanthemi 3937. Molecular Plant-Microbe Interactions, 2005, 18, 1205-1214.	2.6	30
56	Definition of a Consensus DNA-binding Site for PecS, a Global Regulator of Virulence Gene Expression in Erwinia chrysanthemi and Identification of New Members of the PecS Regulon. Journal of Biological Chemistry, 2004, 279, 30158-30167.	3.4	51
57	N-Sulfonyl homoserine lactones as antagonists of bacterial quorum sensing. Bioorganic and Medicinal Chemistry Letters, 2004, 14, 5145-5149.	2.2	109
58	PehN, a Polygalacturonase Homologue with a Low Hydrolase Activity, Is Coregulated with the Other Erwinia chrysanthemi Polygalacturonases. Journal of Bacteriology, 2002, 184, 2664-2673.	2.2	24
59	Characterization of Indigoidine Biosynthetic Genes in <i>Erwinia chrysanthemi</i> and Role of This Blue Pigment in Pathogenicity. Journal of Bacteriology, 2002, 184, 654-665.	2.2	177
60	H-NS-dependent activation of pectate lyases synthesis in the phytopathogenic bacteriumErwinia chrysanthemiis mediated by the PecT repressor. Molecular Microbiology, 2002, 43, 733-748.	2.5	61
61	Transcriptional regulation of fis operon involves a module of multiple coupled promoters. EMBO Journal, 2002, 21, 715-724.	7.8	24
62	Role of the Nucleoid-Associated Protein H-NS in the Synthesis of Virulence Factors in the Phytopathogenic Bacterium Erwinia chrysanthemi. Molecular Plant-Microbe Interactions, 2001, 14, 10-20.	2.6	47
63	CRP Modulates fis Transcription by Alternate Formation of Activating and Repressing Nucleoprotein Complexes. Journal of Biological Chemistry, 2001, 276, 17878-17886.	3.4	72
64	Erwinia carotovora has two KdgR-like proteins belonging to the IclR family of transcriptional regulators: identification and characterization of the RexZ activator and the KdgR repressor of pathogenesis. Microbiology (United Kingdom), 1999, 145, 1531-1545.	1.8	39
65	Analysis of three clustered polygalacturonase genes in Erwinia chrysanthemi 3937 revealed an anti-repressor function for the PecS regulator. Molecular Microbiology, 1999, 34, 641-650.	2.5	47
66	Positive co-regulation of the Escherichia coli carnitine pathway cai and fix operons by CRP and the CaiF activator. Molecular Microbiology, 1999, 34, 562-575.	2.5	34
67	Self-regulation of Pir, a Regulatory Protein Responsible for Hyperinduction of Pectate Lyase in Erwinia chrysanthemi EC16. Molecular Plant-Microbe Interactions, 1999, 12, 385-390.	2.6	12
68	Regulation of <i>pelD</i> and <i>pelE</i> , Encoding Major Alkaline Pectate Lyases in <i>Erwinia chrysanthemi</i> : Involvement of the Main Transcriptional Factors. Journal of Bacteriology, 1999, 181, 5948-5957.	2.2	36
69	The PecT repressor interacts with regulatory regions of pectate lyase genes in Erwinia chrysanthemi. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1998, 1442, 148-160.	2.4	15
70	Characterization of the <i>Erwinia chrysanthemi expIâ€“expR</i> locus directing the synthesis of two <i>N</i>â€acylâ€homoserine lactone signal molecules. Molecular Microbiology, 1998, 29, 1391-1405.	2.5	173
71	Integration of the quorumâ€sensing system in the regulatory networks controlling virulence factor synthesis inErwinia chrysanthemi. Molecular Microbiology, 1998, 29, 1407-1418.	2.5	99
72	The pir gene of Erwinia chrysanthemi EC16 regulates hyperinduction of pectate lyase virulence genes in response to plant signals. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 14034-14039.	7.1	56

#	Article	IF	Citations
73	Comparative analysis of the five major Erwinia chrysanthemi pectate lyases: enzyme characteristics and potential inhibitors. Journal of Bacteriology, 1997, 179, 2503-2511.	2.2	137
74	The cyclic AMP receptor protein is the main activator of pectinolysis genes in Erwinia chrysanthemi. Journal of Bacteriology, 1997, 179, 3500-3508.	2.2	96
75	Mutual control of the PecS/PecM couple, two proteins regulating virulenceâ€factor synthesis in Erwinia chrysanthemi. Molecular Microbiology, 1997, 24, 803-814.	2.5	36
76	Antagonistic effect of CRP and KdgR in the transcription control of the Erwinia chrysanthemi pectinolysis genes. Molecular Microbiology, 1997, 26, 1071-1082.	2.5	60
77	The PecM protein is necessary for the DNA-binding capacity of the PecS repressor, one of the regulators of virulence-factor synthesis in Erwinia chrysanthemi. FEMS Microbiology Letters, 1997, 154, 265-270.	1.8	1
78	Regulation of pectinase biosynthesis in Erwinia chrysanthemi. Progress in Biotechnology, 1996, , 311-330.	0.2	2
79	REGULATION OF PECTINOLYSIS INERWINIA CHRYSANTHEMI. Annual Review of Microbiology, 1996, 50, 213-257.	7.3	401
80	Heavy-metal-responsive genes in maize: identification and comparison of their expression upon various forms of abiotic stress. Planta, 1996, 199, 1-8.	3.2	80
81	Purification and functional characterization of PecS, a regulator of virulence-factor synthesis in Erwinia chrysanthemi. Molecular Microbiology, 1996, 20, 391-402.	2.5	80
82	Purification and characterization of the nuclease NucM of Erwinia chrysanthemi. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1995, 1262, 133-138.	2.4	5
83	The structure of Bacillus subtilis pectate lyase in complex with calcium. Nature Structural and Molecular Biology, 1994, 1, 717-723.	8.2	173
84	pecS: a locus controlling pectinase, cellulase and blue pigment production in Erwinia chrysanthemi. Molecular Microbiology, 1994, 11, 1127-1139.	2.5	151
85	Specific Interactions of Erwinia chrysanthemi KdgR Repressor with Different Operators of Genes Involved in Pectinolysis. Journal of Molecular Biology, 1994, 236, 427-440.	4.2	110
86	Molecular characterization of the Erwinia chrysanthemi kdgK gene involved in pectin degradation. Journal of Bacteriology, 1994, 176, 2386-2392.	2.2	25
87	Pectate lyase fromBacillus subtilis: molecular characterization of the gene, and properties of the cloned enzyme. FEBS Letters, 1993, 335, 319-326.	2.8	60
88	Crystallization and preliminary X-ray studies of the pectate lyase from Bacillus subtilis. Journal of Molecular Biology, 1992, 228, 1255-1258.	4.2	4
89	Purification and functional characterization of the KdgR protein, a major repressor of pectinolysis genes of Erwinia chrysanthemi. Molecular Microbiology, 1992, 6, 257-265.	2.5	87
90	Characterization ofkdgR, a gene ofErwinia chrysanthemithat regulates pectin degradation. Molecular Microbiology, 1991, 5, 2203-2216.	2.5	112

#	Article	IF	Citations
91	Inducing properties of analogs of 2-keto-3-deoxygluconate on the expression of pectinase genes ofErwinia chrysanthemi. FEMS Microbiology Letters, 1991, 81, 73-78.	1.8	42
92	Nouvelle Synthese de L'Acide 3-Desoxy-D-Erythro-2-Hexulosonique (KDG). A Partir De La D-Glucono-1,5-Lactone Synthese Et Etude De RMN De Derives O-Methyles Du KDG. Journal of Carbohydrate Chemistry, 1991, 10, 787-811.	1.1	15
93	Inducing properties of analogs of 2-keto-3-deoxygluconate on the expression of pectinase genes of Erwinia chrysanthemi. FEMS Microbiology Letters, 1991, 81, 73-78.	1.8	10
94	Purification and characterization of extracellular pectate lyase from Bacillus subtilis. Biochimie, 1990, 72, 689-695.	2.6	59
95	Maize pathogenesis-related proteins: characterization and cellular distribution of 1,3-Î²-glucanases and chitinases induced by brome mosaic virus infection or mercuric chloride treatment. Physiological and Molecular Plant Pathology, 1990, 36, 1-14.	2.5	71
96	Identification and characterization of maize pathogenesis-related proteins. Four maize PR proteins are chitinases. Plant Molecular Biology, 1988, 11, 529-538.	3.9	82
97	DNA Sequence-Directed Cooperation between Nucleoid-Associated Proteins. SSRN Electronic Journal, 0, , .	0.4	0