

Ralf Koebnik

List of Publications by Year in descending order

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128
papers

8,135
citations

61984

43
h-index

53230

85
g-index

139
all docs

139
docs citations

139
times ranked

6318
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>Xanthomonas hortorum</i> “beyond gardens: Current taxonomy, genomics, and virulence repertoires. <i>Molecular Plant Pathology</i> , 2022, 23, 597-621.	4.2	20
2	Phenotypic and Molecular-Phylogenetic Analyses Reveal Distinct Features of Crown Gall-Associated <i>Xanthomonas</i> Strains. <i>Microbiology Spectrum</i> , 2022, 10, e0057721.	3.0	11
3	Taxonomic Refinement of <i>Xanthomonas arboricola</i> . <i>Phytopathology</i> , 2022, 112, 1630-1639.	2.2	8
4	Complete Genome Sequence of <i>Xanthomonas campestris</i> pv. <i>campestris</i> SB80, a Race 4 Strain Isolated from White Head Cabbage in Turkey. <i>Microbiology Resource Announcements</i> , 2022, 11, e0002222.	0.6	1
5	Complete Genome Sequence Resource for <i>Xanthomonas translucens</i> pv. <i>undulosa</i> MAI5034, a Wheat Pathogen from Uruguay. <i>Phytopathology</i> , 2022, , PHYTO01220025A.	2.2	2
6	<i>Xanthomonas bonasiae</i> sp. nov. and <i>Xanthomonas youngii</i> sp. nov., isolated from crown gall tissues. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	1.7	16
7	The Complete Genome Sequence of <i>Xanthomonas theicola</i> , the Causal Agent of Canker on Tea Plants, Reveals Novel Secretion Systems in Clade-1 <i>Xanthomonads</i> . <i>Phytopathology</i> , 2021, 111, 611-616.	2.2	17
8	Molecular Epidemiology of <i>Xanthomonas euvesicatoria</i> Strains from the Balkan Peninsula Revealed by a New Multiple-Locus Variable-Number Tandem-Repeat Analysis Scheme. <i>Microorganisms</i> , 2021, 9, 536.	3.6	10
9	Genomics-informed multiplex PCR scheme for rapid identification of rice-associated bacteria of the genus <i>Pantoea</i> . <i>Plant Disease</i> , 2021, 105, 2389-2394.	1.4	10
10	Trends in Molecular Diagnosis and Diversity Studies for Phytosanitary Regulated <i>Xanthomonas</i> . <i>Microorganisms</i> , 2021, 9, 862.	3.6	22
11	Development of two loop-mediated isothermal amplification (LAMP) genomics-informed diagnostic protocols for rapid detection of <i>Pantoea</i> species on rice. <i>MethodsX</i> , 2021, 8, 101216.	1.6	4
12	Integrating science on <i>Xanthomonadaceae</i> for sustainable plant disease management in Europe. <i>Molecular Plant Pathology</i> , 2021, 22, 1461-1463.	4.2	6
13	An atypical class of non-coding small RNAs is produced in rice leaves upon bacterial infection. <i>Scientific Reports</i> , 2021, 11, 24141.	3.3	3
14	Complete Genome Assemblies of All <i>Xanthomonas translucens</i> Pathotype Strains Reveal Three Genetically Distinct Clades. <i>Frontiers in Microbiology</i> , 2021, 12, 817815.	3.5	19
15	Genome Resource of Barley Bacterial Blight and Leaf Streak Pathogen <i>Xanthomonas translucens</i> pv. <i>translucens</i> strain UPB886. <i>Plant Disease</i> , 2020, 104, 13-15.	1.4	12
16	High-Quality Genome Resource of <i>Xanthomonas hyacinthi</i> Generated via Long-Read Sequencing. <i>Plant Disease</i> , 2020, 104, 1011-1012.	1.4	7
17	Repeated gain and loss of a single gene modulates the evolution of vascular plant pathogen lifestyles. <i>Science Advances</i> , 2020, 6, .	10.3	58
18	The Rice DNA-Binding Protein ZBED Controls Stress Regulators and Maintains Disease Resistance After a Mild Drought. <i>Frontiers in Plant Science</i> , 2020, 11, 1265.	3.6	6

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19	Design of a new multiplex PCR assay for rice pathogenic bacteria detection and its application to infer disease incidence and detect co-infection in rice fields in Burkina Faso. PLoS ONE, 2020, 15, e0232115.	2.5	16
20	Genome Resources of Three West African Strains of <i>Pantoea ananatis</i> Causing Bacterial Blight and Grain Discoloration of Rice. Phytopathology, 2020, 110, 1500-1502.	2.2	7
21	Phylogenetic distribution and evolutionary dynamics of nod and T3SS genes in the genus <i>Bradyrhizobium</i> . Microbial Genomics, 2020, 6, .	2.0	9
22	A semi-selective medium to isolate and identify bacteria of the genus <i>Pantoea</i> . Journal of General Plant Pathology, 2019, 85, 424-427.	1.0	14
23	Molecular Typing Reveals High Genetic Diversity of <i>Xanthomonas translucens</i> Strains Infecting Small-Grain Cereals in Iran. Applied and Environmental Microbiology, 2019, 85, .	3.1	37
24	A Pathovar of <i>Xanthomonas oryzae</i> Infecting Wild Grasses Provides Insight Into the Evolution of Pathogenicity in Rice Agroecosystems. Frontiers in Plant Science, 2019, 10, 507.	3.6	18
25	A TonB-dependent transporter is required for secretion of protease PopC across the bacterial outer membrane. Nature Communications, 2019, 10, 1360.	12.8	43
26	An Optimized Microsatellite Scheme for Assessing Populations of <i>Xanthomonas phaseoli</i> pv. <i>manihotis</i> . Phytopathology, 2019, 109, 859-869.	2.2	9
27	Addressing the New Global Threat of <i>Xylella fastidiosa</i> . Phytopathology, 2019, 109, 172-174.	2.2	30
28	The rhizobial type III effector ErnA confers the ability to form nodules in legumes. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 21758-21768.	7.1	65
29	CRISPR elements provide a new framework for the genealogy of the citrus canker pathogen <i>Xanthomonas citri</i> pv. <i>citri</i> . BMC Genomics, 2019, 20, 917.	2.8	16
30	First Report of Bacterial Blight of Peony Caused by <i>Xanthomonas hortorum</i> in Ohio. Plant Disease, 2019, 103, 2940.	1.4	3
31	Multilocus sequence analysis reveals a novel phylogroup of <i>Xanthomonas euvesicatoria</i> pv. <i>perforans</i> causing bacterial spot of tomato in Iran. Plant Pathology, 2018, 67, 1601-1611.	2.4	19
32	Pathogenicity and phylogenetic analysis of <i>Clavibacter michiganensis</i> strains associated with tomato plants in Iran. Plant Pathology, 2018, 67, 957-970.	2.4	37
33	<i>Enterobacter cloacae</i> , an Emerging Plant-Pathogenic Bacterium Affecting Chili Pepper Seedlings. Plant Pathology Journal, 2018, 34, 1-10.	1.7	49
34	Efficient enrichment cloning of TAL effector genes from <i>Xanthomonas</i> . MethodsX, 2018, 5, 1027-1032.	1.6	10
35	Functional analysis of African <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> TALomes reveals a new susceptibility gene in bacterial leaf blight of rice. PLoS Pathogens, 2018, 14, e1007092.	4.7	86
36	Horizontal gene transfer plays a major role in the pathological convergence of <i>Xanthomonas</i> lineages on common bean. BMC Genomics, 2018, 19, 606.	2.8	38

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37	Functional and Genome Sequence-Driven Characterization of tal Effector Gene Repertoires Reveals Novel Variants With Altered Specificities in Closely Related Malian <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> Strains. <i>Frontiers in Microbiology</i> , 2018, 9, 1657.	3.5	40
38	Characterization of the <i>Xanthomonas translucens</i> Complex Using Draft Genomes, Comparative Genomics, Phylogenetic Analysis, and Diagnostic LAMP Assays. <i>Phytopathology</i> , 2017, 107, 519-527.	2.2	61
39	Transcriptome and proteome analysis reveal new insight into proximal and distal responses of wheat to foliar infection by <i>Xanthomonas translucens</i> . <i>Scientific Reports</i> , 2017, 7, 10157.	3.3	25
40	Targeted promoter editing for rice resistance to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> reveals differential activities for <i>SWEET14</i> inducing <i>TAL</i> effectors. <i>Plant Biotechnology Journal</i> , 2017, 15, 306-317.	8.3	176
41	Effector Mimics and Integrated Decoys, the Never-Ending Arms Race between Rice and <i>Xanthomonas oryzae</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 431.	3.6	31
42	Comparative Genomics Identifies a Novel Conserved Protein, HpaT, in Proteobacterial Type III Secretion Systems that Do Not Possess the Putative Translocon Protein HrpF. <i>Frontiers in Microbiology</i> , 2017, 8, 1177.	3.5	26
43	High-Quality Draft Genome Sequence of <i>Curtobacterium</i> sp. Strain Ferrero. <i>Genome Announcements</i> , 2017, 5, .	0.8	4
44	First Report of a New Bacterial Leaf Blight of Rice Caused by <i>Pantoea ananatis</i> and <i>Pantoea stewartii</i> in Togo. <i>Plant Disease</i> , 2017, 101, 241.	1.4	27
45	First Report of a New Bacterial Leaf Blight of Rice Caused by <i>Pantoea ananatis</i> and <i>Pantoea stewartii</i> in Benin. <i>Plant Disease</i> , 2017, 101, 242-242.	1.4	24
46	Whole-Genome Sequences of <i>Xanthomonas euvesicatoria</i> Strains Clarify Taxonomy and Reveal a Stepwise Erosion of Type 3 Effectors. <i>Frontiers in Plant Science</i> , 2016, 7, 1805.	3.6	56
47	Ectopic activation of the rice <i>NLR</i> heteropair <i>RGA4/RGA5</i> confers resistance to bacterial blight and bacterial leaf streak diseases. <i>Plant Journal</i> , 2016, 88, 43-55.	5.7	27
48	AnnoTALE: bioinformatics tools for identification, annotation and nomenclature of TALEs from <i>Xanthomonas</i> genomic sequences. <i>Scientific Reports</i> , 2016, 6, 21077.	3.3	119
49	High-Quality Draft Genome Sequences of Two <i>Xanthomonas</i> Pathotype Strains Infecting Aroid Plants. <i>Genome Announcements</i> , 2016, 4, .	0.8	7
50	Using Ecology, Physiology, and Genomics to Understand Host Specificity in <i>Xanthomonas</i> . <i>Annual Review of Phytopathology</i> , 2016, 54, 163-187.	7.8	157
51	First Report of Bacterial Leaf Blight of Rice Caused by <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> in Benin. <i>Plant Disease</i> , 2016, 100, 515-515.	1.4	8
52	Genomics and transcriptomics of <i>Xanthomonas campestris</i> species challenge the concept of core type III effectome. <i>BMC Genomics</i> , 2015, 16, 975.	2.8	62
53	A knowledge-based molecular screen uncovers a broad spectrum <i>OsSWEET14</i> resistance allele to bacterial blight from wild rice. <i>Plant Journal</i> , 2015, 84, 694-703.	5.7	181
54	Draft Genome Sequence of <i>Xanthomonas translucens</i> pv. <i>graminis</i> Pathotype Strain CFBP 2053. <i>Genome Announcements</i> , 2015, 3, .	0.8	7

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55	Draft Genome Sequences of Two <i>Xanthomonas vesicatoria</i> Strains from the Balkan Peninsula. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
56	New Multilocus Variable-Number Tandem-Repeat Analysis Tool for Surveillance and Local Epidemiology of Bacterial Leaf Blight and Bacterial Leaf Streak of Rice Caused by <i>Xanthomonas oryzae</i> . <i>Applied and Environmental Microbiology</i> , 2015, 81, 688-698.	3.1	69
57	High-Quality Draft Genome Sequence of the <i>Xanthomonas translucens</i> pv. <i>cerealis</i> Pathotype Strain CFBP 2541. <i>Genome Announcements</i> , 2015, 3, .	0.8	24
58	Comparative genomics of a cannabis pathogen reveals insight into the evolution of pathogenicity in <i>Xanthomonas</i> . <i>Frontiers in Plant Science</i> , 2015, 6, 431.	3.6	47
59	Draft Genome Sequences of Two <i>Xanthomonas euvesicatoria</i> Strains from the Balkan Peninsula. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
60	Confirmation of Bacterial Leaf Streak of Rice Caused by <i>Xanthomonas oryzae</i> pv. <i>oryzicola</i> in Vietnam. <i>Plant Disease</i> , 2015, 99, 1853-1853.	1.4	3
61	Draft Genome Sequence of <i>Xanthomonas axonopodis</i> pv. <i>allii</i> Strain CFBP 6369. <i>Genome Announcements</i> , 2014, 2, .	0.8	7
62	Draft Genome Sequence of the Flagellated <i>Xanthomonas fuscans</i> subsp. <i>fuscans</i> Strain CFBP 4884. <i>Genome Announcements</i> , 2014, 2, .	0.8	7
63	Comparative proteomics reveal new HrpX-regulated proteins of <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . <i>Journal of Proteomics</i> , 2014, 97, 256-264.	2.4	14
64	The Genomics of <i>Xanthomonas oryzae</i> . , 2014, , 127-150.		7
65	Population typing of the causal agent of cassava bacterial blight in the Eastern Plains of Colombia using two types of molecular markers. <i>BMC Microbiology</i> , 2014, 14, 161.	3.3	16
66	Analysis of <i>Xanthomonas oryzae</i> pv. <i>oryzicola</i> Population in Mali and Burkina Faso Reveals a High Level of Genetic and Pathogenic Diversity. <i>Phytopathology</i> , 2014, 104, 520-531.	2.2	49
67	Confirmation of Bacterial Leaf Streak Caused by <i>Xanthomonas oryzae</i> pv. <i>oryzicola</i> on Rice in Madagascar. <i>Plant Disease</i> , 2014, 98, 1423-1423.	1.4	16
68	First Report of <i>Xanthomonas oryzae</i> pv. <i>oryzicola</i> Causing Bacterial Leaf Streak of Rice in Burundi. <i>Plant Disease</i> , 2014, 98, 1426-1426.	1.4	4
69	First Report of <i>Xanthomonas oryzae</i> pv. <i>oryzicola</i> Causing Bacterial Leaf Streak of Rice in Uganda. <i>Plant Disease</i> , 2014, 98, 1579-1579.	1.4	10
70	A MLVA Genotyping Scheme for Global Surveillance of the Citrus Pathogen <i>Xanthomonas citri</i> pv. <i>citri</i> Suggests a Worldwide Geographical Expansion of a Single Genetic Lineage. <i>PLoS ONE</i> , 2014, 9, e98129.	2.5	70
71	The <i>Xanthomonas</i> Ax21 protein is processed by the general secretory system and is secreted in association with outer membrane vesicles. <i>PeerJ</i> , 2014, 2, e242.	2.0	48
72	Five phylogenetically close rice <i>SWEET</i> genes confer TAL effector-mediated susceptibility to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . <i>New Phytologist</i> , 2013, 200, 808-819.	7.3	312

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73	Genome sequence of <i>Xanthomonas fuscans</i> subsp. <i>fuscans</i> strain 4834-R reveals that flagellar motility is not a general feature of xanthomonads. <i>BMC Genomics</i> , 2013, 14, 761.	2.8	55
74	<sc>TAL</sc>1 from <i>Xanthomonas axonopodis</i> pv. <i>manihotis</i> acts as a transcriptional activator in plant cells and is important for pathogenicity in cassava plants. <i>Molecular Plant Pathology</i> , 2013, 14, 84-95.	4.2	37
75	Identification of non-TAL effectors in <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> Chinese strain 13751 and analysis of their role in the bacterial virulence. <i>World Journal of Microbiology and Biotechnology</i> , 2013, 29, 733-744.	3.6	15
76	High-Quality Draft Genome Sequences of Two <i>Xanthomonas citri</i> pv. <i>malvacearum</i> Strains. <i>Genome Announcements</i> , 2013, 1, .	0.8	8
77	Draft Genome Sequence of the <i>Xanthomonas cassavae</i> Type Strain CFBP 4642. <i>Genome Announcements</i> , 2013, 1, .	0.8	7
78	High-Quality Draft Genome Sequence of <i>Xanthomonas alfalfae</i> subsp. <i>alfalfae</i> Strain CFBP 3836. <i>Genome Announcements</i> , 2013, 1, .	0.8	7
79	Genome mining reveals the genus <i>Xanthomonas</i> to be a promising reservoir for new bioactive non-ribosomally synthesized peptides. <i>BMC Genomics</i> , 2013, 14, 658.	2.8	21
80	High-Quality Draft Genome Sequences of <i>Xanthomonas axonopodis</i> pv. <i>glycines</i> Strains CFBP 2526 and CFBP 7119. <i>Genome Announcements</i> , 2013, 1, .	0.8	26
81	An Improved Method for TAL Effectors DNA-Binding Sites Prediction Reveals Functional Convergence in TAL Repertoires of <i>Xanthomonas oryzae</i> Strains. <i>PLoS ONE</i> , 2013, 8, e68464.	2.5	102
82	Genomic Survey of Pathogenicity Determinants and VNTR Markers in the Cassava Bacterial Pathogen <i>Xanthomonas axonopodis</i> pv. <i>Manihotis</i> Strain CIO151. <i>PLoS ONE</i> , 2013, 8, e79704.	2.5	42
83	Development of a Variable Number of Tandem Repeats Typing Scheme for the Bacterial Rice Pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzicola</i> . <i>Phytopathology</i> , 2012, 102, 948-956.	2.2	51
84	Genomic insights into strategies used by <i>Xanthomonas albilineans</i> with its reduced artillery to spread within sugarcane xylem vessels. <i>BMC Genomics</i> , 2012, 13, 658.	2.8	50
85	Multilocus sequence analysis and type III effector repertoire mining provide new insights into the evolutionary history and virulence of <i>Xanthomonas oryzae</i>. <i>Molecular Plant Pathology</i> , 2012, 13, 288-302.	4.2	56
86	Two New Complete Genome Sequences Offer Insight into Host and Tissue Specificity of Plant Pathogenic <i>Xanthomonas</i> spp. <i>Journal of Bacteriology</i> , 2011, 193, 5450-5464.	2.2	189
87	Colonization of Rice Leaf Blades by an African Strain of <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> Depends on a New TAL Effector That Induces the Rice Nodulin-3 <i>Os11N3</i> Gene. <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 1102-1113.	2.6	179
88	Comparative genomics reveals diversity among xanthomonads infecting tomato and pepper. <i>BMC Genomics</i> , 2011, 12, 146.	2.8	167
89	Adhesion Mechanisms of Plant-Pathogenic Xanthomonadaceae. <i>Advances in Experimental Medicine and Biology</i> , 2011, 715, 71-89.	1.6	56
90	Membrane topology of conserved components of the type III secretion system from the plant pathogen <i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> . <i>Microbiology (United Kingdom)</i> , 2010, 156, 1963-1974.	1.8	31

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91	The complete genome sequence of <i>Xanthomonas albilineans</i> provides new insights into the reductive genome evolution of the xylem-limited Xanthomonadaceae. <i>BMC Genomics</i> , 2009, 10, 616.	2.8	142
92	The type III effectors of <i>Xanthomonas</i> . <i>Molecular Plant Pathology</i> , 2009, 10, 749-766.	4.2	303
93	Genome sequence and rapid evolution of the rice pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> PXO99A. <i>BMC Genomics</i> , 2008, 9, 204.	2.8	327
94	The missing link: <i>Bordetella petrii</i> is endowed with both the metabolic versatility of environmental bacteria and virulence traits of pathogenic <i>Bordetellae</i> . <i>BMC Genomics</i> , 2008, 9, 449.	2.8	85
95	Genome sequence and rapid evolution of the rice pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> PXO99A. <i>BMC Genomics</i> , 2008, 9, 534.	2.8	33
96	Refinement of the <i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> hrpD and hrpE Operon Structure. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 559-567.	2.6	25
97	A Minimal Transmembrane β -Barrel Platform Protein Studied by Nuclear Magnetic Resonance. <i>Biochemistry</i> , 2007, 46, 1128-1140.	2.5	31
98	Positive Selection of the Hrp Pilin HrpE of the Plant Pathogen <i>Xanthomonas</i> . <i>Journal of Bacteriology</i> , 2006, 188, 1405-1410.	2.2	29
99	Specific Binding of the <i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> AraC-Type Transcriptional Activator HrpX to Plant-Inducible Promoter Boxes. <i>Journal of Bacteriology</i> , 2006, 188, 7652-7660.	2.2	148
100	Domain Structure of HrpE, the Hrp Pilus Subunit of <i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> . <i>Journal of Bacteriology</i> , 2005, 187, 6175-6186.	2.2	32
101	The Type III-Dependent Hrp Pilus Is Required for Productive Interaction of <i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> with Pepper Host Plants. <i>Journal of Bacteriology</i> , 2005, 187, 2458-2468.	2.2	63
102	TonB-dependent trans-envelope signalling: the exception or the rule?. <i>Trends in Microbiology</i> , 2005, 13, 343-347.	7.7	190
103	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
104	The role of bacterial pili in protein and DNA translocation. <i>Trends in Microbiology</i> , 2001, 9, 586-590.	7.7	33
105	Sucrose transport through maltoporin mutants of <i>Escherichia coli</i> . <i>Protein Engineering, Design and Selection</i> , 2001, 14, 943-948.	2.1	12
106	Structure and function of bacterial outer membrane proteins: barrels in a nutshell. <i>Molecular Microbiology</i> , 2000, 37, 239-253.	2.5	1,026
107	Sugar Transport through Maltoporin of <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2000, 275, 19747-19751.	3.4	31
108	Extended Sugar Slide Function for the Periplasmic Coiled Coil Domain of ScrY. <i>Journal of Molecular Biology</i> , 2000, 300, 687-695.	4.2	15

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109	Membrane assembly of the Escherichia coli outer membrane protein OmpA: exploring sequence constraints on transmembrane β -strands 1 Edited by W. Baumeister. Journal of Molecular Biology, 1999, 285, 1801-1810.	4.2	42
110	Structural and Functional Roles of the Surface-Exposed Loops of the β -Barrel Membrane Protein OmpA from <i>Escherichia coli</i> . Journal of Bacteriology, 1999, 181, 3688-3694.	2.2	90
111	Coupling site-directed mutagenesis with high-level expression: large scale production of mutant porins from <i>E. coli</i> . FEMS Microbiology Letters, 1998, 163, 65-72.	1.8	221
112	Transmembrane Signaling across the Ligand-Gated FhuA Receptor. Cell, 1998, 95, 771-778.	28.9	527
113	Stability of Trimeric OmpF Porin: The Contributions of the Latching Loop L2. Biochemistry, 1998, 37, 15663-15670.	2.5	101
114	Coupling site-directed mutagenesis with high-level expression: large scale production of mutant porins from <i>E. coli</i> . FEMS Microbiology Letters, 1998, 163, 65-72.	1.8	2
115	Identification and Characterization of Two Quiescent Porin Genes, <i>nmpC</i> and <i>ompN</i> , in <i>Escherichia coli</i> B ^E . Journal of Bacteriology, 1998, 180, 3388-3392.	2.2	73
116	In vivo membrane assembly of split variants of the <i>E. coli</i> outer membrane protein OmpA.. EMBO Journal, 1996, 15, 3529-3537.	7.8	45
117	In vivo membrane assembly of split variants of the <i>E. coli</i> outer membrane protein OmpA. EMBO Journal, 1996, 15, 3529-37.	7.8	11
118	Proposal for a peptidoglycan-associating alpha-helical motif in the C-terminal regions of some bacterial cell-surface proteins. Molecular Microbiology, 1995, 16, 1269-1270.	2.5	171
119	Membrane Assembly of Circularly Permuted Variants of the <i>E. coli</i> Outer Membrane Protein OmpA. Journal of Molecular Biology, 1995, 250, 617-626.	4.2	55
120	Membrane topology and assembly of the outer membrane protein OmpA of <i>Escherichia coli</i> K12. Molecular Genetics and Genomics, 1994, 243, 127-135.	2.4	74
121	Chapter 18 Outer membrane proteins of <i>Escherichia coli</i> : mechanism of sorting and regulation of synthesis. New Comprehensive Biochemistry, 1994, , 381-395.	0.1	9
122	The TonB protein of <i>Yersinia enterocolitica</i> and its interactions with TonB-box proteins. Molecular Genetics and Genomics, 1993, 237-237, 152-160.	2.4	43
123	The TonB-dependent ferrichrome receptor FcuA of <i>Yersinia enterocolitica</i> : evidence against a strict co-evolution of receptor structure and substrate specificity. Molecular Microbiology, 1993, 7, 383-393.	2.5	44
124	The molecular interaction between components of the TonB-ExbBD-dependent and of the TolQRA-dependent bacterial uptake systems. Molecular Microbiology, 1993, 9, 219-219.	2.5	33
125	Structural organization of TonB-dependent receptors. Trends in Microbiology, 1993, 1, 201.	7.7	5
126	Survey on Newly Characterized Iron Uptake Systems of <i>Yersinia enterocolitica</i> . Zentralblatt Fur Bakteriologie: International Journal of Medical Microbiology, 1993, 278, 416-424.	0.5	32

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127	Insertion derivatives containing segments of up to 16 amino acids identify surface- and periplasm-exposed regions of the FhuA outer membrane receptor of Escherichia coli K-12. Journal of Bacteriology, 1993, 175, 826-839.	2.2	100
128	CHAPTER 21: Targeting of the rice transcriptome by TAL effectors of <i>Xanthomonas oryzae</i> , 0, , 193-206.		0