Renato Morona

List of Publications by Year
in descending order

135 papers	6,870 citations	57758 44 h-index	71685 76 g-index
135 all docs	135 docs citations	135 times ranked	4412 citing authors

#	Article	IF	Citations
1	Detection of a disulphide bond and conformational changes in Shigella flexneri Wzy, and the role of cysteine residues in polymerase activity. Biochimica Et Biophysica Acta - Biomembranes, 2022, 1864, 183871.	2.6	5
2	Bacteriophage Sf6 host range mutant that infects Shigella flexneri serotype 2a2 strains. FEMS Microbiology Letters, 2022, 369, .	1.8	3
3	Interdependence of Shigella flexneri O Antigen and Enterobacterial Common Antigen Biosynthetic Pathways. Journal of Bacteriology, 2022, 204, e0054621.	2.2	12
4	Topology of the Shigella flexneri Enterobacterial Common Antigen polymerase WzyE. Microbiology (United Kingdom), 2022, 168, .	1.8	2
5	Polysaccharide Copolymerase WzzB/WzzE Chimeras Reveal that the Transmembrane 2 Region of WzzB Is Important for Interaction with WzyB. Journal of Bacteriology, 2021, 203, .	2.2	9
6	Large Metabolic Rewiring from Small Genomic Changes between Strains of Shigella flexneri. Journal of Bacteriology, 2021, 203, .	2.2	6
7	Identification of a Region in Shigella flexneri WzyB Disrupting the Interaction with Wzz _{pHS2}. Journal of Bacteriology, 2021, 203, e0041321.	2.2	5
8	Specific blood group antibodies inhibit Shigella flexneri interaction with human cells in the absence of spinoculation. Biochemical and Biophysical Research Communications, 2020, 521, 131-136.	2.1	5
9	The virulence domain of Shigella IcsAÂcontains a subregion with specific host cell adhesion function. PLoS ONE, 2020, 15, e0227425.	2.5	13
10	Shigella flexneri Targets Human Colonic Goblet Cells by O Antigen Binding to Sialyl-Tn and Tn Antigens via Glycanâ€“Glycan Interactions. ACS Infectious Diseases, 2020, 6, 2604-2615.	3.8	7
11	Influence of Shigella flexneri 2a O Antigen Acetylation on Its Bacteriophage Sf6 Receptor Activity and Bacterial Interaction with Human Cells. Journal of Bacteriology, 2020, 202, .	2.2	7
12	In vitro characterization and identification of potential substrates of a low molecular weight protein tyrosine phosphatase in Streptococcus pneumoniae. Microbiology (United Kingdom), 2018, 164, 697-703.	1.8	4
13	Role of Streptococcus pneumoniae OM001 operon in capsular polysaccharide production, virulence and survival in human saliva. PLoS ONE, 2018, 13, e0190402.	2.5	3
14	Unprecedented Abundance of Protein Tyrosine Phosphorylation Modulates Shigella flexneri Virulence. Journal of Molecular Biology, 2016, 428, 4197-4208.	4.2	19
15	Conserved transmembrane glycine residues in the Shigella flexneri polysaccharide co-polymerase protein WzzB influence proteinâ€“protein interactions. Microbiology (United Kingdom), 2016, 162, 921-929.	1.8	5
16	Shigella flexneri cell-to-cell spread, and growth and inflammation in mice, is limited by the outer membrane protease IcsP. FEMS Microbiology Letters, 2015, 362, fnv088.	1.8	1
17	Glycan:glycan interactions: High affinity biomolecular interactions that can mediate binding of pathogenic bacteria to host cells. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E7266-75.	7.1	96
18	Protection against Shiga-Toxigenic Escherichia coli by Non-Genetically Modified Organism Receptor Mimic Bacterial Ghosts. Infection and Immunity, 2015, 83, 3526-3533.	2.2	7

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19	Capsule Structure, Synthesis, and Regulation. , 2015, , 169-179.		1
20	The passengerâ€associated transport repeat promotes virulence factor secretion efficiency and delineates a distinct autotransporter subtype. Molecular Microbiology, 2015, 97, 315-329.	2.5	9
21	Topology of Streptococcus pneumoniae CpsC, a Polysaccharide Copolymerase and Bacterial Protein Tyrosine Kinase Adaptor Protein. Journal of Bacteriology, 2015, 197, 120-127.	2.2	6
22	Lipopolysaccharide surface structure does not influence IcsA polarity. FEMS Microbiology Letters, 2015, 362, fnv042.	1.8	2
23	Mutational Analysis of the Shigella flexneri O-Antigen Polymerase Wzy: Identification of Wzz-Dependent Wzy Mutants. Journal of Bacteriology, 2015, 197, 108-119.	2.2	14
24	Mutational analysis of the major periplasmic loops of Shigella flexneri Wzy: identification of the residues affecting O antigen modal chain length control, and Wzz-dependent polymerization activity. Microbiology (United Kingdom), 2015, 161, 774-785.	1.8	18
25	Detection of Wzy/Wzz interaction in Shigella flexneri. Microbiology (United Kingdom), 2015, 161, 1797-1805.	1.8	28
26	A small conserved motif supports polarity augmentation of Shigella flexneri IcsA. Microbiology (United Kingdom), 2015, 161, 2087-2097.	1.8	8
27	Structural and Biochemical Analysis of a Single Amino-Acid Mutant of WzzBSF That Alters Lipopolysaccharide O-Antigen Chain Length in Shigella flexneri. PLoS ONE, 2015, 10, e0138266.	2.5	8
28	Relationship between O-antigen chain length and resistance to colicin E2 in Shigella flexneri. Microbiology (United Kingdom), 2014, 160, 589-601.	1.8	28
29	Myosin IIA is essential forShigella flexnericell-to-cell spread. Pathogens and Disease, 2014, 72, n/a-n/a.	2.0	18
30	Progress in understanding the assembly process of bacterial O-antigen. FEMS Microbiology Reviews, 2014, 38, 1048-1065.	8.6	96
31	The Role of Bacterial Protein Tyrosine Phosphatases in the Regulation of the Biosynthesis of Secreted Polysaccharides. Antioxidants and Redox Signaling, 2014, 20, 2274-2289.	5.4	39
32	Tyrosine phosphorylation enhances activity of pneumococcal autolysin LytA. Microbiology (United) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.8	16
33	IcsA Is a Shigella flexneri Adhesin Regulated by the Type III Secretion System and Required for Pathogenesis. Cell Host and Microbe, 2014, 15, 435-445.	11.0	88
34	Dynamin-related protein Drp1 and mitochondria are important for Shigella flexneri infection. International Journal of Medical Microbiology, 2014, 304, 530-541.	3.6	28
35	Residues located inside the Escherichia coli FepE protein oligomer are essential for lipopolysaccharide O-antigen modal chain length regulation. Microbiology (United Kingdom), 2013, 159, 701-714.	1.8	16
36	Dual inhibition of DNA polymerase PolC and protein tyrosine phosphatase CpsB uncovers a novel antibiotic target. Biochemical and Biophysical Research Communications, 2013, 430, 167-172.	2.1	15

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37	Encapsulating Bacteria. Structure, 2013, 21, 692-693.	3.3	1
38	Complete Genome Sequence of SfII, a Serotype-Converting Bacteriophage of the Highly Prevalent Shigella flexneri Serotype 2a. Genome Announcements, 2013, 1, .	0.8	14
39	LPS Unmasking of Shigella flexneri Reveals Preferential Localisation of Tagged Outer Membrane Protease IcsP to Septa and New Poles. PLoS ONE, 2013, 8, e70508.	2.5	15
40	Impact of Dynasore an Inhibitor of Dynamin II on Shigella flexneri Infection. PLoS ONE, 2013, 8, e84975.	2.5	9
41	Identification of Shigella flexneri IcsA Residues Affecting Interaction with N-WASP, and Evidence for IcsA-IcsA Co-Operative Interaction. PLoS ONE, 2013, 8, e55152.	2.5	21
42	Absence of O antigen suppresses Shigella flexneri IcsA autochaperone region mutations. Microbiology (United Kingdom), 2012, 158, 2835-2850.	1.8	12
43	Wzy-Dependent Bacterial Capsules as Potential Drug Targets. Current Drug Targets, 2012, 13, 1421-1431.	2.1	13
44	Escherichia coli 83972 Expressing a P fimbriae Oligosaccharide Receptor Mimic Impairs Adhesion of Uropathogenic E. coli. Journal of Infectious Diseases, 2012, 206, 1242-1249.	4.0	25
45	Selective inhibition of Biotin Protein Ligase from Staphylococcus aureus. Journal of Biological Chemistry, 2012, 287, 17823-17832.	3.4	56
46	Bioengineered microbes in disease therapy. Trends in Molecular Medicine, 2012, 18, 417-425.	6.7	44
47	Self-association of the Shigella flexneri IcsA autotransporter protein. Microbiology (United) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5	1.8	9
48	Chemical Inhibition of Bacterial Protein Tyrosine Phosphatase Suppresses Capsule Production. PLoS ONE, 2012, 7, e36312.	2.5	28
49	5-Benzylidenerhodanine and 5-benzylidene-2-4-thiazolidinedione based antibacterials. Bioorganic and Medicinal Chemistry Letters, 2012, 22, 2720-2722.	2.2	34
50	IcsA autotransporter passenger promotes increased fusion protein expression on the cell surface. Microbial Cell Factories, 2012, 11, 20.	4.0	15
51	Identification of Streptococcus pneumoniae Cps2C Residues That Affect Capsular Polysaccharide Polymerization, Cell Wall Ligation, and Cps2D Phosphorylation. Journal of Bacteriology, 2011, 193, 2341-2346.	2.2	17
52	Designer Probiotics and Enteric Cytoprotection. , 2011, , 429-443.		0
53	Bioengineered bugs expressing oligosaccharide receptor mimics: Toxin-binding probiotics for treatment and prevention of enteric infections. Bioengineered Bugs, 2010, 1, 172-177.	1.7	29
54	Mutagenesis and Chemical Cross-Linking Suggest that Wzz Dimer Stability and Oligomerization Affect Lipopolysaccharide O-Antigen Modal Chain Length Control. Journal of Bacteriology, 2010, 192, 3385-3393.	2.2	30

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55	Receptor-mimic probiotics: potential therapeutics for bacterial toxin-mediated enteric diseases. Expert Review of Gastroenterology and Hepatology, 2010, 4, 253-255.	3.0	4
56	Sequence-structure relationships in polysaccharide co-polymerase (PCP) proteins. Trends in Biochemical Sciences, 2009, 34, 78-84.	7.5	76
57	Differential immunogenicity of Vibrio cholerae O139 variants expressing different combinations of naturally occurring and atypical forms of the serogroup polysaccharide. Vaccine, 2009, 27, 1055-1061.	3.8	4
58	Bacterial polysaccharide co-polymerases share a common framework for control of polymer length. Nature Structural and Molecular Biology, 2008, 15, 130-138.	8.2	103
59	Coiled-coil regions play a role in the function of the Shigella flexneri O-antigen chain length regulator WzzpHS2. Microbiology (United Kingdom), 2008, 154, 1104-1116.	1.8	33
60	Mutagenesis of theShigella flexneriAutotransporter IcsA Reveals Novel Functional Regions Involved in IcsA Biogenesis and Recruitment of Host Neural Wiscott-Aldrich Syndrome Protein. Journal of Bacteriology, 2008, 190, 4666-4676.	2.2	43
61	A Recombinant Probiotic for Treatment and Prevention of Cholera. Gastroenterology, 2006, 130, 1688-1695.	1.3	88
62	Designer probiotics for prevention of enteric infections. Nature Reviews Microbiology, 2006, 4, 193-200.	28.6	89
63	Role of oxyR in the Oral Anaerobe Porphyromonas gingivalis. Journal of Bacteriology, 2006, 188, 2454-2462.	2.2	80
64	Attachment of capsular polysaccharide to the cell wall of Streptococcus pneumoniae type 2 is required for invasive disease. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 8505-8510.	7.1	139
65	Altering the Length of the Lipopolysaccharide O Antigen Has an Impact on the Interaction of Salmonella enterica Serovar Typhimurium with Macrophages and Complement. Journal of Bacteriology, 2006, 188, 2735-2739.	2.2	152
66	Inducible serum resistance in Salmonella typhimurium is dependent on wzzfepE-regulated very long O antigen chains. Microbes and Infection, 2005, 7, 1296-1304.	1.9	58
67	Topological analysis of GtrA and GtrB proteins encoded by the serotype-converting cassette of Shigella flexneri. Biochemical and Biophysical Research Communications, 2005, 328, 1252-1260.	2.1	36
68	Recombinant Probiotics for Treatment and Prevention of Enterotoxigenic Escherichia coli Diarrhea. Gastroenterology, 2005, 128, 1219-1228.	1.3	89
69	Refinement of a Therapeutic Shiga Toxinâ€“Binding Probiotic for Human Trials. Journal of Infectious Diseases, 2004, 189, 1547-1555.	4.0	41
70	The Effect That Mutations in the Conserved Capsular Polysaccharide Biosynthesis GenescpsA, cpsB,andcpsDHave on Virulence ofStreptococcus pneumoniae. Journal of Infectious Diseases, 2004, 189, 1905-1913.	4.0	122
71	The Chromosome of Shigella flexneri Bacteriophage Sf6: Complete Nucleotide Sequence, Genetic Mosaicism, and DNA Packaging. Journal of Molecular Biology, 2004, 339, 379-394.	4.2	131
72	Lipopolysaccharide O antigen chains mask IcsA (VirG) inShigella flexneri. FEMS Microbiology Letters, 2003, 221, 173-180.	1.8	31

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73	MulticopyicsAis able to suppress the virulence defect caused by thewzzSFmutation inShigella flexneri. FEMS Microbiology Letters, 2003, 221, 213-219.	1.8	12
74	Regulation of Salmonella typhimurium lipopolysaccharide O antigen chain length is required for virulence; identification of FepE as a second Wzz. Molecular Microbiology, 2003, 47, 1395-1406.	2.5	194
75	The actin-based motility defect of a Shigella flexneri rmlD rough LPS mutant is not due to loss of IcsA polarity. Microbial Pathogenesis, 2003, 35, 11-18.	2.9	25
76	Mutational Analysis of the Carboxy-Terminal (YGX)₄Repeat Domain of CpsD, an Autophosphorylating Tyrosine Kinase Required for Capsule Biosynthesis inStreptococcus pneumoniae. Journal of Bacteriology, 2003, 185, 3009-3019.	2.2	85
77	The Tailspike Protein of Shigella Phage Sf6. Journal of Biological Chemistry, 2003, 278, 1542-1548.	3.4	48
78	Genetic modulation of Shigella flexneri 2a lipopolysaccharide O antigen modal chain length reveals that it has been optimized for virulence. Microbiology (United Kingdom), 2003, 149, 925-939.	1.8	101
79	Streptococcus pneumoniaeCapsule Biosynthesis Protein CpsB Is a Novel Manganese-Dependent Phosphotyrosine-Protein Phosphatase. Journal of Bacteriology, 2002, 184, 577-583.	2.2	116
80	Neutralization of Shiga Toxins Stx1, Stx2c, and Stx2e by Recombinant Bacteria Expressing Mimics of Globotriose and Globotetraose. Infection and Immunity, 2001, 69, 1967-1970.	2.2	67
81	Oral Administration of Formaldehyde-Killed Recombinant Bacteria Expressing a Mimic of the Shiga Toxin Receptor Protects Mice from Fatal Challenge with Shiga-ToxigenicEscherichia coli. Infection and Immunity, 2001, 69, 1389-1393.	2.2	45
82	A new biological agent for treatment of Shiga toxigenic Escherichia coli infections and dysentery in humans. Nature Medicine, 2000, 6, 265-270.	30.7	196
83	Tyrosine phosphorylation of CpsD negatively regulates capsular polysaccharide biosynthesis in Streptococcus pneumoniae. Molecular Microbiology, 2000, 35, 1431-1442.	2.5	189
84	Evaluation of Wzz/MPA1/MPA2 proteins based on the presence of coiled-coil regions. Microbiology (United Kingdom), 2000, 146, 1-4.	1.8	96
85	The Shigella flexneri bacteriophage Sf6 tailspike protein (TSP)/endorhamnosidase is related to the bacteriophage P22 TSP and has a motif common to exo- and endoglycanases, and C-5 epimerases. Microbiology (United Kingdom), 1999, 145, 1649-1659.	1.8	41
86	Molecular and genetic characterization of the capsule biosynthesis locus of Streptococcus pneumoniae type 23F. Microbiology (United Kingdom), 1999, 145, 781-789.	1.8	33
87	The Salmonella typhi melittin resistance gene pqaB affects intracellular growth in PMA-differentiated U937 cells, polymyxin B resistance and lipopolysaccharide. Microbiology (United Kingdom), 1999, 145, 367-378.	1.8	75
88	Analysis of Shigella flexneri Wzz (Rol) function by mutagenesis and cross-linking: Wzz is able to oligomerize. Molecular Microbiology, 1999, 34, 181-194.	2.5	91
89	Analysis of the 5â€² Portion of the Type 19A Capsule Locus Identifies Two Classes of cpsC , cpsD , and cpsE Genes in Streptococcus pneumoniae. Journal of Bacteriology, 1999, 181, 3599-3605.	2.2	45
90	Comparative Genetics of Capsular Polysaccharide Biosynthesis in Streptococcus pneumoniae Types Belonging to Serogroup 19. Journal of Bacteriology, 1999, 181, 5355-5364.	2.2	56

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91	Recombinational exchanges at the capsular polysaccharide biosynthetic locus lead to frequent serotype changes among natural isolates of Streptococcus pneumoniae. Molecular Microbiology, 1998, 27, 73-83.	2.5	303
92	Overexpression and topology of the Shigella flexneri O-antigen polymerase (Rfc/Wzy). Molecular Microbiology, 1998, 28, 1211-1222.	2.5	181
93	Molecular and genetic characterization of the capsule biosynthesis locus of Streptococcus pneumoniae type 19B. Journal of Bacteriology, 1997, 179, 4953-4958.	2.2	47
94	PhoP/Q regulated genes inSalmonella typhi: identification of melittin sensitive mutants. Microbial Pathogenesis, 1997, 22, 165-179.	2.9	35
95	Characterization of the Capsular Polysaccharide Biosynthesis Locus ofStreptococcus pneumoniaeType 19F. Microbial Drug Resistance, 1997, 3, 89-99.	2.0	5
96	Regulation of Oâ€antigen chain length is required for Shigella flexneri virulence. Molecular Microbiology, 1997, 23, 765-775.	2.5	111
97	Characterization of the locus encoding the Streptococcus pneumoniae type 19F capsular polysaccharide biosynthetic pathway. Molecular Microbiology, 1997, 23, 751-763.	2.5	126
98	Mechanism of bacteriophage SfIIâ€mediated serotype conversion in Shigella flexneri. Molecular Microbiology, 1997, 26, 939-950.	2.5	106
99	Genetic rearrangements in the rfb regions of Vibrio cholerae O1 and O139.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 10374-10378.	7.1	107
100	Release of chloramphenicol acetyl transferase from recombinant Escherichia coli by sonication and the French press. Biotechnology Letters, 1995, 9, 477-480.	0.5	6
101	Lipopolysaccharide with an altered O-antigen produced inEscherichia coliK-12 harbouring mutated, clonedShigella flexneri rfbgenes. Molecular Microbiology, 1995, 18, 209-223.	2.5	34
102	Molecular, genetic, and topological characterization of O-antigen chain length regulation in Shigella flexneri. Journal of Bacteriology, 1995, 177, 1059-1068.	2.2	177
103	Genetic analysis of the rfbX gene of shigella flexneri. Gene, 1995, 155, 9-17.	2.2	38
104	In vibrio cholerae serogroup O 1, rfaD is closely linked to the rfb operon. Gene, 1995, 155, 67-72.	2.2	18
105	Putative O-antigen transport genes within the rfb region of Vibrio cholerae O1 are homologous to those for capsule transport. Gene, 1995, 158, 1-7.	2.2	37
106	A putative pathway for biosynthesis of the O-antigen component, 3-deoxy-L-glycero-tetronic acid, based on the sequence of the Vibrio cholerae 01 rfb region. Gene, 1995, 166, 19-31.	2.2	13
107	A putative pathway for perosamine biosynthesis is the first function encoded within the rfb region of Vibrio cholerae O1. Gene, 1995, 166, 33-42.	2.2	55
108	Characterization of the rfc region of Shigella flexneri. Journal of Bacteriology, 1994, 176, 733-747.	2.2	153

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109	Characterization of the dTDP-rhamnose biosynthetic genes encoded in the rfb iocus of Shigella flexneri. Molecular Microbiology, 1994, 11, 281-292.	2.5	86
110	Construction of K88- and K99-expressing clones of Salmonella typhimurium G30: immunogenicity following oral administration to pigs. Vaccine, 1994, 12, 513-517.	3.8	22
111	Isolation, characterization, and nucleotide sequence of IS1202, an insertion sequence of Streptococcus pneumoniae. Journal of Bacteriology, 1994, 176, 4437-4443.	2.2	47
112	Nucleotide sequence analysis of genes essential for capsular polysaccharide biosynthesis in Streptococcus pneumoniae type 19F. Infection and Immunity, 1994, 62, 5384-5396.	2.2	139
113	Immunization of mice with Salmonella typhimurium C5 aroA expressing a genetically toxoided derivative of the pneumococcal toxin pneumolysin. Microbial Pathogenesis, 1993, 14, 95-102.	2.9	8
114	Bacteriophage Lambda as a Delivery Vector for Tn 10 -Derived Transposons in Xenorhabdus bovienii. Applied and Environmental Microbiology, 1993, 59, 3050-3055.	3.1	11
115	Serotype conversion in Vibrio cholerae O1.. Proceedings of the National Academy of Sciences of the United States of America, 1992, 89, 2566-2570.	7.1	199
116	Construction of plasmid vectors with a non-antibiotic selection system based on the Escherichia coli thyA+ gene: application to cholera vaccine development. Gene, 1991, 107, 139-144.	2.2	39
117	Genetic analysis of the rfb region of Shigella flexneri encoding the Y serotype O-antigen specificity. Molecular Microbiology, 1991, 5, 1491-1499.	2.5	46
118	Effect of lipopolysaccharide core synthesis mutations on the production ofVibrio choleraeO-antigen inEscherixhia coliK-12. FEMS Microbiology Letters, 1991, 82, 279-285.	1.8	35
119	Effect of lipopolysaccharide core synthesis mutations on the production of Vibrio cholerae O-antigen in Escherixhia coli K-12. FEMS Microbiology Letters, 1991, 82, 279-285.	1.8	13
120	Regions of the cloned Vibrio cholerae rfb genes needed to determine the Ogawa form of the O-antigen. Molecular Genetics and Genomics, 1990, 224, 405-412.	2.4	8
121	Surface co-expression of Vibrio cholerae and Salmonella typhi O-antigens on Ty21a clone EX210. Microbial Pathogenesis, 1990, 8, 177-188.	2.9	28
122	Immunogenicity of a Candidate Live Oral Typhoid/Cholera Hybrid Vaccine in Humans. Journal of Infectious Diseases, 1989, 159, 145-146.	4.0	53
123	Towards a live oral vaccine against enterotoxigenic Escherichia coli of swine. Vaccine, 1988, 6, 387-389.	3.8	26
124	A galE via (Vi antigen-negative) mutant of Salmonella typhi Ty2 retains virulence in humans. Infection and Immunity, 1988, 56, 1326-1333.	2.2	191
125	Contruction of Defined galE Mutants of Salmonella for Use as Vaccines. Journal of Infectious Diseases, 1987, 156, 167-174.	4.0	84
126	A physical map of the chromosomal region determining O-antigen biosynthesis in Vibrio cholerae 01. Gene, 1987, 55, 197-204.	2.2	33

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127	New locus (ttr) in Escherichia coli K-12 affecting sensitivity to bacteriophage T2 and growth on oleate as the sole carbon source. Journal of Bacteriology, 1986, 168, 534-540.	2.2	23
128	Detection of an OmpA-like protein inVibrio cholerae. FEMS Microbiology Letters, 1986, 37, 99-104.	1.8	15
129	The nature of ompA mutants of Escherichia coli K12 exhibiting temperature-sensitive bacteriophage resistance. Molecular Genetics and Genomics, 1985, 201, 357-359.	2.4	0
130	Demonstration of a bacteriophage receptor site on the Escherichia coli K12 outer-membrane protein OmpC by the use of a protease. FEBS Journal, 1985, 150, 161-169.	0.2	47
131	Detection of several diisopropylfluorophosphate-binding proteins in the outer membrane ofEscherichia coliK-12. FEMS Microbiology Letters, 1984, 23, 179-182.	1.8	5
132	Escherichia coli K-12 outer membrane protein (OmpA) as a bacteriophage receptor: analysis of mutant genes expressing altered proteins. Journal of Bacteriology, 1984, 159, 570-578.	2.2	195
133	A new locus, stc, which affects the phenotype of tolC mutants of Escherichia coli K-12. Molecular Genetics and Genomics, 1982, 187, 335-341.	2.4	9
134	Molecular cloning of the tolC locus of Escherichia coli K-12 with the use of transposon Tn10. Molecular Genetics and Genomics, 1981, 184, 430-433.	2.4	29
135	Molecular Basis for O-Antigen Biosynthesis inVibrio choleraeO1: Ogawa-Inaba Switching. , 0, , 77-94.		74