Peter R Reeves

List of Publications by Year
in descending order

172	12,632	26567	28224
papers	citations	56 h-index	105 g-index

176	176	176	8908
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Single-gene long-read sequencing illuminates Escherichia coli strain dynamics in the human intestinal microbiome. Cell Reports, 2022, 38, 110239.	2.9	9
2	The low level of O antigen in Salmonella enterica Paratyphi A is due to inefficiency of the glycosyltransferase WbaV. FEMS Microbiology Letters, 2021, 368, .	0.7	1
3	Living Trees: High-Quality Reproducible and Reusable Construction of Bacterial Phylogenetic Trees. Molecular Biology and Evolution, 2020, 37, 563-575.	3.5	17
4	Structure and genetics ofEscherichia coliO antigens. FEMS Microbiology Reviews, 2020, 44, 655-683.	3.9	143
5	The Remarkable Dual-Level Diversity of Prokaryotic Flagellins. MSystems, 2020, 5, .	1.7	11
6	Wzx flippases exhibiting complex Oâ€unit preferences require a new model for Wzxâ€“substrate interactions. MicrobiologyOpen, 2019, 8, e00655.	1.2	14
7	Two extremely divergent sequence forms of the genes that define Escherichia coli group 3 capsules suggest a very long history since their common ancestor. FEMS Microbiology Letters, 2019, 366, .	0.7	3
8	Customizable Cloning of Whole Polysaccharide Gene Clusters by Yeast Homologous Recombination. Methods in Molecular Biology, 2019, 1954, 1-14.	0.4	0
9	Changing Molecular Epidemiology of Vibrio cholerae Outbreaks in Shanghai, China. MSystems, 2019, 4, .	1.7	7
10	Progress in Our Understanding of Wzx Flippase for Translocation of Bacterial Membrane Lipid-Linked Oligosaccharide. Journal of Bacteriology, 2018, 200, .	1.0	38
11	Genetics and evolution of Yersinia pseudotuberculosis O-specific polysaccharides: a novel pattern of O-antigen diversity. FEMS Microbiology Reviews, 2017, 41, 200-217.	3.9	48
12	Rapid customised operon assembly by yeast recombinational cloning. Applied Microbiology and Biotechnology, 2017, 101, 4569-4580.	1.7	8
13	Serotype O:8 isolates in the Yersinia pseudotuberculosis complex have different O-antigen gene clusters and produce various forms of rough LPS. Innate Immunity, 2016, 22, 205-217.	1.1	4
14	Origins of the current seventh cholera pandemic. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E7730-E7739.	3.3	150
15	Model for the Controlled Synthesis of O-Antigen Repeat Units Involving the WaaL Ligase. MSphere, 2016, 1, .	1.3	18
16	Inefficient translocation of a truncated O unit by a Salmonella Wzx affects both O-antigen production and cell growth. FEMS Microbiology Letters, 2015, 362, .	0.7	20
17	Three Wzy polymerases are specific for particular forms of an internal linkage in otherwise identical O units. Microbiology (United Kingdom), 2015, 161, 1639-1647.	0.7	23
18	Diversity of O-Antigen Repeat Unit Structures Can Account for the Substantial Sequence Variation of Wzx Translocases. Journal of Bacteriology, 2014, 196, 1713-1722.	1.0	57

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19	Structural diversity inSalmonellaO antigens and its genetic basis. FEMS Microbiology Reviews, 2014, 38, 56-89.	3.9	175
20	The O-specific polysaccharide structure and gene cluster of serotype O:12 of the Yersinia pseudotuberculosis complex, and the identification of a novel L-quinovose biosynthesis gene. Glycobiology, 2013, 23, 346-353.	1.3	18
21	The WbaK acetyltransferase of Salmonella enterica group E gives insights into O antigen evolution. Microbiology (United Kingdom), 2013, 159, 2316-2322.	0.7	12
22	Genomic diversity and adaptation of Salmonella enterica serovar Typhimurium from analysis of six genomes of different phage types. BMC Genomics, 2013, 14, 718.	1.2	34
23	The Wzy O-antigen polymerase ofYersinia pseudotuberculosisO:2a has a dependence on the Wzz chain-length determinant for efficient polymerization. FEMS Microbiology Letters, 2013, 349, 163-170.	0.7	11
24	Mutation accumulation and fitness in mutator subpopulations ofEscherichia coli. Biology Letters, 2013, 9, 20120961.	1.0	14
25	Biosynthesis of UDP-GlcNAc, UndPP-GlcNAc and UDP-GlcNAcA Involves Three Easily Distinguished 4-Epimerase Enzymes, Gne, Gnu and GnaB. PLoS ONE, 2013, 8, e67646.	1.1	47
26	Genetics and Evolution of the Salmonella Galactose-Initiated Set of O Antigens. PLoS ONE, 2013, 8, e69306.	1.1	44
27	Diversity in the Major Polysaccharide Antigen of Acinetobacter Baumannii Assessed by DNA Sequencing, and Development of a Molecular Serotyping Scheme. PLoS ONE, 2013, 8, e70329.	1.1	116
28	Population Structure and Evolution of Non-O1/Non-O139 Vibrio cholerae by Multilocus Sequence Typing. PLoS ONE, 2013, 8, e65342.	1.1	77
29	Characterization of the CDP-d-mannitol biosynthetic pathway in Streptococcus pneumoniae 35A. Glycobiology, 2012, 22, 1760-1767.	1.3	3
30	Development of a Multiplex PCR Assay for Detection and Genogrouping of Neisseria meningitidis. Journal of Clinical Microbiology, 2012, 50, 46-51.	1.8	47
31	Genetic Relationships of Phage Types and Single Nucleotide Polymorphism Typing of Salmonella enterica Serovar Typhimurium. Journal of Clinical Microbiology, 2012, 50, 727-734.	1.8	23
32	The multiplicity of divergence mechanisms in a single evolving population. Genome Biology, 2012, 13, R41.	13.9	55
33	Biochemical Characterization of the CDP-D-Arabinitol Biosynthetic Pathway in Streptococcus pneumoniae 17F. Journal of Bacteriology, 2012, 194, 1868-1874.	1.0	5
34	Multi-locus variable number tandem repeat analysis of 7th pandemic Vibrio cholerae. BMC Microbiology, 2012, 12, 82.	1.3	36
35	The Wzx translocases for Salmonella enterica Oâ€antigen processing have unexpected serotype specificity. Molecular Microbiology, 2012, 84, 620-630.	1.2	49
36	Evolution of Lipopolysaccharide Biosynthesis Genes. , 2011, , 339-370.		10

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37	Rates of Mutation and Host Transmission for an Escherichia coli Clone over 3 Years. PLoS ONE, 2011, 6, e26907.	1.1	132
38	Insight into Evolution of Bordetella pertussis from Comparative Genomic Analysis: Evidence of Vaccine-Driven Selection. Molecular Biology and Evolution, 2011, 28, 707-715.	3.5	78
39	The genetics and structure of the O-specific polysaccharide of Yersinia pseudotuberculosis serotype O:10 and its relationship with Escherichia coli O111 and Salmonella enterica O35. Glycobiology, 2011, 21, 1131-1139.	1.3	14
40	Genetic characterisation and structural analysis of the O-specific polysaccharide of Yersinia pseudotuberculosis serotype O:1c. Innate Immunity, 2011, 17, 183-190.	1.1	13
41	Genetic analysis of the O-antigen gene clusters of Yersinia pseudotuberculosis O:6 and O:7. Glycobiology, 2011, 21, 1140-1146.	1.3	10
42	Divergence Involving Global Regulatory Gene Mutations in an Escherichia coli Population Evolving under Phosphate Limitation. Genome Biology and Evolution, 2010, 2, 478-487.	1.1	82
43	The Variation of O Antigens in Gram-Negative Bacteria. Sub-Cellular Biochemistry, 2010, 53, 123-152.	1.0	79
44	Structure and genetics ofShigellaO antigens: Table 1. FEMS Microbiology Reviews, 2010, 34, 606-606.	3.9	5
45	Derivation of Escherichia coli O157:H7 from Its O55:H7 Precursor. PLoS ONE, 2010, 5, e8700.	1.1	109
46	Biosynthesis of O-antigen chains and assembly. , 2010, , 319-335.		11
47	Genomic Identification of a Novel Mutation in hfq That Provides Multiple Benefits in Evolving Glucose-Limited Populations of Escherichia coli. Journal of Bacteriology, 2010, 192, 4517-4521.	1.0	21
48	Bordetella pertussisClones Identified by Multilocus Variable-Number Tandem-Repeat Analysis. Emerging Infectious Diseases, 2010, 16, 297-300.	2.0	32
49	Evolution of Seventh Cholera Pandemic and Origin of 1991 Epidemic, Latin America. Emerging Infectious Diseases, 2010, 16, 1130-1132.	2.0	40
50	Population structure, origins and evolution of major Salmonella enterica clones. Infection, Genetics and Evolution, 2009, 9, 996-1005.	1.0	101
51	The O-specific polysaccharide structure and biosynthetic gene cluster of Yersinia pseudotuberculosis serotype O:11. Carbohydrate Research, 2009, 344, 1533-1540.	1.1	17
52	Rapid and accurate typing of Bordetella pertussis targeting genes encoding acellular vaccine antigens using real time PCR and High Resolution Melt analysis. Journal of Microbiological Methods, 2009, 77, 326-329.	0.7	15
53	Genomic Sequencing Reveals Regulatory Mutations and Recombinational Events in the Widely Used MC4100 Lineage ofEscherichia coliK-12. Journal of Bacteriology, 2009, 191, 4025-4029.	1.0	98
54	Membrane topology of theSalmonella entericaserovar Typhimurium Group B O-antigen translocase Wzx. FEMS Microbiology Letters, 2008, 287, 76-84.	0.7	27

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55	Importation of the major pilin TcpA gene and frequent recombination drive the divergence of theVibriopathogenicity island inVibrio cholerae. FEMS Microbiology Letters, 2008, 289, 210-218.	0.7	13
56	Structure and genetics ofShigellaO antigens. FEMS Microbiology Reviews, 2008, 32, 627-653.	3.9	305
57	Genome-wide analysis of single nucleotide polymorphisms in Bordetella pertussis using comparative genomic sequencing. Research in Microbiology, 2008, 159, 602-608.	1.0	22
58	Determination of Glycosyltransferase Specificities for the Escherichia coli O111 O Antigen by a Generic Approach. Applied and Environmental Microbiology, 2008, 74, 1294-1298.	1.4	16
59	A Recalibrated Molecular Clock and Independent Origins for the Cholera Pandemic Clones. PLoS ONE, 2008, 3, e4053.	1.1	140
60	Genetic Relatedness of theStreptococcus pneumoniaeCapsular Biosynthetic Loci. Journal of Bacteriology, 2007, 189, 7841-7855.	1.0	118
61	Predicted Functions and Linkage Specificities of the Products of theStreptococcus pneumoniaeCapsular Biosynthetic Loci. Journal of Bacteriology, 2007, 189, 7856-7876.	1.0	114
62	The Yersinia kristensenii O11 O-Antigen Gene Cluster was Acquired by Lateral Gene Transfer and Incorporated at a Novel Chromosomal Locus. Molecular Biology and Evolution, 2007, 24, 1355-1365.	3.5	18
63	A group of Escherichia coli and Salmonella enterica O antigens sharing a common backbone structure. Microbiology (United Kingdom), 2007, 153, 2159-2167.	0.7	59
64	Molecular markers with potential to replace phage typing for Salmonella enterica serovar typhimurium. Journal of Microbiological Methods, 2007, 68, 145-156.	0.7	12
65	Structural and genetic evidence that the Escherichia coli O148 O antigen is the precursor of the Shigella dysenteriae type 1 O antigen and identification of a glucosyltransferase gene. Microbiology (United Kingdom), 2007, 153, 139-147.	0.7	36
66	Amplified Fragment Length Polymorphism Analysis of Salmonella enterica. Methods in Molecular Biology, 2007, 394, 119-132.	0.4	5
67	Sex and virulence in Escherichia coli: an evolutionary perspective. Molecular Microbiology, 2006, 60, 1136-1151.	1.2	1,806
68	Genetic Analysis of the Capsular Biosynthetic Locus from All 90 Pneumococcal Serotypes. PLoS Genetics, 2006, 2, e31.	1.5	661
69	Adaptation of Multilocus Sequencing for Studying Variation Within a Major Clone: Evolutionary Relationships of Salmonella enterica Serovar Typhimurium. Genetics, 2006, 172, 743-750.	1.2	22
70	Evolutionary origins and sequence of theEscherichia coliO4 O-antigen gene cluster. FEMS Microbiology Letters, 2005, 244, 27-32.	0.7	11
71	Vibrio choleraePathogenic Clones. Emerging Infectious Diseases, 2005, 11, 1758-1760.	2.0	50
72	Structural and Genetic Characterization of the Shigella boydii Type 10 and Type 6 O Antigens. Journal of Bacteriology, 2005, 187, 2551-2554.	1.0	19

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73	Structural and Genetic Characterization of Enterohemorrhagic Escherichia coli O145 O Antigen and Development of an O145 Serogroup-Specific PCR Assay. Journal of Bacteriology, 2005, 187, 758-764.	1.0	61
74	Evolutionary Changes of the flhDC Flagellar Master Operon in Shigella Strains. Journal of Bacteriology, 2005, 187, 4295-4302.	1.0	26
75	Molecular Evolutionary Relationships of Enteroinvasive Escherichia coli and Shigella spp. Infection and Immunity, 2004, 72, 5080-5088.	1.0	189
76	Molecular Basis of the Indole-Negative Reaction in Shigella Strains: Extensive Damages to the tna Operon by Insertion Sequences. Journal of Bacteriology, 2004, 186, 7460-7465.	1.0	23
77	Relationships of the Escherichia coli O157, O111, and O55 O-Antigen Gene Clusters with Those of Salmonella enterica and Citrobacter freundii, Which Express Identical O Antigens. Journal of Bacteriology, 2004, 186, 6536-6543.	1.0	64
78	Synthesis of the Heteropolysaccharide O Antigen of Escherichia coli O52 Requires an ABC Transporter: Structural and Genetic Evidence. Journal of Bacteriology, 2004, 186, 4510-4519.	1.0	58
79	Structural and Genetic Characterization of the Shigella boydii Type 13 O Antigen. Journal of Bacteriology, 2004, 186, 383-392.	1.0	81
80	Deletion of the Escherichia coli O14:K7 O antigen gene cluster. Canadian Journal of Microbiology, 2004, 50, 299-302.	0.8	10
81	Structure of the Shigella dysenteriae 7 O antigen gene cluster and identification of its antigen specific genes. Microbial Pathogenesis, 2004, 36, 109-115.	1.3	33
82	Biosynthesis of O-antigens: genes and pathways involved in nucleotide sugar precursor synthesis and O-antigen assembly. Carbohydrate Research, 2003, 338, 2503-2519.	1.1	457
83	AFLP analysis of Salmonella enterica serovar Typhimurium isolates of phage types DT 9Âand DT 135: diversity within phage types and its epidemiological significance. Microbes and Infection, 2003, 5, 841-850.	1.0	10
84	Comparison of Two Major Forms of the Shigella Virulence Plasmid pINV: Positive Selection Is a Major Force Driving the Divergence. Infection and Immunity, 2003, 71, 6298-6306.	1.0	30
85	Species-Wide Variation in the Escherichia coli Flagellin (H-Antigen) Gene. Journal of Bacteriology, 2003, 185, 2936-2943.	1.0	136
86	The variation of dTDP-l-rhamnose pathway genes in Vibrio cholerae. Microbiology (United Kingdom), 2003, 149, 2463-2474.	0.7	19
87	O Antigen Gene Clusters of Yersinia pseudotuberculosis. , 2003, 529, 199-206.		20
88	Extensive Variation in the O-Antigen Gene Cluster within One Salmonella enterica Serogroup Reveals an Unexpected Complex History. Journal of Bacteriology, 2002, 184, 1669-1677.	1.0	55
89	Relationship of Yersinia pseudotuberculosis O Antigens IA, IIA, and IVB: the IIA Gene Cluster Was Derived from That of IVB. Infection and Immunity, 2002, 70, 3271-3276.	1.0	39
90	Fluorescent Amplified Fragment Length Polymorphism Analysis of Salmonella enterica Serovar Typhimurium Reveals Phage-Type- Specific Markers and Potential for Microarray Typing. Journal of Clinical Microbiology, 2002, 40, 3406-3415.	1.8	32

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91	The O-Antigen Gene Cluster of Escherichia coli O55:H7 and Identification of a New UDP-GlcNAc C4 Epimerase Gene. Journal of Bacteriology, 2002, 184, 2620-2625.	1.0	81
92	Sequence of the Escherichia coli O26 O antigen gene cluster and identification of O26 specific genes. Gene, 2002, 297, 123-127.	1.0	62
93	Escherichia coli in disguise: molecular origins of Shigella. Microbes and Infection, 2002, 4, 1125-1132.	1.0	219
94	Pandemic Spread of Cholera: Genetic Diversity and Relationships within the Seventh Pandemic Clone of Vibrio cholerae Determined by Amplified Fragment Length Polymorphism. Journal of Clinical Microbiology, 2002, 40, 172-181.	1.8	56
95	Sequence of the E. coli O104 antigen gene cluster and identification of O104 specific genes. Gene, 2001, 270, 231-236.	1.0	56
96	When does a clone deserve a name? A perspective on bacterial species based on population genetics. Trends in Microbiology, 2001, 9, 419-424.	3.5	143
97	Sequence Analysis of Four Shigella boydii O-Antigen Loci: Implication for Escherichia coli and Shigella Relationships. Infection and Immunity, 2001, 69, 6923-6930.	1.0	54
98	Comparison of Vibrio choleraePathogenicity Islands in Sixth and Seventh Pandemic Strains. Infection and Immunity, 2001, 69, 1947-1952.	1.0	79
99	Molecular Characterization of Streptococcus pneumoniae Type 4, 6B, 8, and 18C Capsular Polysaccharide Gene Clusters. Infection and Immunity, 2001, 69, 1244-1255.	1.0	105
100	Molecular Evolution of Large Virulence Plasmid in Shigella Clones and Enteroinvasive Escherichia coli. Infection and Immunity, 2001, 69, 6303-6309.	1.0	86
101	Molecular evolution of the GDP-mannose pathway genes (manB and manC) in Salmonella enterica The GenBank accession numbers for the sequences reported in this paper are AY012160â€“AY012201.. Microbiology (United Kingdom), 2001, 147, 599-610.	0.7	34
102	Population genetics of Escherichia coli in a natural population of native Australian rats. Environmental Microbiology, 2000, 2, 594-610.	1.8	28
103	The colanic acid gene cluster ofSalmonella entericahas a complex history. FEMS Microbiology Letters, 2000, 191, 11-16.	0.7	35
104	Unique Adaptor Design for AFLP Fingerprinting. BioTechniques, 2000, 29, 745-750.	0.8	14
105	Genetic variation of dTDP-l-rhamnose pathway genes in Salmonella enterica The GenBank accession numbers for the sequences reported in this paper are AF279615â€“AF279625 for the rml gene sets and AF279626â€“AF279648 for the rmlB gene fragments.. Microbiology (United Kingdom), 2000, 146, 2291-2307.	0.7	74
106	Comparison of O-Antigen Gene Clusters of Escherichia coli (Shigella) Sonnei and Plesiomonas shigelloides O17: Sonnei Gained Its Current Plasmid-Borne O-Antigen Genes from P. shigelloides in a Recent Event. Infection and Immunity, 2000, 68, 6056-6061.	1.0	102
107	The Escherichia coli O111 and Salmonella enterica O35 Gene Clusters: Gene Clusters Encoding the Same Colitose-Containing O Antigen Are Highly Conserved. Journal of Bacteriology, 2000, 182, 5256-5261.	1.0	49
108	Rotavirus VP7 epitope mapping using fragments of VP7 displayed on phages. Vaccine, 2000, 18, 2257-2265.	1.7	15

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109	Intraspecies variation in bacterial genomes: the need for a species genome concept. Trends in Microbiology, 2000, 8, 396-401.	3.5	242
110	Sequence Diversity of the Escherichia coli H7 fliC Genes: Implication for a DNA-Based Typing Scheme for E. coli O157:H7. Journal of Clinical Microbiology, 2000, 38, 1786-1790.	1.8	49
111	Bacterial expression of the major antigenic regions of porcine rotavirus VP7 induces a neutralizing immune response in mice. Vaccine, 1999, 17, 2636-2645.	1.7	15
112	Immunization of mice with live oral vaccine based on aSalmonella enterica(sv Typhimurium)aroAstrain expressing theEscherichia coliO111 O antigen. Microbial Pathogenesis, 1999, 27, 55-59.	1.3	10
113	Evolutionary Relationships of Pathogenic Clones of Vibrio cholerae by Sequence Analysis of Four Housekeeping Genes. Infection and Immunity, 1999, 67, 1116-1124.	1.0	87
114	Expression of the O antigen gene cluster is regulated by RfaH through the JUMPstart sequence. FEMS Microbiology Letters, 1998, 165, 201-206.	0.7	42
115	Domain organisation in phosphomannose isomerases (types I and II). BBA - Proteins and Proteomics, 1998, 1382, 5-7.	2.1	50
116	Recombination between rRNA operons created most of the ribotype variation observed in the seventh pandemic clone of Vibrio cholerae. Microbiology (United Kingdom), 1998, 144, 1213-1221.	0.7	74
117	Cholera in the 1990s. British Medical Bulletin, 1998, 54, 611-623.	2.7	20
118	Molecular Basis of Ribotype Variation in the Seventh Pandemic Clone and its O139 Variant of Vibrio cholerae. Memorias Do Instituto Oswaldo Cruz, 1998, 93, 595-600.	0.8	1
119	Organization of Escherichia coli O157 O Antigen Gene Cluster and Identification of Its Specific Genes. Infection and Immunity, 1998, 66, 3545-3551.	1.0	229
120	The Wzz (Cld) Protein in Escherichia coli : Amino Acid Sequence Variation Determines O-Antigen Chain Length Specificity. Journal of Bacteriology, 1998, 180, 2670-2675.	1.0	85
121	Escherichia coli Clone Sonnei (Shigella sonnei) Had a Chromosomal O-Antigen Gene Cluster Prior to Gaining Its Current Plasmid-Borne O-Antigen Genes. Journal of Bacteriology, 1998, 180, 2983-2986.	1.0	28
122	Relationships among the O-Antigen Gene Clusters of Salmonella enterica Groups B, D1, D2, and D3. Journal of Bacteriology, 1998, 180, 1002-1007.	1.0	51
123	Identification of the Fucose Synthetase Gene in the Colanic Acid Gene Cluster of Escherichia coli K-12. Journal of Bacteriology, 1998, 180, 998-1001.	1.0	92
124	Sequencing of Escherichia coli O111 O-Antigen Gene Cluster and Identification of O111-Specific Genes. Journal of Clinical Microbiology, 1998, 36, 3182-3187.	1.8	63
125	The relationship between the structures of the O polysaccharides from Escherichia coli O17 and O16. Carbohydrate Research, 1997, 303, 313-318.	1.1	7
126	Periplasmic expression of part of the major rotavirus capsid protein VP7 containing all the three antigenic regions in Escherichia coli. Gene, 1996, 177, 155-162.	1.0	4

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127	Bacterial polysaccharide synthesis and gene nomenclature. Trends in Microbiology, 1996, 4, 495-503.	3.5	508
128	A plasmid-borne O-antigen chain length determinant and its relationship to other chain length determinants. FEMS Microbiology Letters, 1995, 125, 23-30.	0.7	52
129	Genetic organisation and evolution of Yersinia pseudotuberculosis 3,6-dideoxyhexose biosynthetic genes. Biochimica Et Biophysica Acta - General Subjects, 1995, 1245, 273-277.	1.1	24
130	Sequence and analysis of the O antigen gene (rfb) cluster of Escherichia coli 0111. Gene, 1995, 164, 17-23.	1.0	147
131	Role of O-antigen variation in the immune response. Trends in Microbiology, 1995, 3, 381-386.	3.5	116
132	MULTICOMP: a program for preparing sequence data for phylogenetic analysis. Bioinformatics, 1994, 10, 281-284.	1.8	30
133	The JUMPstart sequence: a 39 bp element common to several polysaccharide gene clusters. Molecular Microbiology, 1994, 12, 855-856.	1.2	172
134	In vitro Synthesis of CDP-D-Abequose Using Salmonella Enzymes of Cloned rfb Genes. Production of CDP-6-Deoxy-D-Xylo -4-Hexulose, CDP-3,6-Dideoxy-D-Xylo -4-Hexulose and CDP-3,6-Dideoxy-D-Galactose, and Isolation by HPLC. FEBS Journal, 1994, 225, 863-872.	0.2	16
135	Chapter 13 Biosynthesis and assembly of lipopolysaccharide. New Comprehensive Biochemistry, 1994, , 281-317.	0.1	75
136	Repeat unit polysaccharides of bacteria: a model for polymerization resembling that of ribosomes and fatty acid synthetase, with a novel mechanism for determining chain length. Molecular Microbiology, 1993, 7, 725-734.	1.2	196
137	Purification, characterization and HPLC assay of Salmonella glucose-1-phosphate thymidylyltransferase from the cloned rfbA gene. FEBS Journal, 1993, 211, 763-770.	0.2	70
138	Evolution of Salmonella O antigen variation by interspecific gene transfer on a large scale. Trends in Genetics, 1993, 9, 17-22.	2.9	254
139	Enzymatic synthesis and isolation of thymidine diphosphate-6-deoxy-D-xylo-4-hexulose and thymidine diphosphate-L-rhamnose. Production using cloned gene products and separation by HPLC. FEBS Journal, 1992, 204, 539-545.	0.2	68
140	Variation in O-antigens, niche-specific selection and bacterial populations. FEMS Microbiology Letters, 1992, 100, 509-516.	0.7	42
141	High level expression and purification of dThymidine diphospho-D-glucose 4,6-dehydratase (rfbB) from Salmonella serovar typhimurium LT2. Biochemical and Biophysical Research Communications, 1991, 174, 846-852.	1.0	19
142	The cps gene cluster of Salmonella strain LT2 includes a second mannose pathway: sequence of two genes and relationship to genes in the rfb gene cluster. Molecular Genetics and Genomics, 1991, 227, 173-180.	2.4	69
143	Molecular cloning and expression in Escherichia coli K-12 of chromosomal genes determining the O antigen of an E. coli O2: K1 strain. FEMS Microbiology Letters, 1991, 66, 345-51.	0.7	8
144	The use of a drug resistance cartridge forin vitro insertion and deletion mutagenesis of a cosmid clone. Plasmid, 1990, 24, 149-152.	0.4	1

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145	Cloning and nucleotide sequence of the Salmonella typhimurium LT2 gnd gene and its homology with the corresponding sequence of Escherichia coli K12. Molecular Genetics and Genomics, 1989, 217, 182-184.	2.4	17
146	Chloramphenicol resistance cloning vector based on pUC9. Plasmid, 1987, 17, 54-57.	0.4	44
147	A low copy number cosmid. Plasmid, 1987, 18, 170-172.	0.4	21
148	Cloning part of the region encoding biosynthetic enzymes for surface antigen (O-antigen) of Salmonella typhimurium. Molecular Genetics and Genomics, 1986, 203, 172-176.	2.4	23
149	Intermediates in the synthesis of TolC protein include an incomplete peptide stalled at a rare Arg codon. FEBS Journal, 1985, 152, 151-155.	0.2	29
150	High-level synthesis of the phage lambda outer-membrane protein from the cloned lom gene. Gene, 1985, 38, 253-258.	1.0	6
151	Detection of several diisopropylfluorophosphate-binding proteins in the outer membrane ofEscherichia coliK-12. FEMS Microbiology Letters, 1984, 23, 179-182.	0.7	5
152	A class of ompA mutants of Escherichia coliK12 affected in the interaction of OmpA protein and the core region of lipopolysaccharide. Molecular Genetics and Genomics, 1983, 189, 162-165.	2.4	9
153	The TolC protein ofEscherichia coliK12 is synthesised in a precursor form. FEBS Letters, 1983, 156, 307-310.	1.3	20
154	Primary structure of toetolCgene that codes for an outer membrane protein ofEscherichia coliK12. Nucleic Acids Research, 1983, 11, 6487-6495.	6.5	42
155	Regulation of the pho regulon of Escherichia coli K-12. Journal of Molecular Biology, 1982, 157, 265-274.	2.0	90
156	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
157	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
158	Outer membrane proteins of Escherichia coli K-12: Isolation of a common receptor protein for bacteriophage T6 and colicin K. Molecular Genetics and Genomics, 1978, 158, 279-286.	2.4	34
159	Comparison of Colicins B-K260 and D-CA23: Purification and Characterization of the Colicins and Examination of Colicin Immunity in the Producing Strains. Antimicrobial Agents and Chemotherapy, 1977, 11, 345-358.	1.4	30
160	Defective growth functions in mutants of Escherichia coli K12 lacking a major outer membrane protein. Journal of Molecular Biology, 1977, 116, 285-300.	2.0	73
161	Outer membrane of Echerichiacoli K-12: Demonstration of the temperature sensitivity of a mutant in one of the major outer membrane proteins. Biochemical and Biophysical Research Communications, 1976, 72, 694-700.	1.0	3
162	Outer membrane of Escherichia coli K-12: Tsx mutants (resistant to bacteriophage T6 and colicin K) lack an outer membrane protein. Biochemical and Biophysical Research Communications, 1976, 71, 466-471.	1.0	48

#	Article	IF	Citations
163	F Factor-Mediated Immunity to Lethal Zygosis in Escherichia coli K-12. Journal of Bacteriology, 1974, 117, 100-106.	1.0	30
164	Con â˜' Mutants: Class of Mutants in Escherichia coli K-12 Lacking a Major Cell Wall Protein and Defective in Conjugation and Adsorption of a Bacteriophage. Journal of Bacteriology, 1974, 119, 726-735.	1.0	244
165	Plasmid Specificity of The Origin of Transfer of Sex Factor F. Journal of Bacteriology, 1974, 120, 125-130.	1.0	33
166	Characterization of Lethal Zygosis Associated with Conjugation in Escherichia coli K-12. Journal of Bacteriology, 1973, 113, 58-70.	1.0	67
167	Physiology of Escherichia coli K-12 During Conjugation: Altered Recipient Cell Functions Associated with Lethal Zygosis. Journal of Bacteriology, 1973, 114, 11-17.	1.0	33
168	Sensitivity of Intracellular Bacteriophage Î» to Colicin CA42-E2. Journal of Virology, 1971, 8, 355-362.	1.5	9
169	Mode of Action of Colicins of Types E ₁ , E ₂ , E ₃ , and K. Journal of Bacteriology, 1968, 96, 1700-1703.	1.0	27
170	MUTANTS RESISTANT TO COLICIN CA42â€E₂: CROSS RESISTANCE AND GENETIC MAPPING OF A SPECIAL CLASS OF MUTANTS. The Australian Journal of Experimental Biology and Medical Science, 1966, 44, 301-316.	0.7	48
171	The Bacteriocins. Bacteriological Reviews, 1965, 29, 24-45.	7.7	183
172	Evolution of Enteric Pathogens. , 0, , 273-299.		1