## Peter R Reeves

List of Publications by Year in descending order

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172 12,632 papers citations

176

all docs

176
docs citations

56 h-index

26567

176 times ranked 28224 105 g-index

8908 citing authors

#	Article	IF	CITATIONS
1	Sex and virulence in Escherichia coli: an evolutionary perspective. Molecular Microbiology, 2006, 60, 1136-1151.	1.2	1,806
2	Genetic Analysis of the Capsular Biosynthetic Locus from All 90 Pneumococcal Serotypes. PLoS Genetics, 2006, 2, e31.	1.5	661
3	Bacterial polysaccharide synthesis and gene nomenclature. Trends in Microbiology, 1996, 4, 495-503.	3.5	508
4	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
5	Structure and genetics of <i>Shigella </i> O antigens. FEMS Microbiology Reviews, 2008, 32, 627-653.	3.9	305
6	Evolution of Salmonella O antigen variation by interspecific gene transfer on a large scale. Trends in Genetics, 1993, 9, 17-22.	2.9	254
7	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
8	Intraspecies variation in bacterial genomes: the need for a species genome concept. Trends in Microbiology, 2000, 8, 396-401.	3.5	242
9	Organization of <i>Escherichia coli</i> O157 O Antigen Gene Cluster and Identification of Its Specific Genes. Infection and Immunity, 1998, 66, 3545-3551.	1.0	229
10	Escherichia coli in disguise: molecular origins of Shigella. Microbes and Infection, 2002, 4, 1125-1132.	1.0	219
11	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
12	Molecular Evolutionary Relationships of Enteroinvasive Escherichia coli and Shigella spp. Infection and Immunity, 2004, 72, 5080-5088.	1.0	189
13	The Bacteriocins. Bacteriological Reviews, 1965, 29, 24-45.	7.7	183
14	Structural diversity in <i>Salmonella</i> O antigens and its genetic basis. FEMS Microbiology Reviews, 2014, 38, 56-89.	3.9	175
15	The JUMPstart sequence: a 39 bp element common to several polysaccharide gene clusters. Molecular Microbiology, 1994, 12, 855-856.	1.2	172
16	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
17	Sequence and analysis of the O antigen gene (rfb) cluster of Escherichia coli 0111. Gene, 1995, 164, 17-23.	1.0	147
18	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

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19	Structure and genetics of <i>Escherichia coli </i> O antigens. FEMS Microbiology Reviews, 2020, 44, 655-683.	3.9	143
20	A Recalibrated Molecular Clock and Independent Origins for the Cholera Pandemic Clones. PLoS ONE, 2008, 3, e4053.	1.1	140
21	Species-Wide Variation in the Escherichia coli Flagellin (H-Antigen) Gene. Journal of Bacteriology, 2003, 185, 2936-2943.	1.0	136
22	Rates of Mutation and Host Transmission for an Escherichia coli Clone over 3 Years. PLoS ONE, 2011, 6, e26907.	1.1	132
23	Genetic Relatedness of the <i>Streptococcus pneumoniae </i> Capsular Biosynthetic Loci. Journal of Bacteriology, 2007, 189, 7841-7855.	1.0	118
24	Role of O-antigen variation in the immune response. Trends in Microbiology, 1995, 3, 381-386.	3.5	116
25	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
26	Predicted Functions and Linkage Specificities of the Products of the <i>Streptococcus pneumoniae </i> Capsular Biosynthetic Loci. Journal of Bacteriology, 2007, 189, 7856-7876.	1.0	114
27	Derivation of Escherichia coli O157:H7 from Its O55:H7 Precursor. PLoS ONE, 2010, 5, e8700.	1.1	109
28	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
29	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
30	Population structure, origins and evolution of major Salmonella enterica clones. Infection, Genetics and Evolution, 2009, 9, 996-1005.	1.0	101
31	Genomic Sequencing Reveals Regulatory Mutations and Recombinational Events in the Widely Used MC4100 Lineage of <i>Escherichia coli </i>	1.0	98
32	Identification of the Fucose Synthetase Gene in the Colanic Acid Gene Cluster of <i>Escherichia coli</i> K-12. Journal of Bacteriology, 1998, 180, 998-1001.	1.0	92
33	Regulation of the pho regulon of Escherichia coli K-12. Journal of Molecular Biology, 1982, 157, 265-274.	2.0	90
34	Evolutionary Relationships of Pathogenic Clones of <i>Vibrio cholerae</i> by Sequence Analysis of Four Housekeeping Genes. Infection and Immunity, 1999, 67, 1116-1124.	1.0	87
35	Molecular Evolution of Large Virulence Plasmid in Shigella Clones and Enteroinvasive Escherichia coli. Infection and Immunity, 2001, 69, 6303-6309.	1.0	86
36	The Wzz (Cld) Protein in <i>Escherichia coli</i> : Amino Acid Sequence Variation Determines O-Antigen Chain Length Specificity. Journal of Bacteriology, 1998, 180, 2670-2675.	1.0	85

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37	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
38	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
39	Structural and Genetic Characterization of the Shigella boydii Type 13 O Antigen. Journal of Bacteriology, 2004, 186, 383-392.	1.0	81
40	Comparison of Vibrio choleraePathogenicity Islands in Sixth and Seventh Pandemic Strains. Infection and Immunity, 2001, 69, 1947-1952.	1.0	79
41	The Variation of O Antigens in Gram-Negative Bacteria. Sub-Cellular Biochemistry, 2010, 53, 123-152.	1.0	79
42	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
43	Population Structure and Evolution of Non-O1/Non-O139 Vibrio cholerae by Multilocus Sequence Typing. PLoS ONE, 2013, 8, e65342.	1.1	77
44	Chapter 13 Biosynthesis and assembly of lipopolysaccharide. New Comprehensive Biochemistry, 1994, , 281-317.	0.1	75
45	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
46	Genetic variation of dTDP-l-rhamnose pathway genes in Salmonella enterica The GenBank accession numbers for the sequences reported in this paper are AF279615–AF279625 for the rml gene sets and AF279626–AF279648 for the rmlB gene fragments Microbiology (United Kingdom), 2000, 146, 2291-2307.	0.7	74
47	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
48	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
49	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
50	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
51	Characterization of Lethal Zygosis Associated with Conjugation in Escherichia coli K-12. Journal of Bacteriology, 1973, 113, 58-70.	1.0	67
52	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
53	Sequencing of <i>Escherichia coli</i> Oll1 O-Antigen Gene Cluster and Identification of Oll1-Specific Genes. Journal of Clinical Microbiology, 1998, 36, 3182-3187.	1.8	63
54	Sequence of the Escherichia coli O26 O antigen gene cluster and identification of O26 specific genes. Gene, 2002, 297, 123-127.	1.0	62

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55	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
56	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
57	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
58	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
59	Sequence of the E. coli O104 antigen gene cluster and identification of O104 specific genes. Gene, 2001, 270, 231-236.	1.0	56
60	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
61	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
62	The multiplicity of divergence mechanisms in a single evolving population. Genome Biology, 2012, 13, R41.	13.9	55
63	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
64	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
65	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
66	Domain organisation in phosphomannose isomerases (types I and II). BBA - Proteins and Proteomics, 1998, 1382, 5-7.	2.1	50
67	Vibrio choleraePathogenic Clones. Emerging Infectious Diseases, 2005, 11, 1758-1760.	2.0	50
68	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
69	The Wzx translocases for <i>Salmonella enterica</i> Oâ€antigen processing have unexpected serotype specificity. Molecular Microbiology, 2012, 84, 620-630.	1.2	49
70	Sequence Diversity of the <i>Escherichia coli</i> H7 <i>fliC</i> Genes: Implication for a DNA-Based Typing Scheme for <i>E. coli</i> O157:H7. Journal of Clinical Microbiology, 2000, 38, 1786-1790.	1.8	49
71	MUTANTS RESISTANT TO COLICIN CA42â€E <sub>2</sub> : 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
72	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

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73	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
74	Development of a Multiplex PCR Assay for Detection and Genogrouping of Neisseria meningitidis. Journal of Clinical Microbiology, 2012, 50, 46-51.	1.8	47
75	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
76	Chloramphenicol resistance cloning vector based on pUC9. Plasmid, 1987, 17, 54-57.	0.4	44
77	Genetics and Evolution of the Salmonella Galactose-Initiated Set of O Antigens. PLoS ONE, 2013, 8, e69306.	1.1	44
78	Primary structure of toetolCgene that codes for an outer membrane protein ofEscherichia coliK12. Nucleic Acids Research, 1983, 11, 6487-6495.	<b>6.</b> 5	42
79	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
80	Variation in O-antigens, niche-specific selection and bacterial populations. FEMS Microbiology Letters, 1992, 100, 509-516.	0.7	42
81	Evolution of Seventh Cholera Pandemic and Origin of 1991 Epidemic, Latin America. Emerging Infectious Diseases, 2010, 16, 1130-1132.	2.0	40
82	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
83	Progress in Our Understanding of Wzx Flippase for Translocation of Bacterial Membrane Lipid-Linked Oligosaccharide. Journal of Bacteriology, 2018, 200, .	1.0	38
84	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
85	Multi-locus variable number tandem repeat analysis of 7th pandemic Vibrio cholerae. BMC Microbiology, 2012, 12, 82.	1.3	36
86	The colanic acid gene cluster of Salmonella entericahas a complex history. FEMS Microbiology Letters, 2000, 191, 11-16.	0.7	35
87	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
88	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
89	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 AY012160–AY012201 Microbiology (United Kingdom), 2001, 147, 599-610.	0.7	34
90	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

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91	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
92	Plasmid Specificity of The Origin of Transfer of Sex Factor F. Journal of Bacteriology, 1974, 120, 125-130.	1.0	33
93	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
94	Bordetella pertussisClones Identified by Multilocus Variable-Number Tandem-Repeat Analysis. Emerging Infectious Diseases, 2010, 16, 297-300.	2.0	32
95	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
96	MULTICOMP: a program for preparing sequence data for phylogenetic analysis. Bioinformatics, 1994, 10, 281-284.	1.8	30
97	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
98	F Factor-Mediated Immunity to Lethal Zygosis in <i>Escherichia coli</i> K-12. Journal of Bacteriology, 1974, 117, 100-106.	1.0	30
99	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
100	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
101	Population genetics of Escherichia coli in a natural population of native Australian rats. Environmental Microbiology, 2000, 2, 594-610.	1.8	28
102	<i>Escherichia coli</i> Clone Sonnei ( <i>Shigella sonnei</i> ) 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
103	Membrane topology of theSalmonella entericaserovar Typhimurium Group B O-antigen translocase Wzx. FEMS Microbiology Letters, 2008, 287, 76-84.	0.7	27
104	Mode of Action of Colicins of Types E <code><sub>1</sub></code> , E <code><sub>2</sub></code> , E <code><sub>3</sub></code> , and K. Journal of Bacteriology, 1968, 96, 1700-1703.	1.0	27
105	Evolutionary Changes of the flhDC Flagellar Master Operon in Shigella Strains. Journal of Bacteriology, 2005, 187, 4295-4302.	1.0	26
106	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
107	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
108	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

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109	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
110	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
111	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
112	Genome-wide analysis of single nucleotide polymorphisms in Bordetella pertussis using comparative genomic sequencing. Research in Microbiology, 2008, 159, 602-608.	1.0	22
113	A low copy number cosmid. Plasmid, 1987, 18, 170-172.	0.4	21
114	Genomic Identification of a Novel Mutation in <i>hfq</i> That Provides Multiple Benefits in Evolving Glucose-Limited Populations of <i>Escherichia coli</i> Journal of Bacteriology, 2010, 192, 4517-4521.	1.0	21
115	The TolC protein of Escherichia coliK12 is synthesised in a precursor form. FEBS Letters, 1983, 156, 307-310.	1.3	20
116	Cholera in the 1990s. British Medical Bulletin, 1998, 54, 611-623.	2.7	20
117	O Antigen Gene Clusters of Yersinia pseudotuberculosis. , 2003, 529, 199-206.		20
118	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
119	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
120	The variation of dTDP-l-rhamnose pathway genes in Vibrio cholerae. Microbiology (United Kingdom), 2003, 149, 2463-2474.	0.7	19
121	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
122	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
123	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
124	Model for the Controlled Synthesis of O-Antigen Repeat Units Involving the WaaL Ligase. MSphere, 2016, 1, .	1.3	18
125	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
126	The O-specific polysaccharide structure and biosynthetic gene cluster of Yersinia pseudotuberculosis serotype O:11. Carbohydrate Research, 2009, 344, 1533-1540.	1.1	17

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127	Living Trees: High-Quality Reproducible and Reusable Construction of Bacterial Phylogenetic Trees. Molecular Biology and Evolution, 2020, 37, 563-575.	3.5	17
128	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
129	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
130	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
131	Rotavirus VP7 epitope mapping using fragments of VP7 displayed on phages. Vaccine, 2000, 18, 2257-2265.	1.7	15
132	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
133	Unique Adaptor Design for AFLP Fingerprinting. BioTechniques, 2000, 29, 745-750.	0.8	14
134	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
135	Mutation accumulation and fitness in mutator subpopulations of <i>Escherichia coli </i> Letters, 2013, 9, 20120961.	1.0	14
136	Wzx flippases exhibiting complex Oâ€unit preferences require a new model for Wzx–substrate interactions. MicrobiologyOpen, 2019, 8, e00655.	1.2	14
137	Importation of the major pilin TcpA gene and frequent recombination drive the divergence of the Vibriopathogenicity island in Vibrio cholerae. FEMS Microbiology Letters, 2008, 289, 210-218.	0.7	13
138	Genetic characterisation and structural analysis of the O-specific polysaccharide of <i>Yersinia pseudotuberculosis</i> serotype O:1c. Innate Immunity, 2011, 17, 183-190.	1.1	13
139	Molecular markers with potential to replace phage typing for Salmonella enterica serovar typhimurium. Journal of Microbiological Methods, 2007, 68, 145-156.	0.7	12
140	The WbaK acetyltransferase of Salmonella enterica group E gives insights into O antigen evolution. Microbiology (United Kingdom), 2013, 159, 2316-2322.	0.7	12
141	Evolutionary origins and sequence of the Escherichia coli O4 O-antigen gene cluster. FEMS Microbiology Letters, 2005, 244, 27-32.	0.7	11
142	Biosynthesis of O-antigen chains and assembly. , 2010, , 319-335.		11
143	The Wzy O-antigen polymerase of Yersinia pseudotuberculosis O:2a has a dependence on the Wzz chain-length determinant for efficient polymerization. FEMS Microbiology Letters, 2013, 349, 163-170.	0.7	11
144	The Remarkable Dual-Level Diversity of Prokaryotic Flagellins. MSystems, 2020, 5, .	1.7	11

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145	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
146	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
147	Deletion of the Escherichia coli O14:K7 O antigen gene cluster. Canadian Journal of Microbiology, 2004, 50, 299-302.	0.8	10
148	Evolution of Lipopolysaccharide Biosynthesis Genes. , 2011, , 339-370.		10
149	Genetic analysis of the O-antigen gene clusters of Yersinia pseudotuberculosis O:6 and O:7. Glycobiology, 2011, 21, 1140-1146.	1.3	10
150	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
151	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
152	Sensitivity of Intracellular Bacteriophage λ to Colicin CA42-E2. Journal of Virology, 1971, 8, 355-362.	1.5	9
153	Single-gene long-read sequencing illuminates Escherichia coli strain dynamics in the human intestinal microbiome. Cell Reports, 2022, 38, 110239.	2.9	9
154	Rapid customised operon assembly by yeast recombinational cloning. Applied Microbiology and Biotechnology, 2017, 101, 4569-4580.	1.7	8
155	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
156	The relationship between the structures of the O polysaccharides from Escherichia coli O17 and O16. Carbohydrate Research, 1997, 303, 313-318.	1.1	7
157	Changing Molecular Epidemiology of Vibrio cholerae Outbreaks in Shanghai, China. MSystems, 2019, 4,	1.7	7
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