Nigel P Minton

List of Publications by Year
in descending order

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235 papers	14,282 citations	22146 59 h-index	25787 108 g-index
247 all docs	247 docs citations	247 times ranked	8701 citing authors

#	Article	IF	Citations
1	The multidrug-resistant human pathogen Clostridium difficile has a highly mobile, mosaic genome. Nature Genetics, 2006, 38, 779-786.	21.4	821
2	The role of toxin A and toxin B in Clostridium difficile infection. Nature, 2010, 467, 711-713.	27.8	727
3	The ClosTron: A universal gene knock-out system for the genus Clostridium. Journal of Microbiological Methods, 2007, 70, 452-464.	1.6	598
4	The pMTL nicâ˜ cloning vectors. I. Improved pUC polylinker regions to facilitate the use of sonicated DNA for nucleotide sequencing. Gene, 1988, 68, 139-149.	2.2	460
5	A modular system for Clostridium shuttle plasmids. Journal of Microbiological Methods, 2009, 78, 79-85.	1.6	410
6	The ClosTron: Mutagenesis in Clostridium refined and streamlined. Journal of Microbiological Methods, 2010, 80, 49-55.	1.6	363
7	Improved plasmid vectors for the isolation of translational lac gene fusions. Gene, 1984, 31, 269-273.	2.2	347
8	Multiple Factors Modulate Biofilm Formation by the Anaerobic Pathogen Clostridium difficile. Journal of Bacteriology, 2013, 195, 545-555.	2.2	247
9	Genome sequence of a proteolytic (Group I) Clostridium botulinum strain Hall A and comparative analysis of the clostridial genomes. Genome Research, 2007, 17, 1082-1092.	5.5	228
10	Conjugative transfer of clostridial shuttle vectors fromEscherichia colitoClostridium difficilethrough circumvention of the restriction barrier. Molecular Microbiology, 2002, 46, 439-452.	2.5	220
11	Precise Manipulation of the Clostridium difficile Chromosome Reveals a Lack of Association between the tcdC Genotype and Toxin Production. Applied and Environmental Microbiology, 2012, 78, 4683-4690.	3.1	209
12	Expression of the bacterial nitroreductase enzyme in mammalian cells renders them selectively sensitive to killing by the prodrug CB1954. European Journal of Cancer, 1995, 31, 2362-2370.	2.8	198
13	Importance of Toxin A, Toxin B, and CDT in Virulence of an Epidemic Clostridium difficile Strain. Journal of Infectious Diseases, 2014, 209, 83-86.	4.0	198
14	Femtomolar Sensitivity of a NO Sensor from Clostridium botulinum. Science, 2004, 306, 1550-1553.	12.6	195
15	Anticancer efficacy of systemically delivered anaerobic bacteria as gene therapy vectors targeting tumor hypoxia/necrosis. Gene Therapy, 2002, 9, 291-296.	4.5	178
16	Metabolic engineering of Clostridium autoethanogenum for selective alcohol production. Metabolic Engineering, 2017, 40, 104-114.	7.0	178
17	The complete amino acid sequence of the Clostridium botulinum type A neurotoxin, deduced by nucleotide sequence analysis of the encoding gene. FEBS Journal, 1990, 189, 73-81.	0.2	176
18	Anaerobic bacteria as a gene delivery system that is controlled by the tumor microenvironment. Gene Therapy, 1997, 4, 791-796.	4.5	171

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19	CRISPR/Cas9-Based Efficient Genome Editing in Clostridium ljungdahlii, an Autotrophic Gas-Fermenting Bacterium. ACS Synthetic Biology, 2016, 5, 1355-1361.	3.8	171
20	Integration of DNA into bacterial chromosomes from plasmids without a counter-selection marker. Nucleic Acids Research, 2012, 40, e59-e59.	14.5	154
21	CRISPRâ€based genome editing and expression control systems in Clostridium acetobutylicum and Clostridium beijerinckii. Biotechnology Journal, 2016, 11, 961-972.	3.5	153
22	Functional Intestinal Bile Acid 7Î±-Dehydroxylation by Clostridium scindens Associated with Protection from Clostridium difficile Infection in a Gnotobiotic Mouse Model. Frontiers in Cellular and Infection Microbiology, 2016, 6, 191.	3.9	151
23	Expanding the Repertoire of Gene Tools for Precise Manipulation of the Clostridium difficile Genome: Allelic Exchange Using pyrE Alleles. PLoS ONE, 2013, 8, e56051.	2.5	146
24	The binary toxin CDT enhances Clostridium difficile virulence by suppressing protective colonic eosinophilia. Nature Microbiology, 2016, 1, 16108.	13.3	140
25	Clostridia in cancer therapy. Nature Reviews Microbiology, 2003, 1, 237-242.	28.6	137
26	Targeted mutagenesis of the Clostridium acetobutylicum acetoneâ€“butanolâ€“ethanol fermentation pathway. Metabolic Engineering, 2012, 14, 630-641.	7.0	135
27	Multiple orphan histidine kinases interact directly with Spo0A to control the initiation of endospore formation in Clostridium acetobutylicum. Molecular Microbiology, 2011, 80, 641-654.	2.5	126
28	A m ariner -Based Transposon System for In Vivo Random Mutagenesis of Clostridium difficile. Applied and Environmental Microbiology, 2010, 76, 1103-1109.	3.1	124
29	A simple procedure for gel electrophoresis and Northern blotting of RNA. Nucleic Acids Research, 1995, 23, 3357-3358.	14.5	123
30	The Role of Flagella in Clostridium difficile Pathogenesis: Comparison between a Non-Epidemic and an Epidemic Strain. PLoS ONE, 2013, 8, e73026.	2.5	117
31	Physical characterisation of the replication region of the Streptococcus faecalis plasmid pAMÎ²1. Gene, 1990, 87, 79-90.	2.2	115
32	Introduction of plasmids into whole cells of Clostridium acetobutylicum by electroporation. FEMS Microbiology Letters, 1988, 56, 83-88.	1.8	114
33	Cloning, expression and complete nucleotide sequence of the Bacillus stearothermophilusl-lactate dehydrogenase gene. Gene, 1986, 46, 47-55.	2.2	111
34	Enhanced solvent production by metabolic engineering of a twin-clostridial consortium. Metabolic Engineering, 2017, 39, 38-48.	7.0	110
35	The role of flagella in Clostridium difficile pathogenicity. Trends in Microbiology, 2015, 23, 275-282.	7.7	109
36	Regulation of Neurotoxin Production and Sporulation by a Putative agrBD Signaling System in Proteolytic Clostridium botulinum. Applied and Environmental Microbiology, 2010, 76, 4448-4460.	3.1	108

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37	The analysis of para-cresol production and tolerance in Clostridium difficile 027 and 012 strains. BMC Microbiology, 2011, 11, 86.	3.3	105
38	Recent advances in the genetics of the clostridia. FEMS Microbiology Letters, 1989, 63, 301-325.	1.8	104
39	Repeated cycles of Clostridium-directed enzyme prodrug therapy result in sustained antitumour effects in vivo. British Journal of Cancer, 2006, 95, 1212-1219.	6.4	103
40	SleC Is Essential for Germination of Clostridium difficile Spores in Nutrient-Rich Medium Supplemented with the Bile Salt Taurocholate. Journal of Bacteriology, 2010, 192, 657-664.	2.2	103
41	Spores of Clostridium difficile Clinical Isolates Display a Diverse Germination Response to Bile Salts. PLoS ONE, 2012, 7, e32381.	2.5	99
42	The complete nucleotide sequence of the Pseudomonas gene coding for carboxypeptidase G2. Gene, 1984, 31, 31-38.	2.2	95
43	The emergence of â€˜hypervirulenceâ€™ in Clostridium difficile. International Journal of Medical Microbiology, 2010, 300, 387-395.	3.6	94
44	A roadmap for gene system development in Clostridium. Anaerobe, 2016, 41, 104-112.	2.1	90
45	Reconsidering the Sporulation Characteristics of Hypervirulent Clostridium difficile BI/NAP1/027. PLoS ONE, 2011, 6, e24894.	2.5	89
46	The complete amino acid sequence of the Clostridium botulinum type-E neurotoxin, derived by nucleotide-sequence analysis of the encoding gene. FEBS Journal, 1992, 204, 657-667.	0.2	85
47	The Rnf Complex Is an Energy-Coupled Transhydrogenase Essential To Reversibly Link Cellular NADH and Ferredoxin Pools in the Acetogen Acetobacterium woodii. Journal of Bacteriology, 2018, 200, .	2.2	85
48	AnagrQuorum Sensing System That Regulates Granulose Formation and Sporulation in Clostridium acetobutylicum. Applied and Environmental Microbiology, 2012, 78, 1113-1122.	3.1	83
49	Insights into CO ₂ Fixation Pathway of Clostridium autoethanogenum by Targeted Mutagenesis. MBio, 2016, 7, .	4.1	83
50	A novel approach to generate a recombinant toxoid vaccine against Clostridium difficile. Microbiology (United Kingdom), 2013, 159, 1254-1266.	1.8	81
51	Advances in metabolic engineering in the microbial production of fuels and chemicals from C1 gas. Current Opinion in Biotechnology, 2018, 50, 174-181.	6.6	80
52	What's a SNP between friends: The influence of single nucleotide polymorphisms on virulence and phenotypes ofClostridium difficilestrain 630 and derivatives. Virulence, 2017, 8, 767-781.	4.4	76
53	Spores of Clostridium engineered for clinical efficacy and safety cause regression and cure of tumors in vivo. Oncotarget, 2014, 5, 1761-1769.	1.8	72
54	Chemotherapeutic tumour targeting using clostridial spores. FEMS Microbiology Reviews, 1995, 17, 357-364.	8.6	71

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55	Modifying an immunogenic epitope on a therapeutic protein: a step towards an improved system for antibody-directed enzyme prodrug therapy (ADEPT). British Journal of Cancer, 2004, 90, 2402-2410.	6.4	70
56	Characterization of a region of the Enterococcus faecalis plasmid pAMÎ²1 which enhances the segregational stability of pAMÎ²1-derived cloning vectors in Bacillus subtilis. Plasmid, 1991, 26, 209-221.	1.4	69
57	RiboCas: A Universal CRISPR-Based Editing Tool for Clostridium. ACS Synthetic Biology, 2019, 8, 1379-1390.	3.8	69
58	Quorum sensing in Clostridium difficile: analysis of a luxS-type signalling system. Journal of Medical Microbiology, 2005, 54, 119-127.	1.8	68
59	Sequence of the adenine methylase gene of theStreptococcus faecalisplasmid pAMÎ²1. Nucleic Acids Research, 1987, 15, 3177-3177.	14.5	65
60	Both, toxin A and toxin B, are important inClostridium difficileinfection.. Gut Microbes, 2011, 2, 252-255.	9.8	63
61	Disruption of the acetate kinase (ack) gene of Clostridium acetobutylicum results in delayed acetate production. Applied Microbiology and Biotechnology, 2012, 94, 729-741.	3.6	63
62	Lipoprotein CD0873 Is a Novel Adhesin of Clostridium difficile. Journal of Infectious Diseases, 2014, 210, 274-284.	4.0	63
63	In vitro and in vivo characterisation of a recombinant carboxypeptidase G2::anti-CEA scFv fusion protein. Immunotechnology: an International Journal of Immunological Engineering, 1996, 2, 47-57.	2.4	61
64	Towards improved butanol production through targeted genetic modification of Clostridium pasteurianum. Metabolic Engineering, 2017, 40, 124-137.	7.0	61
65	The diverse sporulation characteristics of Clostridium difficile clinical isolates are not associated with type. Anaerobe, 2010, 16, 618-622.	2.1	60
66	Microbial solvent formation revisited by comparative genome analysis. Biotechnology for Biofuels, 2017, 10, 58.	6.2	60
67	Entry of spores into intestinal epithelial cells contributes to recurrence of Clostridioides difficile infection. Nature Communications, 2021, 12, 1140.	12.8	60
68	Nucleotide sequence of the Erwinia chrysanthemi NCPPB 1066 l-asparaginase gene. Gene, 1986, 46, 25-35.	2.2	59
69	Release of TcdA and TcdB from Clostridium difficile cdi 630 is not affected by functional inactivation of the tcdE gene. Microbial Pathogenesis, 2012, 52, 92-100.	2.9	59
70	Clostridium difficile Modulates Host Innate Immunity via Toxin-Independent and Dependent Mechanism(s). PLoS ONE, 2013, 8, e69846.	2.5	59
71	Inflammasome Activation Contributes to Interleukin-23 Production in Response to Clostridium difficile. MBio, 2015, 6, .	4.1	59
72	Clostridium difficile secreted Proâ€Pro endopeptidase PPEPâ€1 (ZMP1/CD2830) modulates adhesion through cleavage of the collagen binding protein CD2831. FEBS Letters, 2015, 589, 3952-3958.	2.8	59

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73	Mutant generation by allelic exchange and genome resequencing of the biobutanol organism Clostridium acetobutylicum ATCC 824. Biotechnology for Biofuels, 2016, 9, 4.	6.2	58
74	Physical characterisation of the Escherichia coli B gene encoding nitroreductase and its over-expression in Escherichia coli K12. FEMS Microbiology Letters, 1994, 124, 195-202.	1.8	57
75	ClosTron-Targeted Mutagenesis. Methods in Molecular Biology, 2010, 646, 165-182.	0.9	57
76	CRISPRâ€“Cas9^{D10A} nickaseâ€assisted base editing in the solvent producer Clostridium beijerinckii. Biotechnology and Bioengineering, 2019, 116, 1475-1483.	3.3	57
77	Sporulation studies in Clostridium difficile. Journal of Microbiological Methods, 2011, 87, 133-138.	1.6	56
78	Whole genome sequence and manual annotation of Clostridium autoethanogenum, an industrially relevant bacterium. BMC Genomics, 2015, 16, 1085.	2.8	56
79	Genetic characterisation of the botulinum toxin complex of Clostridium botulinum strain NCTC 2916. FEMS Microbiology Letters, 1996, 140, 151-158.	1.8	55
80	ClosTron-mediated engineering of Clostridium. Bioengineered, 2012, 3, 247-254.	3.2	55
81	Nucleotide sequence analysis of the gene for protein A from Staphylococcus aureus Cowan 1 (NCTC8530) and its enhanced expression in Escherichia coli. Gene, 1987, 58, 283-295.	2.2	53
82	A Transcription Factor-Based Biosensor for Detection of Itaconic Acid. ACS Synthetic Biology, 2018, 7, 1436-1446.	3.8	51
83	Genome Sequencing Shows that European Isolates of Francisella tularensis Subspecies tularensis Are Almost Identical to US Laboratory Strain Schu S4. PLoS ONE, 2007, 2, e352.	2.5	51
84	A genome-wide approach for identification and characterisation of metabolite-inducible systems. Nature Communications, 2020, 11, 1213.	12.8	49
85	The SOS Response Master Regulator LexA Is Associated with Sporulation, Motility and Biofilm Formation in Clostridium difficile. PLoS ONE, 2015, 10, e0144763.	2.5	49
86	Sustained tumor regression of human colorectal cancer xenografts using a multifunctional mannosylated fusion protein in antibody-directed enzyme prodrug therapy. Clinical Cancer Research, 2005, 11, 814-25.	7.0	48
87	Clostridium difficile spore germination: an update. Research in Microbiology, 2010, 161, 730-734.	2.1	47
88	Secretion and assembly of functional mini-cellulosomes from synthetic chromosomal operons in Clostridium acetobutylicum ATCC 824. Biotechnology for Biofuels, 2013, 6, 117.	6.2	47
89	Cloning, sequencing, and expression in Escherichia coli of the Clostridium tetanomorphum gene encoding .beta.-methylaspartase and characterization of the recombinant protein. Biochemistry, 1992, 31, 10747-10756.	2.5	45
90	A strategy for mapping and neutralizing conformational immunogenic sites on protein therapeutics. Proteomics, 2002, 2, 271.	2.2	45

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91	Complete nucleotide sequence of the Rhodosporidium toruloides gene coding for phenylalanine ammonia-lyase. Gene, 1987, 58, 189-199.	2.2	44
92	Molecular analysis of a Clostridium butyricum NCIMB 7423 gene encoding 4-Î±-glucanotransferase and characterization of the recombinant enzyme produced in Escherichia coli. Microbiology (United) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 6	1.8	42
93	Characterisation of a 3-hydroxypropionic acid-inducible system from Pseudomonas putida for orthogonal gene expression control in Escherichia coli and Cupriavidus necator. Scientific Reports, 2017, 7, 1724.	3.3	41
94	Cellular Uptake and Mode-of-Action of Clostridium difficile Toxins. Advances in Experimental Medicine and Biology, 2018, 1050, 77-96.	1.6	41
95	The Flagellin FliC of Clostridium difficile Is Responsible for Pleiotropic Gene Regulation during In Vivo Infection. PLoS ONE, 2014, 9, e96876.	2.5	40
96	Inactivation of the dnaK gene in Clostridium difficile 630 Î”erm yields a temperature-sensitive phenotype and increases biofilm-forming ability. Scientific Reports, 2017, 7, 17522.	3.3	38
97	Development of an integrative vector for the expression of antisense RNA in Clostridium difficile. Journal of Microbiological Methods, 2003, 55, 617-624.	1.6	37
98	Introduction of genes for leucine biosynthesis from Clostridium pasteurianum into C. acetobutylicum by cointegrate conjugal transfer. Molecular Genetics and Genomics, 1988, 214, 177-179.	2.4	36
99	Important Role of Class I Heat Shock Genes hrcA and dnaK in the Heat Shock Response and the Response to pH and NaCl Stress of Group I Clostridium botulinum Strain ATCC 3502. Applied and Environmental Microbiology, 2011, 77, 2823-2830.	3.1	35
100	Fluoroquinolone Resistance Does Not Impose a Cost on the Fitness of Clostridium difficile In Vitro. Antimicrobial Agents and Chemotherapy, 2015, 59, 1794-1796.	3.2	35
101	Synthetic Biology on Acetogenic Bacteria for Highly Efficient Conversion of C1 Gases to Biochemicals. International Journal of Molecular Sciences, 2020, 21, 7639.	4.1	35
102	Cloning, expression and evaluation of a recombinant sub-unit vaccine against Clostridium botulinum type F toxin. Vaccine, 2000, 19, 288-297.	3.8	34
103	A Universal Mariner Transposon System for Forward Genetic Studies in the Genus Clostridium. PLoS ONE, 2015, 10, e0122411.	2.5	34
104	Functional Genetic Elements for Controlling Gene Expression in Cupriavidus necator H16. Applied and Environmental Microbiology, 2018, 84, .	3.1	34
105	Cloning and complete nucleotide sequence of the Bacillus stearothermophilus tryptophanyi tRNA synthetase gene. Gene, 1986, 46, 37-45.	2.2	33
106	Sequence of the gene for alkaline phosphatase fromEscherichia coliJM83. Nucleic Acids Research, 1986, 14, 8689-8689.	14.5	33
107	The potential of clostridial spores as therapeutic delivery vehicles in tumour therapy. Research in Microbiology, 2015, 166, 244-254.	2.1	33
108	ClosTron-Mediated Engineering of Clostridium. Methods in Molecular Biology, 2011, 765, 389-407.	0.9	33

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109	A novel conjugal donor strain for improved DNA transfer into Clostridium spp.. Anaerobe, 2019, 59, 184-191.	2.1	32
110	Genetic and metabolic engineering challenges of C1-gas fermenting acetogenic chassis organisms. FEMS Microbiology Reviews, 2021, 45, .	8.6	32
111	Construction of a Nontoxigenic Clostridium botulinum Strain for Food Challenge Studies. Applied and Environmental Microbiology, 2010, 76, 387-393.	3.1	31
112	Two-Component Signal Transduction System CBO0787/CBO0786 Represses Transcription from Botulinum Neurotoxin Promoters in Clostridium botulinum ATCC 3502. PLoS Pathogens, 2013, 9, e1003252.	4.7	31
113	Syngas Biorefinery and Syngas Utilization. Advances in Biochemical Engineering/Biotechnology, 2017, 166, 247-280.	1.1	31
114	13C-assisted metabolic flux analysis to investigate heterotrophic and mixotrophic metabolism in Cupriavidus necator H16. Metabolomics, 2018, 14, 9.	3.0	31
115	Variability in Arsenic Methylation Efficiency across Aerobic and Anaerobic Microorganisms. Environmental Science & Technology, 2020, 54, 14343-14351.	10.0	31
116	Cloning and sequence analysis of the genes encoding phoshotransbutyrylase and butyrate kinase from Clostridium acetobutylicum NCIMB 8052. Gene, 1993, 131, 107-112.	2.2	30
117	Production of a functional cell wall-anchored minicellulosome by recombinant Clostridium acetobutylicum ATCC 824. Biotechnology for Biofuels, 2016, 9, 109.	6.2	30
118	Homologous overexpression of hydrogenase and glycerol dehydrogenase in Clostridium pasteurianum to enhance hydrogen production from crude glycerol. Bioresource Technology, 2019, 284, 168-177.	9.6	30
119	A Sustainable Chemicals Manufacturing Paradigm Using CO2 and Renewable H2. IScience, 2020, 23, 101218.	4.1	30
120	High-level expression of the phenylalanine ammonia lyase-encoding gene from Rhodosporidium toruloides in Saccharomyces cerevisiae and Escherichia coli using a bifunctional expression system. Gene, 1994, 143, 13-20.	2.2	29
121	Regulation of lactate metabolism in the acetogenic bacterium Acetobacterium woodii. Environmental Microbiology, 2018, 20, 4587-4595.	3.8	29
122	cspB encodes a major cold shock protein in Clostridium botulinum ATCC 3502. International Journal of Food Microbiology, 2011, 146, 23-30.	4.7	28
123	Advancing Clostridia to Clinical Trial: Past Lessons and Recent Progress. Cancers, 2016, 8, 63.	3.7	28
124	Bacillus amyloliquefaciens orthologue of Bacillus subtilis ywrO encodes a nitroreductase enzyme which activates the prodrug CB 1954 The GenBank accession number for the sequence reported in this paper is AF373598.. Microbiology (United Kingdom), 2002, 148, 297-306.	1.8	28
125	A Gene System for Glucitol Transport and Metabolism in Clostridium beijerinckii NCIMB 8052. Applied and Environmental Microbiology, 1998, 64, 1612-1619.	3.1	28
126	Clostridium difficile-mediated effects on human intestinal epithelia: Modelling host-pathogen interactions in a vertical diffusion chamber. Anaerobe, 2016, 37, 96-102.	2.1	25

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127	Progress towards platform chemical production using Clostridium autoethanogenum. Biochemical Society Transactions, 2018, 46, 523-535.	3.4	25
128	Quantitative Isotope-Dilution High-Resolution-Mass-Spectrometry Analysis of Multiple Intracellular Metabolites in Clostridium autoethanogenum with Uniformly 13C-Labeled Standards Derived from Spirulina. Analytical Chemistry, 2018, 90, 4470-4477.	6.5	25
129	Engineering of vitamin prototrophy in Clostridium ljungdahlii and Clostridium autoethanogenum. Applied Microbiology and Biotechnology, 2019, 103, 4633-4648.	3.6	25
130	Engineering Geobacillus thermoglucosidasius for direct utilisation of holocellulose from wheat straw. Biotechnology for Biofuels, 2019, 12, 199.	6.2	24
131	Selection of novel TB vaccine candidates and their evaluation as DNA vaccines against aerosol challenge. Vaccine, 2006, 24, 6340-6350.	3.8	23
132	Array comparative hybridisation reveals a high degree of similarity between UK and European clinical isolates of hypervirulent Clostridium difficile. BMC Genomics, 2010, 11, 389.	2.8	23
133	Characterization of the impact of rpoB mutations on the in vitro and in vivo competitive fitness of Clostridium difficile and susceptibility to fidaxomicin. Journal of Antimicrobial Chemotherapy, 2018, 73, 973-980.	3.0	23
134	Genetic characterisation of the botulinum toxin complex of Clostridium botulinum strain NCTC 2916. FEMS Microbiology Letters, 1996, 140, 151-158.	1.8	22
135	The glucosyltransferase activity of C. difficile Toxin B is required for disease pathogenesis. PLoS Pathogens, 2020, 16, e1008852.	4.7	21
136	Binding of the Anticancer Prodrug CB1954 to the Activating Enzyme NQO2 Revealed by the Crystal Structure of Their Complex. Journal of Medicinal Chemistry, 2005, 48, 7714-7719.	6.4	20
137	Complete Genome Sequence of the Nitrogen-Fixing and Solvent-Producing Clostridium pasteurianum DSM 525. Genome Announcements, 2015, 3, .	0.8	20
138	Generation of a fully erythromycin-sensitive strain of Clostridioides difficile using a novel CRISPR-Cas9 genome editing system. Scientific Reports, 2019, 9, 8123.	3.3	20
139	Genetics of Clostridium. , 1989, , 63-103.		20
140	Involvement of Two-Component System CBO0366/CBO0365 in the Cold Shock Response and Growth of Group I (Proteolytic) Clostridium botulinum ATCC 3502 at Low Temperatures. Applied and Environmental Microbiology, 2012, 78, 5466-5470.	3.1	19
141	Genomeâ€scale model of C. autoethanogenum reveals optimal bioprocess conditions for highâ€value chemical production from carbon monoxide. Engineering Biology, 2019, 3, 32-40.	1.8	19
142	Riboswitch (T-box)-mediated Control of tRNA-dependent Amidation in Clostridium acetobutylicum Rationalizes Gene and Pathway Redundancy for Asparagine and Asparaginyl-tRNAAsn Synthesis. Journal of Biological Chemistry, 2012, 287, 20382-20394.	3.4	18
143	Complete Genome Sequence of Cupriavidus necator H16 (DSM 428). Microbiology Resource Announcements, 2019, 8, .	0.6	18
144	Molecular cloning and nucleotide sequence determination of the Bacillus stearothermophilus NCA 1503 superoxide dismutase gene and its overexpression in Escherichia coli. Applied Microbiology and Biotechnology, 1991, 36, 358-63.	3.6	17

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145	Nucleotide Sequence of the Gene Coding for Proteolytic (Group I) Clostridium botulinum Type F Neurotoxin: Genealogical Comparison with other Clostridial Neurotoxins. Systematic and Applied Microbiology, 1995, 18, 23-31.	2.8	17
146	Development of an inducible transposon system for efficient random mutagenesis inClostridium acetobutylicum. FEMS Microbiology Letters, 2016, 363, fnw065.	1.8	17
147	The genetic basis of 3-hydroxypropanoate metabolism in Cupriavidus necator H16. Biotechnology for Biofuels, 2019, 12, 150.	6.2	17
148	Autotrophic lactate production from H2â€‰+â€‰CO2 using recombinant and fluorescent FAST-tagged Acetobacterium woodii strains. Applied Microbiology and Biotechnology, 2022, 106, 1447-1458.	3.6	17
149	The Genetic Basis of Toxin Production in Clostridium botulinum and Clostridium tetani. , 1997, , 261-294.		16
150	Gene transfer intoClostridium difficileCD630 and characterisation of its methylase genes. FEMS Microbiology Letters, 2003, 229, 103-110.	1.8	16
151	Comparison of culture based methods for the isolation of Clostridium difficile from stool samples in a research setting. Anaerobe, 2014, 28, 226-229.	2.1	16
152	Optimal spore germination in Clostridium botulinum ATCC 3502 requires the presence of functional copies of SleB and YpeB, but not CwlJ. Anaerobe, 2015, 34, 86-93.	2.1	16
153	Biosensor-informed engineering of Cupriavidus necator H16 for autotrophic D-mannitol production. Metabolic Engineering, 2022, 72, 24-34.	7.0	16
154	Cloning and nucleotide sequences of themdhandsucDgenes fromThermus aquaticusB. FEMS Microbiology Letters, 1990, 70, 7-13.	1.8	15
155	Closed Genome Sequence of Clostridium pasteurianum ATCC 6013. Genome Announcements, 2015, 3, .	0.8	15
156	The development of Clostridium difficile genetic systems. Anaerobe, 2004, 10, 75-84.	2.1	14
157	Coenzyme A-transferase-independent butyrate re-assimilation in Clostridium acetobutylicumâ€”evidence from a mathematical model. Applied Microbiology and Biotechnology, 2014, 98, 9059-9072.	3.6	14
158	The role of small acid-soluble proteins (SASPs) in protection of spores of Clostridium botulinum against nitrous acid. International Journal of Food Microbiology, 2016, 216, 25-30.	4.7	14
159	Development of Clostridium difficile R20291Î”PaLoc model strains and inÂvitro methodologies reveals CdtR is required for the production of CDT to cytotoxic levels. Anaerobe, 2017, 44, 51-54.	2.1	14
160	A Novel Bacteriophage with Broad Host Range against Clostridioides difficile Ribotype 078 Supports SlpA as the Likely Phage Receptor. Microbiology Spectrum, 2022, 10, e0229521.	3.0	14
161	Establishing Mixotrophic Growth of Cupriavidus necator H16 on CO2 and Volatile Fatty Acids. Fermentation, 2022, 8, 125.	3.0	14
162	Physical characterization of the replication origin of the cryptic plasmid pCB101 isolated from Clostridium butyricum NCIB 7423. Plasmid, 1992, 28, 1-13.	1.4	13

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