Nigel P Minton

List of Publications by Year
in descending order

234 papers	14,282 citations	25423 59 h-index	29333 108 g-index
247 all docs	247 docs citations	247 times ranked	9591 citing authors

#	Article	IF	Citations
1	Use of an optimised enzyme/prodrug combination for Clostridia directed enzyme prodrug therapy induces a significant growth delay in necrotic tumours. Cancer Gene Therapy, 2022, 29, 178-188.	2.2	9
2	Agr Quorum Sensing influences the Wood-Ljungdahl pathway in Clostridium autoethanogenum. Scientific Reports, 2022, 12, 411.	1.6	8
3	Autotrophic lactate production from H2â€‰+â€‰CO2 using recombinant and fluorescent FAST-tagged Acetobacterium woodii strains. Applied Microbiology and Biotechnology, 2022, 106, 1447-1458.	1.7	17
4	Construction and validation of safe Clostridium botulinum Group II surrogate strain producing inactive botulinum neurotoxin type E toxoid. Scientific Reports, 2022, 12, 1790.	1.6	8
5	A Novel Bacteriophage with Broad Host Range against Clostridioides difficile Ribotype 078 Supports SlpA as the Likely Phage Receptor. Microbiology Spectrum, 2022, 10, e0229521.	1.2	14
6	Biosensor-informed engineering of Cupriavidus necator H16 for autotrophic D-mannitol production. Metabolic Engineering, 2022, 72, 24-34.	3.6	16
7	Establishing Mixotrophic Growth of Cupriavidus necator H16 on CO2 and Volatile Fatty Acids. Fermentation, 2022, 8, 125.	1.4	14
8	Required Gene Set for Autotrophic Growth of Clostridium autoethanogenum. Applied and Environmental Microbiology, 2022, 88, e0247921.	1.4	9
9	Design, Analysis, and Implementation of a Novel Biochemical Pathway for Ethylene Glycol Production in Clostridium autoethanogenum. ACS Synthetic Biology, 2022, 11, 1790-1800.	1.9	6
10	A genome-scale metabolic model of Cupriavidus necator H16 integrated with TraDIS and transcriptomic data reveals metabolic insights for biotechnological applications. PLoS Computational Biology, 2022, 18, e1010106.	1.5	10
11	A clean in-frame knockout system for gene deletion in Acetobacterium woodii. Journal of Biotechnology, 2022, 353, 9-18.	1.9	7
12	Isolation and characterisation of Methylocystis spp. for poly-3-hydroxybutyrate production using waste methane feedstocks. AMB Express, 2021, 11, 6.	1.4	5
13	Entry of spores into intestinal epithelial cells contributes to recurrence of Clostridioides difficile infection. Nature Communications, 2021, 12, 1140.	5.8	60
14	Genetic and metabolic engineering challenges of C1-gas fermenting acetogenic chassis organisms. FEMS Microbiology Reviews, 2021, 45, .	3.9	32
15	Colonisation Factor CD0873, an Attractive Oral Vaccine Candidate against Clostridioides difficile. Microorganisms, 2021, 9, 306.	1.6	6
16	Development of Clostridium saccharoperbutylacetonicum as a Whole Cell Biocatalyst for Production of Chirally Pure (R)-1,3-Butanediol. Frontiers in Bioengineering and Biotechnology, 2021, 9, 659895.	2.0	4
17	Quantitative Bioreactor Monitoring of Intracellular Bacterial Metabolites in Clostridium autoethanogenum Using Liquid Chromatographyâ€“Isotope Dilution Mass Spectrometry. ACS Omega, 2021, 6, 13518-13526.	1.6	4
18	Development of a Suite of Tools for Genome Editing in Parageobacillus thermoglucosidasius and Their Use to Identify the Potential of a Native Plasmid in the Generation of Stable Engineered Strains. ACS Synthetic Biology, 2021, 10, 1739-1749.	1.9	9

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19	Engineering improved ethylene production: Leveraging systems biology and adaptive laboratory evolution. Metabolic Engineering, 2021, 67, 308-320.	3.6	8
20	What's a SNP between friends: The lineage of Clostridioides difficile R20291 can effect research outcomes. Anaerobe, 2021, 71, 102422.	1.0	11
21	The pMTL70000 modular, plasmid vector series for strain engineering in Cupriavidus necator H16. Journal of Microbiological Methods, 2021, 189, 106323.	0.7	10
22	CRISPR-Cas9-Based Toolkit for Clostridium botulinum Group II Spore and Sporulation Research. Frontiers in Microbiology, 2021, 12, 617269.	1.5	8
23	Biosynthesis of Poly(3HB-co-3HP) with Variable Monomer Composition in Recombinant Cupriavidus necator H16. ACS Synthetic Biology, 2021, , .	1.9	9
24	A Sustainable Chemicals Manufacturing Paradigm Using CO2 and Renewable H2. IScience, 2020, 23, 101218.	1.9	30
25	Synthetic Biology on Acetogenic Bacteria for Highly Efficient Conversion of C1 Gases to Biochemicals. International Journal of Molecular Sciences, 2020, 21, 7639.	1.8	35
26	Variability in Arsenic Methylation Efficiency across Aerobic and Anaerobic Microorganisms. Environmental Science & Technology, 2020, 54, 14343-14351.	4.6	31
27	The glucosyltransferase activity of C. difficile Toxin B is required for disease pathogenesis. PLoS Pathogens, 2020, 16, e1008852.	2.1	21
28	Using singular perturbation theory to determine kinetic parameters in a non-standard coupled enzyme assay. Journal of Mathematical Biology, 2020, 81, 649-690.	0.8	0
29	A genome-wide approach for identification and characterisation of metabolite-inducible systems. Nature Communications, 2020, 11, 1213.	5.8	49
30	A Gold Standard, CRISPR/Cas9-Based Complementation Strategy Reliant on 24 Nucleotide Bookmark Sequences. Genes, 2020, 11, 458.	1.0	10
31	RRNPP-type quorum sensing affects solvent formation and sporulation in Clostridium acetobutylicum. Microbiology (United Kingdom), 2020, 166, 579-592.	0.7	13
32	Phosphorylation and functionality of CdtR in Clostridium difficile. Anaerobe, 2019, 58, 103-109.	1.0	10
33	The carbonic anhydrase of Clostridium autoethanogenum represents a new subclass of Î²-carbonic anhydrases. Applied Microbiology and Biotechnology, 2019, 103, 7275-7286.	1.7	11
34	A novel conjugal donor strain for improved DNA transfer into Clostridium spp.. Anaerobe, 2019, 59, 184-191.	1.0	32
35	Complete Genome Sequence of Cupriavidus necator H16 (DSM 428). Microbiology Resource Announcements, 2019, 8, .	0.3	18
36	Engineering Geobacillus thermoglucosidasius for direct utilisation of holocellulose from wheat straw. Biotechnology for Biofuels, 2019, 12, 199.	6.2	24

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37	The genetic basis of 3-hydroxypropanoate metabolism in Cupriavidus necator H16. Biotechnology for Biofuels, 2019, 12, 150.	6.2	17
38	Heterologous gene expression in the human gut bacteria Eubacterium rectale and Roseburia inulinivorans by means of conjugative plasmids. Anaerobe, 2019, 59, 131-140.	1.0	8
39	RiboCas: A Universal CRISPR-Based Editing Tool for Clostridium. ACS Synthetic Biology, 2019, 8, 1379-1390.	1.9	69
40	Generation of a fully erythromycin-sensitive strain of Clostridioides difficile using a novel CRISPR-Cas9 genome editing system. Scientific Reports, 2019, 9, 8123.	1.6	20
41	Engineering of vitamin prototrophy in Clostridium ljungdahlii and Clostridium autoethanogenum. Applied Microbiology and Biotechnology, 2019, 103, 4633-4648.	1.7	25
42	Homologous overexpression of hydrogenase and glycerol dehydrogenase in Clostridium pasteurianum to enhance hydrogen production from crude glycerol. Bioresource Technology, 2019, 284, 168-177.	4.8	30
43	Design, cloning and characterization of transcription factor-based inducible gene expression systems. Methods in Enzymology, 2019, 621, 153-169.	0.4	9
44	CRISPRâ€“Cas9^{D10A} nickaseâ€assisted base editing in the solvent producer Clostridium beijerinckii. Biotechnology and Bioengineering, 2019, 116, 1475-1483.	1.7	57
45	Gsmodutils: a python based framework for test-driven genome scale metabolic model development. Bioinformatics, 2019, 35, 3397-3403.	1.8	2
46	Genomeâ€scale model of C. autoethanogenum reveals optimal bioprocess conditions for highâ€value chemical production from carbon monoxide. Engineering Biology, 2019, 3, 32-40.	0.8	19
47	Progress towards platform chemical production using Clostridium autoethanogenum. Biochemical Society Transactions, 2018, 46, 523-535.	1.6	25
48	The Butanol Producing Microbe Clostridium beijerinckii NCIMB 14988 Manipulated Using Forward and Reverse Genetic Tools. Biotechnology Journal, 2018, 13, e1700711.	1.8	8
49	A Transcription Factor-Based Biosensor for Detection of Itaconic Acid. ACS Synthetic Biology, 2018, 7, 1436-1446.	1.9	51
50	Advances in metabolic engineering in the microbial production of fuels and chemicals from C1 gas. Current Opinion in Biotechnology, 2018, 50, 174-181.	3.3	80
51	Cellular Uptake and Mode-of-Action of Clostridium difficile Toxins. Advances in Experimental Medicine and Biology, 2018, 1050, 77-96.	0.8	41
52	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.	1.3	23
53	Upscaling Diffusion Through First-Order Volumetric Sinks: A Homogenization of Bacterial Nutrient Uptake. SIAM Journal on Applied Mathematics, 2018, 78, 1300-1329.	0.8	11
54	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.	3.2	25

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55	13C-assisted metabolic flux analysis to investigate heterotrophic and mixotrophic metabolism in Cupriavidus necator H16. Metabolomics, 2018, 14, 9.	1.4	31
56	Applying asymptotic methods to synthetic biology: Modelling the reaction kinetics of the mevalonate pathway. Journal of Theoretical Biology, 2018, 439, 39-49.	0.8	6
57	Multi-timescale analysis of a metabolic network in synthetic biology: a kinetic model for 3-hydroxypropionic acid production via beta-alanine. Journal of Mathematical Biology, 2018, 77, 165-199.	0.8	4
58	Regulation of lactate metabolism in the acetogenic bacterium Acetobacterium woodii. Environmental Microbiology, 2018, 20, 4587-4595.	1.8	29
59	Effect of antibiotic treatment on the formation of non-spore Clostridium difficile persister-like cells. Journal of Antimicrobial Chemotherapy, 2018, 73, 2396-2399.	1.3	4
60	Functional Genetic Elements for Controlling Gene Expression in Cupriavidus necator H16. Applied and Environmental Microbiology, 2018, 84, .	1.4	34
61	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, .	1.0	85
62	Recombinant expression and characterisation of the oxygen-sensitive 2-enoate reductase from Clostridium sporogenes. Microbiology (United Kingdom), 2018, 164, 122-132.	0.7	10
63	Metabolic engineering of Clostridium autoethanogenum for selective alcohol production. Metabolic Engineering, 2017, 40, 104-114.	3.6	178
64	Towards improved butanol production through targeted genetic modification of Clostridium pasteurianum. Metabolic Engineering, 2017, 40, 124-137.	3.6	61
65	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.	1.6	41
66	Syngas Biorefinery and Syngas Utilization. Advances in Biochemical Engineering/Biotechnology, 2017, 166, 247-280.	0.6	31
67	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.	1.0	14
68	Making Clostridia Great Again. Industrial Biotechnology, 2017, 13, 52-56.	0.5	3
69	Improving gene transfer in Clostridium pasteurianum through the isolation of rare hypertransformable variants. Anaerobe, 2017, 48, 203-205.	1.0	7
70	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.	1.6	38
71	Microbial solvent formation revisited by comparative genome analysis. Biotechnology for Biofuels, 2017, 10, 58.	6.2	60
72	Enhanced solvent production by metabolic engineering of a twin-clostridial consortium. Metabolic Engineering, 2017, 39, 38-48.	3.6	110

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73	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.	1.8	76
74	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.	1.8	151
75	Advancing Clostridia to Clinical Trial: Past Lessons and Recent Progress. Cancers, 2016, 8, 63.	1.7	28
76	Complete Genome Sequence of Geobacillus thermoglucosidasius NCIMB 11955, the Progenitor of a Bioethanol Production Strain. Genome Announcements, 2016, 4, .	0.8	10
77	Development of an inducible transposon system for efficient random mutagenesis inClostridium acetobutylicum. FEMS Microbiology Letters, 2016, 363, fnw065.	0.7	17
78	A roadmap for gene system development in Clostridium. Anaerobe, 2016, 41, 104-112.	1.0	90
79	Production of a functional cell wall-anchored minicellulosome by recombinant Clostridium acetobutylicum ATCC 824. Biotechnology for Biofuels, 2016, 9, 109.	6.2	30
80	Improving the reproducibility of the NAP1/B1/027 epidemic strain R20291 in the hamster model of infection. Anaerobe, 2016, 39, 51-53.	1.0	12
81	SBRC-Nottingham: sustainable routes to platform chemicals from C1 waste gases. Biochemical Society Transactions, 2016, 44, 684-686.	1.6	0
82	A genetic assay for gene essentiality in Clostridium. Anaerobe, 2016, 42, 40-43.	1.0	1
83	Clostridium difficile Genome Editing Using pyrE Alleles. Methods in Molecular Biology, 2016, 1476, 35-52.	0.4	8
84	CRISPRâ€based genome editing and expression control systems in Clostridium acetobutylicum and Clostridium beijerinckii. Biotechnology Journal, 2016, 11, 961-972.	1.8	153
85	Coinfection and Emergence of Rifamycin Resistance during a Recurrent Clostridium difficile Infection. Journal of Clinical Microbiology, 2016, 54, 2689-2694.	1.8	6
86	The binary toxin CDT enhances Clostridium difficile virulence by suppressing protective colonic eosinophilia. Nature Microbiology, 2016, 1, 16108.	5.9	140
87	CRISPR/Cas9-Based Efficient Genome Editing in Clostridium ljungdahlii, an Autotrophic Gas-Fermenting Bacterium. ACS Synthetic Biology, 2016, 5, 1355-1361.	1.9	171
88	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
89	Insights into CO ₂ Fixation Pathway of Clostridium autoethanogenum by Targeted Mutagenesis. MBio, 2016, 7, .	1.8	83
90	Clostridium difficile-mediated effects on human intestinal epithelia: Modelling host-pathogen interactions in a vertical diffusion chamber. Anaerobe, 2016, 37, 96-102.	1.0	25

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91	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.	2.1	14
92	Whole genome sequence and manual annotation of Clostridium autoethanogenum, an industrially relevant bacterium. BMC Genomics, 2015, 16, 1085.	1.2	56
93	A Universal Mariner Transposon System for Forward Genetic Studies in the Genus Clostridium. PLoS ONE, 2015, 10, e0122411.	1.1	34
94	New Tools for the Genetic Modification of Industrial Clostridia. , 2015, , 241-289.		0
95	Inflammasome Activation Contributes to Interleukin-23 Production in Response to Clostridium difficile. MBio, 2015, 6, .	1.8	59
96	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.	1.0	16
97	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.	1.3	59
98	Complete Genome Sequence of the Nitrogen-Fixing and Solvent-Producing Clostridium pasteurianum DSM 525. Genome Announcements, 2015, 3, .	0.8	20
99	Closed Genome Sequence of Clostridium pasteurianum ATCC 6013. Genome Announcements, 2015, 3, .	0.8	15
100	The role of flagella in Clostridium difficile pathogenicity. Trends in Microbiology, 2015, 23, 275-282.	3.5	109
101	The potential of clostridial spores as therapeutic delivery vehicles in tumour therapy. Research in Microbiology, 2015, 166, 244-254.	1.0	33
102	Fluoroquinolone Resistance Does Not Impose a Cost on the Fitness of Clostridium difficile In Vitro. Antimicrobial Agents and Chemotherapy, 2015, 59, 1794-1796.	1.4	35
103	Genome Sequence of the Solvent-Producing Clostridium beijerinckii Strain 59B, Isolated from Staffordshire Garden Soil. Genome Announcements, 2015, 3, .	0.8	3
104	Complete Genome Sequence of the Nonpathogenic Soil-Dwelling Bacterium Clostridium sporogenes Strain NCIMB 10696. Genome Announcements, 2015, 3, .	0.8	4
105	The SOS Response Master Regulator LexA Is Associated with Sporulation, Motility and Biofilm Formation in Clostridium difficile. PLoS ONE, 2015, 10, e0144763.	1.1	49
106	The Cold-Induced Two-Component System CBO0366/CBO0365 Regulates Metabolic Pathways with Novel Roles in Group I Clostridium botulinum ATCC 3502 Cold Tolerance. Applied and Environmental Microbiology, 2014, 80, 306-319.	1.4	11
107	Comparison of culture based methods for the isolation of Clostridium difficile from stool samples in a research setting. Anaerobe, 2014, 28, 226-229.	1.0	16
108	Lipoprotein CD0873 Is a Novel Adhesin of Clostridium difficile. Journal of Infectious Diseases, 2014, 210, 274-284.	1.9	63

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109	Importance of Toxin A, Toxin B, and CDT in Virulence of an Epidemic Clostridium difficile Strain. Journal of Infectious Diseases, 2014, 209, 83-86.	1.9	198
110	Coenzyme A-transferase-independent butyrate re-assimilation in Clostridium acetobutylicumâ€"evidence from a mathematical model. Applied Microbiology and Biotechnology, 2014, 98, 9059-9072.	1.7	14
111	The Flagellin FliC of Clostridium difficile Is Responsible for Pleiotropic Gene Regulation during In Vivo Infection. PLoS ONE, 2014, 9, e96876.	1.1	40
112	Spores of Clostridium engineered for clinical efficacy and safety cause regression and cure of tumors in vivo. Oncotarget, 2014, 5, 1761-1769.	0.8	72
113	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
114	Multiple Factors Modulate Biofilm Formation by the Anaerobic Pathogen Clostridium difficile. Journal of Bacteriology, 2013, 195, 545-555.	1.0	247
115	The putative influence of the agr operon upon survival mechanisms used by Clostridium acetobutylicum. Mathematical Biosciences, 2013, 243, 223-239.	0.9	10
116	A novel approach to generate a recombinant toxoid vaccine against Clostridium difficile. Microbiology (United Kingdom), 2013, 159, 1254-1266.	0.7	81
117	Two-Component Signal Transduction System CBO0787/CBO0786 Represses Transcription from Botulinum Neurotoxin Promoters in Clostridium botulinum ATCC 3502. PLoS Pathogens, 2013, 9, e1003252.	2.1	31
118	Regulation of cel Genes of C. cellulolyticum: Identification of GlyR2, a Transcriptional Regulator Regulating cel5D Gene Expression. PLoS ONE, 2013, 8, e44708.	1.1	6
119	Expanding the Repertoire of Gene Tools for Precise Manipulation of the Clostridium difficile Genome: Allelic Exchange Using pyrE Alleles. PLoS ONE, 2013, 8, e56051.	1.1	146
120	Clostridium difficile Modulates Host Innate Immunity via Toxin-Independent and Dependent Mechanism(s). PLoS ONE, 2013, 8, e69846.	1.1	59
121	The Role of Flagella in Clostridium difficile Pathogenesis: Comparison between a Non-Epidemic and an Epidemic Strain. PLoS ONE, 2013, 8, e73026.	1.1	117
122	ClosTron-mediated engineering of Clostridium. Bioengineered, 2012, 3, 247-254.	1.4	55
123	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.	1.4	19
124	Integration of DNA into bacterial chromosomes from plasmids without a counter-selection marker. Nucleic Acids Research, 2012, 40, e59-e59.	6.5	154
125	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.	1.6	18
126	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.	1.4	209

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127	AnagrQuorum Sensing System That Regulates Granulose Formation and Sporulation in Clostridium acetobutylicum. Applied and Environmental Microbiology, 2012, 78, 1113-1122.	1.4	83
128	Targeted mutagenesis of the Clostridium acetobutylicum acetoneâ€“butanolâ€“ethanol fermentation pathway. Metabolic Engineering, 2012, 14, 630-641.	3.6	135
129	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.	1.3	59
130	Disruption of the acetate kinase (ack) gene of Clostridium acetobutylicum results in delayed acetate production. Applied Microbiology and Biotechnology, 2012, 94, 729-741.	1.7	63
131	Spores of Clostridium difficile Clinical Isolates Display a Diverse Germination Response to Bile Salts. PLoS ONE, 2012, 7, e32381.	1.1	99
132	Sporulation studies in Clostridium difficile. Journal of Microbiological Methods, 2011, 87, 133-138.	0.7	56
133	Multiple orphan histidine kinases interact directly with Spo0A to control the initiation of endospore formation in Clostridium acetobutylicum. Molecular Microbiology, 2011, 80, 641-654.	1.2	126
134	cspB encodes a major cold shock protein in Clostridium botulinum ATCC 3502. International Journal of Food Microbiology, 2011, 146, 23-30.	2.1	28
135	The analysis of para-cresol production and tolerance in Clostridium difficile 027 and 012 strains. BMC Microbiology, 2011, 11, 86.	1.3	105
136	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.	1.4	35
137	Both, toxin A and toxin B, are important inClostridium difficileinfection.. Gut Microbes, 2011, 2, 252-255.	4.3	63
138	ClosTron-Mediated Engineering of Clostridium. Methods in Molecular Biology, 2011, 765, 389-407.	0.4	33
139	Solvent production â€“ not to be sniffed at!: Biobutanol: 21st Century biofuel. Biochemist, 2011, 33, 8-13.	0.2	1
140	Reconsidering the Sporulation Characteristics of Hypervirulent Clostridium difficile BI/NAP1/027. PLoS ONE, 2011, 6, e24894.	1.1	89
141	Array comparative hybridisation reveals a high degree of similarity between UK and European clinical isolates of hypervirulent Clostridium difficile. BMC Genomics, 2010, 11, 389.	1.2	23
142	The diverse sporulation characteristics of Clostridium difficile clinical isolates are not associated with type. Anaerobe, 2010, 16, 618-622.	1.0	60
143	The role of toxin A and toxin B in Clostridium difficile infection. Nature, 2010, 467, 711-713.	13.7	727
144	Construction of a Nontoxigenic Clostridium botulinum Strain for Food Challenge Studies. Applied and Environmental Microbiology, 2010, 76, 387-393.	1.4	31

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145	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.	1.0	103
146	A m ariner -Based Transposon System for In Vivo Random Mutagenesis of Clostridium difficile. Applied and Environmental Microbiology, 2010, 76, 1103-1109.	1.4	124
147	Regulation of Neurotoxin Production and Sporulation by a Putative agrBD Signaling System in Proteolytic Clostridium botulinum. Applied and Environmental Microbiology, 2010, 76, 4448-4460.	1.4	108
148	The ClosTron: Mutagenesis in Clostridium refined and streamlined. Journal of Microbiological Methods, 2010, 80, 49-55.	0.7	363
149	The emergence of â€˜hypervirulenceâ€™ in Clostridium difficile. International Journal of Medical Microbiology, 2010, 300, 387-395.	1.5	94
150	Clostridium difficile spore germination: an update. Research in Microbiology, 2010, 161, 730-734.	1.0	47
151	ClosTron-Targeted Mutagenesis. Methods in Molecular Biology, 2010, 646, 165-182.	0.4	57
152	A modular system for Clostridium shuttle plasmids. Journal of Microbiological Methods, 2009, 78, 79-85.	0.7	410
153	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.	2.4	228
154	The ClosTron: A universal gene knock-out system for the genus Clostridium. Journal of Microbiological Methods, 2007, 70, 452-464.	0.7	598
155	Crystallization and preliminary X-ray characterization of theBacillus amyloliquefaciensYwrO enzyme. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 746-750.	0.7	2
156	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.	1.1	51
157	Selection of novel TB vaccine candidates and their evaluation as DNA vaccines against aerosol challenge. Vaccine, 2006, 24, 6340-6350.	1.7	23
158	The multidrug-resistant human pathogen Clostridium difficile has a highly mobile, mosaic genome. Nature Genetics, 2006, 38, 779-786.	9.4	821
159	Repeated cycles of Clostridium-directed enzyme prodrug therapy result in sustained antitumour effects in vivo. British Journal of Cancer, 2006, 95, 1212-1219.	2.9	103
160	Clostridia in Cancer Therapy. , 2005, , 251-270.		3
161	Quorum sensing in Clostridium difficile: analysis of a luxS-type signalling system. Journal of Medical Microbiology, 2005, 54, 119-127.	0.7	68
162	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.	2.9	20

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163	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.	3.2	48
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