Fernando De La Cruz

List of Publications by Year
in descending order

208 papers	14,853 citations	18482 62 h-index	24982 109 g-index
221 all docs	221 docs citations	221 times ranked	9006 citing authors

#	Article	IF	Citations
1	Mobility of Plasmids. Microbiology and Molecular Biology Reviews, 2010, 74, 434-452.	6.6	919
2	The diversity of conjugative relaxases and its application in plasmid classification. FEMS Microbiology Reviews, 2009, 33, 657-687.	8.6	500
3	Construction and properties of a family of pACYC184-derived cloning vectors compatible with pBR322 and its derivatives. Gene, 1991, 102, 75-78.	2.2	489
4	Horizontal gene transfer and the origin of species: lessons from bacteria. Trends in Microbiology, 2000, 8, 128-133.	7.7	474
5	Bacterial conjugation: a two-step mechanism for DNA transport. Molecular Microbiology, 2002, 45, 1-8.	2.5	341
6	The Repertoire of ICE in Prokaryotes Underscores the Unity, Diversity, and Ubiquity of Conjugation. PLoS Genetics, 2011, 7, e1002222.	3.5	329
7	pACYC184-derived cloning vectors containing the multiple cloning site and lacZÎ± reporter gene of pUC8/9 and pUC18/19 plasmids. Gene, 1988, 68, 159-162.	2.2	325
8	The bacterial conjugation protein TrwB resembles ring helicases and F1-ATPase. Nature, 2001, 409, 637-641.	27.8	318
9	Conjugative DNA metabolism in Gram-negative bacteria. FEMS Microbiology Reviews, 2010, 34, 18-40.	8.6	318
10	A classification scheme for mobilization regions of bacterial plasmids. FEMS Microbiology Reviews, 2004, 28, 79-100.	8.6	308
11	Dissemination of Cephalosporin Resistance Genes between Escherichia coli Strains from Farm Animals and Humans by Specific Plasmid Lineages. PLoS Genetics, 2014, 10, e1004776.	3.5	276
12	Breaking and joining single-stranded DNA: the HUH endonuclease superfamily. Nature Reviews Microbiology, 2013, 11, 525-538.	28.6	244
13	Pathways for horizontal gene transfer in bacteria revealed by a global map of their plasmids. Nature Communications, 2020, 11, 3602.	12.8	211
14	Genetic evidence of a coupling role for the TraG protein family in bacterial conjugation. Molecular Genetics and Genomics, 1997, 254, 400-406.	2.4	210
15	Key components of the eight classes of type IV secretion systems involved in bacterial conjugation or protein secretion. Nucleic Acids Research, 2014, 42, 5715-5727.	14.5	200
16	Towards an integrated model of bacterial conjugation. FEMS Microbiology Reviews, 2014, 39, n/a-n/a.	8.6	195
17	Evolution of Conjugation and Type IV Secretion Systems. Molecular Biology and Evolution, 2013, 30, 315-331.	8.9	193
18	Identification of bacterial plasmids based on mobility and plasmid population biology. FEMS Microbiology Reviews, 2011, 35, 936-956.	8.6	187

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19	Plasmid Flux in Escherichia coli ST131 Sublineages, Analyzed by Plasmid Constellation Network (PLACNET), a New Method for Plasmid Reconstruction from Whole Genome Sequences. PLoS Genetics, 2014, 10, e1004766.	3.5	179
20	Ecology and Evolution as Targets: the Need for Novel Eco-Evo Drugs and Strategies To Fight Antibiotic Resistance. Antimicrobial Agents and Chemotherapy, 2011, 55, 3649-3660.	3.2	171
21	The Tn21 subgroup of bacterial transposable elements. Plasmid, 1990, 24, 163-189.	1.4	168
22	Why is entry exclusion an essential feature of conjugative plasmids?. Plasmid, 2008, 60, 1-18.	1.4	167
23	Dynamics of the IncW genetic backbone imply general trends in conjugative plasmid evolution. FEMS Microbiology Reviews, 2006, 30, 942-966.	8.6	139
24	Recognition and processing of the origin of transfer DNA by conjugative relaxase TrwC. Nature Structural and Molecular Biology, 2003, 10, 1002-1010.	8.2	132
25	Conjugative coupling proteins interact with cognate and heterologous VirB10-like proteins while exhibiting specificity for cognate relaxosomes. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 10465-10470.	7.1	131
26	Transcription factor-based biosensors enlightened by the analyte. Frontiers in Microbiology, 2015, 6, 648.	3.5	121
27	Transposon Tn21 encodes a RecA-independent site-specific integration system. Molecular Genetics and Genomics, 1988, 211, 320-325.	2.4	116
28	PLACNETw: a web-based tool for plasmid reconstruction from bacterial genomes. Bioinformatics, 2017, 33, 3796-3798.	4.1	115
29	In-depth resistome analysis by targeted metagenomics. Microbiome, 2018, 6, 11.	11.1	115
30	A bacterial conjugation machinery recruited for pathogenesis. Molecular Microbiology, 2003, 49, 1253-1266.	2.5	112
31	Spread of <i>bla</i> _{CTX-M-14} Is Driven Mainly by IncK Plasmids Disseminated among <i>Escherichia coli</i> Phylogroups A, B1, and D in Spain. Antimicrobial Agents and Chemotherapy, 2009, 53, 5204-5212.	3.2	112
32	Site-specific recombinase and integrase activities of a conjugative relaxase in recipient cells. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 16385-16390.	7.1	100
33	Unsaturated fatty acids are inhibitors of bacterial conjugation. Microbiology (United Kingdom), 2005, 151, 3517-3526.	1.8	100
34	TrwB, the coupling protein involved in DNA transport during bacterial conjugation, is a DNA-dependent ATPase. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 8156-8161.	7.1	99
35	Release of lipid vesicle contents by the bacterial protein toxin Î±-haemolysin. Biochimica Et Biophysica Acta - Biomembranes, 1993, 1147, 81-88.	2.6	97
36	Characterization of ATP and DNA Binding Activities of TrwB, the Coupling Protein Essential in Plasmid R388 Conjugation. Journal of Biological Chemistry, 1999, 274, 36117-36124.	3.4	97

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37	Toward minimal bacterial cells: evolution vs. design. FEMS Microbiology Reviews, 2009, 33, 225-235.	8.6	97
38	The hha gene modulates haemolysin expression in Escherichia coli. Molecular Microbiology, 1991, 5, 1285-1293.	2.5	96
39	A Degenerate Primer MOB Typing (DPMT) Method to Classify Gamma-Proteobacterial Plasmids in Clinical and Environmental Settings. PLoS ONE, 2012, 7, e40438.	2.5	96
40	Coupling Factors in Macromolecular Type-IV Secretion Machineries. Current Pharmaceutical Design, 2004, 10, 1551-1565.	1.9	94
41	Differential roles of the transposon termini in IS91 transposition.. Proceedings of the National Academy of Sciences of the United States of America, 1994, 91, 1922-1926.	7.1	93
42	Genetic Organization of the Conjugal DNA Processing Region of the IncW Plasmid R388. Journal of Molecular Biology, 1994, 235, 448-464.	4.2	92
43	Enzymology of Type IV Macromolecule Secretion Systems: the Conjugative Transfer Regions of Plasmids RP4 and R388 and the <i>cag</i> Pathogenicity Island of <i>Helicobacter pylori</i> Encode Structurally and Functionally Related Nucleoside Triphosphate Hydrolases. Journal of Bacteriology, 2000, 182, 2761-2770.	2.2	90
44	TrwD, a Protein Encoded by the IncW Plasmid R388, Displays an ATP Hydrolase Activity Essential for Bacterial Conjugation. Journal of Biological Chemistry, 1997, 272, 25583-25590.	3.4	88
45	MOBscan: Automated Annotation of MOB Relaxases. Methods in Molecular Biology, 2020, 2075, 295-308.	0.9	88
46	Escherichia coli genes affecting recipient ability in plasmid conjugation: Are there any?. BMC Genomics, 2009, 10, 71.	2.8	87
47	General organization of the conjugal transfer genes of the IncW plasmid R388 and interactions between R388 and IncN and IncP plasmids. Journal of Bacteriology, 1990, 172, 5795-5802.	2.2	82
48	Comparative Genomics of the Conjugation Region of F-like Plasmids: Five Shades of F. Frontiers in Molecular Biosciences, 2016, 3, 71.	3.5	82
49	Carriage of Extended-Spectrum Beta-Lactamase-Plasmids Does Not Reduce Fitness but Enhances Virulence in Some Strains of Pandemic E. coli Lineages. Frontiers in Microbiology, 2016, 7, 336.	3.5	81
50	PipX, the coactivator of NtcA, is a global regulator in cyanobacteria. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E2423-30.	7.1	80
51	Hemolysis determinant common to Escherichia coli hemolytic plasmids of different incompatibility groups. Journal of Bacteriology, 1980, 143, 825-833.	2.2	78
52	Two active-site tyrosyl residues of protein TrwC act sequentially at the origin of transfer during plasmid R388 conjugation. Journal of Molecular Biology, 2000, 295, 1163-1172.	4.2	76
53	Four Main Virotypes among Extended-Spectrum-Î²-Lactamase-Producing Isolates of Escherichia coli O25b:H4-B2-ST131: Bacterial, Epidemiological, and Clinical Characteristics. Journal of Clinical Microbiology, 2013, 51, 3358-3367.	3.9	76
54	Complementation of transposition of tnpA mutants of Tn3, Tn21, Tn501, and Tn1721. Plasmid, 1982, 8, 276-286.	1.4	75

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55	Nicking Activity of TrwC Directed Against the Origin of Transfer of the IncW Plasmid R388. Journal of Molecular Biology, 1995, 246, 54-62.	4.2	75
56	Conjugative Plasmid Protein TrwB, an Integral Membrane Type IV Secretion System Coupling Protein. Journal of Biological Chemistry, 2002, 277, 7556-7566.	3.4	75
57	Requirements for mobilization of plasmids RSF1010 and ColE1 by the IncW plasmid R388: trwB and RP4 traG are interchangeable. Journal of Bacteriology, 1994, 176, 4455-4458.	2.2	74
58	Functional Domains in Protein TrwC of Plasmid R388: Dissected DNA Strand Transferase and DNA Helicase Activities Reconstitute Protein Function. Journal of Molecular Biology, 1996, 264, 56-67.	4.2	73
59	The ATPase Activity of the DNA Transporter TrwB Is Modulated by Protein TrwA. Journal of Biological Chemistry, 2007, 282, 25569-25576.	3.4	72
60	Different Pathways to Acquiring Resistance Genes Illustrated by the Recent Evolution of IncW Plasmids. Antimicrobial Agents and Chemotherapy, 2008, 52, 1472-1480.	3.2	71
61	Unveiling the Molecular Mechanism of a Conjugative Relaxase: The Structure of TrwC Complexed with a 27-mer DNA Comprising the Recognition Hairpin and the Cleavage Site. Journal of Molecular Biology, 2006, 358, 857-869.	4.2	68
62	Plasmid Diversity and Adaptation Analyzed by Massive Sequencing of Escherichia coli Plasmids. Microbiology Spectrum, 2014, 2, .	3.0	68
63	The Carboxyl Terminus of Protein TraD Adds Specificity and Efficiency to F-Plasmid Conjugative Transfer. Journal of Bacteriology, 1998, 180, 6039-6042.	2.2	68
64	Secondary sites for integration mediated by the Tn21 integrase. Molecular Microbiology, 1993, 10, 823-828.	2.5	66
65	The Hexameric Structure of a Conjugative VirB4 Protein ATPase Provides New Insights for a Functional and Phylogenetic Relationship with DNA Translocases. Journal of Biological Chemistry, 2012, 287, 39925-39932.	3.4	66
66	COPLA, a taxonomic classifier of plasmids. BMC Bioinformatics, 2021, 22, 390.	2.6	66
67	Conjugative transfer can be inhibited by blocking relaxase activity within recipient cells with intrabodies. Molecular Microbiology, 2007, 63, 404-416.	2.5	65
68	Genomic analysis of the emergence and evolution of multidrug resistance during a Klebsiella pneumoniae outbreak including carbapenem and colistin resistance. Journal of Antimicrobial Chemotherapy, 2014, 69, 632-636.	3.0	65
69	Bacterial conjugation: a potential tool for genomic engineering. Research in Microbiology, 2005, 156, 1-6.	2.1	64
70	Molecular epidemiology and virulence of Escherichia coli O16:H5-ST131: Comparison with H30 and H30-Rx subclones of O25b:H4-ST131. International Journal of Medical Microbiology, 2014, 304, 1247-1257.	3.6	64
71	Towards a taxonomy of conjugative plasmids. Current Opinion in Microbiology, 2017, 38, 106-113.	5.1	64
72	Purification and Properties of TrwB, a Hexameric, ATP-binding Integral Membrane Protein Essential for R388 Plasmid Conjugation. Journal of Biological Chemistry, 2002, 277, 46456-46462.	3.4	63

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73	Multicellular Computing Using Conjugation for Wiring. PLoS ONE, 2013, 8, e65986.	2.5	61
74	The IntI1 Integron Integrase Preferentially Binds Single-Stranded DNA of the <i>attC</i> Site. Journal of Bacteriology, 1999, 181, 6844-6849.	2.2	61
75	OriT-processing and regulatory roles of TrwA protein in ploasmid R388 conjugation. Journal of Molecular Biology, 1997, 270, 188-200.	4.2	59
76	Transcription Modulation of Salmonella enterica Serovar Typhimurium Promoters by Sub-MIC Levels of Rifampin. Journal of Bacteriology, 2006, 188, 7988-7991.	2.2	59
77	Synthetic Fatty Acids Prevent Plasmid-Mediated Horizontal Gene Transfer. MBio, 2015, 6, e01032-15.	4.1	59
78	Natural and Artificial Strategies To Control the Conjugative Transmission of Plasmids. Microbiology Spectrum, 2018, 6, .	3.0	59
79	Single-stranded DNA intermediates in IS91 rolling-circle transposition. Molecular Microbiology, 2001, 39, 494-502.	2.5	58
80	Conjugation-independent, site-specific recombination at the oriT of the IncW plasmid R388 mediated by TrwC. Journal of Bacteriology, 1994, 176, 3210-3217.	2.2	57
81	Host Range and Genetic Plasticity Explain the Coexistence of Integrative and Extrachromosomal Mobile Genetic Elements. Molecular Biology and Evolution, 2018, 35, 2230-2239.	8.9	57
82	IS91 transposase is related to the rolling-circle-type replication proteins of the pUB110 family of plasmids. Nucleic Acids Research, 1992, 20, 3521-3521.	14.5	56
83	The Calcium-binding C-terminal Domain of Escherichia coli Î±-Hemolysin Is a Major Determinant in the Surface-active Properties of the Protein. Journal of Biological Chemistry, 2007, 282, 11827-11835.	3.4	56
84	The stb Operon Balances the Requirements for Vegetative Stability and Conjugative Transfer of Plasmid R388. PLoS Genetics, 2011, 7, e1002073.	3.5	56
85	Incompatibility among Î±-hemolytic plasmids studied after inactivation of the Î±-hemolysin gene by transposition of Tn802. Plasmid, 1979, 2, 507-519.	1.4	55
86	Genes involved in conjugative DNA processing of plasmid R6K. Molecular Microbiology, 1997, 24, 1157-1168.	2.5	53
87	Analysis of DNA processing reactions in bacterial conjugation by using suicide oligonucleotides. EMBO Journal, 2007, 26, 3847-3857.	7.8	53
88	Plasmid typing and genetic context of AmpC Î²-lactamases in Enterobacteriaceae lacking inducible chromosomal ampC genes: findings from a Spanish hospital 1999â€"2007. Journal of Antimicrobial Chemotherapy, 2012, 67, 115-122.	3.0	53
89	Functional Interactions of VirB11 Traffic ATPases with VirB4 and VirD4 Molecular Motors in Type IV Secretion Systems. Journal of Bacteriology, 2013, 195, 4195-4201.	2.2	53
90	Negative Feedback and Transcriptional Overshooting in a Regulatory Network for Horizontal Gene Transfer. PLoS Genetics, 2014, 10, e1004171.	3.5	53

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91	Î±-Haemolysin fromE. colipurification and self-aggregation properties. FEBS Letters, 1991, 280, 195-198.	2.8	51
92	Purification and Biochemical Characterization of TrwC, the Helicase Involved in Plasmid R388 Conjugal DNA Transfer. FEBS Journal, 1994, 226, 403-412.	0.2	51
93	Viral replication in patients with concomitant hepatitis B and C virus infections. European Journal of Clinical Microbiology and Infectious Diseases, 1997, 16, 445-451.	2.9	51
94	Two atypical mobilization proteins are involved in plasmid CloDF13 relaxation. Molecular Microbiology, 2001, 39, 1088-1099.	2.5	51
95	Physical and genetic map of the IncW plasmid R388. Plasmid, 1988, 20, 155-157.	1.4	50
96	Escherichia coli hha mutants, DNA supercoiling and expression of the haemolysin genes from the recombinant plasmid pANN202-312. Molecular Microbiology, 1993, 9, 1011-1018.	2.5	48
97	Severe clinical course of de novo hepatitis B infection after liver transplantation. Liver Transplantation, 1999, 5, 175-183.	1.8	48
98	AcCNET (<u>Ac</u>cessory Genome <u>C</u>onstellation <u>Net</u>work): comparative genomics software for accessory genome analysis using bipartite networks. Bioinformatics, 2017, 33, 283-285.	4.1	48
99	Functional Dissection of the Conjugative Coupling Protein TrwB. Journal of Bacteriology, 2010, 192, 2655-2669.	2.2	47
100	Association of Composite IS <i>26-sul3</i> Elements with Highly Transmissible IncI1 Plasmids in Extended-Spectrum-Î²-Lactamase-Producing Escherichia coli Clones from Humans. Antimicrobial Agents and Chemotherapy, 2011, 55, 2451-2457.	3.2	47
101	Escherichia coli alpha-haemolysin synthesis and export genes are flanked by a direct repetition of IS91-like elements. Molecular Genetics and Genomics, 1984, 197, 90-97.	2.4	46
102	Plasmids containing one inverted repeat of Tn21 can fuse with other plasmids in the presence of Tn21 transposase. Molecular Genetics and Genomics, 1984, 195, 288-293.	2.4	46
103	Structural and functional analysis of the origin of conjugal transfer of the broad-host-range IneW plasmid R388 and comparison with the related IncN plasmid R46. Molecular Genetics and Genomics, 1991, 226, 473-483.	2.4	46
104	Functional interactions between type IV secretion systems involved in DNA transfer and virulence. Microbiology (United Kingdom), 2005, 151, 3505-3516.	1.8	46
105	DNA binding properties of protein TrwA, a possible structural variant of the Arc repressor superfamily. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2004, 1701, 15-23.	2.3	45
106	Regulation of finP Transcription by DNA Adenine Methylation in the Virulence Plasmid of Salmonella enterica. Journal of Bacteriology, 2005, 187, 5691-5699.	2.2	45
107	ATPase Activity and Oligomeric State of TrwK, the VirB4 Homologue of the Plasmid R388 Type IV Secretion System. Journal of Bacteriology, 2008, 190, 5472-5479.	2.2	44
108	Conjugation Inhibitors and Their Potential Use to Prevent Dissemination of Antibiotic Resistance Genes in Bacteria. Frontiers in Microbiology, 2017, 8, 2329.	3.5	44

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109	Evolution of Plasmid Mobility: Origin and Fate of Conjugative and Nonconjugative Plasmids. Molecular Biology and Evolution, 2022, 39, .	8.9	44
110	Determination of conjugation rates on solid surfaces. Plasmid, 2012, 67, 174-182.	1.4	43
111	Genomic and metagenomic technologies to explore the antibiotic resistance mobilome. Annals of the New York Academy of Sciences, 2017, 1388, 26-41.	3.8	43
112	Plasmid R6K Contains Two FunctionaloriTswhich can Assemble Simultaneously in Relaxosomesin vivo. Journal of Molecular Biology, 1996, 261, 135-143.	4.2	42
113	Role of IncHI2 plasmids harbouring blaVIM-1, blaCTX-M-9, aac(6â€²)-Ib and qnrA genes in the spread of multiresistant Enterobacter cloacae and Klebsiella pneumoniae strains in different units at Hospital Vall dâ€™Hebron, Barcelona, Spain. International Journal of Antimicrobial Agents, 2012, 39, 514-517.	2.5	42
114	Type IV traffic ATPase TrwD as molecular target to inhibit bacterial conjugation. Molecular Microbiology, 2016, 100, 912-921.	2.5	42
115	Orthogonal Protein Assembly on DNA Nanostructures Using Relaxases. Angewandte Chemie - International Edition, 2016, 55, 4348-4352.	13.8	40
116	Purification of Î±-hemolysin from an overproducing E. coli strain. Molecular Genetics and Genomics, 1985, 199, 106-110.	2.4	39
117	Engineering the fatty acid synthesis pathway in Synechococcus elongatus PCC 7942 improves omega-3 fatty acid production. Biotechnology for Biofuels, 2018, 11, 239.	6.2	39
118	Purification of Escherichia coli Pro-Haemolysin, and a Comparison with the Properties of Mature alpha-haemolysin. FEBS Journal, 1996, 238, 418-422.	0.2	38
119	Distribution of IS91 family insertion sequences in bacterial genomes: evolutionary implications. FEMS Microbiology Ecology, 2002, 42, 303-313.	2.7	38
120	Ordering the bestiary of genetic elements transmissible by conjugation. Mobile Genetic Elements, 2013, 3, e24263.	1.8	38
121	Specificity of insertion of IS91, an insertion sequence present in ?-haemolysin plasmids of Escherichia coli. Molecular Microbiology, 1989, 3, 979-984.	2.5	37
122	Structure and role of coupling proteins in conjugal DNA transfer. Research in Microbiology, 2002, 153, 199-204.	2.1	37
123	A new domain of conjugative relaxase TrwC responsible for efficient oriT-specific recombination on minimal target sequences. Molecular Microbiology, 2006, 62, 984-996.	2.5	37
124	Tanzawaic Acids, a Chemically Novel Set of Bacterial Conjugation Inhibitors. PLoS ONE, 2016, 11, e0148098.	2.5	37
125	TrwB: An F1-ATPase-like molecular motor involved in DNA transport during bacterial conjugation. Research in Microbiology, 2006, 157, 299-305.	2.1	36
126	Relaxases and Plasmid Transfer in Gram-Negative Bacteria. Current Topics in Microbiology and Immunology, 2017, 413, 93-113.	1.1	35

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127	Analysis of ColE1 MbeC Unveils an Extended Ribbon-Helix-Helix Family of Nicking Accessory Proteins. Journal of Bacteriology, 2009, 191, 1446-1455.	2.2	34
128	Junction sequences generated by â€˜one-ended transpositionâ€™. Nucleic Acids Research, 1985, 13, 3335-3342.	14.5	33
129	Plasmid R1 Conjugative DNA Processing Is Regulated at the Coupling Protein Interface. Journal of Bacteriology, 2009, 191, 6877-6887.	2.2	33
130	The Conjugative DNA Translocase TrwB Is a Structure-specific DNA-binding Protein. Journal of Biological Chemistry, 2010, 285, 17537-17544.	3.4	32
131	CRISPR-Cas systems preferentially target the leading regions of MOB_Fconjugative plasmids. RNA Biology, 2013, 10, 749-761.	3.1	32
132	Biochemical interactions between LPS and LPS-binding molecules. Critical Reviews in Biotechnology, 2020, 40, 292-305.	9.0	32
133	Genetic and biochemical characterization of MbeA, the relaxase involved in plasmid ColE1 conjugative mobilization. Molecular Microbiology, 2003, 48, 481-493.	2.5	30
134	Relaxase DNA Binding and Cleavage Are Two Distinguishable Steps in Conjugative DNA Processing That Involve Different Sequence Elements of the nic Site. Journal of Biological Chemistry, 2010, 285, 8918-8926.	3.4	30
135	Plasmid segregation without partition. Mobile Genetic Elements, 2011, 1, 236-241.	1.8	30
136	Role of the Transmembrane Domain in the Stability of TrwB, an Integral Protein Involved in Bacterial Conjugation. Journal of Biological Chemistry, 2004, 279, 10955-10961.	3.4	28
137	Construction of a family of Mycobacterium/Escherichia coli shuttle vectors derived from pAL5000 and pACYC184: their use for cloning an antibiotic-resistance gene from Mycobacterium fortuitum. Gene, 1996, 176, 23-26.	2.2	27
138	Cointegrates are not obligatory intermediates in transposition of Tn3 and Tn21. Nature, 1983, 305, 743-744.	27.8	26
139	Whole genome sequencing, molecular typing and in vivo virulence of OXA-48-producing Escherichia coli isolates including ST131 H30-Rx, H22 and H41 subclones. Scientific Reports, 2017, 7, 12103.	3.3	26
140	The transmembrane domain provides nucleotide binding specificity to the bacterial conjugation protein TrwB. FEBS Letters, 2006, 580, 3075-3082.	2.8	25
141	Catalytic domain of plasmid pAD1 relaxase TraX defines a group of relaxases related to restriction endonucleases. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 13606-13611.	7.1	25
142	IHF protein inhibits cleavage but not assembly of plasmid R388 relaxosomes. Molecular Microbiology, 1999, 31, 1643-1652.	2.5	24
143	Use of Limited Proteolysis and Mutagenesis To Identify Folding Domains and Sequence Motifs Critical for Wax Ester Synthase/Acyl Coenzyme A:Diacylglycerol Acyltransferase Activity. Applied and Environmental Microbiology, 2014, 80, 1132-1141.	3.1	24
144	TrwD, the Hexameric Traffic ATPase Encoded by Plasmid R388, Induces Membrane Destabilization and Hemifusion of Lipid Vesicles. Journal of Bacteriology, 2002, 184, 1661-1668.	2.2	23

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145	Conjugation inhibitors compete with palmitic acid for binding to the conjugative traffic ATPase TrwD, providing a mechanism to inhibit bacterial conjugation. Journal of Biological Chemistry, 2018, 293, 16923-16930.	3.4	23
146	Function of the Ti-Plasmid Vir Proteins: T-Complex Formation and Transfer to the Plant Cell. , 1998, , 281-301.		23
147	Characterization of the new insertion sequence IS91 from an alpha-hemolysin plasmid of Escherichia coli. Molecular Genetics and Genomics, 1984, 193, 493-499.	2.4	22
148	A Role for Gut Microbiome Fermentative Pathways in Fatty Liver Disease Progression. Journal of Clinical Medicine, 2020, 9, 1369.	2.4	22
149	The Relaxase of the Rhizobium etli Symbiotic Plasmid Shows nic Site cis -Acting Preference. Journal of Bacteriology, 2006, 188, 7488-7499.	2.2	21
150	The transmembrane domain of the T4SS coupling protein TrwB and its role in proteinâ€"protein interactions. Biochimica Et Biophysica Acta - Biomembranes, 2013, 1828, 2015-2025.	2.6	21
151	Intramolecular transposition of insertion sequence IS91 results in second-site simple insertions. Molecular Microbiology, 1999, 33, 223-234.	2.5	20
152	Degenerate primer MOB typing of multiresistant clinical isolates of E. coli uncovers new plasmid backbones. Plasmid, 2015, 77, 17-27.	1.4	20
153	Population genomics and antimicrobial resistance dynamics of Escherichia coli in wastewater and river environments. Communications Biology, 2021, 4, 457.	4.4	20
154	In vivoâ€ƒtransmission of a plasmid coharbouring blaDHA-1 and qnrB genes between Escherichia coliâ€ƒand Serratia marcescens. FEMS Microbiology Letters, 2010, 308, 24-28.	1.8	19
155	ArdC, a ssDNA-binding protein with a metalloprotease domain, overpasses the recipient hsdRMS restriction system broadening conjugation host range. PLoS Genetics, 2020, 16, e1008750.	3.5	19
156	Membrane insertion stabilizes the structure of TrwB, the R388 conjugative plasmid coupling protein. Biochimica Et Biophysica Acta - Biomembranes, 2011, 1808, 1032-1039.	2.6	18
157	Autoinhibitory Regulation of TrwK, an Essential VirB4 ATPase in Type IV Secretion Systems. Journal of Biological Chemistry, 2011, 286, 17376-17382.	3.4	18
158	Regulation of the Type IV Secretion ATPase TrwD by Magnesium. Journal of Biological Chemistry, 2012, 287, 17408-17414.	3.4	18
159	A high security double lock and key mechanism in HUH relaxases controls oriT-processing for plasmid conjugation. Nucleic Acids Research, 2014, 42, 10632-10643.	14.5	18
160	Reconstitution in liposome bilayers enhances nucleotide binding affinity and ATP-specificity of TrwB conjugative coupling protein. Biochimica Et Biophysica Acta - Biomembranes, 2010, 1798, 2160-2169.	2.6	17
161	Genomics of high molecular weight plasmids isolated from an on-farm biopurification system. Scientific Reports, 2016, 6, 28284.	3.3	17
162	PifC and Osa, Plasmid Weapons against Rival Conjugative Coupling Proteins. Frontiers in Microbiology, 2017, 8, 2260.	3.5	17

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163	Structural independence of conjugative coupling protein TrwB from its Type IV secretion machinery. Plasmid, 2013, 70, 146-153.	1.4	16
164	Cis-Acting Relaxases Guarantee Independent Mobilization of MOBQ4 Plasmids. Frontiers in Microbiology, 2019, 10, 2557.	3.5	16
165	Conjugation Inhibitors Effectively Prevent Plasmid Transmission in Natural Environments. MBio, 2021, 12, e0127721.	4.1	16
166	Plasmid Conjugation from Proteobacteria as Evidence for the Origin of Xenologous Genes in Cyanobacteria. Journal of Bacteriology, 2014, 196, 1551-1559.	2.2	15
167	A Bacterial TrwC Relaxase Domain Contains a Thermally Stable Î±-Helical Core. Journal of Bacteriology, 2003, 185, 4226-4232.	2.2	13
168	Changing the recognition site of a conjugative relaxase by rational design. Biotechnology Journal, 2009, 4, 554-557.	3.5	13
169	Nutrient starvation leading to triglyceride accumulation activates the Entner Doudoroff pathway in Rhodococcus jostii RHA1. Microbial Cell Factories, 2017, 16, 35.	4.0	13
170	The molecular relatedness among Î±-hemolytic plasmids from various incompatibility groups. Plasmid, 1980, 4, 76-81.	1.4	12
171	Correlation between hepatitis B viremia and the clinical and histological activity of chronic delta hepatitis. Medical Microbiology and Immunology, 1994, 183, 159-167.	4.8	12
172	Interaction between relaxase MbeA and accessory protein MbeC of the conjugally mobilizable plasmid ColE1. FEBS Letters, 2012, 586, 675-679.	2.8	12
173	Rebooting the genome: The role of negative feedback in horizontal gene transfer. Mobile Genetic Elements, 2014, 4, 1-6.	1.8	11
174	Subcellular location of the coupling protein TrwB and the role of its transmembrane domain. Biochimica Et Biophysica Acta - Biomembranes, 2014, 1838, 223-230.	2.6	11
175	Bacterial computing with engineered populations. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2015, 373, 20140218.	3.4	9
176	On the Transposition and Evolution of Tn1721 and its Relatives. , 1985, 30, 79-91.		9
177	Blueprint for a minimal photoautotrophic cell: conserved and variable genes in Synechococcus elongatus PCC 7942. BMC Genomics, 2011, 12, 25.	2.8	8
178	Deletion of a single helix from the transmembrane domain causes large changes in membrane insertion properties and secondary structure of the bacterial conjugation protein TrwB. Biochimica Et Biophysica Acta - Biomembranes, 2012, 1818, 3158-3166.	2.6	8
179	Horizontal Gene Transfer. Methods in Molecular Biology, 2020, , .	0.9	8
180	Heterologous expression of a thermophilic diacylglycerol acyltransferase triggers triglyceride accumulation in Escherichia coli. PLoS ONE, 2017, 12, e0176520.	2.5	8

#	Article	IF	Citations
181	Genetics of the replication and maintenance functions of the hemolytic plasmid pSU316. Cloning of an IncFIII determinant. Plasmid, 1983, 10, 175-183.	1.4	6
182	Tn5tac1 insertion polarity in Escherichia coli. Plasmid, 1991, 26, 222-224.	1.4	6
183	Concerted action of NIC relaxase and auxiliary protein MobC in RA3 plasmid conjugation. Molecular Microbiology, 2016, 101, 439-456.	2.5	6
184	Substrate translocation involves specific lysine residues of the central channel of the conjugative coupling protein TrwB. Molecular Genetics and Genomics, 2017, 292, 1037-1049.	2.1	6
185	Negative feedback increases information transmission, enabling bacteria to discriminate sublethal antibiotic concentrations. Science Advances, 2018, 4, eaat5771.	10.3	6
186	Plasmid Diversity and Adaptation Analyzed by Massive Sequencing of<i>Escherichia coli</i>Plasmids. , 0, , 219-235.		6
187	Site-specific recombination and shuffling of resistance genes in transposon Tn21. Research in Microbiology, 1991, 142, 701-704.	2.1	5
188	Numbers on the edges: A simplified and scalable method for quantifying the Gene Regulation Function. BioEssays, 2010, 32, 346-355.	2.5	5
189	fabH deletion increases DHA production in Escherichia coli expressing Pfa genes. Microbial Cell Factories, 2018, 17, 88.	4.0	5
190	Dynamical Task Switching in Cellular Computers. Life, 2019, 9, 14.	2.4	5
191	Factors that affect transposition mediated by the Tn21 transposase. Plasmid, 1988, 20, 54-60.	1.4	4
192	Integrated strategy for the separation of endotoxins from biofluids. LPS capture on newly synthesized protein. Separation and Purification Technology, 2021, 255, 117689.	7.9	4
193	Genomic Insights into Drug Resistance and Virulence Platforms, CRISPR-Cas Systems and Phylogeny of Commensal E. coli from Wildlife. Microorganisms, 2021, 9, 999.	3.6	4
194	Design of Novel Relaxase Substrates Based on Rolling Circle Replicases for Bioconjugation to DNA Nanostructures. PLoS ONE, 2016, 11, e0152666.	2.5	4
195	Synechococcus elongatus PCC 7942 as a Platform for Bioproduction of Omega-3 Fatty Acids. Life, 2022, 12, 810.	2.4	4
196	Plasmid Reconstruction from Next-Gen Data: A Detailed Protocol for the Use of PLACNETw for the Reconstruction of Plasmids from WGS Datasets. Methods in Molecular Biology, 2020, 2075, 323-339.	0.9	3
197	Identification of Xenologs and Their Characteristic Low Expression Levels in the Cyanobacterium Synechococcus elongatus. Journal of Molecular Evolution, 2015, 80, 292-304.	1.8	2
198	Microbial Oils as Nutraceuticals and Animal Feeds. , 2020, , 401-445.		2

#	Article	IF	Citations
199	PLASmid TAXonomic PCR (PlasTax-PCR), a Multiplex Relaxase MOB Typing to Assort Plasmids into Taxonomic Units. Methods in Molecular Biology, 2022, 2392, 127-142.	0.9	2
200	Membrane insertion stabilizes TrwB, the coupling protein of the conjugative plasmid R388. Chemistry and Physics of Lipids, 2010, 163, S47.	3.2	0
201	Nanobiotechnology. Current Opinion in Biotechnology, 2012, 23, 501-502.	6.6	0
202	Natural and Artificial Strategies to Control the Conjugative Transmission of Plasmids. , 2019, , 33-64.		0
203	Conjugative Transfer Systems and Classifying Plasmid Genomes. , 2014, , 1-5.		0
204	Transposition-Like Events Mediated by Single-Ended Derivatives of Transposon Tn21. , 1985, , 121-132.		0
205	Purification and Some Properties of E. coli Î±-Haemolysin. , 1991, , 155-176.		0
206	Transcriptional Regulation of Î±-Hemolysin Genetic Expression: hly M, a sequence contained in hly C, modulates hemolysin transcription. Developments in Plant Pathology, 1994, , 379-397.	0.1	0
207	Conjugative Transfer Systems and Classifying Plasmid Genomes. , 2018, , 115-118.		0
208	Five Complete <i>Salmonella enterica</i> Serotype Reading Genomes Recovered from Patients in the United States. Microbiology Resource Announcements, 0, , .	0.6	0