Fernando De La Cruz

List of Publications by Year
in descending order

208	14,853	62	109
papers	citations	h-index	g-index
		18482	24982

221	221	221	9006
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	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
2	Synechococcus elongatus PCC 7942 as a Platform for Bioproduction of Omega-3 Fatty Acids. Life, 2022, 12, 810.	2.4	4
3	Evolution of Plasmid Mobility: Origin and Fate of Conjugative and Nonconjugative Plasmids. Molecular Biology and Evolution, 2022, 39, .	8.9	44
4	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
5	Population genomics and antimicrobial resistance dynamics of Escherichia coli in wastewater and river environments. Communications Biology, 2021, 4, 457.	4.4	20
6	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
7	COPLA, a taxonomic classifier of plasmids. BMC Bioinformatics, 2021, 22, 390.	2.6	66
8	Conjugation Inhibitors Effectively Prevent Plasmid Transmission in Natural Environments. MBio, 2021, 12, e0127721.	4.1	16
9	Horizontal Gene Transfer. Methods in Molecular Biology, 2020, , .	0.9	8
10	Pathways for horizontal gene transfer in bacteria revealed by a global map of their plasmids. Nature Communications, 2020, 11, 3602.	12.8	211
11	A Role for Gut Microbiome Fermentative Pathways in Fatty Liver Disease Progression. Journal of Clinical Medicine, 2020, 9, 1369.	2.4	22
12	Biochemical interactions between LPS and LPS-binding molecules. Critical Reviews in Biotechnology, 2020, 40, 292-305.	9.0	32
13	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
14	MOBscan: Automated Annotation of MOB Relaxases. Methods in Molecular Biology, 2020, 2075, 295-308.	0.9	88
15	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
16	Microbial Oils as Nutraceuticals and Animal Feeds. , 2020, , 401-445.		2
17	Natural and Artificial Strategies to Control the Conjugative Transmission of Plasmids. , 2019, , 33-64.		0
18	Cis-Acting Relaxases Guarantee Independent Mobilization of MOBQ4 Plasmids. Frontiers in Microbiology, 2019, 10, 2557.	3.5	16

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19	Dynamical Task Switching in Cellular Computers. Life, 2019, 9, 14.	2.4	5
20	Natural and Artificial Strategies To Control the Conjugative Transmission of Plasmids. Microbiology Spectrum, 2018, 6, .	3.0	59
21	Negative feedback increases information transmission, enabling bacteria to discriminate sublethal antibiotic concentrations. Science Advances, 2018, 4, eaat5771.	10.3	6
22	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
23	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
24	In-depth resistome analysis by targeted metagenomics. Microbiome, 2018, 6, 11.	11.1	115
25	fabH deletion increases DHA production in Escherichia coli expressing Pfa genes. Microbial Cell Factories, 2018, 17, 88.	4.0	5
26	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
27	Conjugative Transfer Systems and Classifying Plasmid Genomes. , 2018, , 115-118.		0
28	Nutrient starvation leading to triglyceride accumulation activates the Entner Doudoroff pathway in Rhodococcus jostii RHA1. Microbial Cell Factories, 2017, 16, 35.	4.0	13
29	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
30	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
31	PLACNETw: a web-based tool for plasmid reconstruction from bacterial genomes. Bioinformatics, 2017, 33, 3796-3798.	4.1	115
32	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
33	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
34	Relaxases and Plasmid Transfer in Gram-Negative Bacteria. Current Topics in Microbiology and Immunology, 2017, 413, 93-113.	1.1	35
35	PifC and Osa, Plasmid Weapons against Rival Conjugative Coupling Proteins. Frontiers in Microbiology, 2017, 8, 2260.	3.5	17
36	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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37	Towards a taxonomy of conjugative plasmids. Current Opinion in Microbiology, 2017, 38, 106-113.	5.1	64
38	Heterologous expression of a thermophilic diacylglycerol acyltransferase triggers triglyceride accumulation in Escherichia coli. PLoS ONE, 2017, 12, e0176520.	2.5	8
39	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
40	Comparative Genomics of the Conjugation Region of F-like Plasmids: Five Shades of F. Frontiers in Molecular Biosciences, 2016, 3, 71.	3.5	82
41	Tanzawaic Acids, a Chemically Novel Set of Bacterial Conjugation Inhibitors. PLoS ONE, 2016, 11, e0148098.	2.5	37
42	Concerted action of NIC relaxase and auxiliary protein MobC in RA3 plasmid conjugation. Molecular Microbiology, 2016, 101, 439-456.	2.5	6
43	Type IV traffic ATPase TrwD as molecular target to inhibit bacterial conjugation. Molecular Microbiology, 2016, 100, 912-921.	2.5	42
44	Genomics of high molecular weight plasmids isolated from an on-farm biopurification system. Scientific Reports, 2016, 6, 28284.	3.3	17
45	Orthogonal Protein Assembly on DNA Nanostructures Using Relaxases. Angewandte Chemie - International Edition, 2016, 55, 4348-4352.	13.8	40
46	Design of Novel Relaxase Substrates Based on Rolling Circle Replicases for Bioconjugation to DNA Nanostructures. PLoS ONE, 2016, 11, e0152666.	2.5	4
47	Transcription factor-based biosensors enlightened by the analyte. Frontiers in Microbiology, 2015, 6, 648.	3.5	121
48	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
49	Bacterial computing with engineered populations. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2015, 373, 20140218.	3.4	9
50	Synthetic Fatty Acids Prevent Plasmid-Mediated Horizontal Gene Transfer. MBio, 2015, 6, e01032-15.	4.1	59
51	Degenerate primer MOB typing of multiresistant clinical isolates of E. coli uncovers new plasmid backbones. Plasmid, 2015, 77, 17-27.	1.4	20
52	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
53	Negative Feedback and Transcriptional Overshooting in a Regulatory Network for Horizontal Gene Transfer. PLoS Genetics, 2014, 10, e1004171.	3.5	53
54	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

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55	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
56	Rebooting the genome: The role of negative feedback in horizontal gene transfer. Mobile Genetic Elements, 2014, 4, 1-6.	1.8	11
57	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
58	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
59	Towards an integrated model of bacterial conjugation. FEMS Microbiology Reviews, 2014, 39, n/a-n/a.	8.6	195
60	Plasmid Conjugation from Proteobacteria as Evidence for the Origin of Xenologous Genes in Cyanobacteria. Journal of Bacteriology, 2014, 196, 1551-1559.	2.2	15
61	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
62	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
63	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
64	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
65	Plasmid Diversity and Adaptation Analyzed by Massive Sequencing of Escherichia coli Plasmids. Microbiology Spectrum, 2014, 2, .	3.0	68
66	Conjugative Transfer Systems and Classifying Plasmid Genomes. , 2014, , 1-5.		0
67	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
68	Structural independence of conjugative coupling protein TrwB from its Type IV secretion machinery. Plasmid, 2013, 70, 146-153.	1.4	16
69	CRISPR-Cas systems preferentially target the leading regions of MOB_Fconjugative plasmids. RNA Biology, 2013, 10, 749-761.	3.1	32
70	Breaking and joining single-stranded DNA: the HUH endonuclease superfamily. Nature Reviews Microbiology, 2013, 11, 525-538.	28.6	244
71	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
72	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

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73	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
74	Evolution of Conjugation and Type IV Secretion Systems. Molecular Biology and Evolution, 2013, 30, 315-331.	8.9	193
75	Ordering the bestiary of genetic elements transmissible by conjugation. Mobile Genetic Elements, 2013, 3, e24263.	1.8	38
76	Multicellular Computing Using Conjugation for Wiring. PLoS ONE, 2013, 8, e65986.	2.5	61
77	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
78	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
79	Regulation of the Type IV Secretion ATPase TrwD by Magnesium. Journal of Biological Chemistry, 2012, 287, 17408-17414.	3.4	18
80	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
81	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
82	Nanobiotechnology. Current Opinion in Biotechnology, 2012, 23, 501-502.	6.6	0
83	Interaction between relaxase MbeA and accessory protein MbeC of the conjugally mobilizable plasmid ColE1. FEBS Letters, 2012, 586, 675-679.	2.8	12
84	Determination of conjugation rates on solid surfaces. Plasmid, 2012, 67, 174-182.	1.4	43
85	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
86	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
87	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
88	Identification of bacterial plasmids based on mobility and plasmid population biology. FEMS Microbiology Reviews, 2011, 35, 936-956.	8.6	187
89	Blueprint for a minimal photoautotrophic cell: conserved and variable genes in Synechococcus elongatus PCC 7942. BMC Genomics, 2011, 12, 25.	2.8	8
90	Plasmid segregation without partition. Mobile Genetic Elements, 2011, 1, 236-241.	1.8	30

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91	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
92	Autoinhibitory Regulation of TrwK, an Essential VirB4 ATPase in Type IV Secretion Systems. Journal of Biological Chemistry, 2011, 286, 17376-17382.	3.4	18
93	The stb Operon Balances the Requirements for Vegetative Stability and Conjugative Transfer of Plasmid R388. PLoS Genetics, 2011, 7, e1002073.	3.5	56
94	The Repertoire of ICE in Prokaryotes Underscores the Unity, Diversity, and Ubiquity of Conjugation. PLoS Genetics, 2011, 7, e1002222.	3.5	329
95	Numbers on the edges: A simplified and scalable method for quantifying the Gene Regulation Function. BioEssays, 2010, 32, 346-355.	2.5	5
96	Membrane insertion stabilizes TrwB, the coupling protein of the conjugative plasmid R388. Chemistry and Physics of Lipids, 2010, 163, S47.	3.2	0
97	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
98	Conjugative DNA metabolism in Gram-negative bacteria. FEMS Microbiology Reviews, 2010, 34, 18-40.	8.6	318
99	Functional Dissection of the Conjugative Coupling Protein TrwB. Journal of Bacteriology, 2010, 192, 2655-2669.	2.2	47
100	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
101	The Conjugative DNA Translocase TrwB Is a Structure-specific DNA-binding Protein. Journal of Biological Chemistry, 2010, 285, 17537-17544.	3.4	32
102	Mobility of Plasmids. Microbiology and Molecular Biology Reviews, 2010, 74, 434-452.	6.6	919
103	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
104	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
105	Plasmid R1 Conjugative DNA Processing Is Regulated at the Coupling Protein Interface. Journal of Bacteriology, 2009, 191, 6877-6887.	2.2	33
106	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
107	Escherichia coli genes affecting recipient ability in plasmid conjugation: Are there any?. BMC Genomics, 2009, 10, 71.	2.8	87
108	Toward minimal bacterial cells: evolution vs. design. FEMS Microbiology Reviews, 2009, 33, 225-235.	8.6	97

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109	The diversity of conjugative relaxases and its application in plasmid classification. FEMS Microbiology Reviews, 2009, 33, 657-687.	8.6	500
110	Changing the recognition site of a conjugative relaxase by rational design. Biotechnology Journal, 2009, 4, 554-557.	3.5	13
111	Why is entry exclusion an essential feature of conjugative plasmids?. Plasmid, 2008, 60, 1-18.	1.4	167
112	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
113	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
114	The ATPase Activity of the DNA Transporter TrwB Is Modulated by Protein TrwA. Journal of Biological Chemistry, 2007, 282, 25569-25576.	3.4	72
115	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
116	Analysis of DNA processing reactions in bacterial conjugation by using suicide oligonucleotides. EMBO Journal, 2007, 26, 3847-3857.	7.8	53
117	Conjugative transfer can be inhibited by blocking relaxase activity within recipient cells with intrabodies. Molecular Microbiology, 2007, 63, 404-416.	2.5	65
118	The transmembrane domain provides nucleotide binding specificity to the bacterial conjugation protein TrwB. FEBS Letters, 2006, 580, 3075-3082.	2.8	25
119	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
120	TrwB: An F1-ATPase-like molecular motor involved in DNA transport during bacterial conjugation. Research in Microbiology, 2006, 157, 299-305.	2.1	36
121	Dynamics of the IncW genetic backbone imply general trends in conjugative plasmid evolution. FEMS Microbiology Reviews, 2006, 30, 942-966.	8.6	139
122	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
123	The Relaxase of the Rhizobium etli Symbiotic Plasmid Shows nic Site cis -Acting Preference. Journal of Bacteriology, 2006, 188, 7488-7499.	2.2	21
124	Transcription Modulation of Salmonella enterica Serovar Typhimurium Promoters by Sub-MIC Levels of Rifampin. Journal of Bacteriology, 2006, 188, 7988-7991.	2.2	59
125	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
126	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

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127	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
128	Bacterial conjugation: a potential tool for genomic engineering. Research in Microbiology, 2005, 156, 1-6.	2.1	64
129	Unsaturated fatty acids are inhibitors of bacterial conjugation. Microbiology (United Kingdom), 2005, 151, 3517-3526.	1.8	100
130	Functional interactions between type IV secretion systems involved in DNA transfer and virulence. Microbiology (United Kingdom), 2005, 151, 3505-3516.	1.8	46
131	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
132	A classification scheme for mobilization regions of bacterial plasmids. FEMS Microbiology Reviews, 2004, 28, 79-100.	8.6	308
133	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
134	Coupling Factors in Macromolecular Type-IV Secretion Machineries. Current Pharmaceutical Design, 2004, 10, 1551-1565.	1.9	94
135	A bacterial conjugation machinery recruited for pathogenesis. Molecular Microbiology, 2003, 49, 1253-1266.	2.5	112
136	Genetic and biochemical characterization of MbeA, the relaxase involved in plasmid ColE1 conjugative mobilization. Molecular Microbiology, 2003, 48, 481-493.	2.5	30
137	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
138	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
139	A Bacterial TrwC Relaxase Domain Contains a Thermally Stable Î±-Helical Core. Journal of Bacteriology, 2003, 185, 4226-4232.	2.2	13
140	Conjugative Plasmid Protein TrwB, an Integral Membrane Type IV Secretion System Coupling Protein. Journal of Biological Chemistry, 2002, 277, 7556-7566.	3.4	75
141	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
142	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
143	Structure and role of coupling proteins in conjugal DNA transfer. Research in Microbiology, 2002, 153, 199-204.	2.1	37
144	Bacterial conjugation: a two-step mechanism for DNA transport. Molecular Microbiology, 2002, 45, 1-8.	2.5	341

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146	Single-stranded DNA intermediates in IS91 rolling-circle transposition. Molecular Microbiology, 2001, 39, 494-502.	2.5	58
147	Two atypical mobilization proteins are involved in plasmid CloDF13 relaxation. Molecular Microbiology, 2001, 39, 1088-1099.	2.5	51
148	The bacterial conjugation protein TrwB resembles ring helicases and F1-ATPase. Nature, 2001, 409, 637-641.	27.8	318
149	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
150	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
151	Horizontal gene transfer and the origin of species: lessons from bacteria. Trends in Microbiology, 2000, 8, 128-133.	7.7	474
152	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
153	IHF protein inhibits cleavage but not assembly of plasmid R388 relaxosomes. Molecular Microbiology, 1999, 31, 1643-1652.	2.5	24
154	Intramolecular transposition of insertion sequence IS91 results in second-site simple insertions. Molecular Microbiology, 1999, 33, 223-234.	2.5	20
155	Severe clinical course of de novo hepatitis B infection after liver transplantation. Liver Transplantation, 1999, 5, 175-183.	1.8	48
156	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
157	Function of the Ti-Plasmid Vir Proteins: T-Complex Formation and Transfer to the Plant Cell. , 1998, , 281-301.		23
158	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
159	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
160	OriT-processing and regulatory roles of TrwA protein in ploasmid R388 conjugation. Journal of Molecular Biology, 1997, 270, 188-200.	4.2	59
161	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
162	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

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163	Genes involved in conjugative DNA processing of plasmid R6K. Molecular Microbiology, 1997, 24, 1157-1168.	2.5	53
164	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
165	Plasmid R6K Contains Two FunctionaloriTswhich can Assemble Simultaneously in Relaxosomesin vivo. Journal of Molecular Biology, 1996, 261, 135-143.	4.2	42
166	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
167	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
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