

Kenn Gerdes

List of Publications by Year in descending order

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160
papers

21,184
citations

8755

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169
docs citations

169
times ranked

10418
citing authors

#	ARTICLE	IF	CITATIONS
1	Hibernation factors directly block ribonucleases from entering the ribosome in response to starvation. <i>Nucleic Acids Research</i> , 2021, 49, 2226-2239.	14.5	21
2	Structural Basis for Regulation of Toxin Activity via Dual Phosphorylation in the Tripartite HipBST Toxin-Antitoxin System. <i>FASEB Journal</i> , 2021, 35, .	0.5	0
3	Phylogeny Reveals Novel HipA-Homologous Kinase Families and Toxin-Antitoxin Gene Organizations. <i>MBio</i> , 2021, 12, e0105821.	4.1	12
4	Proteome Dynamics during Antibiotic Persistence and Resuscitation. <i>MSystems</i> , 2021, 6, e0054921.	3.8	4
5	PasT of <i>Escherichia coli</i> sustains antibiotic tolerance and aerobic respiration as a bacterial homolog of mitochondrial Coq10. <i>MicrobiologyOpen</i> , 2020, 9, e1064.	3.0	13
6	Type II and type IV toxin-antitoxin systems show different evolutionary patterns in the global <i>Klebsiella pneumoniae</i> population. <i>Nucleic Acids Research</i> , 2020, 48, 4357-4370.	14.5	14
7	Fatty acid starvation activates RelA by depleting lysine precursor pyruvate. <i>Molecular Microbiology</i> , 2019, 112, 1339-1349.	2.5	26
8	Toxin-antitoxin operon <i>kacAT</i> of <i>Klebsiella pneumoniae</i> is regulated by conditional cooperativity via a W-shaped <i>KacA-KacT</i> complex. <i>Nucleic Acids Research</i> , 2019, 47, 7690-7702.	14.5	20
9	The <i>E. coli</i> <i>HicB</i> Antitoxin Contains a Structurally Stable Helix-Turn-Helix DNA Binding Domain. <i>Structure</i> , 2019, 27, 1675-1685.e3.	3.3	23
10	Serine-Threonine Kinases Encoded by Split <i>hipA</i> Homologs Inhibit Tryptophanyl-tRNA Synthetase. <i>MBio</i> , 2019, 10, .	4.1	25
11	(p)ppGpp Regulates a Bacterial Nucleosidase by an Allosteric Two-Domain Switch. <i>Molecular Cell</i> , 2019, 74, 1239-1249.e4.	9.7	39
12	CRP Interacts Specifically With Sxy to Activate Transcription in <i>Escherichia coli</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2053.	3.5	5
13	The RES domain toxins of <i>RES-Xre</i> toxin-antitoxin modules induce cell stasis by degrading NAD ⁺ . <i>Molecular Microbiology</i> , 2019, 111, 221-236.	2.5	46
14	Novel (p)ppGpp Binding and Metabolizing Proteins of <i>Escherichia coli</i> . <i>MBio</i> , 2018, 9, .	4.1	132
15	Activation of the Stringent Response by Loading of RelA-tRNA Complexes at the Ribosomal A-Site. <i>Molecular Cell</i> , 2018, 70, 95-105.e4.	9.7	97
16	Toxins, Targets, and Triggers: An Overview of Toxin-Antitoxin Biology. <i>Molecular Cell</i> , 2018, 70, 768-784.	9.7	521
17	Ribosome Hibernation. <i>Annual Review of Genetics</i> , 2018, 52, 321-348.	7.6	110
18	Transcriptome-Wide Analysis of Protein-RNA and RNA-RNA Interactions in Pathogenic Bacteria. <i>Methods in Enzymology</i> , 2018, 612, 467-488.	1.0	7

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19	The kinases HipA and HipA7 phosphorylate different substrate pools in <i>Escherichia coli</i> to promote multidrug tolerance. <i>Science Signaling</i> , 2018, 11, .	3.6	52
20	SLING: a tool to search for linked genes in bacterial datasets. <i>Nucleic Acids Research</i> , 2018, 46, e128.	14.5	18
21	Hic toxin of <i>Escherichia coli</i> derepresses AB transcription to selectively produce HicB antitoxin. <i>Molecular Microbiology</i> , 2017, 104, 781-792.	2.5	45
22	Peptide nucleotide antibiotic Microcin C is a potent inducer of stringent response and persistence in both sensitive and producing cells. <i>Molecular Microbiology</i> , 2017, 104, 463-471.	2.5	21
23	Ribosome-dependent <i>Vibrio cholerae</i> mRNAse HigB2 is regulated by a λ^2 -strand sliding mechanism. <i>Nucleic Acids Research</i> , 2017, 45, 4972-4983.	14.5	43
24	Prophages and Growth Dynamics Confound Experimental Results with Antibiotic-Tolerant Persister Cells. <i>MBio</i> , 2017, 8, .	4.1	190
25	VapCs of <i>Mycobacterium tuberculosis</i> cleave RNAs essential for translation. <i>Nucleic Acids Research</i> , 2016, 44, 9860-9871.	14.5	106
26	Alarmone (p)ppGpp regulates the transition from pathogenicity to mutualism in <i>Pseudomonas fluorescens</i> . <i>Molecular Microbiology</i> , 2016, 100, 735-747.	2.5	19
27	Mechanisms of bacterial persistence during stress and antibiotic exposure. <i>Science</i> , 2016, 354, .	12.6	640
28	Back to the Roots: Deep View into the Evolutionary History of ADP-Ribosylation Opened by the DNA-Targeting Toxin-Antitoxin Module DarTG. <i>Molecular Cell</i> , 2016, 64, 1020-1021.	9.7	4
29	Pumping persisters. <i>Nature</i> , 2016, 534, 41-42.	27.8	37
30	Rapid Curtailing of the Stringent Response by Toxin-Antitoxin Module-Encoded mRNases. <i>Journal of Bacteriology</i> , 2016, 198, 1918-1926.	2.2	27
31	Hypothesis: type I toxin-antitoxin genes enter the persistence field—a feedback mechanism explaining membrane homeostasis. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20160189.	4.0	18
32	Cell age dependent concentration of <i>Escherichia coli</i> divisome proteins analyzed with ImageJ and ObjectJ. <i>Frontiers in Microbiology</i> , 2015, 6, 586.	3.5	92
33	Crystallization of two operator complexes from the <i>Vibrio cholerae</i> HigBA2 toxin-antitoxin module. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 226-233.	0.8	2
34	Remarkable Functional Convergence: Alarmone ppGpp Mediates Persistence by Activating Type I and II Toxin-Antitoxins. <i>Molecular Cell</i> , 2015, 59, 1-3.	9.7	52
35	Stochastic induction of persister cells by HipA through (p)ppGpp-mediated activation of mRNA endonucleases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5171-5176.	7.1	132
36	Recent functional insights into the role of (p)ppGpp in bacterial physiology. <i>Nature Reviews Microbiology</i> , 2015, 13, 298-309.	28.6	703

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37	Adenylylation of Gyrase and Topo IV by FicT Toxins Disrupts Bacterial DNA Topology. <i>Cell Reports</i> , 2015, 12, 1497-1507.	6.4	92
38	<scp>CRP</scp>-dependent Positive Autoregulation and Proteolytic Degradation Regulate Competence Activator Sxy of <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 2015, 95, 833-845.	2.5	30
39	Competing ParA Structures Space Bacterial Plasmids Equally over the Nucleoid. <i>PLoS Computational Biology</i> , 2014, 10, e1004009.	3.2	60
40	ZapE Is a Novel Cell Division Protein Interacting with FtsZ and Modulating the Z-Ring Dynamics. <i>MBio</i> , 2014, 5, e00022-14.	4.1	54
41	Molecular Mechanisms Underlying Bacterial Persisters. <i>Cell</i> , 2014, 157, 539-548.	28.9	538
42	Direct interaction of FtsZ and MreB is required for septum synthesis and cell division in <i>Escherichia coli</i> . <i>EMBO Journal</i> , 2013, 32, 1953-1965.	7.8	121
43	A problem of persistence: still more questions than answers?. <i>Nature Reviews Microbiology</i> , 2013, 11, 587-591.	28.6	228
44	Molecular Mechanism of Bacterial Persistence by HipA. <i>Molecular Cell</i> , 2013, 52, 248-254.	9.7	326
45	VapC20 of <i>Mycobacterium tuberculosis</i> cleaves the Sarcin-Ricin loop of 23S rRNA. <i>Nature Communications</i> , 2013, 4, 2796.	12.8	112
46	Killing the survivors. <i>Nature</i> , 2013, 503, 347-349.	27.8	10
47	Type II Toxin-Antitoxins Loci: The relBE Family. , 2013, , 69-92.		3
48	Conditional Cooperativity of Toxin - Antitoxin Regulation Can Mediate Bistability between Growth and Dormancy. <i>PLoS Computational Biology</i> , 2013, 9, e1003174.	3.2	55
49	Protein expression, crystallization and preliminary X-ray crystallographic analysis of the isolated <i>Shigella flexneri</i> VapC toxin. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 762-765.	0.7	6
50	Crystallization of the HigBA2 toxin-antitoxin complex from <i>Vibrio cholerae</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 1052-1059.	0.7	9
51	Regulation of Enteric vapBC Transcription: Induction by VapC Toxin Dimer-Breaking. <i>Nucleic Acids Research</i> , 2012, 40, 4347-4357.	14.5	70
52	Conditional cooperativity in toxin-antitoxin regulation prevents random toxin activation and promotes fast translational recovery. <i>Nucleic Acids Research</i> , 2012, 40, 6424-6434.	14.5	78
53	FtsZ-ZapA-ZapB Interactome of <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2012, 194, 292-302.	2.2	78
54	Bacterial Persistence and Toxin-Antitoxin Loci. <i>Annual Review of Microbiology</i> , 2012, 66, 103-123.	7.3	346

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55	ParA ATPases can move and position DNA and subcellular structures. <i>Current Opinion in Microbiology</i> , 2011, 14, 712-718.	5.1	40
56	Crystal Structure of the VapBC Toxin-Antitoxin Complex from <i>Shigella flexneri</i> Reveals a Hetero-Octameric DNA-Binding Assembly. <i>Journal of Molecular Biology</i> , 2011, 414, 713-722.	4.2	75
57	Bacterial persistence by RNA endonucleases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 13206-13211.	7.1	450
58	Enteric virulence associated protein VapC inhibits translation by cleavage of initiator tRNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 7403-7407.	7.1	234
59	Three new RelE-homologous mRNA interferases of <i>Escherichia coli</i> differentially induced by environmental stresses. <i>Molecular Microbiology</i> , 2010, 75, 333-348.	2.5	205
60	Spatial resolution of two bacterial cell division proteins: ZapA recruits ZapB to the inner face of the Z-ring. <i>Molecular Microbiology</i> , 2010, 76, 1514-1526.	2.5	94
61	What is the mechanism of ParA-mediated DNA movement?. <i>Molecular Microbiology</i> , 2010, 78, 9-12.	2.5	18
62	Pushing and Pulling in Prokaryotic DNA Segregation. <i>Cell</i> , 2010, 141, 927-942.	28.9	281
63	Movement and equi-positioning of plasmids by ParA filament disassembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 19369-19374.	7.1	171
64	HicA of <i>Escherichia coli</i> Defines a Novel Family of Translation-Independent mRNA Interferases in Bacteria and Archaea. <i>Journal of Bacteriology</i> , 2009, 191, 1191-1199.	2.2	218
65	Ectopic production of VapCs from <i>Enterobacteria</i> inhibits translation and activates YoeB mRNA interferase. <i>Molecular Microbiology</i> , 2009, 72, 918-930.	2.5	60
66	RodZ, a new player in bacterial cell morphogenesis. <i>EMBO Journal</i> , 2009, 28, 171-172.	7.8	22
67	The Structural Basis for mRNA Recognition and Cleavage by the Ribosome-Dependent Endonuclease RelE. <i>Cell</i> , 2009, 139, 1084-1095.	28.9	194
68	RelB and RelE of <i>Escherichia coli</i> Form a Tight Complex That Represses Transcription via the Ribbon-Helix Motif in RelB. <i>Journal of Molecular Biology</i> , 2009, 394, 183-196.	4.2	102
69	Novel coiled-coil cell division factor ZapB stimulates Z ring assembly and cell division. <i>Molecular Microbiology</i> , 2008, 68, 720-735.	2.5	113
70	Messenger RNA interferase RelE controls <i>relBE</i> transcription by conditional cooperativity. <i>Molecular Microbiology</i> , 2008, 69, 841-857.	2.5	178
71	Chapter 25 RNA Decay by Messenger RNA Interferases. <i>Methods in Enzymology</i> , 2008, 447, 521-535.	1.0	24
72	Translation affects YoeB and MazF messenger RNA interferase activities by different mechanisms. <i>Nucleic Acids Research</i> , 2008, 36, 6472-6481.	14.5	57

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73	Doc of Prophage P1 Is Inhibited by Its Antitoxin Partner Phd through Fold Complementation. <i>Journal of Biological Chemistry</i> , 2008, 283, 30821-30827.	3.4	103
74	Plasmid segregation: spatial awareness at the molecular level. <i>Journal of Cell Biology</i> , 2007, 179, 813-815.	5.2	10
75	Regulatory Cross-talk in the Double par Locus of Plasmid pB171. <i>Journal of Biological Chemistry</i> , 2007, 282, 3134-3145.	3.4	30
76	Centromere Pairing by a Plasmid-encoded Type I ParB Protein. <i>Journal of Biological Chemistry</i> , 2007, 282, 28216-28225.	3.4	22
77	RNA antitoxins. <i>Current Opinion in Microbiology</i> , 2007, 10, 117-124.	5.1	216
78	Structural and Thermodynamic Characterization of the <i>Escherichia coli</i> RelBE Toxin ⁺ Antitoxin System: A ⁺ Indication for a Functional Role of Differential Stability. <i>Biochemistry</i> , 2007, 46, 12152-12163.	2.5	32
79	Structural analysis of the ParR/parC plasmid partition complex. <i>EMBO Journal</i> , 2007, 26, 4413-4422.	7.8	71
80	Competitive inhibition of natural antisense Sok-RNA interactions activates Hok-mediated cell killing in <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2006, 34, 5915-5922.	14.5	60
81	The chromosomal relBE2 toxin-antitoxin locus of <i>Streptococcus pneumoniae</i> : characterization and use of a bioluminescence resonance energy transfer assay to detect toxin-antitoxin interaction. <i>Molecular Microbiology</i> , 2006, 59, 1280-1296.	2.5	48
82	Regular cellular distribution of plasmids by oscillating and filament-forming ParA ATPase of plasmid pB171. <i>Molecular Microbiology</i> , 2006, 61, 1428-1442.	2.5	108
83	Two hgbA loci in the <i>Vibrio cholerae</i> superintegron encode mRNA cleaving enzymes and can stabilize plasmids. <i>Molecular Microbiology</i> , 2006, 62, 397-411.	2.5	166
84	Actin homolog MreB and RNA polymerase interact and are both required for chromosome segregation in <i>Escherichia coli</i> . <i>Genes and Development</i> , 2006, 20, 113-124.	5.9	115
85	The morphogenetic MreBCD proteins of <i>Escherichia coli</i> form an essential membrane-bound complex. <i>Molecular Microbiology</i> , 2005, 55, 78-89.	2.5	333
86	Partition-associated incompatibility caused by random assortment of pure plasmid clusters. <i>Molecular Microbiology</i> , 2005, 56, 1430-1440.	2.5	32
87	Prokaryotic toxin ⁺ antitoxin stress response loci. <i>Nature Reviews Microbiology</i> , 2005, 3, 371-382.	28.6	950
88	Bacterial DNA segregation by the actin-like MreB protein. <i>Trends in Cell Biology</i> , 2005, 15, 343-345.	7.9	46
89	Plasmid Segregation Mechanisms. <i>Annual Review of Genetics</i> , 2005, 39, 453-479.	7.6	226
90	Toxin-antitoxin loci are highly abundant in free-living but lost from host-associated prokaryotes. <i>Nucleic Acids Research</i> , 2005, 33, 966-976.	14.5	809

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91	Centromere parC of plasmid R1 is curved. <i>Nucleic Acids Research</i> , 2004, 32, 5907-5915.	14.5	13
92	MICROBIOLOGY: Dynamic Instability of a Bacterial Engine. <i>Science</i> , 2004, 306, 987-989.	12.6	4
93	Bacterial mitosis: partitioning protein ParA oscillates in spiral-shaped structures and positions plasmids at mid-cell. <i>Molecular Microbiology</i> , 2004, 52, 385-398.	2.5	128
94	Delayed-relaxed response explained by hyperactivation of RelE. <i>Molecular Microbiology</i> , 2004, 53, 587-597.	2.5	53
95	Overproduction of the Lon protease triggers inhibition of translation in <i>Escherichia coli</i> : involvement of the yefM-yoeB toxin-antitoxin system. <i>Molecular Microbiology</i> , 2004, 51, 1705-1717.	2.5	211
96	Bacterial Mitotic Machineries. <i>Cell</i> , 2004, 116, 359-366.	28.9	113
97	Clustering versus random segregation of plasmids lacking a partitioning function: a plasmid paradox?. <i>Plasmid</i> , 2003, 50, 95-101.	1.4	37
98	RelE toxins from Bacteria and Archaea cleave mRNAs on translating ribosomes, which are rescued by tmRNA. <i>Molecular Microbiology</i> , 2003, 48, 1389-1400.	2.5	314
99	Dysfunctional MreB inhibits chromosome segregation in <i>Escherichia coli</i> . <i>EMBO Journal</i> , 2003, 22, 5283-5292.	7.8	249
100	A Mechanism for ParB-dependent Waves of ParA, a Protein Related to DNA Segregation during Cell Division in Prokaryotes. <i>Journal of Molecular Biology</i> , 2003, 329, 35-43.	4.2	21
101	Toxin-antitoxin Loci as Stress-response-elements: ChpAK/MazF and ChpBK Cleave Translated RNAs and are Counteracted by tmRNA. <i>Journal of Molecular Biology</i> , 2003, 332, 809-819.	4.2	349
102	The Bacterial Toxin RelE Displays Codon-Specific Cleavage of mRNAs in the Ribosomal A Site. <i>Cell</i> , 2003, 112, 131-140.	28.9	500
103	Bacterial Mitosis. <i>Molecular Cell</i> , 2003, 12, 1477-1487.	9.7	192
104	Spot 42 RNA mediates discoordinate expression of the <i>E. coli</i> galactose operon. <i>Genes and Development</i> , 2002, 16, 1696-1706.	5.9	268
105	A pH-jump approach for investigating secondary structure refolding kinetics in RNA. <i>Nucleic Acids Research</i> , 2002, 30, 63e-63.	14.5	19
106	Bacterial toxin RelE induces apoptosis in human cells. <i>FEBS Letters</i> , 2002, 519, 191-194.	2.8	42
107	The antisense RNA of the par locus of pAD1 regulates the expression of a 33-amino-acid toxic peptide by an unusual mechanism. <i>Molecular Microbiology</i> , 2002, 37, 652-660.	2.5	69
108	Rapid induction and reversal of a bacteriostatic condition by controlled expression of toxins and antitoxins. <i>Molecular Microbiology</i> , 2002, 45, 501-510.	2.5	338

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109	Prokaryotic DNA segregation by an actin-like filament. <i>EMBO Journal</i> , 2002, 21, 3119-3127.	7.8	235
110	F-actin-like filaments formed by plasmid segregation protein ParM. <i>EMBO Journal</i> , 2002, 21, 6935-6943.	7.8	229
111	Antisense RNA regulation of the par post-segregational killing system: structural analysis and mechanism of binding of the antisense RNA, RNAI and its target, RNAI. <i>Molecular Microbiology</i> , 2001, 42, 527-537.	2.5	60
112	The double par locus of virulence factor pB171: DNA segregation is correlated with oscillation of ParA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 15078-15083.	7.1	131
113	RelE, a global inhibitor of translation, is activated during nutritional stress. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 14328-14333.	7.1	403
114	Temporal Translational Control by a Metastable RNA Structure. <i>Journal of Biological Chemistry</i> , 2001, 276, 35707-35713.	3.4	32
115	Coupled nucleotide covariations reveal dynamic RNA interaction patterns. <i>Rna</i> , 2000, 6, 1483-1491.	3.5	14
116	Toxin-Antitoxin Modules May Regulate Synthesis of Macromolecules during Nutritional Stress. <i>Journal of Bacteriology</i> , 2000, 182, 561-572.	2.2	266
117	Bacterial Toxin-Antitoxin Gene System as Containment Control in Yeast Cells. <i>Applied and Environmental Microbiology</i> , 2000, 66, 5524-5526.	3.1	67
118	U-turns and regulatory RNAs. <i>Current Opinion in Microbiology</i> , 2000, 3, 159-164.	5.1	64
119	Plasmid and chromosome segregation in prokaryotes. <i>Trends in Microbiology</i> , 2000, 8, 313-320.	7.7	75
120	Plasmid and chromosome partitioning: surprises from phylogeny. <i>Molecular Microbiology</i> , 2000, 37, 455-466.	2.5	394
121	Metastable structures and refolding kinetics in hok mRNA of plasmid R1. <i>Rna</i> , 1999, 5, 1408-1418.	3.5	43
122	Mechanism of DNA segregation in prokaryotes: ParM partitioning protein of plasmid R1 co-localizes with its replicon during the cell cycle. <i>EMBO Journal</i> , 1999, 18, 4076-4084.	7.8	97
123	Ribonuclease III Processing of Coaxially Stacked RNA Helices. <i>Journal of Biological Chemistry</i> , 1999, 274, 26572-26578.	3.4	25
124	Multiple hok genes on the chromosome of <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 1999, 32, 1090-1102.	2.5	160
125	Toxin-antitoxin systems homologous with relBE of <i>Escherichia coli</i> plasmid P307 are ubiquitous in prokaryotes 1 Edited by M. Gottesman. <i>Journal of Molecular Biology</i> , 1999, 285, 1401-1415.	4.2	92
126	Antisense RNA regulation in prokaryotes: rapid RNA/RNA interaction facilitated by a general U-turn loop structure. <i>Journal of Molecular Biology</i> , 1999, 294, 1115-1125.	4.2	154

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127	The <i>Escherichia coli</i> relBE genes belong to a new toxin-antitoxin gene family. <i>Molecular Microbiology</i> , 1998, 29, 1065-1076.	2.5	300
128	Targeting of nucleic acid junctions: addressing to a branch point an oligodeoxynucleotide conjugated with an intercalator. <i>Nucleic Acids Research</i> , 1998, 26, 4919-4924.	14.5	4
129	Mechanism of DNA segregation in prokaryotes: Replicon pairing by parC of plasmid R1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 8550-8555.	7.1	97
130	ANTISENSE RNA-REGULATED PROGRAMMED CELL DEATH. <i>Annual Review of Genetics</i> , 1997, 31, 1-31.	7.6	209
131	Programmed cell death by hok/sok of plasmid R1: Processing at the hok mRNA 3'-end triggers structural rearrangements that allow translation and antisense RNA binding. <i>Journal of Molecular Biology</i> , 1997, 273, 38-51.	4.2	96
132	Programmed cell death by hok/sok of plasmid R1: Coupled nucleotide covariations reveal a phylogenetically conserved folding pathway in the hok family of mRNAs. <i>Journal of Molecular Biology</i> , 1997, 273, 26-37.	4.2	51
133	Partitioning of plasmid R1. The ParM protein exhibits ATPase activity and interacts with the centromere-like ParR-parC complex. <i>Journal of Molecular Biology</i> , 1997, 269, 505-513.	4.2	111
134	Copper-dependent reciprocal transcriptional regulation of methane monooxygenase genes in <i>Methylococcus capsulatus</i> and <i>Methylosinus trichosporium</i> . <i>Molecular Microbiology</i> , 1997, 25, 399-409.	2.5	141
135	Sok antisense RNA from plasmid R1 is functionally inactivated by RNase E and polyadenylated by poly(A) polymerase I. <i>Molecular Microbiology</i> , 1997, 26, 311-320.	2.5	60
136	Plasmid Stabilization by Post-Segregational Killing. , 1997, 19, 49-61.		32
137	Combining the hok/sok, parDE, and pnd postsegregational killer loci to enhance plasmid stability. <i>Applied and Environmental Microbiology</i> , 1997, 63, 1917-1924.	3.1	58
138	The centromere-like parC locus of plasmid R1. <i>Molecular Microbiology</i> , 1996, 20, 581-592.	2.5	40
139	Programmed cell death in bacteria: translational repression by mRNA end pairing. <i>Molecular Microbiology</i> , 1996, 21, 1049-1060.	2.5	59
140	Regulation of bacterial methane oxidation: transcription of the soluble methane mono-oxygenase operon of <i>Methylococcus capsulatus</i> (Bath) is repressed by copper ions. <i>Microbiology (United Kingdom)</i> , 1996, 140, 1011-1017.	10.7	101
141	Programmed cell death in bacteria: proteic plasmid stabilization systems. <i>Molecular Microbiology</i> , 1995, 17, 205-210.	2.5	318
142	Comparison of ccd of F, parDE of RP4, and parD of R1 using a novel conditional replication control system of plasmid R1. <i>Molecular Microbiology</i> , 1995, 17, 211-220.	2.5	84
143	Mechanism of Post-segregational Killing: Secondary Structure Analysis of the Entire Hok mRNA from Plasmid R1 Suggests a Fold-back Structure that Prevents Translation and Antisense RNA Binding. <i>Journal of Molecular Biology</i> , 1995, 247, 859-873.	4.2	48
144	Mechanism of post-segregational killing by hok-homologue pnd of plasmid R483: Two translational control elements in the pnd mRNA. <i>Journal of Molecular Biology</i> , 1995, 249, 270-282.	4.2	16

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145	Partitioning of plasmid R1 Ten direct repeats flanking the parA promoter constitute a centromere-like partition site parC, that expresses incompatibility. <i>Journal of Molecular Biology</i> , 1994, 236, 1289-1298.	4.2	94
146	Partitioning of plasmid R1 The parA operon is autoregulated by parR and its transcription is highly stimulated by a downstream activating element. <i>Journal of Molecular Biology</i> , 1994, 236, 1299-1309.	4.2	60
147	Mechanism of killer gene activation. Antisense RNA-dependent RNase III cleavage ensures rapid turn-over of the stable Hok, SrnB and PndA effector messenger RNAs. <i>Journal of Molecular Biology</i> , 1992, 226, 637-649.	4.2	126
148	Mechanism of post-segregational killing by the hok/sok system of plasmid R1. <i>Journal of Molecular Biology</i> , 1992, 223, 41-54.	4.2	107
149	The rifampicin-inducible genes srn6 from F and pnd from R483 are regulated by antisense RNAs and mediate plasmid maintenance by killing of plasmid-free segregants. <i>Molecular Microbiology</i> , 1991, 5, 1961-1973.	2.5	60
150	The kis and kid genes of the parD maintenance system of plasmid R1 form an operon that is autoregulated at the level of transcription by the co-ordinated action of the Kis and Kid proteins. <i>Molecular Microbiology</i> , 1991, 5, 2685-2693.	2.5	77
151	Mechanism of post-segregational killing by the hok/sok system of plasmid R1: sok antisense RNA regulates formation of a hok mRNA species correlated with killing of plasmid-free cells. <i>Molecular Microbiology</i> , 1990, 4, 1807-1818.	2.5	109
152	The parB (hok/sok) Locus of Plasmid R1: A General Purpose Plasmid Stabilization System. <i>Nature Biotechnology</i> , 1988, 6, 1402-1405.	17.5	79
153	Translational control and differential RNA decay are key elements regulating postsegregational expression of the killer protein encoded by the parB locus of plasmid R1. <i>Journal of Molecular Biology</i> , 1988, 203, 119-129.	4.2	71
154	Effects of genes exerting growth inhibition and plasmid stability on plasmid maintenance. <i>Journal of Bacteriology</i> , 1987, 169, 4646-4650.	2.2	75
155	Genetic analysis of the parB + locus of plasmid R1. <i>Molecular Genetics and Genomics</i> , 1987, 209, 122-128.	2.4	33
156	Partitioning of plasmid R1. <i>Journal of Molecular Biology</i> , 1986, 190, 269-279.	4.2	118
157	Unique type of plasmid maintenance function: postsegregational killing of plasmid-free cells.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1986, 83, 3116-3120.	7.1	607
158	Stable inheritance of plasmid R1 requires two different loci. <i>Journal of Bacteriology</i> , 1985, 161, 292-298.	2.2	175
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