

Didier Mazel

List of Publications by Year in descending order

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125
papers

10,672
citations

30070

54
h-index

34986

98
g-index

159
all docs

159
docs citations

159
times ranked

7785
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrans: agents of bacterial evolution. <i>Nature Reviews Microbiology</i> , 2006, 4, 608-620.	28.6	896
2	Integrans. <i>Annual Review of Genetics</i> , 2010, 44, 141-166.	7.6	442
3	A Distinctive Class of Integron in the <i>Vibrio cholerae</i> Genome. <i>Science</i> , 1998, 280, 605-608.	12.6	361
4	The SOS Response Controls Integron Recombination. <i>Science</i> , 2009, 324, 1034-1034.	12.6	359
5	SOS, the formidable strategy of bacteria against aggressions. <i>FEMS Microbiology Reviews</i> , 2014, 38, 1126-1145.	8.6	312
6	Antibiotic Resistance in the ECOR Collection: Integrans and Identification of a Novel <i>aad</i> Gene. <i>Antimicrobial Agents and Chemotherapy</i> , 2000, 44, 1568-1574.	3.2	304
7	Molecular Analysis of Antibiotic Resistance Gene Clusters in <i>Vibrio cholerae</i> O139 and O1 SXT Constins. <i>Antimicrobial Agents and Chemotherapy</i> , 2001, 45, 2991-3000.	3.2	300
8	Silent Mischief: Bacteriophage Mu Insertions Contaminate Products of <i>Escherichia coli</i> Random Mutagenesis Performed Using Suicidal Transposon Delivery Plasmids Mobilized by Broad-Host-Range RP4 Conjugative Machinery. <i>Journal of Bacteriology</i> , 2010, 192, 6418-6427.	2.2	276
9	A new family of mobilizable suicide plasmids based on broad host range R388 plasmid (IncW) and RP4 plasmid (IncP1±) conjugative machineries and their cognate <i>Escherichia coli</i> host strains. <i>Research in Microbiology</i> , 2005, 156, 245-255.	2.1	270
10	Construction of a <i>Vibrio splendidus</i> Mutant Lacking the Metalloprotease Gene <i>vsm</i> by Use of a Novel Counterselectable Suicide Vector. <i>Applied and Environmental Microbiology</i> , 2007, 73, 777-784.	3.1	240
11	Conjugative DNA Transfer Induces the Bacterial SOS Response and Promotes Antibiotic Resistance Development through Integron Activation. <i>PLoS Genetics</i> , 2010, 6, e1001165.	3.5	228
12	The evolutionary history of chromosomal super-integrans provides an ancestry for multiresistant integrans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 652-657.	7.1	224
13	Bacterial resistance evolution by recruitment of super-integron gene cassettes. <i>Molecular Microbiology</i> , 2002, 43, 1657-1669.	2.5	207
14	Comparative Analysis of Superintegrans: Engineering Extensive Genetic Diversity in the Vibrionaceae. <i>Genome Research</i> , 2003, 13, 428-442.	5.5	199
15	The role of integrans in antibiotic resistance gene capture. <i>International Journal of Medical Microbiology</i> , 2002, 292, 115-125.	3.6	196
16	<i>Vibrio cholerae</i> Triggers SOS and Mutagenesis in Response to a Wide Range of Antibiotics: a Route towards Multiresistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 2438-2441.	3.2	185
17	Adaptive eradication of methionine and cysteine from cyanobacterial light-harvesting proteins. <i>Nature</i> , 1989, 341, 245-248.	27.8	173
18	Inverse Correlation between Promoter Strength and Excision Activity in Class 1 Integrans. <i>PLoS Genetics</i> , 2010, 6, e1000793.	3.5	166

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19	Chromosomal toxin-antitoxin loci can diminish large-scale genome reductions in the absence of selection. <i>Molecular Microbiology</i> , 2007, 63, 1588-1605.	2.5	162
20	Folded DNA in Action: Hairpin Formation and Biological Functions in Prokaryotes. <i>Microbiology and Molecular Biology Reviews</i> , 2010, 74, 570-588.	6.6	161
21	Multicopy plasmids potentiate the evolution of antibiotic resistance in bacteria. <i>Nature Ecology and Evolution</i> , 2017, 1, 10.	7.8	147
22	The Single-Stranded Genome of Phage CTX Is the Form Used for Integration into the Genome of <i>Vibrio cholerae</i> . <i>Molecular Cell</i> , 2005, 19, 559-566.	9.7	146
23	Genome Engineering in <i>Vibrio cholerae</i> : A Feasible Approach to Address Biological Issues. <i>PLoS Genetics</i> , 2012, 8, e1002472.	3.5	136
24	The emergence of <i>Vibrio</i> pathogens in Europe: ecology, evolution, and pathogenesis (Paris, 11 th -12 th) Tj ETQq0 0,0,rgBT /Overlock 10	3.5	136
25	Green light induces transcription of the phycoerythrin operon in the cyanobacterium <i>Calothrix</i> 7601. <i>Nucleic Acids Research</i> , 1986, 14, 8279-8290.	14.5	132
26	An end-joining repair mechanism in <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 2141-2146.	7.1	132
27	Highly repetitive DNA sequences in cyanobacterial genomes. <i>Journal of Bacteriology</i> , 1990, 172, 2755-2761.	2.2	131
28	Structural basis for broad DNA-specificity in integron recombination. <i>Nature</i> , 2006, 440, 1157-1162.	27.8	131
29	Integrans: natural tools for bacterial genome evolution. <i>Current Opinion in Microbiology</i> , 2001, 4, 565-569.	5.1	124
30	Integron cassette insertion: a recombination process involving a folded single strand substrate. <i>EMBO Journal</i> , 2005, 24, 4356-4367.	7.8	122
31	A checkpoint control orchestrates the replication of the two chromosomes of <i>Vibrio cholerae</i> . <i>Science Advances</i> , 2016, 2, e1501914.	10.3	122
32	Integron-Associated Antibiotic Resistance and Phylogenetic Grouping of <i>Escherichia coli</i> Isolates from Healthy Subjects Free of Recent Antibiotic Exposure. <i>Antimicrobial Agents and Chemotherapy</i> , 2005, 49, 3062-3065.	3.2	115
33	Super-integrans. <i>Research in Microbiology</i> , 1999, 150, 641-651.	2.1	114
34	Evidence for Induction of Integron-Based Antibiotic Resistance by the SOS Response in a Clinical Setting. <i>PLoS Pathogens</i> , 2012, 8, e1002778.	4.7	109
35	Engineered toxin-intein antimicrobials can selectively target and kill antibiotic-resistant bacteria in mixed populations. <i>Nature Biotechnology</i> , 2019, 37, 755-760.	17.5	107
36	Prevalence of SOS-mediated control of integron integrase expression as an adaptive trait of chromosomal and mobile integrans. <i>Mobile DNA</i> , 2011, 2, 6.	3.6	104

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37	Resistance gene capture. <i>Current Opinion in Microbiology</i> , 1999, 2, 483-488.	5.1	102
38	<i>Vibrio splendidus</i> as the Source of Plasmid-Mediated QnrS-Like Quinolone Resistance Determinants. <i>Antimicrobial Agents and Chemotherapy</i> , 2007, 51, 2650-2651.	3.2	100
39	Photoregulation of gene expression in the filamentous cyanobacterium <i>Calothrix</i> sp. PCC 7601: light-harvesting complexes and cell differentiation. <i>Photosynthesis Research</i> , 1988, 18, 99-132.	2.9	99
40	Genome sequence of <i>Vibrio splendidus</i> : an abundant planctonic marine species with a large genotypic diversity. <i>Environmental Microbiology</i> , 2009, 11, 1959-1970.	3.8	98
41	The major outer membrane protein OmpU of <i>Vibrio splendidus</i> contributes to host antimicrobial peptide resistance and is required for virulence in the oyster <i>Crassostrea gigas</i> . <i>Environmental Microbiology</i> , 2010, 12, 951-963.	3.8	98
42	The Integron: Adaptation On Demand. <i>Microbiology Spectrum</i> , 2015, 3, MDNA3-0019-2014.	3.0	95
43	Molecular cloning and nucleotide sequence of a developmentally regulated gene from the cyanobacterium <i>Calothrix</i> PCC 7601: a gas vesicle protein gene. <i>Nucleic Acids Research</i> , 1985, 13, 7223-7236.	14.5	88
44	A multigene family in <i>Calothrix</i> sp. PCC 7601 encodes phycocyanin, the major component of the cyanobacterial light-harvesting antenna. <i>Molecular Genetics and Genomics</i> , 1988, 211, 296-304.	2.4	88
45	Erythromycin Esterase Gene <i>ere(A)</i> Is Located in a Functional Gene Cassette in an Unusual Class 2 Integron. <i>Antimicrobial Agents and Chemotherapy</i> , 2003, 47, 3326-3331.	3.2	88
46	Comparative Study of Class 1 Integron and <i>Vibrio cholerae</i> Superintegron Integrase Activities. <i>Journal of Bacteriology</i> , 2005, 187, 1740-1750.	2.2	88
47	<i>RpoS</i> Plays a Central Role in the SOS Induction by Sub-Lethal Aminoglycoside Concentrations in <i>Vibrio cholerae</i> . <i>PLoS Genetics</i> , 2013, 9, e1003421.	3.5	86
48	Metalloprotease <i>Vsm</i> Is the Major Determinant of Toxicity for Extracellular Products of <i>Vibrio splendidus</i> . <i>Applied and Environmental Microbiology</i> , 2008, 74, 7108-7117.	3.1	85
49	A role for <i>cpeYZ</i> in cyanobacterial phycoerythrin biosynthesis. <i>Journal of Bacteriology</i> , 1997, 179, 998-1006.	2.2	84
50	Comprehensive Functional Analysis of the 18 <i>Vibrio cholerae</i> N16961 Toxin-Antitoxin Systems Substantiates Their Role in Stabilizing the Superintegron. <i>Journal of Bacteriology</i> , 2015, 197, 2150-2159.	2.2	78
51	Connecting Environment and Genome Plasticity in the Characterization of Transformation-Induced SOS Regulation and Carbon Catabolite Control of the <i>Vibrio cholerae</i> Integron Integrase. <i>Journal of Bacteriology</i> , 2012, 194, 1659-1667.	2.2	71
52	<i>Vibrio aestuarianus</i> zinc metalloprotease causes lethality in the Pacific oyster <i>Crassostrea gigas</i> and impairs the host cellular immune defenses. <i>Fish and Shellfish Immunology</i> , 2010, 29, 753-758.	3.6	69
53	A survey of polypeptide deformylase function throughout the eubacterial lineage. <i>Journal of Molecular Biology</i> , 1997, 266, 939-949.	4.2	60
54	Identification of key structural determinants of the <i>IntI1</i> integron integrase that influence <i>attC</i> — <i>attI1</i> recombination efficiency. <i>Nucleic Acids Research</i> , 2007, 35, 6475-6489.	14.5	58

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55	A single regulatory gene is sufficient to alter <i>Vibrio aestuarianus</i> pathogenicity in oysters. <i>Environmental Microbiology</i> , 2015, 17, 4189-4199.	3.8	58
56	Structural Features of Single-Stranded Integron Cassette attC Sites and Their Role in Strand Selection. <i>PLoS Genetics</i> , 2009, 5, e1000632.	3.5	56
57	Functional Interactions between Coexisting Toxin-Antitoxin Systems of the ccd Family in <i>Escherichia coli</i> O157:H7. <i>Journal of Bacteriology</i> , 2007, 189, 2712-2719.	2.2	55
58	High-Level Gene Cassette Transcription Prevents Integrase Expression in Class 1 Integrons. <i>Journal of Bacteriology</i> , 2011, 193, 5675-5682.	2.2	55
59	Characterization of the <i>phd-doc</i> and <i>ccd</i> Toxin-Antitoxin Cassettes from <i>Vibrio</i> Superintegrons. <i>Journal of Bacteriology</i> , 2013, 195, 2270-2283.	2.2	46
60	Management of multipartite genomes: the <i>Vibrio cholerae</i> model. <i>Current Opinion in Microbiology</i> , 2014, 22, 120-126.	5.1	45
61	Translation regulation of integrons gene cassette expression by the attC sites. <i>Molecular Microbiology</i> , 2009, 72, 1475-1486.	2.5	44
62	Replicative resolution of integron cassette insertion. <i>Nucleic Acids Research</i> , 2012, 40, 8361-8370.	14.5	39
63	Fuse or die: how to survive the loss of Dam in <i>Vibrio cholerae</i> . <i>Molecular Microbiology</i> , 2014, 91, 665-678.	2.5	39
64	Efficiency of integron cassette insertion in correct orientation is ensured by the interplay of the three unpaired features of attC recombination sites. <i>Nucleic Acids Research</i> , 2016, 44, 7792-7803.	14.5	38
65	Construction of an improved RP4 (RK2)-based conjugative system. <i>Research in Microbiology</i> , 2008, 159, 545-549.	2.1	37
66	Synonymous Genes Explore Different Evolutionary Landscapes. <i>PLoS Genetics</i> , 2008, 4, e1000256.	3.5	36
67	Genomic Location of the Major Ribosomal Protein Gene Locus Determines <i>Vibrio cholerae</i> Global Growth and Infectivity. <i>PLoS Genetics</i> , 2015, 11, e1005156.	3.5	36
68	Real-time tracking of bacterial membrane vesicles reveals enhanced membrane traffic upon antibiotic exposure. <i>Science Advances</i> , 2021, 7, .	10.3	36
69	The synthetic integron: an in vivo genetic shuffling device. <i>Nucleic Acids Research</i> , 2010, 38, e153-e153.	14.5	35
70	Replicate Once Per Cell Cycle: Replication Control of Secondary Chromosomes. <i>Frontiers in Microbiology</i> , 2018, 9, 1833.	3.5	35
71	Multiple Pathways of Genome Plasticity Leading to Development of Antibiotic Resistance. <i>Antibiotics</i> , 2013, 2, 288-315.	3.7	34
72	Expansion of the SOS regulon of <i>Vibrio cholerae</i> through extensive transcriptome analysis and experimental validation. <i>BMC Genomics</i> , 2018, 19, 373.	2.8	34

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73	Cellular pathways controlling integron cassette site folding. EMBO Journal, 2010, 29, 2623-2634.	7.8	32
74	Identification of genes involved in low aminoglycoside-induced SOS response in <i>Vibrio cholerae</i> : a role for transcription stalling and Mfd helicase. Nucleic Acids Research, 2014, 42, 2366-2379.	14.5	32
75	Virulence of an emerging pathogenic lineage of <i>Vibrio nigripulchritudo</i> is dependent on two plasmids. Environmental Microbiology, 2011, 13, 296-306.	3.8	31
76	A Natural System of Chromosome Transfer in <i>Yersinia pseudotuberculosis</i> . PLoS Genetics, 2012, 8, e1002529.	3.5	31
77	Comparative genomics of pathogenic lineages of <i>Vibrio nigripulchritudo</i> identifies virulence-associated traits. ISME Journal, 2013, 7, 1985-1996.	9.8	30
78	Differences in Integron Cassette Excision Dynamics Shape a Trade-Off between Evolvability and Genetic Capacitance. MBio, 2017, 8, .	4.1	27
79	Sleeping ribosomes: Bacterial signaling triggers RaiA mediated persistence to aminoglycosides. IScience, 2021, 24, 103128.	4.1	25
80	Complete nucleotide sequence of the red-light specific set of phycocyanin genes from the cyanobacterium <i>Calothrix</i> PCC 7601. Nucleic Acids Research, 1988, 16, 1626-1626.	14.5	24
81	Unmasking the ancestral activity of integron integrases reveals a smooth evolutionary transition during functional innovation. Nature Communications, 2016, 7, 10937.	12.8	24
82	Dynamic stepwise opening of integron attC DNA hairpins by SSB prevents toxicity and ensures functionality. Nucleic Acids Research, 2017, 45, 10555-10563.	14.5	23
83	Correlation between Detection of a Plasmid and High-Level Virulence of <i>Vibrio nigripulchritudo</i> , a Pathogen of the Shrimp <i>Litopenaeus stylirostris</i> . Applied and Environmental Microbiology, 2008, 74, 3038-3047.	3.1	21
84	The relaxed requirements of the integron cleavage site allow predictable changes in integron target specificity. Nucleic Acids Research, 2010, 38, 559-569.	14.5	21
85	A new family of conditional replicating plasmids and their cognate <i>Escherichia coli</i> host strains. Research in Microbiology, 2004, 155, 455-461.	2.1	19
86	Gene capture in <i>Vibrio cholerae</i> . Trends in Microbiology, 1999, 7, 93-95.	7.7	18
87	Structural heterogeneity of attC integron recombination sites revealed by optical tweezers. Nucleic Acids Research, 2019, 47, 1861-1870.	14.5	18
88	Metagenomic strategies identify diverse integron integrase and antibiotic resistance genes in the Antarctic environment. MicrobiologyOpen, 2021, 10, e1219.	3.0	18
89	<i>Vibrio</i> 2005: the First International Conference on the Biology of Vibrios. Journal of Bacteriology, 2006, 188, 4592-4596.	2.2	17
90	Delineation of the recombination sites necessary for integration of pathogenicity islands II and III into the <i>Escherichia coli</i> 536 chromosome. Molecular Microbiology, 2008, 68, 139-151.	2.5	17

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91	The Integron Integrase Efficiently Prevents the Melting Effect of Escherichia coli Single-Stranded DNA-Binding Protein on Folded <i>attC</i> Sites. Journal of Bacteriology, 2014, 196, 762-771.	2.2	17
92	RadD Contributes to R-Loop Avoidance in Sub-MIC Tobramycin. MBio, 2019, 10, .	4.1	17
93	Enhanced emergence of antibiotic-resistant pathogenic bacteria after in vitro induction with cancer chemotherapy drugs. Journal of Antimicrobial Chemotherapy, 2019, 74, 1572-1577.	3.0	17
94	Structure-specific DNA recombination sites: Design, validation, and machine learning-based refinement. Science Advances, 2020, 6, eaay2922.	10.3	17
95	Cassette recruitment in the chromosomal Integron of <i>Vibrio cholerae</i> . Nucleic Acids Research, 2021, 49, 5654-5670.	14.5	17
96	<i>Vibrio cholerae</i> chromosome 2 copy number is controlled by the methylation-independent binding of its monomeric initiator to the chromosome 1 <i>crtS</i> site. Nucleic Acids Research, 2018, 46, 10145-10156.	14.5	16
97	The Proximity of Ribosomal Protein Genes to <i>oriC</i> Enhances <i>Vibrio cholerae</i> Fitness in the Absence of Multifork Replication. MBio, 2017, 8, .	4.1	14
98	The Superintegron Integrase and the Cassette Promoters Are Co-Regulated in <i>Vibrio cholerae</i> . PLoS ONE, 2014, 9, e91194.	2.5	14
99	Integrans as Adaptive Devices. Grand Challenges in Biology and Biotechnology, 2018, , 199-239.	2.4	11
100	Deficiency in cytosine DNA methylation leads to high chaperonin expression and tolerance to aminoglycosides in <i>Vibrio cholerae</i> . PLoS Genetics, 2021, 17, e1009748.	3.5	11
101	Macromolecular crowding links ribosomal protein gene dosage to growth rate in <i>Vibrio cholerae</i> . BMC Biology, 2020, 18, 43.	3.8	10
102	Unbridled Integrans: A Matter of Host Factors. Cells, 2022, 11, 925.	4.1	10
103	Integron Identification in Bacterial Genomes and Cassette Recombination Assays. Methods in Molecular Biology, 2020, 2075, 189-208.	0.9	9
104	Cellular pathways controlling integron cassette site folding. EMBO Journal, 2010, 29, 3745-3745.	7.8	8
105	The coordinated replication of <i>Vibrio cholerae</i> 's two chromosomes required the acquisition of a unique domain by the RctB initiator. Nucleic Acids Research, 2021, 49, 11119-11133.	14.5	8
106	Genomic Plasticity of <i>Vibrio cholerae</i> . International Microbiology, 2017, 20, 138-148.	2.4	8
107	Interplay between Sublethal Aminoglycosides and Quorum Sensing: Consequences on Survival in <i>V. cholerae</i> . Cells, 2021, 10, 3227.	4.1	8
108	The Integron: Adaptation On Demand. , 0, , 139-161.		7

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109	Primary and promiscuous functions coexist during evolutionary innovation through whole protein domain acquisitions. <i>ELife</i> , 2020, 9, .	6.0	7
110	Shuffling of DNA Cassettes in a Synthetic Integron. <i>Methods in Molecular Biology</i> , 2013, 1073, 169-174.	0.9	5
111	Bacteria from Fildes Peninsula carry class 1 integrons and antibiotic resistance genes in conjugative plasmids. <i>Antarctic Science</i> , 2018, 30, 22-28.	0.9	5
112	The Adaptive Genetic Arsenal of Pathogenic <i>Vibrio</i> Species: the Role of Integrons. , 0, , 95-111.		5
113	Gene capture in <i>Vibrio cholerae</i> : Response. <i>Trends in Microbiology</i> , 1999, 7, 95.	7.7	4
114	Antibiotics as physiological stress inducers and bacterial response to the challenge. <i>Current Opinion in Microbiology</i> , 2012, 15, 553-554.	5.1	4
115	An att site-based recombination reporter system for genome engineering and synthetic DNA assembly. <i>BMC Biotechnology</i> , 2017, 17, 62.	3.3	4
116	Recoding of synonymous genes to expand evolutionary landscapes requires control of secondary structure affecting translation. <i>Biotechnology and Bioengineering</i> , 2018, 115, 184-191.	3.3	4
117	A qnr-plasmid allows aminoglycosides to induce SOS in <i>Escherichia coli</i> . <i>ELife</i> , 2022, 11, .	6.0	4
118	The Evolution of Antibiotic Resistance. , 0, , 221-241.		3
119	Influence of very short patch mismatch repair on SOS inducing lesions after aminoglycoside treatment in <i>Escherichia coli</i> . <i>Research in Microbiology</i> , 2014, 165, 476-480.	2.1	2
120	Tn5469 Mutagenesis of Chromatic Adaptation Genes in <i>Calothrix</i> sp. strain PCC 7601. , 1995, , 2393-2396.		2
121	Séquences d'ADN mobiles altérant l'expression des gènes des phycobiliprotéines chez <i>Calothrix</i> 7601. <i>Bulletin De La Société Botanique De France Actualités Botaniques</i> , 1989, 136, 165-167.	0.0	0
122	DNA Secondary Structure Formation in Bacterial Gene Capture Systems at Single-Molecule Resolution. <i>Biophysical Journal</i> , 2014, 106, 272a-273a.	0.5	0
123	Evolution of Integrons and Evolution of Antibiotic Resistance. , 2014, , 139-154.		0
124	Photoregulation of gene expression in the filamentous cyanobacterium <i>Calothrix</i> sp. PCC 7601: light-harvesting complexes and cell differentiation. , 1988, , 195-228.		0
125	Cholera-causing bacteria have defences that degrade plasmid invaders. <i>Nature</i> , 2022, 604, 250-252.	27.8	0