

Gilles Vergnaud

List of Publications by Year in descending order

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162
papers

13,299
citations

29994

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111
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168
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168
docs citations

168
times ranked

11288
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic diversity of <i>Francisella tularensis</i> subsp. <i>holarctica</i> in Kazakhstan. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009419.	1.3	5
2	Whole-Genome Sequence of a <i>Brucella pinnipedialis</i> Sequence Type 54 Strain Isolated from a Hooded Seal (<i>Cystophora cristata</i>) from the North Atlantic Ocean, Norway. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	2
3	<i>Bacillus anthracis</i> Phylogeography: New Clues From Kazakhstan, Central Asia. <i>Frontiers in Microbiology</i> , 2021, 12, 778225.	1.5	6
4	CoxBase: an Online Platform for Epidemiological Surveillance, Visualization, Analysis, and Typing of <i>Coxiella burnetii</i> Genomic Sequences. <i>MSystems</i> , 2021, 6, e0040321.	1.7	5
5	CRISPRCasdb a successor of CRISPRdb containing CRISPR arrays and <i>cas</i> genes from complete genome sequences, and tools to download and query lists of repeats and spacers. <i>Nucleic Acids Research</i> , 2020, 48, D535-D544.	6.5	88
6	Characterization of sixteen <i>Achromobacter xylosoxidans</i> phages from Abidjan, Côte d'Ivoire, isolated on a single clinical strain. <i>Archives of Virology</i> , 2020, 165, 725-730.	0.9	8
7	Draft Genome Sequences of Three <i>Pasteurella multocida</i> Strains Isolated from Domestic Animals in Kazakhstan. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	0
8	Draft Genome Sequence of the Strain <i>Francisella tularensis</i> subsp. <i>mediasiatica</i> 240, Isolated in Kazakhstan. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
9	Draft Genome Sequence of <i>Moraxella bovoculi</i> Strain KZ-1, Isolated from Cattle in North Kazakhstan. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	3
10	A Review of Arguments for the Existence of Latent Infections of <i>Bacillus anthracis</i> , and Research Needed to Understand Their Role in the Outbreaks of Anthrax. <i>Microorganisms</i> , 2020, 8, 800.	1.6	4
11	Omp2b Porin Alteration in the Course of Evolution of <i>Brucella</i> spp.. <i>Frontiers in Microbiology</i> , 2020, 11, 284.	1.5	1
12	The Basis for Natural Multiresistance to Phage in <i>Pseudomonas aeruginosa</i> . <i>Antibiotics</i> , 2020, 9, 339.	1.5	12
13	<i>Bacillus anthracis</i> evolutionary history: taking advantage of the topology of the phylogenetic tree and of human history to propose dating points. <i>Erciyes Medical Journal</i> , 2020, , .	0.0	6
14	Retrospective Analysis of the Relationship between Two Anthrax Outbreaks in Kazakhstan Based on Genomic Data. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
15	Genetic Diversity of <i>Brucella melitensis</i> in Kazakhstan in Relation to World-Wide Diversity. <i>Frontiers in Microbiology</i> , 2019, 10, 1897.	1.5	21
16	Insights from <i>Bacillus anthracis</i> strains isolated from permafrost in the tundra zone of Russia. <i>PLoS ONE</i> , 2019, 14, e0209140.	1.1	44
17	Molecular characterization of <i>Brucella</i> species from Zimbabwe. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007311.	1.3	34
18	Investigation of <i>Pseudomonas aeruginosa</i> strain Pcyll-10 variants resisting infection by N4-like phage Ab09 in search for genes involved in phage adsorption. <i>PLoS ONE</i> , 2019, 14, e0215456.	1.1	20

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19	And Then There Were Three: Discovering the Role of CRISPRs. <i>CRISPR Journal</i> , 2019, 2, 359-361.	1.4	0
20	Complete Genome Sequences of Five <i>Acinetobacter baumannii</i> Phages from Abidjan, Côte d'Ivoire. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	6
21	Associations between <i>Mycobacterium tuberculosis</i> Beijing genotype and drug resistance to four first-line drugs: a survey in China. <i>Frontiers of Medicine</i> , 2018, 12, 92-97.	1.5	4
22	CRISPRCasFinder, an update of CRISPRFinder, includes a portable version, enhanced performance and integrates search for Cas proteins. <i>Nucleic Acids Research</i> , 2018, 46, W246-W251.	6.5	985
23	Genotypic Expansion Within the Population Structure of Classical <i>Brucella</i> Species Revealed by MLVA16 Typing of 1404 <i>Brucella</i> Isolates From Different Animal and Geographic Origins, 1974-2006. <i>Frontiers in Microbiology</i> , 2018, 9, 1545.	1.5	57
24	Transposition Behavior Revealed by High-Resolution Description of <i>Pseudomonas Aeruginosa</i> Saltovirus Integration Sites. <i>Viruses</i> , 2018, 10, 245.	1.5	4
25	<i>Brucella</i> spp. of amphibians comprise genomically diverse motile strains competent for replication in macrophages and survival in mammalian hosts. <i>Scientific Reports</i> , 2017, 7, 44420.	1.6	96
26	A carrier state is established in <i>Pseudomonas aeruginosa</i> by phage LeviOr01, a newly isolated ssRNA levivirus. <i>Journal of General Virology</i> , 2017, 98, 2181-2189.	1.3	26
27	Large Preferred Region for Packaging of Bacterial DNA by phiC725A, a Novel <i>Pseudomonas aeruginosa</i> F116-Like Bacteriophage. <i>PLoS ONE</i> , 2017, 12, e0169684.	1.1	10
28	Russian isolates enlarge the known geographic diversity of <i>Francisella tularensis</i> subsp. <i>mediasiatica</i> . <i>PLoS ONE</i> , 2017, 12, e0183714.	1.1	28
29	Complete Genome Sequences of <i>Pseudomonas aeruginosa</i> Phages vB_PaeP_PcyII-10_P3P1 and vB_PaeM_PcyII-10_PII10A. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
30	<i>Brucella vulpis</i> sp. nov., isolated from mandibular lymph nodes of red foxes (<i>Vulpes vulpes</i>). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 2090-2098.	0.8	155
31	Pseudolysogeny and sequential mutations build multiresistance to virulent bacteriophages in <i>Pseudomonas aeruginosa</i> . <i>Microbiology (United Kingdom)</i> , 2016, 162, 748-763.	0.7	53
32	Comparison of French and Worldwide <i>Bacillus anthracis</i> Strains Favors a Recent, Post-Columbian Origin of the Predominant North-American Clade. <i>PLoS ONE</i> , 2016, 11, e0146216.	1.1	31
33	Investigation of a Large Collection of <i>Pseudomonas aeruginosa</i> Bacteriophages Collected from a Single Environmental Source in Abidjan, Côte d'Ivoire. <i>PLoS ONE</i> , 2015, 10, e0130548.	1.1	62
34	A novel multiple locus variable number of tandem repeat (VNTR) analysis (MLVA) method for <i>Propionibacterium acnes</i> . <i>Infection, Genetics and Evolution</i> , 2015, 33, 233-241.	1.0	5
35	Development of a Multiple-Locus Variable-Number Tandem-Repeat Typing Scheme for Genetic Fingerprinting of <i>Burkholderia cenocepacia</i> and Application to Nationwide Epidemiological Analysis. <i>Journal of Clinical Microbiology</i> , 2015, 53, 398-409.	1.8	6
36	Generation of a CRISPR database for <i>Yersinia pseudotuberculosis</i> complex and role of CRISPR-based immunity in conjugation. <i>Environmental Microbiology</i> , 2015, 17, 4306-4321.	1.8	24

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37	Molecular Epidemiology of <i>Mycoplasma pneumoniae</i> : Genotyping Using Single Nucleotide Polymorphisms and SNaPshot Technology. <i>Journal of Clinical Microbiology</i> , 2015, 53, 3182-3194.	1.8	27
38	Development of a Multiple Loci Variable Number of Tandem Repeats Analysis (MLVA) to Unravel the Intra-Pathovar Structure of <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> Populations Worldwide. <i>PLoS ONE</i> , 2015, 10, e0135310.	1.1	46
39	Genotyping of French <i>Bacillus anthracis</i> Strains Based on 31-Loci Multi Locus VNTR Analysis: Epidemiology, Marker Evaluation, and Update of the Internet Genotype Database. <i>PLoS ONE</i> , 2014, 9, e95131.	1.1	38
40	Progenitor <i>Mycobacterium canettii</i> Clone Responsible for Lymph Node Tuberculosis Epidemic, Djibouti. <i>Emerging Infectious Diseases</i> , 2014, 20, 21-28.	2.0	62
41	<i>Staphylococcus aureus</i> from 152 cases of bovine, ovine and caprine mastitis investigated by Multiple-locus variable number of tandem repeat analysis (MLVA). <i>Veterinary Research</i> , 2014, 45, 97.	1.1	29
42	<i>Yersinia pseudotuberculosis</i> ST42 (O:1) Strain Misidentified as <i>Yersinia pestis</i> by Mass Spectrometry Analysis. <i>Genome Announcements</i> , 2014, 2, .	0.8	11
43	<i>Brucella papionis</i> sp. nov., isolated from baboons (<i>Papio</i> spp.). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 4120-4128.	0.8	171
44	High-throughput sequencing of <i>Bacillus anthracis</i> in France: investigating genome diversity and population structure using whole-genome SNP discovery. <i>BMC Genomics</i> , 2014, 15, 288.	1.2	50
45	Diversity of β -lactam resistance mechanisms in cystic fibrosis isolates of <i>Pseudomonas aeruginosa</i> : a French multicentre study. <i>Journal of Antimicrobial Chemotherapy</i> , 2013, 68, 1763-1771.	1.3	59
46	Draft Genome Sequences of Two <i>Yersinia pseudotuberculosis</i> ST43 (O:1b) Strains, B-7194 and B-7195. <i>Genome Announcements</i> , 2013, 1, .	0.8	0
47	Draft Genome Sequences of Five <i>Yersinia pseudotuberculosis</i> ST19 Isolates and One Isolate Variant. <i>Genome Announcements</i> , 2013, 1, e0012213.	0.8	3
48	The Susceptibility of <i>Pseudomonas aeruginosa</i> Strains from Cystic Fibrosis Patients to Bacteriophages. <i>PLoS ONE</i> , 2013, 8, e60575.	1.1	73
49	Molecular characterisation of <i>Brucella</i> species. <i>OIE Revue Scientifique Et Technique</i> , 2013, 32, 149-162.	0.5	89
50	Use of multilocus variable-number tandem repeat analysis (MLVA) in eight European countries, 2012. <i>Eurosurveillance</i> , 2013, 18, 20385.	3.9	63
51	Intraspecies Biodiversity of the Genetically Homologous Species <i>Brucella microti</i> . <i>Applied and Environmental Microbiology</i> , 2012, 78, 1534-1543.	1.4	48
52	Rapid Identification of International Multidrug-Resistant <i>Pseudomonas aeruginosa</i> Clones by Multiple-Locus Variable Number of Tandem Repeats Analysis and Investigation of Their Susceptibility to Lytic Bacteriophages. <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 6175-6180.	1.4	27
53	MLVA16 Typing of Portuguese Human and Animal <i>Brucella melitensis</i> and <i>Brucella abortus</i> Isolates. <i>PLoS ONE</i> , 2012, 7, e42514.	1.1	52
54	A new highly discriminatory multiplex capillary-based MLVA assay as a tool for the epidemiological survey of <i>Pseudomonas aeruginosa</i> in cystic fibrosis patients. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2012, 31, 2247-2256.	1.3	30

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55	Diversity of <i>Acinetobacter baumannii</i> in Four French Military Hospitals, as Assessed by Multiple Locus Variable Number of Tandem Repeats Analysis. <i>PLoS ONE</i> , 2012, 7, e44597.	1.1	63
56	<i>Yersinia pestis</i> Lineages in Mongolia. <i>PLoS ONE</i> , 2012, 7, e30624.	1.1	64
57	High Throughput Multiple Locus Variable Number of Tandem Repeat Analysis (MLVA) of <i>Staphylococcus aureus</i> from Human, Animal and Food Sources. <i>PLoS ONE</i> , 2012, 7, e33967.	1.1	41
58	Significance of the Identification in the Horn of Africa of an Exceptionally Deep Branching <i>Mycobacterium tuberculosis</i> Clade. <i>PLoS ONE</i> , 2012, 7, e52841.	1.1	109
59	Épidémiologie de <i>Pseudomonas aeruginosa</i> chez les patients mucoviscidosiques. <i>Revue Francophone Des Laboratoires</i> , 2011, 2011, 41-48.	0.0	0
60	Investigation on <i>Mycobacterium tuberculosis</i> Diversity in China and the Origin of the Beijing Clade. <i>PLoS ONE</i> , 2011, 6, e29190.	1.1	35
61	Molecular epidemiology of human and animal tuberculosis in Ibadan, Southwestern Nigeria. <i>Veterinary Microbiology</i> , 2011, 151, 139-147.	0.8	59
62	High-Throughput Typing Method To Identify a Non-Outbreak-Involved <i>Legionella pneumophila</i> Strain Colonizing the Entire Water Supply System in the Town of Rennes, France. <i>Applied and Environmental Microbiology</i> , 2011, 77, 6899-6907.	1.4	26
63	Investigation of the population structure of <i>Legionella pneumophila</i> by analysis of tandem repeat copy number and internal sequence variation. <i>Microbiology (United Kingdom)</i> , 2011, 157, 2582-2594.	0.7	19
64	Identification of Variable-Number Tandem-Repeat (VNTR) Sequences in <i>Acinetobacter baumannii</i> and Interlaboratory Validation of an Optimized Multiple-Locus VNTR Analysis Typing Scheme. <i>Journal of Clinical Microbiology</i> , 2011, 49, 539-548.	1.8	71
65	Multiple-Locus Variable-Number Tandem-Repeat Analysis Genotyping of Human <i>Brucella</i> Isolates from Turkey. <i>Journal of Clinical Microbiology</i> , 2011, 49, 3276-3283.	1.8	69
66	Characterization of Genetic Diversity of <i>Bacillus anthracis</i> in France by Using High-Resolution Melting Assays and Multilocus Variable-Number Tandem-Repeat Analysis. <i>Journal of Clinical Microbiology</i> , 2011, 49, 4286-4292.	1.8	20
67	<i>Clostridium botulinum</i> Group I Strain Genotyping by 15-Locus Multilocus Variable-Number Tandem-Repeat Analysis. <i>Journal of Clinical Microbiology</i> , 2011, 49, 4252-4263.	1.8	28
68	Longitudinal survey of <i>Staphylococcus aureus</i> in cystic fibrosis patients using a multiple-locus variable-number of tandem-repeats analysis method. <i>BMC Microbiology</i> , 2010, 10, 24.	1.3	19
69	Molecular characteristics of <i>Mycobacterium canettii</i> the smooth <i>Mycobacterium tuberculosis</i> bacilli. <i>Infection, Genetics and Evolution</i> , 2010, 10, 1165-1173.	1.0	61
70	<i>Brucella inopinata</i> sp. nov., isolated from a breast implant infection. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2010, 60, 801-808.	0.8	276
71	Improved Multiple-Locus Variable-Number Tandem-Repeat Assay for <i>Staphylococcus aureus</i> Genotyping, Providing a Highly Informative Technique Together with Strong Phylogenetic Value. <i>Journal of Clinical Microbiology</i> , 2009, 47, 3121-3128.	1.8	44
72	Comparison of two commercial assays for the characterization of <i>rpoB</i> mutations in <i>Mycobacterium tuberculosis</i> and description of new mutations conferring weak resistance to rifampicin. <i>Journal of Antimicrobial Chemotherapy</i> , 2009, 64, 259-262.	1.3	25

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73	MLVA-16 typing of 295 marine mammal <i>Brucella</i> isolates from different animal and geographic origins identifies 7 major groups within <i>Brucella ceti</i> and <i>Brucella pinnipedialis</i> . <i>BMC Microbiology</i> , 2009, 9, 145.	1.3	119
74	A rapid allele variant discrimination method for <i>Yersinia pestis</i> strains based on high-resolution melting curve analysis. <i>Diagnostic Microbiology and Infectious Disease</i> , 2009, 65, 7-13.	0.8	10
75	Validation of ten new polymorphic tandem repeat loci and application to the MLVA typing of <i>Burkholderia pseudomallei</i> isolates collected in Singapore from 1988 to 2004. <i>Journal of Microbiological Methods</i> , 2009, 77, 297-301.	0.7	7
76	Isolation of <i>Brucella microti</i> from Mandibular Lymph Nodes of Red Foxes, <i>Vulpes vulpes</i> , in Lower Austria. <i>Vector-Borne and Zoonotic Diseases</i> , 2009, 9, 153-156.	0.6	103
77	Multiple Locus Variable Number of Tandem Repeats Analysis. <i>Methods in Molecular Biology</i> , 2009, 551, 141-158.	0.4	53
78	Clustered Regularly Interspaced Short Palindromic Repeats (CRISPRs) for the Genotyping of Bacterial Pathogens. <i>Methods in Molecular Biology</i> , 2009, 551, 105-116.	0.4	26
79	Genotyping and Phylogenetic Analysis of <i>Yersinia pestis</i> by MLVA: Insights into the Worldwide Expansion of Central Asia Plague Foci. <i>PLoS ONE</i> , 2009, 4, e6000.	1.1	111
80	High resolution typing of <i>Chlamydomphila psittaci</i> by multilocus VNTR analysis (MLVA). <i>Infection, Genetics and Evolution</i> , 2008, 8, 171-181.	1.0	35
81	Fieldable genotyping of <i>Bacillus anthracis</i> and <i>Yersinia pestis</i> based on 25-loci Multi Locus VNTR Analysis. <i>BMC Microbiology</i> , 2008, 8, 21.	1.3	36
82	<i>Brucella microti</i> sp. nov., isolated from the common vole <i>Microtus arvalis</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008, 58, 375-382.	0.8	300
83	On-line resources for bacterial micro-evolution studies using MLVA or CRISPR typing. <i>Biochimie</i> , 2008, 90, 660-668.	1.3	131
84	CRISPRcompar: a website to compare clustered regularly interspaced short palindromic repeats. <i>Nucleic Acids Research</i> , 2008, 36, W145-W148.	6.5	135
85	Selection and Validation of a Multilocus Variable-Number Tandem-Repeat Analysis Panel for Typing <i>Shigella</i> spp. <i>Journal of Clinical Microbiology</i> , 2008, 46, 1026-1036.	1.8	41
86	Evaluation of a Multilocus Variable-Number Tandem-Repeat Analysis Scheme for Typing Human <i>Brucella</i> Isolates in a Region of Brucellosis Endemicity. <i>Journal of Clinical Microbiology</i> , 2008, 46, 3935-3940.	1.8	79
87	Insight into Microevolution of <i>Yersinia pestis</i> by Clustered Regularly Interspaced Short Palindromic Repeats. <i>PLoS ONE</i> , 2008, 3, e2652.	1.1	150
88	Isolation of <i>Brucella microti</i> from Soil. <i>Emerging Infectious Diseases</i> , 2008, 14, 1316-1317.	2.0	107
89	Multiple-Locus Variable-Number Tandem-Repeat Analysis for Longitudinal Survey of Sources of <i>Pseudomonas aeruginosa</i> Infection in Cystic Fibrosis Patients. <i>Journal of Clinical Microbiology</i> , 2007, 45, 3175-3183.	1.8	79
90	Identification of Variable-Number Tandem-Repeat (VNTR) Sequences in <i>Legionella pneumophila</i> and Development of an Optimized Multiple-Locus VNTR Analysis Typing Scheme. <i>Journal of Clinical Microbiology</i> , 2007, 45, 1190-1199.	1.8	45

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91	Comparison of Multiple-Locus Variable-Number Tandem-Repeat Analysis with Other PCR-Based Methods for Typing <i>Brucella suis</i> Isolates. <i>Journal of Clinical Microbiology</i> , 2007, 45, 4070-4072.	1.8	63
92	Assessment of genetic stability of <i>Brucella melitensis</i> Rev 1 vaccine strain by multiple-locus variable-number tandem repeat analysis. <i>Vaccine</i> , 2007, 25, 2858-2862.	1.7	41
93	Evaluation of <i>Brucella</i> MLVA typing for human brucellosis. <i>Journal of Microbiological Methods</i> , 2007, 69, 137-145.	0.7	246
94	CRISPRFinder: a web tool to identify clustered regularly interspaced short palindromic repeats. <i>Nucleic Acids Research</i> , 2007, 35, W52-W57.	6.5	1,799
95	Analysis of the Three <i>Yersinia pestis</i> CRISPR Loci Provides New Tools for Phylogenetic Studies and Possibly for the Investigation of Ancient DNA. <i>Advances in Experimental Medicine and Biology</i> , 2007, 603, 327-338.	0.8	55
96	The CRISPRdb database and tools to display CRISPRs and to generate dictionaries of spacers and repeats. <i>BMC Bioinformatics</i> , 2007, 8, 172.	1.2	890
97	Multiple Locus VNTR (Variable Number of Tandem Repeat) Analysis. , 2006, , 83-104.		27
98	Genotyping of <i>Bacillus anthracis</i> strains based on automated capillary 25-loci multiple locus variable-number tandem repeats analysis. <i>BMC Microbiology</i> , 2006, 6, 33.	1.3	151
99	Molecular characterization of <i>Coxiella burnetii</i> isolates by infrequent restriction site-PCR and MLVA typing. <i>BMC Microbiology</i> , 2006, 6, 38.	1.3	133
100	Evaluation and selection of tandem repeat loci for a <i>Brucella</i> MLVA typing assay. <i>BMC Microbiology</i> , 2006, 6, 9.	1.3	339
101	A nose-only apparatus for airborne delivery of <i>Mycobacterium tuberculosis</i> to mice: calibration of biological parameters. <i>Microbes and Infection</i> , 2005, 7, 457-466.	1.0	4
102	Evaluation and selection of tandem repeat loci for <i>Streptococcus pneumoniae</i> MLVA strain typing. <i>BMC Microbiology</i> , 2005, 5, 66.	1.3	37
103	Minisatellite polymorphism as a tool to distinguish closely related <i>Lactococcus lactis</i> strains. <i>FEMS Microbiology Letters</i> , 2005, 248, 101-109.	0.7	5
104	Comparison of Minisatellite Polymorphisms in the <i>Bacillus cereus</i> Complex: a Simple Assay for Large-Scale Screening and Identification of Strains Most Closely Related to <i>Bacillus anthracis</i> . <i>Applied and Environmental Microbiology</i> , 2005, 71, 6613-6623.	1.4	23
105	Failure of a Short-Term Antibiotic Therapy for Human Brucellosis Using Ciprofloxacin. <i>Chemotherapy</i> , 2005, 51, 352-356.	0.8	31
106	CRISPR elements in <i>Yersinia pestis</i> acquire new repeats by preferential uptake of bacteriophage DNA, and provide additional tools for evolutionary studies. <i>Microbiology (United Kingdom)</i> , 2005, 151, 653-663.	0.7	1,083
107	<i>Yersinia pestis</i> genotyping. <i>Emerging Infectious Diseases</i> , 2005, 11, 1317-8; author reply 1318-9.	2.0	12
108	High Genetic Diversity Revealed by Variable-Number Tandem Repeat Genotyping and Analysis of hsp65 Gene Polymorphism in a Large Collection of <i>Mycobacterium canettii</i> Strains Indicates that the <i>M. tuberculosis</i> Complex Is a Recently Emerged Clone of <i>M. canettii</i> . <i>Journal of Clinical Microbiology</i> , 2004, 42, 3248-3255.	1.8	98

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109	Variable Number of Tandem Repeats in Salmonella enterica subsp. enterica for Typing Purposes. Journal of Clinical Microbiology, 2004, 42, 5722-5730.	1.8	123
110	Identification of polymorphic tandem repeats by direct comparison of genome sequence from different bacterial strains: a web-based resource. BMC Bioinformatics, 2004, 5, 4.	1.2	99
111	Tandem repeats analysis for the high resolution phylogenetic analysis of Yersinia pestis. BMC Microbiology, 2004, 4, 22.	1.3	116
112	Evaluation of the Polymorphisms Associated with Tandem Repeats for Pseudomonas aeruginosa Strain Typing. Journal of Clinical Microbiology, 2003, 41, 4991-4997.	1.8	82
113	DNA-DNA hybridization study of Burkholderia species using genomic DNA macro-array analysis coupled to reverse genome probing. International Journal of Systematic and Evolutionary Microbiology, 2003, 53, 739-746.	0.8	14
114	Predicting Human Minisatellite Polymorphism. Genome Research, 2003, 13, 856-867.	2.4	43
115	Characterization of a Tandem Repeat Polymorphism in Legionella pneumophila and Its Use for Genotyping. Journal of Clinical Microbiology, 2003, 41, 1819-1826.	1.8	60
116	Segmental Polymorphisms in the Proterminal Regions of a Subset of Human Chromosomes. Genome Research, 2002, 12, 1673-1678.	2.4	32
117	High resolution, on-line identification of strains from the Mycobacterium tuberculosis complex based on tandem repeat typing. BMC Microbiology, 2002, 2, 37.	1.3	170
118	A tandem repeats database for bacterial genomes: application to the genotyping of Yersinia pestis and Bacillus anthracis. BMC Microbiology, 2001, 1, 2.	1.3	222
119	Children of Chernobyl Cleanup Workers do not Show Elevated Rates of Mutations in Minisatellite Alleles. Radiation Research, 2001, 155, 74-80.	0.7	72
120	A Dominant Modifier of Transgene Methylation Is Mapped by QTL Analysis to Mouse Chromosome 13. Genome Research, 2001, 11, 382-388.	2.4	9
121	Use of a set of highly polymorphic minisatellite probes for the identification of cryptic 1p36.3 deletions in a large collection of patients with idiopathic mental retardation. Journal of Medical Genetics, 2001, 38, 121-125.	1.5	23
122	The SH2D2A gene encoding the T-cell-specific adapter protein (TSAd) is localized centromeric to the CD1 gene cluster on human Chromosome 1. Immunogenetics, 2000, 51, 179-185.	1.2	16
123	Minisatellites: Mutability and Genome Architecture. Genome Research, 2000, 10, 899-907.	2.4	178
124	Meiotic instability of human minisatellite CEB1 in yeast requires DNA double-strand breaks. Nature Genetics, 1999, 23, 367-371.	9.4	65
125	Linkage and physical mapping of rat microsatellites derived from minisatellite loci. Mammalian Genome, 1999, 10, 405-409.	1.0	11
126	Finding New Human Minisatellite Sequences in the Vicinity of Long CA-Rich Sequences. Genome Research, 1999, 9, 647-653.	2.4	6

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127	Recent Human-Specific Spreading of a Subtelomeric Domain. <i>Genomics</i> , 1998, 51, 165-176.	1.3	45
128	Analysis of Distribution in the Human, Pig, and Rat Genomes Points toward a General Subtelomeric Origin of Minisatellite Structures. <i>Genomics</i> , 1998, 52, 62-71.	1.3	39
129	Molecular-cytogenetic detection of a deletion of 1p36.3.. <i>Journal of Medical Genetics</i> , 1997, 34, 314-317.	1.5	47
130	European Gene Mapping Project (EUROGEM): Breakpoint panels for human chromosomes based on the CEPH reference families. <i>Annals of Human Genetics</i> , 1996, 60, 447-486.	0.3	8
131	Stability of microsatellites and minisatellites in Bloom syndrome, a human syndrome of genetic instability. <i>Mutation Research DNA Repair</i> , 1996, 362, 227-236.	3.8	11
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