

Gilles Vergnaud

List of Publications by Year in descending order

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162
papers

13,299
citations

30070

54
h-index

23533

111
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168
all docs

168
docs citations

168
times ranked

11288
citing authors

#	ARTICLE	IF	CITATIONS
1	CRISPRFinder: a web tool to identify clustered regularly interspaced short palindromic repeats. <i>Nucleic Acids Research</i> , 2007, 35, W52-W57.	14.5	1,799
2	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.	1.8	1,083
3	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.	14.5	985
4	The CRISPRdb database and tools to display CRISPRs and to generate dictionaries of spacers and repeats. <i>BMC Bioinformatics</i> , 2007, 8, 172.	2.6	890
5	Evaluation and selection of tandem repeat loci for a <i>Brucella</i> MLVA typing assay. <i>BMC Microbiology</i> , 2006, 6, 9.	3.3	339
6	A gradient of sex linkage in the pseudoautosomal region of the human sex chromosomes. <i>Nature</i> , 1986, 319, 291-295.	27.8	320
7	<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.	1.7	300
8	<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.	1.7	276
9	Evaluation of <i>Brucella</i> MLVA typing for human brucellosis. <i>Journal of Microbiological Methods</i> , 2007, 69, 137-145.	1.6	246
10	A tandem repeats database for bacterial genomes: application to the genotyping of <i>Yersinia pestis</i> and <i>Bacillus anthracis</i> . <i>BMC Microbiology</i> , 2001, 1, 2.	3.3	222
11	Pseudoautosomal DNA sequences in the pairing region of the human sex chromosomes. <i>Nature</i> , 1985, 317, 692-697.	27.8	212
12	Minisatellites: Mutability and Genome Architecture. <i>Genome Research</i> , 2000, 10, 899-907.	5.5	178
13	<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.	1.7	171
14	High resolution, on-line identification of strains from the <i>Mycobacterium tuberculosis</i> complex based on tandem repeat typing. <i>BMC Microbiology</i> , 2002, 2, 37.	3.3	170
15	<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.	1.7	155
16	The use of synthetic tandem repeats to isolate new VNTR loci: Cloning of a human hypermutable sequence. <i>Genomics</i> , 1991, 11, 135-144.	2.9	151
17	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.	3.3	151
18	Insight into Microevolution of <i>Yersinia pestis</i> by Clustered Regularly Interspaced Short Palindromic Repeats. <i>PLoS ONE</i> , 2008, 3, e2652.	2.5	150

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19	Mapping of quantitative trait loci for blood pressure and cardiac mass in the rat by genome scanning of recombinant inbred strains.. Journal of Clinical Investigation, 1995, 96, 1973-1978.	8.2	146
20	CRISPRcompar: a website to compare clustered regularly interspaced short palindromic repeats. Nucleic Acids Research, 2008, 36, W145-W148.	14.5	135
21	Molecular characterization of <i>Coxiella burnetii</i> isolates by infrequent restriction site-PCR and MLVA typing. BMC Microbiology, 2006, 6, 38.	3.3	133
22	On-line resources for bacterial micro-evolution studies using MLVA or CRISPR typing. Biochimie, 2008, 90, 660-668.	2.6	131
23	Variable Number of Tandem Repeats in <i>Salmonella enterica</i> subsp. <i>enterica</i> for Typing Purposes. Journal of Clinical Microbiology, 2004, 42, 5722-5730.	3.9	123
24	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> . BMC Microbiology, 2009, 9, 145.	3.3	119
25	Tandem repeats analysis for the high resolution phylogenetic analysis of <i>Yersinia pestis</i> . BMC Microbiology, 2004, 4, 22.	3.3	116
26	Genotyping and Phylogenetic Analysis of <i>Yersinia pestis</i> by MLVA: Insights into the Worldwide Expansion of Central Asia Plague Foci. PLoS ONE, 2009, 4, e6000.	2.5	111
27	Significance of the Identification in the Horn of Africa of an Exceptionally Deep Branching <i>Mycobacterium tuberculosis</i> Clade. PLoS ONE, 2012, 7, e52841.	2.5	109
28	A genetic linkage map of the rat derived from recombinant inbred strains. Mammalian Genome, 1996, 7, 117-127.	2.2	108
29	Isolation of <i>Brucella microti</i> from Soil. Emerging Infectious Diseases, 2008, 14, 1316-1317.	4.3	107
30	Isolation of <i>Brucella microti</i> from Mandibular Lymph Nodes of Red Foxes, <i>Vulpes vulpes</i> , in Lower Austria. Vector-Borne and Zoonotic Diseases, 2009, 9, 153-156.	1.5	103
31	Identification of polymorphic tandem repeats by direct comparison of genome sequence from different bacterial strains: a web-based resource. BMC Bioinformatics, 2004, 5, 4.	2.6	99
32	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> . Journal of Clinical Microbiology, 2004, 42, 3248-3255.	3.9	98
33	<i>Brucella</i> spp. of amphibians comprise genomically diverse motile strains competent for replication in macrophages and survival in mammalian hosts. Scientific Reports, 2017, 7, 44420.	3.3	96
34	Physical mapping of the holoprosencephaly critical region on chromosome 7q36. Nature Genetics, 1993, 3, 247-251.	21.4	95
35	Molecular characterisation of <i>Brucella</i> species. OIE Revue Scientifique Et Technique, 2013, 32, 149-162.	1.2	89
36	CRISPRCasdb a successor of CRISPRdb containing CRISPR arrays and cas genes from complete genome sequences, and tools to download and query lists of repeats and spacers. Nucleic Acids Research, 2020, 48, D535-D544.	14.5	88

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37	Evaluation of the Polymorphisms Associated with Tandem Repeats for <i>Pseudomonas aeruginosa</i> Strain Typing. <i>Journal of Clinical Microbiology</i> , 2003, 41, 4991-4997.	3.9	82
38	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.	3.9	79
39	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.	3.9	79
40	Polymers of random short oligonucleotides detect polymorphic loci in the human genome. <i>Nucleic Acids Research</i> , 1989, 17, 7623-7630.	14.5	75
41	The Susceptibility of <i>Pseudomonas aeruginosa</i> Strains from Cystic Fibrosis Patients to Bacteriophages. <i>PLoS ONE</i> , 2013, 8, e60575.	2.5	73
42	Children of Chernobyl Cleanup Workers do not Show Elevated Rates of Mutations in Minisatellite Alleles. <i>Radiation Research</i> , 2001, 155, 74-80.	1.5	72
43	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.	3.9	71
44	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.	3.9	69
45	Meiotic instability of human minisatellite CEB1 in yeast requires DNA double-strand breaks. <i>Nature Genetics</i> , 1999, 23, 367-371.	21.4	65
46	<i>Yersinia pestis</i> Lineages in Mongolia. <i>PLoS ONE</i> , 2012, 7, e30624.	2.5	64
47	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.	3.9	63
48	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.	2.5	63
49	Use of multilocus variable-number tandem repeat analysis (MLVA) in eight European countries, 2012. <i>Eurosurveillance</i> , 2013, 18, 20385.	7.0	63
50	Progenitor <i>Mycobacterium canettii</i> Clone Responsible for Lymph Node Tuberculosis Epidemic, Djibouti. <i>Emerging Infectious Diseases</i> , 2014, 20, 21-28.	4.3	62
51	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.	2.5	62
52	Molecular characteristics of <i>Mycobacterium canettii</i> the smooth <i>Mycobacterium tuberculosis</i> bacilli. <i>Infection, Genetics and Evolution</i> , 2010, 10, 1165-1173.	2.3	61
53	Characterization of a Tandem Repeat Polymorphism in <i>Legionella pneumophila</i> and Its Use for Genotyping. <i>Journal of Clinical Microbiology</i> , 2003, 41, 1819-1826.	3.9	60
54	Molecular epidemiology of human and animal tuberculosis in Ibadan, Southwestern Nigeria. <i>Veterinary Microbiology</i> , 2011, 151, 139-147.	1.9	59

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55	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.	3.0	59
56	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, 1974â€“2006. <i>Frontiers in Microbiology</i> , 2018, 9, 1545.	3.5	57
57	The CEPH Consortium Linkage Map of Human Chromosome 13. <i>Genomics</i> , 1993, 16, 486-496.	2.9	55
58	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.	1.6	55
59	PCR assay for chromosome 1p deletion in small neuroblastoma samples. <i>International Journal of Cancer</i> , 1992, 52, 544-548.	5.1	53
60	Multiple Locus Variable Number of Tandem Repeats Analysis. <i>Methods in Molecular Biology</i> , 2009, 551, 141-158.	0.9	53
61	Pseudolysogeny and sequential mutations build multiresistance to virulent bacteriophages in <i>Pseudomonas aeruginosa</i> . <i>Microbiology (United Kingdom)</i> , 2016, 162, 748-763.	1.8	53
62	MLVA16 Typing of Portuguese Human and Animal <i>Brucella melitensis</i> and <i>Brucella abortus</i> Isolates. <i>PLoS ONE</i> , 2012, 7, e42514.	2.5	52
63	Allelic loss of the short arm of chromosome 4 in neuroblastoma suggests a novel tumour suppressor gene locus. <i>Human Genetics</i> , 1996, 97, 834-837.	3.8	51
64	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.	2.8	50
65	Intraspecies Biodiversity of the Genetically Homologous Species <i>Brucella microti</i> . <i>Applied and Environmental Microbiology</i> , 2012, 78, 1534-1543.	3.1	48
66	Molecular-cytogenetic detection of a deletion of 1p36.3.. <i>Journal of Medical Genetics</i> , 1997, 34, 314-317.	3.2	47
67	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.	2.5	46
68	Recent Human-Specific Spreading of a Subtelomeric Domain. <i>Genomics</i> , 1998, 51, 165-176.	2.9	45
69	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.	3.9	45
70	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.	3.9	44
71	Insights from <i>Bacillus anthracis</i> strains isolated from permafrost in the tundra zone of Russia. <i>PLoS ONE</i> , 2019, 14, e0209140.	2.5	44
72	Predicting Human Minisatellite Polymorphism. <i>Genome Research</i> , 2003, 13, 856-867.	5.5	43

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73	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.	3.8	41
74	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.	3.9	41
75	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.	2.5	41
76	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.	2.9	39
77	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.	2.5	38
78	Evaluation and selection of tandem repeat loci for <i>Streptococcus pneumoniae</i> MLVA strain typing. <i>BMC Microbiology</i> , 2005, 5, 66.	3.3	37
79	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.	3.3	36
80	High resolution typing of <i>Chlamydomydia psittaci</i> by multilocus VNTR analysis (MLVA). <i>Infection, Genetics and Evolution</i> , 2008, 8, 171-181.	2.3	35
81	Investigation on <i>Mycobacterium tuberculosis</i> Diversity in China and the Origin of the Beijing Clade. <i>PLoS ONE</i> , 2011, 6, e29190.	2.5	35
82	Molecular characterization of <i>Brucella</i> species from Zimbabwe. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007311.	3.0	34
83	Segmental Polymorphisms in the Proterminal Regions of a Subset of Human Chromosomes. <i>Genome Research</i> , 2002, 12, 1673-1678.	5.5	32
84	Failure of a Short-Term Antibiotic Therapy for Human Brucellosis Using Ciprofloxacin. <i>Chemotherapy</i> , 2005, 51, 352-356.	1.6	31
85	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.	2.5	31
86	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.	2.9	30
87	Detection of single and multiple polymorphic loci by synthetic tandem repeats of short oligonucleotides. <i>Electrophoresis</i> , 1991, 12, 134-140.	2.4	29
88	<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.	3.0	29
89	<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.	3.9	28
90	Russian isolates enlarge the known geographic diversity of <i>Francisella tularensis</i> subsp. <i>mediasiatica</i> . <i>PLoS ONE</i> , 2017, 12, e0183714.	2.5	28

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91	Multiple Locus VNTR (Variable Number of Tandem Repeat) Analysis. , 2006, , 83-104.		27
92	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.	3.2	27
93	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.	3.9	27
94	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.	3.1	26
95	Clustered Regularly Interspaced Short Palindromic Repeats (CRISPRs) for the Genotyping of Bacterial Pathogens. <i>Methods in Molecular Biology</i> , 2009, 551, 105-116.	0.9	26
96	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.	2.9	26
97	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.	3.0	25
98	CEPH Consortium Map of Chromosome 9. <i>Genomics</i> , 1994, 19, 203-214.	2.9	24
99	Generation of a <sc>CRISPR</sc> database for <sc><i>Y</i></sc><i>ersinia pseudotuberculosis</i></sc> complex and role of <sc>CRISPR</sc>-based immunity in conjugation. <i>Environmental Microbiology</i> , 2015, 17, 4306-4321.	3.8	24
100	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.	3.1	23
101	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. <i>Journal of Medical Genetics</i> , 2001, 38, 121-125.	3.2	23
102	Genetic Diversity of <i>Brucella melitensis</i> in Kazakhstan in Relation to World-Wide Diversity. <i>Frontiers in Microbiology</i> , 2019, 10, 1897.	3.5	21
103	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.	3.9	20
104	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.	2.5	20
105	The CEPH Consortium Linkage Map of Human Chromosome 11. <i>Genomics</i> , 1995, 27, 101-112.	2.9	19
106	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.	3.3	19
107	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.	1.8	19
108	Detection of polymorphic loci in complex genomes with synthetic tandem repeats. <i>Genomics</i> , 1992, 12, 454-458.	2.9	18

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109	The CEPH consortium linkage map of human chromosome 16. <i>Genomics</i> , 1995, 25, 44-58.	2.9	18
110	The SH2D2A gene encoding the T-cell-specific adapter protein (TSA _d) is localized centromeric to the CD1 gene cluster on human Chromosome 1. <i>Immunogenetics</i> , 2000, 51, 179-185.	2.4	16
111	DNA-DNA hybridization study of Burkholderia species using genomic DNA macro-array analysis coupled to reverse genome probing. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2003, 53, 739-746.	1.7	14
112	Genetic mapping of three human homologues of murine t-complex genes localizes TCP10 to 6q27, 15 cM distal to TCP1 and PLC. <i>Genomics</i> , 1992, 12, 826-828.	2.9	13
113	The Basis for Natural Multiresistance to Phage in <i>Pseudomonas aeruginosa</i> . <i>Antibiotics</i> , 2020, 9, 339.	3.7	12
114	<i>Yersinia pestis</i> genotyping. <i>Emerging Infectious Diseases</i> , 2005, 11, 1317-8; author reply 1318-9.	4.3	12
115	CEB 13 detects a VNTR locus (Het: 93%) on chromosome 7q. <i>Human Molecular Genetics</i> , 1992, 1, 64-64.	2.9	11
116	Stability of microsatellites and minisatellites in Bloom syndrome, a human syndrome of genetic instability. <i>Mutation Research DNA Repair</i> , 1996, 362, 227-236.	3.7	11
117	Linkage and physical mapping of rat microsatellites derived from minisatellite loci. <i>Mammalian Genome</i> , 1999, 10, 405-409.	2.2	11
118	<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
119	Isolation of human minisatellite loci detected by synthetic tandem repeat probes: direct comparison with cloned DNA fingerprinting probes. <i>Human Molecular Genetics</i> , 1992, 1, 319-323.	2.9	10
120	The CEPH consortium linkage map of human chromosome 15q. <i>Genomics</i> , 1992, 14, 833-840.	2.9	10
121	The CEPH consortium linkage map of human chromosome 2. <i>Genomics</i> , 1992, 14, 1055-1063.	2.9	10
122	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.	1.8	10
123	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.	2.5	10
124	A Dominant Modifier of Transgene Methylation Is Mapped by QTL Analysis to Mouse Chromosome 13. <i>Genome Research</i> , 2001, 11, 382-388.	5.5	9
125	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.	0.8	8
126	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.	2.1	8

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127	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.	1.6	7
128	A VNTR isolated by size selection of human DNA fragments detects RFLPs at the extremity of 1p and 4q. <i>Nucleic Acids Research</i> , 1991, 19, 4572-4572.	14.5	6
129	A synthetic probe, STR 14C19, detects a new polymorphic locus at 16pter (D16S282). <i>Nucleic Acids Research</i> , 1991, 19, 4015-4015.	14.5	6
130	No Increase in Female Recombination Frequency in the Distal Part of the Human Pseudoautosomal Region. <i>Genomics</i> , 1994, 24, 610-612.	2.9	6
131	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.	3.9	6
132	Complete Genome Sequences of Five <i>Acinetobacter baumannii</i> Phages from Abidjan, Côte d'Ivoire. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	6
133	<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
134	Allelic loss of the short arm of chromosome 4 in neuroblastoma suggests a novel tumour suppressor gene locus. <i>Human Genetics</i> , 1996, 97, 834-837.	3.8	6
135	Finding New Human Minisatellite Sequences in the Vicinity of Long CA-Rich Sequences. <i>Genome Research</i> , 1999, 9, 647-653.	5.5	6
136	<i>Bacillus anthracis</i> Phylogeography: New Clues From Kazakhstan, Central Asia. <i>Frontiers in Microbiology</i> , 2021, 12, 778225.	3.5	6
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