

Christine Pourcel

List of Publications by Year in descending order

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120
papers

12,528
citations

53660

45
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25716

108
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129
all docs

129
docs citations

129
times ranked

11099
citing authors

#	ARTICLE	IF	CITATIONS
1	2-kupl: mapping-free variant detection from DNA-seq data of matched samples. BMC Bioinformatics, 2021, 22, 304.	1.2	1
2	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.	6.5	88
3	Characterization of sixteen Achromobacter xylosoxidans phages from Abidjan, Côte d'Ivoire, isolated on a single clinical strain. Archives of Virology, 2020, 165, 725-730.	0.9	8
4	The Basis for Natural Multiresistance to Phage in Pseudomonas aeruginosa. Antibiotics, 2020, 9, 339.	1.5	12
5	New Insights into CRISPR Arrays. CRISPR Journal, 2020, 3, 422-424.	1.4	1
6	Revised Interpretation of the Hain Lifescience GenoType MTBC To Differentiate Mycobacterium canettii and Members of the Mycobacterium tuberculosis Complex. Antimicrobial Agents and Chemotherapy, 2019, 63, .	1.4	20
7	Impact of FiuA Outer Membrane Receptor Polymorphism on the Resistance of Pseudomonas aeruginosa toward Peptidoglycan Lipid II-Targeting Paem Pyocins. Journal of Bacteriology, 2019, 201, .	1.0	2
8	Investigation of Pseudomonas aeruginosa strain Pcyll-10 variants resisting infection by N4-like phage Ab09 in search for genes involved in phage adsorption. PLoS ONE, 2019, 14, e0215456.	1.1	20
9	Clinical Features of Mycobacterium canettii Infection: A Retrospective Study of 20 Cases Among French Soldiers and Relatives. Clinical Infectious Diseases, 2019, 69, 2003-2010.	2.9	9
10	Complete Genome Sequences of Five Acinetobacter baumannii Phages from Abidjan, Côte d'Ivoire. Microbiology Resource Announcements, 2019, 8, .	0.3	6
11	Associations between Mycobacterium tuberculosis Beijing genotype and drug resistance to four first-line drugs: a survey in China. Frontiers of Medicine, 2018, 12, 92-97.	1.5	4
12	Recovery and Characterization of Bacteria Resisting Infection by Lytic Bacteriophage. Methods in Molecular Biology, 2018, 1693, 85-98.	0.4	4
13	CRISPRCasFinder, an update of CRISPRFinder, includes a portable version, enhanced performance and integrates search for Cas proteins. Nucleic Acids Research, 2018, 46, W246-W251.	6.5	985
14	Genotypic Expansion Within the Population Structure of Classical Brucella Species Revealed by MLVA16 Typing of 1404 Brucella Isolates From Different Animal and Geographic Origins, 1974-2006. Frontiers in Microbiology, 2018, 9, 1545.	1.5	57
15	Transposition Behavior Revealed by High-Resolution Description of Pseudomonas Aeruginosa Saltovirus Integration Sites. Viruses, 2018, 10, 245.	1.5	4
16	Clinical Relevance of Type II Fatty Acid Synthesis Bypass in Staphylococcus aureus. Antimicrobial Agents and Chemotherapy, 2017, 61, .	1.4	26
17	CRISPR-like sequences in Helicobacter pylori and application in genotyping. Gut Pathogens, 2017, 9, 65.	1.6	11
18	A carrier state is established in Pseudomonas aeruginosa by phage LeviOr01, a newly isolated ssRNA levivirus. Journal of General Virology, 2017, 98, 2181-2189.	1.3	26

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19	Fine structure analysis of lipopolysaccharides in bacteriophage-resistant <i>Pseudomonas aeruginosa</i> PAO1 mutants. <i>Microbiology (United Kingdom)</i> , 2017, 163, 848-855.	0.7	22
20	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
21	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
22	Complete Genome Sequence of PM105, a New <i>Pseudomonas aeruginosa</i> B3-Like Transposable Phage. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
23	A new genotyping scheme based on MLVA for inter-laboratory surveillance of <i>Streptococcus pyogenes</i> . <i>Journal of Microbiological Methods</i> , 2016, 127, 176-181.	0.7	3
24	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
25	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
26	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
27	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
28	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
29	Genotyping of <i>Pseudomonas aeruginosa</i> reveals high diversity, stability over time and good outcome of eradication. <i>Journal of Cystic Fibrosis</i> , 2015, 14, 353-360.	0.3	15
30	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
31	A novel <i>Pseudomonas aeruginosa</i> Bacteriophage, Ab31, a Chimera Formed from Temperate Phage PAJU2 and <i>P. putida</i> Lytic Phage AF: Characteristics and Mechanism of Bacterial Resistance. <i>PLoS ONE</i> , 2014, 9, e93777.	1.1	35
32	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
33	<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
34	<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
35	Occurrence, Diversity of CRISPR-Cas Systems and Genotyping Implications. , 2013, , 33-59.		1
36	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

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37	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
38	Optimized Multilocus Variable-Number Tandem-Repeat Analysis Assay and Its Complementarity with Pulsed-Field Gel Electrophoresis and Multilocus Sequence Typing for <i>Listeria monocytogenes</i> Clone Identification and Surveillance. <i>Journal of Clinical Microbiology</i> , 2013, 51, 1868-1880.	1.8	58
39	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
40	Comparative Genomics Reveal That Host-Innate Immune Responses Influence the Clinical Prevalence of <i>Legionella pneumophila</i> Serogroups. <i>PLoS ONE</i> , 2013, 8, e67298.	1.1	33
41	The Susceptibility of <i>Pseudomonas aeruginosa</i> Strains from Cystic Fibrosis Patients to Bacteriophages. <i>PLoS ONE</i> , 2013, 8, e60575.	1.1	73
42	Four Genotyping Schemes for Phylogenetic Analysis of <i>Pseudomonas aeruginosa</i> : Comparison of Their Congruence with Multi-Locus Sequence Typing. <i>PLoS ONE</i> , 2013, 8, e82069.	1.1	34
43	Evidence of Diversity among Epidemiologically Related Carbapenemase-Producing <i>Acinetobacter baumannii</i> Strains Belonging to International Clonal Lineage II. <i>Journal of Clinical Microbiology</i> , 2012, 50, 590-597.	1.8	36
44	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
45	How to Identify CRISPRs in Sequencing Data. <i>Methods in Molecular Biology</i> , 2012, 905, 15-27.	0.4	5
46	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
47	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
48	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
49	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
50	Épidémiologie de <i>Pseudomonas aeruginosa</i> chez les patients mucoviscidosiques. <i>Revue Francophone Des Laboratoires</i> , 2011, 2011, 41-48.	0.0	0
51	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
52	Clinical characteristics of the smooth tubercle bacilli <i>Mycobacterium canettii</i> ™ infection suggest the existence of an environmental reservoir. <i>Clinical Microbiology and Infection</i> , 2011, 17, 1013-1019.	2.8	81
53	Molecular epidemiology of human and animal tuberculosis in Ibadan, Southwestern Nigeria. <i>Veterinary Microbiology</i> , 2011, 151, 139-147.	0.8	59
54	A multi locus variable number of tandem repeat analysis (MLVA) scheme for <i>Streptococcus agalactiae</i> genotyping. <i>BMC Microbiology</i> , 2011, 11, 171.	1.3	40

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55	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
56	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
57	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
58	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
59	Multiple-locus variable-number tandem repeat analysis for molecular typing of <i>Aspergillus fumigatus</i> . <i>BMC Microbiology</i> , 2010, 10, 315.	1.3	22
60	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
61	Alternative Routes for Dissemination of <i>Legionella pneumophila</i> Causing Three Outbreaks in Norway. <i>Environmental Science & Technology</i> , 2010, 44, 8712-8717.	4.6	42
62	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
63	First Insight into Genetic Diversity of the <i>Mycobacterium tuberculosis</i> Complex in Albania Obtained by Multilocus Variable-Number Tandem-Repeat Analysis and Spoligotyping Reveals the Presence of Beijing Multidrug-Resistant Isolates. <i>Journal of Clinical Microbiology</i> , 2009, 47, 1581-1584.	1.8	14
64	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
65	Genotyping of <i>Chlamydophila abortus</i> strains by multilocus VNTR analysis. <i>Veterinary Microbiology</i> , 2009, 137, 335-344.	0.8	30
66	Multiple Locus Variable Number of Tandem Repeats Analysis. <i>Methods in Molecular Biology</i> , 2009, 551, 141-158.	0.4	53
67	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
68	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
69	High resolution typing of <i>Chlamydophila psittaci</i> by multilocus VNTR analysis (MLVA). <i>Infection, Genetics and Evolution</i> , 2008, 8, 171-181.	1.0	35
70	On-line resources for bacterial micro-evolution studies using MLVA or CRISPR typing. <i>Biochimie</i> , 2008, 90, 660-668.	1.3	131
71	CRISPRcompar: a website to compare clustered regularly interspaced short palindromic repeats. <i>Nucleic Acids Research</i> , 2008, 36, W145-W148.	6.5	135
72	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

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73	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
74	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
75	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
76	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
77	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
78	Multiple Locus VNTR (Variable Number of Tandem Repeat) Analysis. , 2006, , 83-104.		27
79	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
80	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
81	Identification of Variable-Number Tandem-Repeat Loci in <i>Leptospira interrogans</i> Sensu Stricto. <i>Journal of Clinical Microbiology</i> , 2005, 43, 539-545.	1.8	115
82	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
83	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
84	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
85	Tandem repeats analysis for the high resolution phylogenetic analysis of <i>Yersinia pestis</i> . <i>BMC Microbiology</i> , 2004, 4, 22.	1.3	116
86	A submicroscopic unbalanced subtelomeric translocation t(2p;10q) identified by fluorescence in situ hybridization: fetus with increased nuchal translucency and normal standard karyotype with later growth and developmental delay, rhombencephalosynapsis (RES). <i>Annales De G�n�tique</i> , 2004, 47, 405-417.	0.4	15
87	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.	1.8	60
88	Transgenic B lymphocytes expressing a human cold agglutinin escape tolerance following experimental infection of mice by <i>Mycoplasma pulmonis</i> . <i>European Journal of Immunology</i> , 2002, 32, 1147-1156.	1.6	13
89	A Dominant Modifier of Transgene Methylation Is Mapped by QTL Analysis to Mouse Chromosome 13. <i>Genome Research</i> , 2001, 11, 382-388.	2.4	9
90	Negative regulation of autoreactive B cells in transgenic mice expressing a human pathogenic cold agglutinin. <i>European Journal of Immunology</i> , 2000, 30, 2290-2299.	1.6	7

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91	A new family of genes and pseudogenes potentially expressing testis- and brain-specific leucine zipper proteins in man and mouse. <i>Gene</i> , 2000, 249, 105-113.	1.0	3
92	ASSOCIATION OF GLUCOCORTICOIDS AND CYCLOSPORIN A OR RAPAMYCIN PREVENTS E-SELECTIN AND IL-8 EXPRESSION DURING LPS- AND TNF α -MEDIATED ENDOTHELIAL CELL ACTIVATION1. <i>Transplantation</i> , 2000, 69, 945-953.	0.5	37
93	Mutated cytochrome b as a determinant of a new monoclonal antibody (H8.98) on renal carcinoma cell lines recognized by a V β 3V β 1+ T-cell clone. , 1999, 82, 562-568.		4
94	Recent Human-Specific Spreading of a Subtelomeric Domain. <i>Genomics</i> , 1998, 51, 165-176.	1.3	45
95	Control of Expression and Methylation of a Hepatitis B Virus Transgene by Strain-Specific Modifiers. <i>DNA and Cell Biology</i> , 1998, 17, 427-435.	0.9	23
96	INTRACELLULAR EXPRESSION IN PIG CELLS OF ANTI- β 1,3GALACTOSYLTRANSFERASE SINGLE-CHAIN FV ANTIBODIES REDUCES GAL β 1,3GAL EXPRESSION AND INHIBITS CYTOTOXICITY MEDIATED BY ANTI-GAL XENOANTIBODIES1. <i>Transplantation</i> , 1998, 66, 1477-1485.	0.5	25
97	Porcine β 1,3-galactosyltransferase: tissue-specific and regulated expression of splicing isoforms. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 1997, 1356, 1-11.	1.9	18
98	La x α onogreffé chez l'homme : acquis et perspectives.. <i>Medecine/Sciences</i> , 1997, 13, 301.	0.0	0
99	Transgenesis in rats: Technical aspects and models. <i>Transgenic Research</i> , 1996, 5, 223-234.	1.3	137
100	Simultaneous expression by porcine aorta endothelial cells of glycosphingolipids bearing the major epitope for human xenoreactive antibodies (Gal β 1 \rightarrow 3Gal), blood group H determinant and N-glycolylneuraminic acid. <i>Glycoconjugate Journal</i> , 1996, 13, 947-953.	1.4	105
101	Inhibition of hepatitis b virus surface antigen gene expression in carcinogen-induced liver tumors from transgenic mice. <i>Molecular Carcinogenesis</i> , 1994, 9, 185-192.	1.3	14
102	Induction of anti-hepatitis B surface antigen (HBsAg) antibodies in HBsAg producing transgenic mice: A possible way of circumventing "nonresponse" to HBsAg. <i>Journal of Medical Virology</i> , 1993, 39, 67-74.	2.5	60
103	Chronic alcohol intoxication decreases the serum level of hepatitis B surface antigen in transgenic mice. <i>Journal of Hepatology</i> , 1992, 15, 118-124.	1.8	18
104	Transgenic mice containing hepatitis B virus sequences are more susceptible to carcinogen-induced hepatocarcinogenesis. <i>Carcinogenesis</i> , 1990, 11, 953-956.	1.3	50
105	Transcription of the S gene in transgenic mice is associated with hypomethylation at specific sites and with DNase I sensitivity. <i>Journal of Virology</i> , 1990, 64, 931-935.	1.5	25
106	Replication and gene expression of hepatitis B virus in a transgenic mouse that contains the complete viral genome. <i>Journal of Virology</i> , 1988, 62, 4144-4152.	1.5	146
107	Hepatitis B surface antigen gene expression is regulated by sex steroids and glucocorticoids in transgenic mice.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1987, 84, 1187-1191.	3.3	136
108	Maternal inhibition of hepatitis B surface antigen gene expression in transgenic mice correlates with de novo methylation. <i>Nature</i> , 1987, 329, 454-456.	13.7	209

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109	Formation of the pool of covalently closed circular viral DNA in hepadnavirus-infected cells. <i>Cell</i> , 1986, 47, 451-460.	13.5	665
110	The hepatitis B virus. <i>Nature</i> , 1985, 317, 489-495.	13.7	1,292
111	Specific expression of hepatitis B surface antigen (HBsAg) in transgenic mice. <i>Science</i> , 1985, 230, 1160-1163.	6.0	166
112	Purification by hydrophobic chromatography of hepatitis B surface antigen particles. <i>Annales De L'Institut Pasteur Virology</i> , 1983, 134, 87-96.	0.5	0
113	Antigenicity and immunogenicity of hepatitis B virus particles produced by mouse cells transfected with cloned viral DNA. <i>Virology</i> , 1982, 121, 175-183.	1.1	9
114	Transcription of the hepatitis B surface antigen gene in mouse cells transformed with cloned viral DNA. <i>Journal of Virology</i> , 1982, 42, 100-105.	1.5	147
115	Excretion of hepatitis B surface antigen particles from mouse cells transformed with cloned viral DNA.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1980, 77, 4549-4553.	3.3	248
116	Presence of integrated hepatitis B virus DNA sequences in cellular DNA of human hepatocellular carcinoma. <i>Nature</i> , 1980, 286, 533-535.	13.7	610
117	Bacteriophage lambda-E. coli K12 vector-host system for gene cloning and expression under lactose promoter control. <i>Molecular Genetics and Genomics</i> , 1979, 170, 161-169.	2.4	26
118	Localization of <i>Streptomyces stanfordii</i> endonuclease I (SstI) cleavage sites on genomes of human adenovirus types two and five. <i>Gene</i> , 1979, 5, 77-83.	1.0	7
119	Cloning in <i>Escherichia coli</i> and physical structure of hepatitis B virion DNA.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1979, 76, 2222-2226.	3.3	187
120	λ-plac5 derivatives, potential vectors for DNA fragments cleaved by <i>Streptomyces stanfordii</i> restriction enzyme (SstI). <i>Gene</i> , 1977, 1, 281-286.	1.0	4