

Jean-Michel Claverie

List of Publications by Year in descending order

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214
papers

28,361
citations

9756

73
h-index

5806

161
g-index

244
all docs

244
docs citations

244
times ranked

30855
citing authors

#	ARTICLE	IF	CITATIONS
1	Phylogeny.fr: robust phylogenetic analysis for the non-specialist. <i>Nucleic Acids Research</i> , 2008, 36, W465-W469.	6.5	4,135
2	The Significance of Digital Gene Expression Profiles. <i>Genome Research</i> , 1997, 7, 986-995.	2.4	2,665
3	The 1.2-Megabase Genome Sequence of Mimivirus. <i>Science</i> , 2004, 306, 1344-1350.	6.0	959
4	Single mimivirus particles intercepted and imaged with an X-ray laser. <i>Nature</i> , 2011, 470, 78-81.	13.7	790
5	A Giant Virus in Amoebae. <i>Science</i> , 2003, 299, 2033-2033.	6.0	742
6	Comparative Genomics of Multidrug Resistance in <i>Acinetobacter baumannii</i> . <i>PLoS Genetics</i> , 2006, 2, e7.	1.5	677
7	The candidate gene for the X-linked Kallmann syndrome encodes a protein related to adhesion molecules. <i>Cell</i> , 1991, 67, 423-435.	13.5	668
8	BLAST-EXPLORER helps you building datasets for phylogenetic analysis. <i>BMC Evolutionary Biology</i> , 2010, 10, 8.	3.2	633
9	Patterns of Variant Polyadenylation Signal Usage in Human Genes. <i>Genome Research</i> , 2000, 10, 1001-1010.	2.4	603
10	Pandoraviruses: Amoeba Viruses with Genomes Up to 2.5 Mb Reaching That of Parasitic Eukaryotes. <i>Science</i> , 2013, 341, 281-286.	6.0	509
11	Thirty-thousand-year-old distant relative of giant icosahedral DNA viruses with a pandoravirus morphology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 4274-4279.	3.3	468
12	Patterns of Rare and Abundant Marine Microbial Eukaryotes. <i>Current Biology</i> , 2014, 24, 813-821.	1.8	450
13	Pan genome of the phytoplankton <i>Emiliania</i> underpins its global distribution. <i>Nature</i> , 2013, 499, 209-213.	13.7	448
14	The <i>Chlorella variabilis</i> NC64A Genome Reveals Adaptation to Photosymbiosis, Coevolution with Viruses, and Cryptic Sex. <i>Plant Cell</i> , 2010, 22, 2943-2955.	3.1	441
15	Mechanisms of Evolution in <i>Rickettsia conorii</i> and <i>R. prowazekii</i> . <i>Science</i> , 2001, 293, 2093-2098.	6.0	408
16	Marine protist diversity in European coastal waters and sediments as revealed by high-throughput sequencing. <i>Environmental Microbiology</i> , 2015, 17, 4035-4049.	1.8	384
17	A Holistic Approach to Marine Eco-Systems Biology. <i>PLoS Biology</i> , 2011, 9, e1001177.	2.6	353
18	Comparative Analysis of <i>Acinetobacters</i> : Three Genomes for Three Lifestyles. <i>PLoS ONE</i> , 2008, 3, e1805.	1.1	315

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19	Distant Mimivirus relative with a larger genome highlights the fundamental features of Megaviridae. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 17486-17491.	3.3	306
20	What If There Are Only 30,000 Human Genes?. Science, 2001, 291, 1255-1257.	6.0	299
21	The genome of the polar eukaryotic microalga <i>Coccomyxa subellipsoidea</i> reveals traits of cold adaptation. Genome Biology, 2012, 13, R39.	13.9	289
22	Genome Sequence of <i>Rickettsia bellii</i> Illuminates the Role of Amoebae in Gene Exchanges between Intracellular Pathogens. PLoS Genetics, 2006, 2, e76.	1.5	286
23	Three-Dimensional Reconstruction of the Giant Mimivirus Particle with an X-Ray Free-Electron Laser. Physical Review Letters, 2015, 114, 098102.	2.9	284
24	In-depth study of <i>Mollivirus sibericum</i> , a new 30,000-y-old giant virus infecting <i>Acanthamoeba</i> . Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5327-35.	3.3	284
25	Characterization of the Naturally Occurring Oxacillinase of <i>Acinetobacter baumannii</i> . Antimicrobial Agents and Chemotherapy, 2005, 49, 4174-4179.	1.4	254
26	Structural and Genomic Correlates of Hyperthermostability. Journal of Biological Chemistry, 2000, 275, 32383-32386.	1.6	246
27	FusionDB: a database for in-depth analysis of prokaryotic gene fusion events. Nucleic Acids Research, 2004, 32, 273D-276.	6.5	245
28	The Genome Sequence of <i>Rickettsia felis</i> Identifies the First Putative Conjugative Plasmid in an Obligate Intracellular Parasite. PLoS Biology, 2005, 3, e248.	2.6	242
29	The rapidly expanding universe of giant viruses: Mimivirus, Pandoravirus, Pithovirus and Mollivirus. FEMS Microbiology Reviews, 2015, 39, 779-796.	3.9	219
30	Large-Scale Statistical Analyses of Rice ESTs Reveal Correlated Patterns of Gene Expression. Genome Research, 1999, 9, 950-959.	2.4	216
31	The human gene damage index as a gene-level approach to prioritizing exome variants. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 13615-13620.	3.3	213
32	Viruses take center stage in cellular evolution. Genome Biology, 2006, 7, 110.	13.9	207
33	Implications of a Fab-like structure for the T-cell receptor. Trends in Immunology, 1989, 10, 10-14.	7.5	200
34	Exploring nucleo-cytoplasmic large DNA viruses in Tara Oceans microbial metagenomes. ISME Journal, 2013, 7, 1678-1695.	4.4	185
35	Genome-based design of a cell-free culture medium for <i>Tropheryma whippelii</i> . Lancet, The, 2003, 362, 447-449.	6.3	180
36	Mimivirus and its Virophage. Annual Review of Genetics, 2009, 43, 49-66.	3.2	178

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37	Genome of <i>Phaeocystis globosa</i> virus PgV-16T highlights the common ancestry of the largest known DNA viruses infecting eukaryotes. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 10800-10805.	3.3	178
38	Fewer Genes, More Noncoding RNA. Science, 2005, 309, 1529-1530.	6.0	177
39	Reductive Genome Evolution from the Mother of Rickettsia. PLoS Genetics, 2007, 3, e14.	1.5	167
40	<i>Tropheryma whipplei</i> Twist: A Human Pathogenic Actinobacteria With a Reduced Genome. Genome Research, 2003, 13, 1800-1809.	2.4	161
41	mRNA deep sequencing reveals 75 new genes and a complex transcriptional landscape in Mimivirus. Genome Research, 2010, 20, 664-674.	2.4	160
42	Mimivirus and the emerging concept of "giant" virus. Virus Research, 2006, 117, 133-144.	1.1	157
43	Positional clustering of differentially expressed genes on human chromosomes 20, 21 and 22. Genome Biology, 2003, 4, P1.	13.9	147
44	The Genome of <i>Borrelia recurrentis</i> , the Agent of Deadly Louse-Borne Relapsing Fever, Is a Degraded Subset of Tick-Borne <i>Borrelia duttonii</i> . PLoS Genetics, 2008, 4, e1000185.	1.5	146
45	Genomic Correlates of Hyperthermostability, an Update. Journal of Biological Chemistry, 2003, 278, 17198-17202.	1.6	142
46	Taxonomic distribution of large DNA viruses in the sea. Genome Biology, 2008, 9, R106.	13.9	140
47	Horizontal gene transfer of an entire metabolic pathway between a eukaryotic alga and its DNA virus. Genome Research, 2009, 19, 1441-1449.	2.4	139
48	Mimivirus Giant Particles Incorporate a Large Fraction of Anonymous and Unique Gene Products. Journal of Virology, 2006, 80, 11678-11685.	1.5	123
49	Lateral gene transfer between obligate intracellular bacteria: Evidence from the <i>Rickettsia massiliae</i> genome. Genome Research, 2007, 17, 1657-1664.	2.4	123
50	Diversity and evolution of the emerging Pandoraviridae family. Nature Communications, 2018, 9, 2285.	5.8	122
51	Molecular Evolution of <i>Rickettsia</i> Surface Antigens: Evidence of Positive Selection. Molecular Biology and Evolution, 2005, 22, 2073-2083.	3.5	119
52	Alternate Polyadenylation in Human mRNAs: A Large-Scale Analysis by EST Clustering. Genome Research, 1998, 8, 524-530.	2.4	117
53	Sedimentation of generalized systems of interacting particles. I. Solution of systems of complete Lamm equations. Biopolymers, 1975, 14, 1685-1700.	1.2	116
54	Selfish DNA in Protein-Coding Genes of <i>Rickettsia</i> . Science, 2000, 290, 347-350.	6.0	113

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55	Metagrowth: a new resource for the building of metabolic hypotheses in microbiology. <i>Nucleic Acids Research</i> , 2004, 33, D321-D324.	6.5	113
56	Information enhancement methods for large scale sequence analysis. <i>Computers & Chemistry</i> , 1993, 17, 191-201.	1.2	109
57	Mimivirus and Mimiviridae: Giant viruses with an increasing number of potential hosts, including corals and sponges. <i>Journal of Invertebrate Pathology</i> , 2009, 101, 172-180.	1.5	109
58	Escherichia coli ykfe ORFan Gene Encodes a Potent Inhibitor of C-type Lysozyme. <i>Journal of Biological Chemistry</i> , 2001, 276, 18437-18441.	1.6	105
59	Transcriptome analysis of functional differentiation between haploid and diploid cells of <i>Emiliania huxleyi</i> , a globally significant photosynthetic calcifying cell. <i>Genome Biology</i> , 2009, 10, R114.	13.9	105
60	Marine mimivirus relatives are probably large algal viruses. <i>Virology Journal</i> , 2008, 5, 12.	1.4	104
61	Mimivirus relatives in the Sargasso sea. <i>Virology Journal</i> , 2005, 2, 62.	1.4	96
62	MHC-Antigen Interaction: What Does the T Cell Receptor See?. <i>Advances in Immunology</i> , 1989, 45, 107-193.	1.1	95
63	Benthic protists: the under-charted majority. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw120.	1.3	94
64	Mimivirus: the emerging paradox of quasi-autonomous viruses. <i>Trends in Genetics</i> , 2010, 26, 431-437.	2.9	93
65	Heuristic informational analysis of sequences. <i>Nucleic Acids Research</i> , 1986, 14, 179-196.	6.5	92
66	Unsupervised classification of single-particle X-ray diffraction snapshots by spectral clustering. <i>Optics Express</i> , 2011, 19, 16542.	1.7	91
67	Noumeavirus replication relies on a transient remote control of the host nucleus. <i>Nature Communications</i> , 2017, 8, 15087.	5.8	91
68	Genome Analysis of the First Marseilleviridae Representative from Australia Indicates that Most of Its Genes Contribute to Virus Fitness. <i>Journal of Virology</i> , 2014, 88, 14340-14349.	1.5	90
69	CaspR: a web server for automated molecular replacement using homology modelling. <i>Nucleic Acids Research</i> , 2004, 32, W606-W609.	6.5	87
70	T-immunogenic peptides are constituted of rare sequence patterns. Use in the identification of T epitopes in the human immunodeficiency virus gag protein. <i>European Journal of Immunology</i> , 1988, 18, 1547-1554.	1.6	83
71	Genomics of Megavirus and the elusive fourth domain of Life. <i>Communicative and Integrative Biology</i> , 2012, 5, 102-106.	0.6	83
72	Breaking the 1000-gene barrier for Mimivirus using ultra-deep genome and transcriptome sequencing. <i>Virology Journal</i> , 2011, 8, 99.	1.4	81

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73	[15] k-tuple frequency analysis: From intron/exon discrimination to T-cell epitope mapping. <i>Methods in Enzymology</i> , 1990, 183, 237-252.	0.4	79
74	Mimivirus gene promoters exhibit an unprecedented conservation among all eukaryotes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 14689-14693.	3.3	79
75	Towards defining the chloroviruses: a genomic journey through a genus of large DNA viruses. <i>BMC Genomics</i> , 2013, 14, 158.	1.2	79
76	Virus-Encoded Aminoacyl-tRNA Synthetases: Structural and Functional Characterization of Mimivirus TyrRS and MetRS. <i>Journal of Virology</i> , 2007, 81, 12406-12417.	1.5	78
77	<i>Brucella microti</i> : the genome sequence of an emerging pathogen. <i>BMC Genomics</i> , 2009, 10, 352.	1.2	77
78	Structure and evolution of the Ivy protein family, unexpected lysozyme inhibitors in Gram-negative bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 6394-6399.	3.3	76
79	Some lessons from Rickettsia genomics. <i>FEMS Microbiology Reviews</i> , 2005, 29, 99-117.	3.9	75
80	Gene Expression in Proliferating Cells of the Dinoflagellate <i>Alexandrium catenella</i> (Dinophyceae). <i>Applied and Environmental Microbiology</i> , 2010, 76, 4521-4529.	1.4	71
81	Life-cycle modification in open oceans accounts for genome variability in a cosmopolitan phytoplankton. <i>ISME Journal</i> , 2015, 9, 1365-1377.	4.4	70
82	The polyadenylation site of Mimivirus transcripts obeys a stringent "hairpin rule". <i>Genome Research</i> , 2009, 19, 1233-1242.	2.4	69
83	Two new subfamilies of DNA mismatch repair proteins (MutS) specifically abundant in the marine environment. <i>ISME Journal</i> , 2011, 5, 1143-1151.	4.4	69
84	Structure of the <i>Escherichia coli</i> TolB protein determined by MAD methods at 1.95 Å resolution. <i>Structure</i> , 1999, 7, 1291-1300.	1.6	68
85	Mimiviridae: An Expanding Family of Highly Diverse Large dsDNA Viruses Infecting a Wide Phylogenetic Range of Aquatic Eukaryotes. <i>Viruses</i> , 2018, 10, 506.	1.5	68
86	Genome Analysis of <i>Minibacterium massiliensis</i> Highlights the Convergent Evolution of Water-Living Bacteria. <i>PLoS Genetics</i> , 2007, 3, e138.	1.5	64
87	Detection of eukaryotic promoters using Markov transition matrices. <i>Computers & Chemistry</i> , 1997, 21, 223-227.	1.2	61
88	Phydbac "Gene Function Predictor": a gene annotation tool based on genomic context analysis. <i>BMC Bioinformatics</i> , 2005, 6, 247.	1.2	59
89	Comparative Genomics of Chrysochromulina Ericina Virus and Other Microalga-Infecting Large DNA Viruses Highlights Their Intricate Evolutionary Relationship with the Established Mimiviridae Family. <i>Journal of Virology</i> , 2017, 91, .	1.5	59
90	A common philosophy and FORTRAN 77 software package for implementing and searching sequence databases. <i>Nucleic Acids Research</i> , 1984, 12, 397-407.	6.5	58

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91	MHC restriction, alloreactivity, and thymic education: A common link?. <i>Cell</i> , 1989, 56, 327-329.	13.5	57
92	Ten good reasons not to exclude giruses from the evolutionary picture. <i>Nature Reviews Microbiology</i> , 2009, 7, 615-615.	13.6	57
93	Structural genomics of highly conserved microbial genes of unknown function in search of new antibacterial targets. <i>Journal of Structural and Functional Genomics</i> , 2003, 4, 141-157.	1.2	56
94	The statistical significance of nucleotide position-weight matrix matches. <i>Bioinformatics</i> , 1996, 12, 431-439.	1.8	54
95	Open Questions About Giant Viruses. <i>Advances in Virus Research</i> , 2013, 85, 25-56.	0.9	53
96	Response to Comment on "The 1.2-Megabase Genome Sequence of Mimivirus". <i>Science</i> , 2005, 308, 1114b-1114b.	6.0	52
97	Remarkable sequence similarity between the dinoflagellate-infecting marine girus and the terrestrial pathogen African swine fever virus. <i>Virology Journal</i> , 2009, 6, 178.	1.4	51
98	Giant viruses: The difficult breaking of multiple epistemological barriers. <i>Studies in History and Philosophy of Science Part C: Studies in History and Philosophy of Biological and Biomedical Sciences</i> , 2016, 59, 89-99.	0.8	50
99	New genomic data and analyses challenge the traditional vision of animal epithelium evolution. <i>BMC Genomics</i> , 2018, 19, 393.	1.2	50
100	Protein Coding Palindromes Are a Unique but Recurrent Feature in <i>Rickettsia</i> . <i>Genome Research</i> , 2002, 12, 808-816.	2.4	49
101	Diatom diversity through HTS-metabarcoding in coastal European seas. <i>Scientific Reports</i> , 2018, 8, 18059.	1.6	48
102	Sedimentation of generalized systems of interacting particles. II. Active enzyme centrifugation?theory and extensions of its validity range. <i>Biopolymers</i> , 1975, 14, 1701-1716.	1.2	47
103	Detecting Frame Shifts by Amino Acid Sequence Comparison. <i>Journal of Molecular Biology</i> , 1993, 234, 1140-1157.	2.0	47
104	The Structure of <i>Acidithiobacillus ferrooxidans</i> c4-Cytochrome. <i>Structure</i> , 2003, 11, 547-555.	1.6	47
105	Structural variability and complexity of the giant Pithovirus sibericum particle revealed by high-voltage electron cryo-tomography and energy-filtered electron cryo-microscopy. <i>Scientific Reports</i> , 2017, 7, 13291.	1.6	47
106	Investigating the Concept and Origin of Viruses. <i>Trends in Microbiology</i> , 2020, 28, 959-967.	3.5	47
107	A Putative Role of de-Mono-ADP-Ribosylation of STAT1 by the SARS-CoV-2 Nsp3 Protein in the Cytokine Storm Syndrome of COVID-19. <i>Viruses</i> , 2020, 12, 646.	1.5	46
108	The insertion of palindromic repeats in the evolution of proteins. <i>Trends in Biochemical Sciences</i> , 2003, 28, 75-80.	3.7	45

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109	Horizontal gene transfer and nucleotide compositional anomaly in large DNA viruses. BMC Genomics, 2007, 8, 456.	1.2	44
110	Sequence patterns in protein kinases. Nature, 1988, 331, 22-22.	13.7	43
111	Quantitative Analysis of the T Cell Repertoire Selected by a Single Peptide—Major Histocompatibility Complex. Journal of Experimental Medicine, 1998, 187, 1871-1883.	4.2	43
112	Unique genes in giant viruses: Regular substitution pattern and anomalously short size. Genome Research, 2007, 17, 1353-1361.	2.4	42
113	In Vivo Evolution of Bacterial Resistance in Two Cases of Enterobacter aerogenes Infections during Treatment with Imipenem. PLoS ONE, 2015, 10, e0138828.	1.1	42
114	Sedimentation of generalized systems of interacting particles. III. Concentration-dependent sedimentation and extension to other transport methods. Biopolymers, 1976, 15, 843-857.	1.2	41
115	Some useful statistical properties of position-weight matrices. Computers & Chemistry, 1994, 18, 287-294.	1.2	41
116	Characterization of Mimivirus DNA Topoisomerase IB Suggests Horizontal Gene Transfer between Eukaryal Viruses and Bacteria. Journal of Virology, 2006, 80, 314-321.	1.5	41
117	SAmBA: An interactive software for optimizing the design of biological macromolecules crystallization experiments. , 1997, 29, 252-257.		40
118	A new example of viral intein in Mimivirus. Virology Journal, 2005, 2, 8.	1.4	40
119	The DNA methylation landscape of giant viruses. Nature Communications, 2020, 11, 2657.	5.8	40
120	Alu alert. Nature, 1994, 371, 752-752.	13.7	39
121	Giant DNA Virus Mimivirus Encodes Pathway for Biosynthesis of Unusual Sugar 4-Amino-4,6-dideoxy-d-glucose (Viosamine). Journal of Biological Chemistry, 2012, 287, 3009-3018.	1.6	38
122	Cryo-EM structure of a Marseilleviridae virus particle reveals a large internal microassembly. Virology, 2018, 516, 239-245.	1.1	37
123	The genome sequence of Brucella pinnipedialis B2/94 sheds light on the evolutionary history of the genus Brucella. BMC Evolutionary Biology, 2011, 11, 200.	3.2	36
124	Biased amino acid distributions in regions of the T cell receptors and MHC molecules potentially involved in their association. International Immunology, 1991, 3, 853-864.	1.8	35
125	Reverse transcriptase genes are highly abundant and transcriptionally active in marine plankton assemblages. ISME Journal, 2016, 10, 1134-1146.	4.4	35
126	Pandoravirus Celtis Illustrates the Microevolution Processes at Work in the Giant Pandoraviridae Genomes. Frontiers in Microbiology, 2019, 10, 430.	1.5	34

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127	Identifying coding exons by similarity search: Alu-derived and other potentially misleading protein sequences. <i>Genomics</i> , 1992, 12, 838-841.	1.3	32
128	A Streamlined Random Sequencing Strategy for Finding Coding Exons. <i>Genomics</i> , 1994, 23, 575-581.	1.3	29
129	Heart-specific genes revealed by expressed sequence tag (EST) sampling. <i>Genome Biology</i> , 2002, 3, research0074.1.	13.9	29
130	Phydbac2: improved inference of gene function using interactive phylogenomic profiling and chromosomal location analysis. <i>Nucleic Acids Research</i> , 2004, 32, W336-W339.	6.5	29
131	Characterization of <i>Mollivirus kamchatka</i> , the First Modern Representative of the Proposed <i>Molliviridae</i> Family of Giant Viruses. <i>Journal of Virology</i> , 2020, 94, .	1.5	29
132	Characterization and Chromosomal Assignment of a Human cDNA Encoding a Protein Related to the Murine 102-kDa Cadherin-Associated Protein (β -Catenin). <i>Genomics</i> , 1993, 15, 13-20.	1.3	28
133	The Megavirus Chilensis Cu,Zn-Superoxide Dismutase: the First Viral Structure of a Typical Cellular Copper Chaperone-Independent Hyperstable Dimeric Enzyme. <i>Journal of Virology</i> , 2015, 89, 824-832.	1.5	27
134	Reverse Transcriptase-Polymerase Chain Reaction Validation of 25 "Orphan" Genes from <i>Escherichia coli</i> K-12 MG1655. <i>Genome Research</i> , 2000, 10, 959-966.	2.4	26
135	Complete Genome Sequence of a New Member of the Marseilleviridae Recovered from the Brackish Submarine Spring in the Cassis Port-Miou Calanque, France. <i>Genome Announcements</i> , 2015, 3, .	0.8	26
136	Distribution patterns of microbial communities in ultramafic landscape: a metagenetic approach highlights the strong relationships between diversity and environmental traits. <i>Molecular Ecology</i> , 2016, 25, 2258-2272.	2.0	26
137	Isolation and characterisation of a murine cDNA clone highly homologous to the yeast L29 ribosomal protein gene. <i>Nucleic Acids Research</i> , 1987, 15, 1019-1029.	6.5	25
138	The difficulty of identifying genes in anonymous vertebrate sequences. <i>Computers & Chemistry</i> , 1997, 21, 203-214.	1.2	25
139	Determination of strongly overlapping signaling activity from microarray data. <i>BMC Bioinformatics</i> , 2006, 7, 99.	1.2	25
140	Translation in Giant Viruses: A Unique Mixture of Bacterial and Eukaryotic Termination Schemes. <i>PLoS Genetics</i> , 2012, 8, e1003122.	1.5	25
141	A strong propensity toward loop formation characterizes the expressed reading frames of the D segments at the Ig H and T cell receptor loci. <i>European Journal of Immunology</i> , 1991, 21, 3021-3025.	1.6	24
142	<i>Rickettsia felis</i> , from Culture to Genome Sequencing. <i>Annals of the New York Academy of Sciences</i> , 2005, 1063, 26-34.	1.8	24
143	CRISPR-Cas-like system in giant viruses: why MIMIVIRE is not likely to be an adaptive immune system. <i>Virologica Sinica</i> , 2016, 31, 193-196.	1.2	24
144	Phosphorylation of Intracellular Fructose in <i>Bacillus subtilis</i> Mediated by Phosphoenolpyruvate-l-Fructose Phosphotransferase. <i>FEBS Journal</i> , 1976, 66, 485-491.	0.2	23

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145	Conformational analysis of t immunogenic peptides by circular dichroism spectroscopy. <i>European Journal of Immunology</i> , 1989, 19, 1969-1972.	1.6	22
146	Identification of a major human immunodeficiency virus-1 reverse transcriptase epitope recognized by mouse CD4+ T lymphocytes. <i>European Journal of Immunology</i> , 1991, 21, 1371-1377.	1.6	22
147	Exploration of the propagation of transpovirons within Mimiviridae reveals a unique example of commensalism in the viral world. <i>ISME Journal</i> , 2020, 14, 727-739.	4.4	22
148	Expanding the Mimiviridae family using asparagine synthase as a sequence bait. <i>Virology</i> , 2014, 466-467, 112-122.	1.1	21
149	Visualizing the competitive recognition of TATA-boxes in vertebrate promoters. <i>Trends in Genetics</i> , 1998, 14, 10-11.	2.9	20
150	Crystal structure of <i>Escherichia coli</i> DkgA, a broad-specificity aldo-keto reductase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 302-307.	1.5	20
151	Tentative Mapping of Transcription-Induced Interchromosomal Interaction using Chimeric EST and mRNA Data. <i>PLoS ONE</i> , 2007, 2, e254.	1.1	20
152	Mimivirus TyrRS: preliminary structural and functional characterization of the first amino-acyl tRNA synthetase found in a virus. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 212-215.	0.7	19
153	Dissecting the Unique Nucleotide Specificity of Mimivirus Nucleoside Diphosphate Kinase. <i>Journal of Virology</i> , 2009, 83, 7142-7150.	1.5	19
154	â€œHiddenâ€•dUTPase Sequence in Human Immunodeficiency Virus Type 1 gp120. <i>Journal of Virology</i> , 1999, 73, 751-753.	1.5	19
155	Variability analysis of the human and mouse T-cell receptor ? chains. <i>Immunogenetics</i> , 1987, 26, 304-308.	1.2	18
156	Discovery of protein-coding palindromic repeats in <i>Wolbachia</i> . <i>Trends in Microbiology</i> , 2005, 13, 253-255.	3.5	18
157	Single-shot diffraction data from the Mimivirus particle using an X-ray free-electron laser. <i>Scientific Data</i> , 2016, 3, 160060.	2.4	18
158	A new protein sequence data bank. <i>Nature</i> , 1985, 318, 19-19.	13.7	17
159	Objective comparison of exon and intron sequences by the mean of 2-dimensional data analysis methods. <i>Nucleic Acids Research</i> , 1988, 16, 1729-1728.	6.5	17
160	The 474-Kilobase-Pair Complete Genome Sequence of CeV-01B, a Virus Infecting <i>Haptolina</i> (<i>Haptolina</i>). <i>Journal of Virology</i> , 2010, 84, 1000-1008.	6.8	17
161	mRNA maturation in giant viruses: variation on a theme. <i>Nucleic Acids Research</i> , 2015, 43, 3776-3788.	6.5	17
162	An appeal for an objective, open, and transparent scientific debate about the origin of SARS-CoV-2. <i>Lancet</i> , 2021, 398, 1402-1404.	6.3	17

#	ARTICLE	IF	CITATIONS
163	[14] Effective large-scale sequence similarity searches. <i>Methods in Enzymology</i> , 1996, 266, 212-227.	0.4	16
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