

Jean-Michel Claverie

List of Publications by Year in descending order

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Version: 2024-02-01

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	Metagenomic survey of the microbiome of ancient Siberian permafrost and modern Kamchatkan cryosols. <i>MicroLife</i> , 2022, 3, .	1.0	5
2	The WHO mission report struggles to trace the origins of the SARS-CoV-2 epidemic. <i>Virologie</i> , 2021, 25, 42-46.	0.1	0
3	An appeal for an objective, open, and transparent scientific debate about the origin of SARS-CoV-2. <i>Lancet, The</i> , 2021, 398, 1402-1404.	6.3	17
4	Validation of predicted anonymous proteins simply using Fisher's exact test. <i>Bioinformatics Advances</i> , 2021, 1, .	0.9	2
5	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
6	Fundamental Difficulties Prevent the Reconstruction of the Deep Phylogeny of Viruses. <i>Viruses</i> , 2020, 12, 1130.	1.5	10
7	Giant viruses. <i>Current Biology</i> , 2020, 30, R1108-R1110.	1.8	13
8	Investigating the Concept and Origin of Viruses. <i>Trends in Microbiology</i> , 2020, 28, 959-967.	3.5	47
9	The DNA methylation landscape of giant viruses. <i>Nature Communications</i> , 2020, 11, 2657.	5.8	40
10	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
11	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
12	Frozen Zoo: a collection of permafrost samples containing viable protists and their viruses. <i>Biodiversity Data Journal</i> , 2020, 8, e51586.	0.4	12
13	ACDtool: a web-server for the generic analysis of large data sets of counts. <i>Bioinformatics</i> , 2019, 35, 170-171.	1.8	5
14	Pandoravirus Celtis Illustrates the Microevolution Processes at Work in the Giant Pandoraviridae Genomes. <i>Frontiers in Microbiology</i> , 2019, 10, 430.	1.5	34
15	Editorial: Viruses, Genetic Exchange, and the Tree of Life. <i>Frontiers in Microbiology</i> , 2019, 10, 2782.	1.5	3
16	A Puzzling Anomaly in the 4-Mer Composition of the Giant Pandoravirus Genomes Reveals a Stringent New Evolutionary Selection Process. <i>Journal of Virology</i> , 2019, 93, .	1.5	9
17	Cryo-EM structure of a Marseilleviridae virus particle reveals a large internal microassembly. <i>Virology</i> , 2018, 516, 239-245.	1.1	37
18	Diatom diversity through HTS-metabarcoding in coastal European seas. <i>Scientific Reports</i> , 2018, 8, 18059.	1.6	48

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19	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
20	Exploring the microbiome of the freshwater diatom <i>Asterionella formosa</i> in a laboratory context. <i>Environmental Microbiology</i> , 2018, 20, 3601-3615.	1.8	6
21	New genomic data and analyses challenge the traditional vision of animal epithelium evolution. <i>BMC Genomics</i> , 2018, 19, 393.	1.2	50
22	Diversity and evolution of the emerging Pandoraviridae family. <i>Nature Communications</i> , 2018, 9, 2285.	5.8	122
23	Noumeavirus replication relies on a transient remote control of the host nucleus. <i>Nature Communications</i> , 2017, 8, 15087.	5.8	91
24	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
25	Complete mitochondrial genome sequence of the freshwater diatom <i>Asterionella formosa</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 97-98.	0.2	13
26	Re-emerging infectious diseases from the past: Hysteria or real risk?. <i>European Journal of Internal Medicine</i> , 2017, 44, 28-30.	1.0	10
27	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
28	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
29	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
30	Benthic protists: the under-charted majority. <i>FEMS Microbiology Ecology</i> , 2016, 92, f1w120.	1.3	94
31	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
32	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
33	Reverse transcriptase genes are highly abundant and transcriptionally active in marine plankton assemblages. <i>ISME Journal</i> , 2016, 10, 1134-1146.	4.4	35
34	Diversité des virus géants. <i>Virologie</i> , 2016, 20, 61-63.	0.1	3
35	The 474-Kilobase-Base Complete Genome Sequence of CeV-01B, a Virus Infecting <i>Haptolina</i> (Tj ETQq1 1 0.784314 rgBT /Overl...	0.8	17
36	Draft Genome Sequence of an Alphaproteobacterium Associated with the Mediterranean Sponge <i>Oscarella lobularis</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	11

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37	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
38	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
39	mRNA maturation in giant viruses: variation on a theme. <i>Nucleic Acids Research</i> , 2015, 43, 3776-3788.	6.5	17
40	Mitochondrial Genome Sequence of the Glass Sponge <i>Oopsacas minuta</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	4
41	From extraordinary endocytobionts to Pandoraviruses. Comment on Scheid et al.: Some secrets are revealed: Parasitic keratitis amoebae as vectors of the scarcely described pandoraviruses to humans. <i>Parasitology Research</i> , 2015, 114, 1625-1627.	0.6	7
42	Three-Dimensional Reconstruction of the Giant Mimivirus Particle with an X-Ray Free-Electron Laser. <i>Physical Review Letters</i> , 2015, 114, 098102.	2.9	284
43	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
44	The rapidly expanding universe of giant viruses: Mimivirus, Pandoravirus, Pithovirus and Mollivirus. <i>FEMS Microbiology Reviews</i> , 2015, 39, 779-796.	3.9	219
45	The human gene damage index as a gene-level approach to prioritizing exome variants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13615-13620.	3.3	213
46	In-depth study of <i>Mollivirus sibericum</i> , a new 30,000-y-old giant virus infecting <i>Acanthamoeba</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E5327-35.	3.3	284
47	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
48	In Vivo Evolution of Bacterial Resistance in Two Cases of <i>Enterobacter aerogenes</i> Infections during Treatment with Imipenem. <i>PLoS ONE</i> , 2015, 10, e0138828.	1.1	42
49	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
50	Patterns of Rare and Abundant Marine Microbial Eukaryotes. <i>Current Biology</i> , 2014, 24, 813-821.	1.8	450
51	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
52	Expanding the Mimiviridae family using asparagine synthase as a sequence bait. <i>Virology</i> , 2014, 466-467, 112-122.	1.1	21
53	Pan genome of the phytoplankton <i>Emiliana</i> underpins its global distribution. <i>Nature</i> , 2013, 499, 209-213.	13.7	448
54	Towards defining the chloroviruses: a genomic journey through a genus of large DNA viruses. <i>BMC Genomics</i> , 2013, 14, 158.	1.2	79

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55	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
56	Pandoraviruses: Amoeba Viruses with Genomes Up to 2.5 Mb Reaching That of Parasitic Eukaryotes. Science, 2013, 341, 281-286.	6.0	509
57	Open Questions About Giant Viruses. Advances in Virus Research, 2013, 85, 25-56.	0.9	53
58	Giant virus in the sea: Extending the realm of Megaviridae to Viridiplantae. Communicative and Integrative Biology, 2013, 6, e25685.	0.6	12
59	Exploring nucleo-cytoplasmic large DNA viruses in Tara Oceans microbial metagenomes. ISME Journal, 2013, 7, 1678-1695.	4.4	185
60	Are viruses viruses, after all?. Virologie, 2013, 17, 217-228.	0.1	1
61	Translation in Giant Viruses: A Unique Mixture of Bacterial and Eukaryotic Termination Schemes. PLoS Genetics, 2012, 8, e1003122.	1.5	25
62	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
63	Genomics of Megavirus and the elusive fourth domain of Life. Communicative and Integrative Biology, 2012, 5, 102-106.	0.6	83
64	The genome of the polar eukaryotic microalga <i>Coccomyxa subellipsoidea</i> reveals traits of cold adaptation. Genome Biology, 2012, 13, R39.	13.9	289
65	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
66	A Holistic Approach to Marine Eco-Systems Biology. PLoS Biology, 2011, 9, e1001177.	2.6	353
67	Breaking the 1000-gene barrier for Mimivirus using ultra-deep genome and transcriptome sequencing. Virology Journal, 2011, 8, 99.	1.4	81
68	Unsupervised classification of single-particle X-ray diffraction snapshots by spectral clustering. Optics Express, 2011, 19, 16542.	1.7	91
69	Two new subfamilies of DNA mismatch repair proteins (MutS) specifically abundant in the marine environment. ISME Journal, 2011, 5, 1143-1151.	4.4	69
70	The Conserved <i>Candida albicans</i> CA3427 Gene Product Defines a New Family of Proteins Exhibiting the Generic Periplasmic Binding Protein Structural Fold. PLoS ONE, 2011, 6, e18528.	1.1	1
71	Single mimivirus particles intercepted and imaged with an X-ray laser. Nature, 2011, 470, 78-81.	13.7	790
72	Mimivirus reveals Mre11/Rad50 fusion proteins with a sporadic distribution in eukaryotes, bacteria, viruses and plasmids. Virology Journal, 2011, 8, 427.	1.4	14

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73	The genome sequence of <i>Brucella pinnipedialis</i> B2/94 sheds light on the evolutionary history of the genus <i>Brucella</i> . <i>BMC Evolutionary Biology</i> , 2011, 11, 200.	3.2	36
74	Mimivirus: the emerging paradox of quasi-autonomous viruses. <i>Trends in Genetics</i> , 2010, 26, 431-437.	2.9	93
75	BLAST-EXPLORER helps you building datasets for phylogenetic analysis. <i>BMC Evolutionary Biology</i> , 2010, 10, 8.	3.2	633
76	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
77	mRNA deep sequencing reveals 75 new genes and a complex transcriptional landscape in Mimivirus. <i>Genome Research</i> , 2010, 20, 664-674.	2.4	160
78	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
79	Distribution of Giant Viruses in Marine Environments. , 2010, , 157-162.		3
80	Horizontal gene transfer of an entire metabolic pathway between a eukaryotic alga and its DNA virus. <i>Genome Research</i> , 2009, 19, 1441-1449.	2.4	139
81	The polyadenylation site of Mimivirus transcripts obeys a stringent "hairpin rule". <i>Genome Research</i> , 2009, 19, 1233-1242.	2.4	69
82	Dissecting the Unique Nucleotide Specificity of Mimivirus Nucleoside Diphosphate Kinase. <i>Journal of Virology</i> , 2009, 83, 7142-7150.	1.5	19
83	<i>Brucella microti</i> : the genome sequence of an emerging pathogen. <i>BMC Genomics</i> , 2009, 10, 352.	1.2	77
84	Ten good reasons not to exclude giruses from the evolutionary picture. <i>Nature Reviews Microbiology</i> , 2009, 7, 615-615.	13.6	57
85	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
86	Mimivirus and its Virophage. <i>Annual Review of Genetics</i> , 2009, 43, 49-66.	3.2	178
87	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
88	Transcriptome analysis of functional differentiation between haploid and diploid cells of <i>Emiliana huxleyi</i> , a globally significant photosynthetic calcifying cell. <i>Genome Biology</i> , 2009, 10, R114.	13.9	105
89	Structural characterization of CA1462, the <i>Candida albicans</i> thiamine pyrophosphokinase. <i>BMC Structural Biology</i> , 2008, 8, 33.	2.3	14
90	Marine mimivirus relatives are probably large algal viruses. <i>Virology Journal</i> , 2008, 5, 12.	1.4	104

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91	Taxonomic distribution of large DNA viruses in the sea. <i>Genome Biology</i> , 2008, 9, R106.	13.9	140
92	How to Infect a Mimivirus. <i>Science</i> , 2008, 321, 1305-1306.	6.0	12
93	Phylogeny.fr: robust phylogenetic analysis for the non-specialist. <i>Nucleic Acids Research</i> , 2008, 36, W465-W469.	6.5	4,135
94	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> . <i>PLoS Genetics</i> , 2008, 4, e1000185.	1.5	146
95	Comparative Analysis of Acinetobacters: Three Genomes for Three Lifestyles. <i>PLoS ONE</i> , 2008, 3, e1805.	1.1	315
96	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
97	Lateral gene transfer between obligate intracellular bacteria: Evidence from the <i>Rickettsia massiliae</i> genome. <i>Genome Research</i> , 2007, 17, 1657-1664.	2.4	123
98	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
99	Reductive Genome Evolution from the Mother of <i>Rickettsia</i> . <i>PLoS Genetics</i> , 2007, 3, e14.	1.5	167
100	Unique genes in giant viruses: Regular substitution pattern and anomalously short size. <i>Genome Research</i> , 2007, 17, 1353-1361.	2.4	42
101	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
102	Horizontal gene transfer and nucleotide compositional anomaly in large DNA viruses. <i>BMC Genomics</i> , 2007, 8, 456.	1.2	44
103	Tentative Mapping of Transcription-Induced Interchromosomal Interaction using Chimeric EST and mRNA Data. <i>PLoS ONE</i> , 2007, 2, e254.	1.1	20
104	Viruses take center stage in cellular evolution. <i>Genome Biology</i> , 2006, 7, 110.	13.9	207
105	Mimivirus and the emerging concept of "giant" virus. <i>Virus Research</i> , 2006, 117, 133-144.	1.1	157
106	The nucleoside diphosphate kinase from mimivirus: a peculiar affinity for deoxypyrimidine nucleotides. <i>Journal of Bioenergetics and Biomembranes</i> , 2006, 38, 247-254.	1.0	9
107	Determination of strongly overlapping signaling activity from microarray data. <i>BMC Bioinformatics</i> , 2006, 7, 99.	1.2	25
108	Impact of the Excision of an Ancient Repeat Insertion on <i>Rickettsia conorii</i> Guanylate Kinase Activity. <i>Molecular Biology and Evolution</i> , 2006, 23, 2112-2122.	3.5	14

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109	Genome Sequence of <i>Rickettsia bellii</i> Illuminates the Role of Amoebae in Gene Exchanges between Intracellular Pathogens. <i>PLoS Genetics</i> , 2006, 2, e76.	1.5	286
110	Characterization of Mimivirus DNA Topoisomerase IB Suggests Horizontal Gene Transfer between Eukaryal Viruses and Bacteria. <i>Journal of Virology</i> , 2006, 80, 314-321.	1.5	41
111	Comparative Genomics of Multidrug Resistance in <i>Acinetobacter baumannii</i> . <i>PLoS Genetics</i> , 2006, 2, e7.	1.5	677
112	Mimivirus Giant Particles Incorporate a Large Fraction of Anonymous and Unique Gene Products. <i>Journal of Virology</i> , 2006, 80, 11678-11685.	1.5	123
113	<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
114	Phydbac "Gene Function Predictor": a gene annotation tool based on genomic context analysis. <i>BMC Bioinformatics</i> , 2005, 6, 247.	1.2	59
115	Some lessons from <i>Rickettsia</i> genomics. <i>FEMS Microbiology Reviews</i> , 2005, 29, 99-117.	3.9	75
116	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
117	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
118	The Genome Sequence of <i>Rickettsia felis</i> Identifies the First Putative Conjugative Plasmid in an Obligate Intracellular Parasite. <i>PLoS Biology</i> , 2005, 3, e248.	2.6	242
119	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
120	Characterization of the Naturally Occurring Oxacillinase of <i>Acinetobacter baumannii</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2005, 49, 4174-4179.	1.4	254
121	Response to Comment on "The 1.2-Megabase Genome Sequence of Mimivirus". <i>Science</i> , 2005, 308, 1114b-1114b.	6.0	52
122	Molecular Evolution of <i>Rickettsia</i> Surface Antigens: Evidence of Positive Selection. <i>Molecular Biology and Evolution</i> , 2005, 22, 2073-2083.	3.5	119
123	Claverie, Jean-Michel. <i>Science</i> , 2005, 307, 1169-1169.	6.0	0
124	Bayesian Decomposition Analysis of Bacterial Phylogenomic Profiles. <i>Molecular Diagnosis and Therapy</i> , 2005, 5, 63-70.	3.3	3
125	Discovery of protein-coding palindromic repeats in <i>Wolbachia</i> . <i>Trends in Microbiology</i> , 2005, 13, 253-255.	3.5	18
126	Fewer Genes, More Noncoding RNA. <i>Science</i> , 2005, 309, 1529-1530.	6.0	177

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127	Mimivirus relatives in the Sargasso sea. <i>Virology Journal</i> , 2005, 2, 62.	1.4	96
128	A new example of viral intein in Mimivirus. <i>Virology Journal</i> , 2005, 2, 8.	1.4	40
129	Genome Analysis of Minibacterium massiliensis Highlights the Convergent Evolution of Water Living Bacteria. <i>PLoS Genetics</i> , 2005, preprint, e138.	1.5	1
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	Metagrowth: a new resource for the building of metabolic hypotheses in microbiology. <i>Nucleic Acids Research</i> , 2004, 33, D321-D324.	6.5	113
132	CaspR: a web server for automated molecular replacement using homology modelling. <i>Nucleic Acids Research</i> , 2004, 32, W606-W609.	6.5	87
133	FusionDB: a database for in-depth analysis of prokaryotic gene fusion events. <i>Nucleic Acids Research</i> , 2004, 32, 273D-276.	6.5	245
134	The 1.2-Megabase Genome Sequence of Mimivirus. <i>Science</i> , 2004, 306, 1344-1350.	6.0	959
135	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
136	The insertion of palindromic repeats in the evolution of proteins. <i>Trends in Biochemical Sciences</i> , 2003, 28, 75-80.	3.7	45
137	The Structure of Acidithiobacillus ferrooxidans c4-Cytochrome. <i>Structure</i> , 2003, 11, 547-555.	1.6	47
138	Genome-based design of a cell-free culture medium for Tropheryma whipplei. <i>Lancet, The</i> , 2003, 362, 447-449.	6.3	180
139	A Giant Virus in Amoebae. <i>Science</i> , 2003, 299, 2033-2033.	6.0	742
140	Positional clustering of differentially expressed genes on human chromosomes 20, 21 and 22. <i>Genome Biology</i> , 2003, 4, P1.	13.9	147
141	Phydbac (phylogenomic display of bacterial genes): an interactive resource for the annotation of bacterial genomes. <i>Nucleic Acids Research</i> , 2003, 31, 3720-3722.	6.5	12
142	Genomic Correlates of Hyperthermostability, an Update. <i>Journal of Biological Chemistry</i> , 2003, 278, 17198-17202.	1.6	142
143	<i>Tropheryma whipplei</i> Twist: A Human Pathogenic Actinobacteria With a Reduced Genome. <i>Genome Research</i> , 2003, 13, 1800-1809.	2.4	161
144	Protein Coding Palindromes Are a Unique but Recurrent Feature in Rickettsia. <i>Genome Research</i> , 2002, 12, 808-816.	2.4	49

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145	Heart-specific genes revealed by expressed sequence tag (EST) sampling. <i>Genome Biology</i> , 2002, 3, research0074.1.	13.9	29
146	In Search of New Anti-bacterial Target Genes: A Comparative/Structural Genomics Approach. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2002, 5, 511-522.	0.6	16
147	Mechanisms of Evolution in <i>Rickettsia conorii</i> and <i>R. prowazekii</i> . <i>Science</i> , 2001, 293, 2093-2098.	6.0	408
148	<i>Escherichia coli</i> ykfE ORFan Gene Encodes a Potent Inhibitor of C-type Lysozyme. <i>Journal of Biological Chemistry</i> , 2001, 276, 18437-18441.	1.6	105
149	Recent advances in computational genomics. <i>Pharmacogenomics</i> , 2001, 2, 361-372.	0.6	6
150	What If There Are Only 30,000 Human Genes?. <i>Science</i> , 2001, 291, 1255-1257.	6.0	299
151	Crystallization and preliminary crystallographic study of b0220, an 'ORFan' protein of unknown function from <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1694-1695.	2.5	5
152	Do we need a huge new centre to annotate the human genome?. <i>Nature</i> , 2000, 403, 12-12.	13.7	10
153	Structural and Genomic Correlates of Hyperthermostability. <i>Journal of Biological Chemistry</i> , 2000, 275, 32383-32386.	1.6	246
154	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
155	Patterns of Variant Polyadenylation Signal Usage in Human Genes. <i>Genome Research</i> , 2000, 10, 1001-1010.	2.4	603
156	Selfish DNA in Protein-Coding Genes of <i>Rickettsia</i> . <i>Science</i> , 2000, 290, 347-350.	6.0	113
157	Large-Scale Statistical Analyses of Rice ESTs Reveal Correlated Patterns of Gene Expression. <i>Genome Research</i> , 1999, 9, 950-959.	2.4	216
158	Crystallization and preliminary crystallographic study of HIP/PAP, a human C-lectin overexpressed in primary liver cancers. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1487-1489.	2.5	13
159	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
160	Hidden dUTPase Sequence in Human Immunodeficiency Virus Type 1 gp120. <i>Journal of Virology</i> , 1999, 73, 751-753.	1.5	19
161	Visualizing the competitive recognition of TATA-boxes in vertebrate promoters. <i>Trends in Genetics</i> , 1998, 14, 10-11.	2.9	20
162	Triple association of CDC25-, Dbl- and Sec7-related domains in mammalian guanine-nucleotide-exchange factors. <i>Trends in Biochemical Sciences</i> , 1998, 23, 472-473.	3.7	6

#	ARTICLE	IF	CITATIONS
163	Computational methods for exon detection. <i>Molecular Biotechnology</i> , 1998, 10, 27-48.	1.3	14
164	Crystallization and preliminary crystallographic study of a component of the Escherichia coli Tol system: TolB. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 102-104.	2.5	8
165	Quantitative Analysis of the T Cell Repertoire Selected by a Single Peptide's Major Histocompatibility Complex. <i>Journal of Experimental Medicine</i> , 1998, 187, 1871-1883.	4.2	43
166	Alternate Polyadenylation in Human mRNAs: A Large-Scale Analysis by EST's Clustering. <i>Genome Research</i> , 1998, 8, 524-530.	2.4	117
167	Exon Detection by Similarity Searches. , 1997, 68, 283-314.		7
168	The Significance of Digital Gene Expression's Profiles. <i>Genome Research</i> , 1997, 7, 986-995.	2.4	2,665
169	The difficulty of identifying genes in anonymous vertebrate sequences. <i>Computers & Chemistry</i> , 1997, 21, 203-214.	1.2	25
170	Detection of eukaryotic promoters using Markov transition matrices. <i>Computers & Chemistry</i> , 1997, 21, 223-227.	1.2	61
171	SAmBA: An interactive software for optimizing the design of biological macromolecules crystallization experiments. , 1997, 29, 252-257.		40
172	[14] Effective large-scale sequence similarity searches. <i>Methods in Enzymology</i> , 1996, 266, 212-227.	0.4	16
173	The statistical significance of nucleotide position-weight matrix matches. <i>Bioinformatics</i> , 1996, 12, 431-439.	1.8	54
174	Progress in Large-Scale Sequence Analysis. , 1996, , 161-208.		3
175	Nef and Gag Synthetic Peptide Priming of Antibody Responses to HIV Type 1 Antigens in Mice and Primates. <i>AIDS Research and Human Retroviruses</i> , 1994, 10, 1241-1250.	0.5	6
176	Some useful statistical properties of position-weight matrices. <i>Computers & Chemistry</i> , 1994, 18, 287-294.	1.2	41
177	Alu alert. <i>Nature</i> , 1994, 371, 752-752.	13.7	39
178	A Streamlined Random Sequencing Strategy for Finding Coding Exons. <i>Genomics</i> , 1994, 23, 575-581.	1.3	29
179	Shallow Shotgun Sequencing as a Strategy for Finding Coding Exons. , 1994, , 229-237.		0
180	Information enhancement methods for large scale sequence analysis. <i>Computers & Chemistry</i> , 1993, 17, 191-201.	1.2	109

#	ARTICLE	IF	CITATIONS
181	Characterization and Chromosomal Assignment of a Human cDNA Encoding a Protein Related to the Murine 102-kDa Cadherin-Associated Protein (\pm -Catenin). <i>Genomics</i> , 1993, 15, 13-20.	1.3	28
182	Detecting Frame Shifts by Amino Acid Sequence Comparison. <i>Journal of Molecular Biology</i> , 1993, 234, 1140-1157.	2.0	47
183	Identifying coding exons by similarity search: Alu-derived and other potentially misleading protein sequences. <i>Genomics</i> , 1992, 12, 838-841.	1.3	32
184	Sequence "signals": Artifact or reality?. <i>Computers & Chemistry</i> , 1992, 16, 89-91.	1.2	5
185	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
186	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
187	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
188	Biased amino acid distributions in regions of the T cell receptors and MHC molecules potentially involved in their association. <i>International Immunology</i> , 1991, 3, 853-864.	1.8	35
189	Smoothing profiles with sliding windows: better to wear a hat!. <i>Bioinformatics</i> , 1991, 7, 113-115.	1.8	5
190	[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
191	Protein instruction. <i>Nature</i> , 1990, 345, 121-122.	13.7	0
192	Conformational analysis of t immunogenic peptides by circular dichroism spectroscopy. <i>European Journal of Immunology</i> , 1989, 19, 1969-1972.	1.6	22
193	Implications of a Fab-like structure for the T-cell receptor. <i>Trends in Immunology</i> , 1989, 10, 10-14.	7.5	200
194	MHC restriction, alloreactivity, and thymic education: A common link?. <i>Cell</i> , 1989, 56, 327-329.	13.5	57
195	MHC-Antigen Interaction: What Does the T Cell Receptor See?. <i>Advances in Immunology</i> , 1989, 45, 107-193.	1.1	95
196	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
197	Sequence patterns in protein kinases. <i>Nature</i> , 1988, 331, 22-22.	13.7	43
198	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

#	ARTICLE	IF	CITATIONS
199	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
200	Variability analysis of the human and mouse T-cell receptor α chains. <i>Immunogenetics</i> , 1987, 26, 304-308.	1.2	18
201	T cells recognize antigen alone and not MHC molecules. <i>Trends in Immunology</i> , 1987, 8, 202-203.	7.5	4
202	Relevance of the lariat model to the splicing of the H-2 gene family. <i>FEBS Journal</i> , 1986, 160, 279-284.	0.2	3
203	Correct translation of protein coding regions in GenBank: a reply. <i>Trends in Biochemical Sciences</i> , 1986, 11, 381.	3.7	1
204	Heuristic informational analysis of sequences. <i>Nucleic Acids Research</i> , 1986, 14, 179-196.	6.5	92
205	A new protein sequence data bank. <i>Nature</i> , 1985, 318, 19-19.	13.7	17
206	Computer generation and statistical analysis of a data bank of protein sequences translated from GenBank. <i>Biochimie</i> , 1985, 67, 437-443.	1.3	14
207	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
208	Models for the rearrangements of immunoglobulin genes: a computer view. <i>Trends in Biochemical Sciences</i> , 1984, 9, 293-296.	3.7	15
209	T lymphoma variants with specifically altered growth in semi-solid media. <i>International Journal of Cancer</i> , 1983, 32, 641-643.	2.3	0
210	A new simple method to determine the diffusion coefficient from Active Enzyme Centrifugation experiments. <i>Archives of Biochemistry and Biophysics</i> , 1980, 202, 160-167.	1.4	6
211	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
212	Sedimentation of generalized systems of interacting particles. III. Concentration-dependent sedimentation and extension to other transport methods. <i>Biopolymers</i> , 1976, 15, 843-857.	1.2	41
213	Sedimentation of generalized systems of interacting particles. I. Solution of systems of complete Lamm equations. <i>Biopolymers</i> , 1975, 14, 1685-1700.	1.2	116
214	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