

# Gustavo Caetano-Anolles

## List of Publications by Year in descending order

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172  
papers

10,537  
citations

71004

43  
h-index

40945

97  
g-index

190  
all docs

190  
docs citations

190  
times ranked

8730  
citing authors

#	ARTICLE	IF	CITATIONS
1	Biological Networks across Scales—The Theoretical and Empirical Foundations for Time-Varying Complex Networks that Connect Structure and Function across Levels of Biological Organization. <i>Integrative and Comparative Biology</i> , 2022, 61, 1991-2010.	0.9	5
2	Recruitment: A Problem of Entangled Temporal Parts. <i>Frontiers in Bioscience</i> , 2022, 27, 128.	0.8	2
3	The emergence of SARS-CoV-2 variants of concern in Australia by haplotype coalescence reveals a continental link to COVID-19 seasonality. <i>Methods in Microbiology</i> , 2022, , 233-268.	0.4	2
4	The seasonal behaviour of COVID-19 and its galectin-like culprit of the viral spike. <i>Methods in Microbiology</i> , 2022, , 27-81.	0.4	3
5	Temperature and Latitude Correlate with SARS-CoV-2 Epidemiological Variables but not with Genomic Change Worldwide. <i>Evolutionary Bioinformatics</i> , 2021, 17, 117693432198969.	0.6	31
6	The tree of life describes a tripartite cellular world. <i>BioEssays</i> , 2021, 43, 2000343.	1.2	8
7	Menzerath—Altmann—™s Law of Syntax in RNA Accretion History. <i>Life</i> , 2021, 11, 489.	1.1	5
8	Evolution of networks of protein domain organization. <i>Scientific Reports</i> , 2021, 11, 12075.	1.6	23
9	The Tree of Life describes a tripartite cellular world: Neglected support from genome structure and codon usage and the fallacy of alignment—dependent phylogenetic interpretations. <i>BioEssays</i> , 2021, 43, 2100130.	1.2	2
10	The Compressed Vocabulary of Microbial Life. <i>Frontiers in Microbiology</i> , 2021, 12, 655990.	1.5	8
11	Tracing protein and proteome history with chronologies and networks: folding recapitulates evolution. <i>Expert Review of Proteomics</i> , 2021, 18, 863-880.	1.3	9
12	Genetic Structure of <i>Ralstonia solanacearum</i> and <i>Ralstonia pseudosolanacearum</i> in Brazil. <i>Plant Disease</i> , 2020, 104, 1019-1025.	0.7	10
13	Dual RNase and $\beta$ -lactamase Activity of a Single Enzyme Encoded in Archaea. <i>Life</i> , 2020, 10, 280.	1.1	12
14	The origin and evolution of viruses inferred from fold family structure. <i>Archives of Virology</i> , 2020, 165, 2177-2191.	0.9	20
15	New Pathways of Mutational Change in SARS-CoV-2 Proteomes Involve Regions of Intrinsic Disorder Important for Virus Replication and Release. <i>Evolutionary Bioinformatics</i> , 2020, 16, 117693432096514.	0.6	39
16	Bacterial Origin and Reductive Evolution of the CPR Group. <i>Genome Biology and Evolution</i> , 2020, 12, 103-121.	1.1	11
17	Editorial: Viruses, Genetic Exchange, and the Tree of Life. , 2020, , .		0
18	Multiple Arbitrary Amplicon Profiling Using Short Oligonucleotide Primers. , 2020, , 29-45.		1

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19	Human metallo-β-lactamase enzymes degrade penicillin. <i>Scientific Reports</i> , 2019, 9, 12173.	1.6	34
20	Genome-Wide Identification and Characterization of the Vacuolar H <sup>+</sup> -ATPase Subunit H Gene Family in Crop Plants. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5125.	1.8	9
21	Emergence of Hierarchical Modularity in Evolving Networks Uncovered by Phylogenomic Analysis. <i>Evolutionary Bioinformatics</i> , 2019, 15, 117693431987298.	0.6	11
22	MANET 3.0: Hierarchy and modularity in evolving metabolic networks. <i>PLoS ONE</i> , 2019, 14, e0224201.	1.1	14
23	Testing Empirical Support for Evolutionary Models that Root the Tree of Life. <i>Journal of Molecular Evolution</i> , 2019, 87, 131-142.	0.8	6
24	Horizontal gene transfer in human-associated microorganisms inferred by phylogenetic reconstruction and reconciliation. <i>Scientific Reports</i> , 2019, 9, 5953.	1.6	55
25	Editorial: Viruses, Genetic Exchange, and the Tree of Life. <i>Frontiers in Microbiology</i> , 2019, 10, 2782.	1.5	3
26	Genome-wide analysis of the MYB-CC gene family of maize. <i>Genetica</i> , 2019, 147, 1-9.	0.5	12
27	Phylogenetic profiling, an untapped resource for the prediction of secreted proteins and its complementation with sequence-based classifiers in bacterial type III, IV and VI secretion systems. <i>Briefings in Bioinformatics</i> , 2019, 20, 1395-1402.	3.2	18
28	Order and polarity in character state transformation models that root the tree of life. <i>Biochimie</i> , 2018, 149, 135-136.	1.3	8
29	Evolution of Macromolecular Structure: A "Double Tale" of Biological Accretion and Diversification. <i>Science Progress</i> , 2018, 101, 360-383.	1.0	9
30	Rooting Phylogenies and the Tree of Life While Minimizing Ad Hoc and Auxiliary Assumptions. <i>Evolutionary Bioinformatics</i> , 2018, 14, 117693431880510.	0.6	40
31	Ancestrality and Mosaicism of Giant Viruses Supporting the Definition of the Fourth TRUC of Microbes. <i>Frontiers in Microbiology</i> , 2018, 9, 2668.	1.5	44
32	Metabolite-Centric Reporter Pathway and Tripartite Network Analysis of Arabidopsis Under Cold Stress. <i>Frontiers in Bioengineering and Biotechnology</i> , 2018, 6, 121.	2.0	15
33	Archaea First and the Co-Evolutionary Diversification of Domains of Life. <i>BioEssays</i> , 2018, 40, e1800036.	1.2	15
34	Commercial Applications of DNA Profiling by Amplification with Arbitrary Oligonucleotide Primers. , 2018, , 131-146.		0
35	Mimivirus: leading the way in the discovery of giant viruses of amoebae. <i>Nature Reviews Microbiology</i> , 2017, 15, 243-254.	13.6	132
36	Long-term evolution of viruses: A Janus-faced balance. <i>BioEssays</i> , 2017, 39, 1700026.	1.2	22

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37	The Compressed Vocabulary of the Proteins of Archaea. , 2017, , 147-174.		7
38	RubisCO and the Search for Biomolecular Culprits of Planetary Change. BioEssays, 2017, 39, 1700174.	1.2	5
39	Phylotype and sequevar variability of <i>Ralstonia solanacearum</i> in Brazil, an ancient centre of diversity of the pathogen. Plant Pathology, 2017, 66, 383-392.	1.2	36
40	Identification of Capsid/Coat Related Protein Folds and Their Utility for Virus Classification. Frontiers in Microbiology, 2017, 8, 380.	1.5	21
41	Phylogenetic Tracings of Proteome Size Support the Gradual Accretion of Protein Structural Domains and the Early Origin of Viruses from Primordial Cells. Frontiers in Microbiology, 2017, 8, 1178.	1.5	32
42	Do Viruses Exchange Genes across Superkingdoms of Life?. Frontiers in Microbiology, 2017, 8, 2110.	1.5	23
43	The natural history of molecular functions inferred from an extensive phylogenomic analysis of gene ontology data. PLoS ONE, 2017, 12, e0176129.	1.1	12
44	Piecemeal Buildup of the Genetic Code, Ribosomes, and Genomes from Primordial tRNA Building Blocks. Life, 2016, 6, 43.	1.1	38
45	Arguments Reinforcing the Three-Domain View of Diversified Cellular Life. Archaea, 2016, 2016, 1-11.	2.3	25
46	Genomic characterization of plant cell wall degrading enzymes and in silico analysis of xylanases and polygalacturonases of <i>Fusarium virguliforme</i> . BMC Microbiology, 2016, 16, 147.	1.3	46
47	The early history and emergence of molecular functions and modular scale-free network behavior. Scientific Reports, 2016, 6, 25058.	1.6	58
48	A Dynamic Model for the Evolution of Protein Structure. Journal of Molecular Evolution, 2016, 82, 230-243.	0.8	11
49	The Phylogenomic Roots of Translation. , 2016, , 9-30.		0
50	Creationism and intelligent design are incompatible with scientific progress: A response to Shanta and VÃ³danta. Communicative and Integrative Biology, 2016, 9, e1123356.	0.6	4
51	Commentary: History of the ribosome and the origin of translation. Frontiers in Molecular Biosciences, 2016, 3, 87.	1.6	13
52	Investigating the Control of Chlorophyll Degradation by Genomic Correlation Mining. PLoS ONE, 2016, 11, e0162327.	1.1	33
53	The organization of domains in proteins obeys Menzerath-Altmann's law of language. BMC Systems Biology, 2015, 9, 44.	3.0	27
54	Ribosomal accretion, apriorism and the phylogenetic method: a response to Petrov and Williams. Frontiers in Genetics, 2015, 6, 194.	1.1	12

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55	Untangling the origin of viruses and their impact on cellular evolution. <i>Annals of the New York Academy of Sciences</i> , 2015, 1341, 61-74.	1.8	30
56	The absence of protein Y4yS affects negatively the abundance of T3SS <i>Mesorhizobium loti</i> secretin, RhcC2, in bacterial membranes. <i>Frontiers in Plant Science</i> , 2015, 6, 12.	1.7	19
57	Lokiarchaeota: eukaryote-like missing links from microbial dark matter?. <i>Trends in Microbiology</i> , 2015, 23, 448-450.	3.5	24
58	Ancestral Insertions and Expansions of rRNA do not Support an Origin of the Ribosome in Its Peptidyl Transferase Center. <i>Journal of Molecular Evolution</i> , 2015, 80, 162-165.	0.8	21
59	A phylogenomic data-driven exploration of viral origins and evolution. <i>Science Advances</i> , 2015, 1, e1500527.	4.7	158
60	Computing the origin and evolution of the ribosome from its structure " Uncovering processes of macromolecular accretion benefiting synthetic biology. <i>Computational and Structural Biotechnology Journal</i> , 2015, 13, 427-447.	1.9	26
61	Archaea: The First Domain of Diversified Life. <i>Archaea</i> , 2014, 2014, 1-26.	2.3	27
62	A Phylogenomic Census of Molecular Functions Identifies Modern Thermophilic Archaea as the Most Ancient Form of Cellular Life. <i>Archaea</i> , 2014, 2014, 1-15.	2.3	21
63	The Origin and Evolution of the Archaeal Domain. <i>Archaea</i> , 2014, 2014, 1-2.	2.3	1
64	The distribution and impact of viral lineages in domains of life. <i>Frontiers in Microbiology</i> , 2014, 5, 194.	1.5	42
65	The natural history of transfer RNA and its interactions with the ribosome. <i>Frontiers in Genetics</i> , 2014, 5, 127.	1.1	27
66	The Natural History of Biocatalytic Mechanisms. <i>PLoS Computational Biology</i> , 2014, 10, e1003642.	1.5	30
67	Global Patterns of Protein Domain Gain and Loss in Superkingdoms. <i>PLoS Computational Biology</i> , 2014, 10, e1003452.	1.5	65
68	A calibrated chronology of biochemistry reveals a stem line of descent responsible for planetary biodiversity. <i>Frontiers in Genetics</i> , 2014, 5, 306.	1.1	11
69	A Tree of Cellular Life Inferred from a Genomic Census of Molecular Functions. <i>Journal of Molecular Evolution</i> , 2014, 79, 240-262.	0.8	25
70	The importance of using realistic evolutionary models for retrodicting proteomes. <i>Biochimie</i> , 2014, 99, 129-137.	1.3	17
71	Fast Folding as a Constraint in the Evolution of Protein Structures. <i>Biophysical Journal</i> , 2013, 104, 370a.	0.2	0
72	Evolutionary Optimization of Protein Folding. <i>PLoS Computational Biology</i> , 2013, 9, e1002861.	1.5	44

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73	The Coevolutionary Roots of Biochemistry and Cellular Organization Challenge the RNA World Paradigm. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2013, 23, 152-177.	1.0	40
74	Phylogenomics Supports a Cellularly Structured Urancestor. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2013, 23, 178-191.	1.0	10
75	Origin and Evolution of Protein Fold Designs Inferred from Phylogenomic Analysis of CATH Domain Structures in Proteomes. <i>PLoS Computational Biology</i> , 2013, 9, e1003009.	1.5	44
76	Widespread Recruitment of Ancient Domain Structures in Modern Enzymes during Metabolic Evolution. <i>Journal of Integrative Bioinformatics</i> , 2013, 10, 1-18.	1.0	4
77	CLUSTOM: A Novel Method for Clustering 16S rRNA Next Generation Sequences by Overlap Minimization. <i>PLoS ONE</i> , 2013, 8, e62623.	1.1	18
78	A General Framework of Persistence Strategies for Biological Systems Helps Explain Domains of Life. <i>Frontiers in Genetics</i> , 2013, 4, 16.	1.1	27
79	Comparative Analysis of Proteomes and Functionomes Provides Insights into Origins of Cellular Diversification. <i>Archaea</i> , 2013, 2013, 1-13.	2.3	17
80	Comparative Analysis of Barophily-Related Amino Acid Content in Protein Domains of <i>Pyrococcus abyssi</i> and <i>Pyrococcus furiosus</i> . <i>Archaea</i> , 2013, 2013, 1-9.	2.3	7
81	Structural Phylogenomics Reveals Gradual Evolutionary Replacement of Abiotic Chemistries by Protein Enzymes in Purine Metabolism. <i>PLoS ONE</i> , 2013, 8, e59300.	1.1	24
82	Structural Phylogenomics Retrodicts the Origin of the Genetic Code and Uncovers the Evolutionary Impact of Protein Flexibility. <i>PLoS ONE</i> , 2013, 8, e72225.	1.1	61
83	Widespread recruitment of ancient domain structures in modern enzymes during metabolic evolution. <i>Journal of Integrative Bioinformatics</i> , 2013, 10, 214.	1.0	10
84	The Impact of Oxygen on Metabolic Evolution: A Chemoinformatic Investigation. <i>PLoS Computational Biology</i> , 2012, 8, e1002426.	1.5	23
85	Viral evolution. <i>Mobile Genetic Elements</i> , 2012, 2, 247-252.	1.8	35
86	Evolution of Protein Architecture for Mechanical Function. <i>Biophysical Journal</i> , 2012, 102, 251a-252a.	0.2	0
87	Stress induces biphasic-rewiring and modularization patterns in the metabolomic networks of <i>Escherichia coli</i> . , 2012, , .		2
88	Structural phylogenomics uncovers the early and concurrent origins of cysteine biosynthesis and iron-sulfur proteins. <i>Journal of Biomolecular Structure and Dynamics</i> , 2012, 30, 542-545.	2.0	6
89	Giant viruses coexisted with the cellular ancestors and represent a distinct supergroup along with superkingdoms Archaea, Bacteria and Eukarya. <i>BMC Evolutionary Biology</i> , 2012, 12, 156.	3.2	110
90	Ribosomal History Reveals Origins of Modern Protein Synthesis. <i>PLoS ONE</i> , 2012, 7, e32776.	1.1	134

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91	Biphasic patterns of diversification and the emergence of modules. <i>Frontiers in Genetics</i> , 2012, 3, 147.	1.1	24
92	Benefits of using molecular structure and abundance in phylogenomic analysis. <i>Frontiers in Genetics</i> , 2012, 3, 172.	1.1	32
93	The Phylogenomic Roots of Modern Biochemistry: Origins of Proteins, Cofactors and Protein Biosynthesis. <i>Journal of Molecular Evolution</i> , 2012, 74, 1-34.	0.8	73
94	Protein Domain Structure Uncovers the Origin of Aerobic Metabolism and the Rise of Planetary Oxygen. <i>Structure</i> , 2012, 20, 67-76.	1.6	53
95	The evolutionary history of protein fold families and proteomes confirms that the archaeal ancestor is more ancient than the ancestors of other superkingdoms. <i>BMC Evolutionary Biology</i> , 2012, 12, 13.	3.2	57
96	Reductive evolution of proteomes and protein structures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11954-11958.	3.3	75
97	A Universal Molecular Clock of Protein Folds and Its Power in Tracing the Early History of Aerobic Metabolism and Planet Oxygenation. <i>Molecular Biology and Evolution</i> , 2011, 28, 567-582.	3.5	127
98	Annotation of Protein Domains Reveals Remarkable Conservation in the Functional Make up of Proteomes Across Superkingdoms. <i>Genes</i> , 2011, 2, 869-911.	1.0	22
99	Proteome Evolution and the Metabolic Origins of Translation and Cellular Life. <i>Journal of Molecular Evolution</i> , 2011, 72, 14-33.	0.8	57
100	Evolution of vacuolar proton pyrophosphatase domains and volutin granules: clues into the early evolutionary origin of the acidocalcisome. <i>Biology Direct</i> , 2011, 6, 50.	1.9	45
101	The proteomic complexity and rise of the primordial ancestor of diversified life. <i>BMC Evolutionary Biology</i> , 2011, 11, 140.	3.2	83
102	Comparative Genomic and Phylogenetic Analyses Reveal the Evolution of the Core Two-Component Signal Transduction Systems in Enterobacteria. <i>Journal of Molecular Evolution</i> , 2010, 70, 167-180.	0.8	15
103	The Origin of Modern 5S rRNA: A Case of Relating Models of Structural History to Phylogenetic Data. <i>Journal of Molecular Evolution</i> , 2010, 71, 3-5.	0.8	8
104	The ancient history of the structure of ribonuclease P and the early origins of Archaea. <i>BMC Bioinformatics</i> , 2010, 11, 153.	1.2	43
105	Exploring the interplay of stability and function in protein evolution. <i>BioEssays</i> , 2010, 32, 655-658.	1.2	15
106	Emergence and Evolution of Modern Molecular Functions Inferred from Phylogenomic Analysis of Ontological Data. <i>Molecular Biology and Evolution</i> , 2010, 27, 1710-1733.	3.5	43
107	History of biological metal utilization inferred through phylogenomic analysis of protein structures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 10567-10572.	3.3	264
108	The Evolutionary Mechanics of Domain Organization in Proteomes and the Rise of Modularity in the Protein World. <i>Structure</i> , 2009, 17, 66-78.	1.6	113

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109	The evolutionary significance of the long variable arm in transfer RNA. <i>Complexity</i> , 2009, 14, 26-39.	0.9	11
110	The Evolutionary History of the Structure of 5S Ribosomal RNA. <i>Journal of Molecular Evolution</i> , 2009, 69, 430-443.	0.8	49
111	The origin, evolution and structure of the protein world. <i>Biochemical Journal</i> , 2009, 417, 621-637.	1.7	201
112	The origin and evolution of modern metabolism. <i>International Journal of Biochemistry and Cell Biology</i> , 2009, 41, 285-297.	1.2	105
113	The Origin and Evolution of tRNA Inferred from Phylogenetic Analysis of Structure. <i>Journal of Molecular Evolution</i> , 2008, 66, 21-35.	0.8	77
114	Evolutionary Patterns in the Sequence and Structure of Transfer RNA: Early Origins of Archaea and Viruses. <i>PLoS Computational Biology</i> , 2008, 4, e1000018.	1.5	40
115	NOBAL: a web server for character coding of geometrical and statistical features in RNA structure. <i>Nucleic Acids Research</i> , 2008, 36, W85-W90.	6.5	13
116	An approach of orthology detection from homologous sequences under minimum evolution. <i>Nucleic Acids Research</i> , 2008, 36, e110-e110.	6.5	26
117	Transfer RNA and the Origins of Diversified Life. <i>Science Progress</i> , 2008, 91, 265-284.	1.0	20
118	Introductory Editorial. <i>Genomics Insights</i> , 2008, 1, 117863100800100.	3.0	0
119	Evolutionary Patterns in the Sequence and Structure of Transfer RNA: A Window into Early Translation and the Genetic Code. <i>PLoS ONE</i> , 2008, 3, e2799.	1.1	29
120	Origins and evolution of modern biochemistry: insights from genomes and molecular structure. <i>Frontiers in Bioscience - Landmark</i> , 2008, Volume, 5212.	3.0	16
121	Evolutionary Genomics: Linking Macromolecular Structure, Genomes and Biological Networks. <i>Soil Biology</i> , 2008, , 155-181.	0.6	0
122	The origin of modern metabolic networks inferred from phylogenomic analysis of protein architecture. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 9358-9363.	3.3	153
123	Reductive evolution of architectural repertoires in proteomes and the birth of the tripartite world. <i>Genome Research</i> , 2007, 17, 1572-1585.	2.4	120
124	Gene-interleaving patterns of synteny in the <i>Saccharomyces cerevisiae</i> genome: are they proof of an ancient genome duplication event?. <i>Biology Direct</i> , 2007, 2, 23.	1.9	8
125	Common evolutionary trends for SINE RNA structures. <i>Trends in Genetics</i> , 2007, 23, 26-33.	2.9	68
126	MANET: tracing evolution of protein architecture in metabolic networks. <i>BMC Bioinformatics</i> , 2006, 7, 351.	1.2	48



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127	A phylogenomic reconstruction of the protein world based on a genomic census of protein fold architecture. <i>Complexity</i> , 2006, 12, 27-40.	0.9	33
128	Global Phylogeny Determined by the Combination of Protein Domains in Proteomes. <i>Molecular Biology and Evolution</i> , 2006, 23, 2444-2454.	3.5	85
129	Universal Sharing Patterns in Proteomes and Evolution of Protein Fold Architecture and Life. <i>Journal of Molecular Evolution</i> , 2005, 60, 484-498.	0.8	46
130	Grass Evolution Inferred from Chromosomal Rearrangements and Geometrical and Statistical Features in RNA Structure. <i>Journal of Molecular Evolution</i> , 2005, 60, 635-652.	0.8	25
131	Evolution of Genome Size in the Grasses. <i>Crop Science</i> , 2005, 45, 1809-1816.	0.8	65
132	An Evolutionarily Structured Universe of Protein Architecture. <i>Genome Research</i> , 2003, 13, 1563-1571.	2.4	146
133	Extensive and specific responses of a eukaryote to bacterial quorum-sensing signals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 1444-1449.	3.3	474
134	Population genetics and spatial structure of the fairy ring fungus <i>Marasmius oreades</i> in a Norwegian sand dune ecosystem. <i>Mycologia</i> , 2003, 95, 1021-1031.	0.8	20
135	Tracing the evolution of RNA structure in ribosomes. <i>Nucleic Acids Research</i> , 2002, 30, 2575-2587.	6.5	105
136	Evolved RNA Secondary Structure and the Rooting of the Universal Tree of Life. <i>Journal of Molecular Evolution</i> , 2002, 54, 333-345.	0.8	74
137	Patterns of evolution in <i>Discaria</i> fungi and the origin of dogwood anthracnose in North America, studied using arbitrarily amplified and ribosomal DNA. <i>Current Genetics</i> , 2001, 39, 346-354.	0.8	14
138	High genome-wide mutation rates in vegetatively propagated bermudagrass. <i>Molecular Ecology</i> , 1999, 8, 1211-1221.	2.0	28
139	Title is missing!. <i>Euphytica</i> , 1998, 101, 165-173.	0.6	22
140	DNA Analysis of Turfgrass Genetic Diversity. <i>Crop Science</i> , 1998, 38, 1415-1424.	0.8	29
141	DAF Optimization Using Taguchi Methods and the Effect of Thermal Cycling Parameters on DNA Amplification. <i>BioTechniques</i> , 1998, 25, 472-480.	0.8	30
142	Molecular dissection and improvement of the nodule symbiosis in legumes. <i>Field Crops Research</i> , 1997, 53, 47-68.	2.3	23
143	The Origin of Bermudagrass ( <i>Cynodon</i> ) Offspring Types Inferred by DNA Amplification Fingerprinting. <i>Crop Science</i> , 1997, 37, 81-87.	0.8	37
144	Generation of Sequence Signatures from DNA Amplification Fingerprints with Mini-Hairpin and Microsatellite Primers. <i>BioTechniques</i> , 1996, 20, 1044-1056.	0.8	30

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145	Advances in the positional cloning of nodulation genes in soybean. <i>Plant and Soil</i> , 1996, 186, 1-7.	1.8	6
146	Scanning of nucleic acids by in vitro amplification: New developments and applications. <i>Nature Biotechnology</i> , 1996, 14, 1668-1674.	9.4	39
147	Nucleic Acid Scanning-by-Hybridization of Enterohemorrhagic <i>Escherichia Coli</i> Isolates Using Oligodeoxynucleotide Arrays. <i>Nucleic Acids Research</i> , 1996, 24, 5056-5057.	6.5	13
148	Advances in the positional cloning of nodulation genes in soybean. , 1996, , 1-7.		1
149	DNA amplification fingerprinting provides evidence that <i>Discula destructiva</i> , the cause of dogwood anthracnose in North America, is an introduced pathogen. <i>Mycologia</i> , 1995, 87, 490-500.	0.8	37
150	DNA Amplification Fingerprinting and Hybridization Analysis of Centipede grass. <i>Crop Science</i> , 1995, 35, 881-885.	0.8	29
151	DNA Amplification Fingerprinting Using Arbitrary Mini-hairpin Oligonucleotide Primers. <i>Nature Biotechnology</i> , 1994, 12, 619-623.	9.4	42
152	Enhanced detection of polymorphic DNA by multiple arbitrary amplicon profiling of endonuclease-digested DNA: identification of markers tightly linked to the supernodulation locus in soybean. <i>Molecular Genetics and Genomics</i> , 1993, 241-241, 57-64.	2.4	42
153	DNA amplification fingerprinting using arbitrary oligonucleotide primers. <i>Applied Biochemistry and Biotechnology</i> , 1993, 42, 189-200.	1.4	44
154	Silver staining of DNA in polyacrylamide gels. <i>Applied Biochemistry and Biotechnology</i> , 1993, 42, 181-188.	1.4	121
155	Amplifying DNA with arbitrary oligonucleotide primers.. <i>Genome Research</i> , 1993, 3, 85-94.	2.4	241
156	Growth and Movement of Spot Inoculated <i>Rhizobium meliloti</i> on the Root Surface of Alfalfa. <i>Plant Physiology</i> , 1992, 98, 1181-1189.	2.3	46
157	Anatomical analysis of nodule development in soybean reveals an additional autoregulatory control point. <i>Plant Science</i> , 1992, 85, 1-7.	1.7	16
158	Primer-template interactions during DNA amplification fingerprinting with single arbitrary oligonucleotides. <i>Molecular Genetics and Genomics</i> , 1992, 235, 157-165.	2.4	111
159	Plant Genetic Control of Nodulation. <i>Annual Review of Microbiology</i> , 1991, 45, 345-382.	2.9	459
160	Excision of Nodules Induced by <i>Rhizobium meliloti</i> Exopolysaccharide Mutants Releases Autoregulation in Alfalfa. <i>Journal of Plant Physiology</i> , 1991, 138, 765-767.	1.6	10
161	Mature Nodules and Root Tips Control Nodulation in Soybean. <i>Journal of Plant Physiology</i> , 1991, 137, 389-396.	1.6	47
162	DNA amplification fingerprinting: A strategy for genome analysis. <i>Plant Molecular Biology Reporter</i> , 1991, 9, 294-307.	1.0	92

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163	Fast and sensitive silver staining of DNA in polyacrylamide gels. Analytical Biochemistry, 1991, 196, 80-83.	1.1	2,497
164	DNA Amplification Fingerprinting Using Very Short Arbitrary Oligonucleotide Primers. Nature Biotechnology, 1991, 9, 553-557.	9.4	514
165	Alfalfa Controls Nodulation during the Onset of <i>Rhizobium</i> -induced Cortical Cell Division. Plant Physiology, 1991, 95, 366-373.	2.3	70
166	Chemotaxis, induced gene expression and competitiveness in the rhizosphere. , 1991, , 155-162.		2
167	Efficiency of Nodule Initiation and Autoregulatory Responses in a Supernodulating Soybean Mutant. Applied and Environmental Microbiology, 1991, 57, 2205-2210.	1.4	26
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