

Graziano Pesole

List of Publications by Year in descending order

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Version: 2024-02-01

330
papers

30,582
citations

12330

69
h-index

5394

164
g-index

355
all docs

355
docs citations

355
times ranked

39216
citing authors

#	ARTICLE	IF	CITATIONS
1	The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla. <i>Nature</i> , 2007, 449, 463-467.	27.8	3,384
2	The Transcriptional Landscape of the Mammalian Genome. <i>Science</i> , 2005, 309, 1559-1563.	12.6	3,227
3	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	27.8	1,886
4	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. <i>Nature</i> , 2002, 420, 563-573.	27.8	1,548
5	Assessing computational tools for the discovery of transcription factor binding sites. <i>Nature Biotechnology</i> , 2005, 23, 137-144.	17.5	1,121
6	Genome sequence of the metazoan plant-parasitic nematode <i>Meloidogyne incognita</i> . <i>Nature Biotechnology</i> , 2008, 26, 909-915.	17.5	1,012
7	Untranslated regions of mRNAs. <i>Genome Biology</i> , 2002, 3, reviews0004.1.	9.6	779
8	Functional annotation of a full-length mouse cDNA collection. <i>Nature</i> , 2001, 409, 685-690.	27.8	653
9	Evolution of the mitochondrial genome of Metazoa as exemplified by comparison of congeneric species. <i>Heredity</i> , 2008, 101, 301-320.	2.6	515
10	Mammalian mitochondrial D-loop region structural analysis: identification of new conserved sequences and their functional and evolutionary implications. <i>Gene</i> , 1997, 205, 125-140.	2.2	437
11	Weeder Web: discovery of transcription factor binding sites in a set of sequences from co-regulated genes. <i>Nucleic Acids Research</i> , 2004, 32, W199-W203.	14.5	435
12	Evolutionary genomics in Metazoa: the mitochondrial DNA as a model system. <i>Gene</i> , 1999, 238, 195-209.	2.2	396
13	Nucleotide Substitution Rate of Mammalian Mitochondrial Genomes. <i>Journal of Molecular Evolution</i> , 1999, 48, 427-434.	1.8	395
14	Pscan: finding over-represented transcription factor binding site motifs in sequences from co-regulated or co-expressed genes. <i>Nucleic Acids Research</i> , 2009, 37, W247-W252.	14.5	377
15	Structural and functional features of eukaryotic mRNA untranslated regions. <i>Gene</i> , 2001, 276, 73-81.	2.2	365
16	Asymmetrical directional mutation pressure in the mitochondrial genome of mammals. <i>Molecular Biology and Evolution</i> , 1998, 15, 957-966.	8.9	342
17	The guinea-pig is not a rodent. <i>Nature</i> , 1996, 381, 597-600.	27.8	339
18	The main regulatory region of mammalian mitochondrial DNA: Structure-function model and evolutionary pattern. <i>Journal of Molecular Evolution</i> , 1991, 33, 83-91.	1.8	305

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19	UTRdb and UTRsite (RELEASE 2010): a collection of sequences and regulatory motifs of the untranslated regions of eukaryotic mRNAs. <i>Nucleic Acids Research</i> , 2010, 38, D75-D80.	14.5	285
20	An algorithm for finding signals of unknown length in DNA sequences. <i>Bioinformatics</i> , 2001, 17, S207-S214.	4.1	279
21	REDIportal: a comprehensive database of A-to-I RNA editing events in humans. <i>Nucleic Acids Research</i> , 2017, 45, D750-D757.	14.5	256
22	Endogenous murine microbiota member <i>Faecalibaculum rodentium</i> and its human homologue protect from intestinal tumour growth. <i>Nature Microbiology</i> , 2020, 5, 511-524.	13.3	248
23	BALB/c and C57BL/6 Mice Differ in Polyreactive IgA Abundance, which Impacts the Generation of Antigen-Specific IgA and Microbiota Diversity. <i>Immunity</i> , 2015, 43, 527-540.	14.3	247
24	REDItools: high-throughput RNA editing detection made easy. <i>Bioinformatics</i> , 2013, 29, 1813-1814.	4.1	243
25	Building essential biodiversity variables (<sc>EBV</sc>s) of species distribution and abundance at a global scale. <i>Biological Reviews</i> , 2018, 93, 600-625.	10.4	218
26	uAUG and uORFs in human and rodent 5' untranslated mRNAs. <i>Gene</i> , 2005, 349, 97-105.	2.2	212
27	Evolutionary analysis of cytochrome b sequences in some perciformes: Evidence for a slower rate of evolution than in mammals. <i>Journal of Molecular Evolution</i> , 1994, 39, 589-597.	1.8	205
28	A transcriptional sketch of a primary human breast cancer by 454 deep sequencing. <i>BMC Genomics</i> , 2009, 10, 163.	2.8	205
29	Profiling RNA editing in human tissues: towards the inosinome Atlas. <i>Scientific Reports</i> , 2015, 5, 14941.	3.3	194
30	UTRdb and UTRsite: specialized databases of sequences and functional elements of 5' and 3' untranslated regions of eukaryotic mRNAs. Update 2002. <i>Nucleic Acids Research</i> , 2002, 30, 335-340.	14.5	176
31	Diversity and temporal patterns of planktonic protist assemblages at a Mediterranean Long Term Ecological Research site. <i>FEMS Microbiology Ecology</i> , 2017, 93, fiw200.	2.7	173
32	MToolBox: a highly automated pipeline for heteroplasmy annotation and prioritization analysis of human mitochondrial variants in high-throughput sequencing. <i>Bioinformatics</i> , 2014, 30, 3115-3117.	4.1	166
33	UTRdb and UTRsite: specialized databases of sequences and functional elements of 5' and 3' untranslated regions of eukaryotic mRNAs. <i>Nucleic Acids Research</i> , 2000, 28, 193-196.	14.5	155
34	SpliceAid-F: a database of human splicing factors and their RNA-binding sites. <i>Nucleic Acids Research</i> , 2013, 41, D125-D131.	14.5	148
35	Tissue-specific mtDNA abundance from exome data and its correlation with mitochondrial transcription, mass and respiratory activity. <i>Mitochondrion</i> , 2015, 20, 13-21.	3.4	146
36	Next generation sequencing of SARS-CoV-2 genomes: challenges, applications and opportunities. <i>Briefings in Bioinformatics</i> , 2021, 22, 616-630.	6.5	143

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37	Bioinformatics approaches for genomics and post genomics applications of next-generation sequencing. <i>Briefings in Bioinformatics</i> , 2010, 11, 181-197.	6.5	141
38	Developmental factor IRF6 exhibits tumor suppressor activity in squamous cell carcinomas. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 13710-13715.	7.1	141
39	UTRdb and UTRsite: a collection of sequences and regulatory motifs of the untranslated regions of eukaryotic mRNAs. <i>Nucleic Acids Research</i> , 2004, 33, D141-D146.	14.5	140
40	Large-scale detection and analysis of RNA editing in grape mtDNA by RNA deep-sequencing. <i>Nucleic Acids Research</i> , 2010, 38, 4755-4767.	14.5	135
41	Identification and functional characterization of two new transcriptional variants of the human p63 gene. <i>Nucleic Acids Research</i> , 2009, 37, 6092-6104.	14.5	130
42	Motif discovery and transcription factor binding sites before and after the next-generation sequencing era. <i>Briefings in Bioinformatics</i> , 2013, 14, 225-237.	6.5	129
43	Metagenomics Reveals Dysbiosis and a Potentially Pathogenic <i>N. flavescens</i> Strain in Duodenum of Adult Celiac Patients. <i>American Journal of Gastroenterology</i> , 2016, 111, 879-890.	0.4	128
44	[35] Influence of base composition on quantitative estimates of gene evolution. <i>Methods in Enzymology</i> , 1990, 183, 570-584.	1.0	126
45	Glutamine synthetase gene evolution: a good molecular clock.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1991, 88, 522-526.	7.1	123
46	Evolution of the mitochondrial genetic system: an overview. <i>Gene</i> , 2000, 261, 153-159.	2.2	122
47	The 67-kDa laminin receptor originated from a ribosomal protein that acquired a dual function during evolution. <i>Molecular Biology and Evolution</i> , 1998, 15, 1017-1025.	8.9	120
48	Discrimination of Non-Protein-Coding Transcripts from Protein-Coding mRNA. <i>RNA Biology</i> , 2006, 3, 40-48.	3.1	118
49	Congruent Mammalian Trees from Mitochondrial and Nuclear Genes Using Bayesian Methods. <i>Molecular Biology and Evolution</i> , 2003, 21, 397-403.	8.9	111
50	Where Do Rodents Fit? Evidence from the Complete Mitochondrial Genome of <i>Sciurus vulgaris</i> . <i>Molecular Biology and Evolution</i> , 2000, 17, 979-983.	8.9	110
51	Lineage-Specific Evolutionary Rate in Mammalian mtDNA. <i>Molecular Biology and Evolution</i> , 2000, 17, 1022-1031.	8.9	107
52	Mitochondrial genomes gleaned from human whole-exome sequencing. <i>Nature Methods</i> , 2012, 9, 523-524.	19.0	102
53	Whole transcriptome profiling of Late-Onset Alzheimer's Disease patients provides insights into the molecular changes involved in the disease. <i>Scientific Reports</i> , 2018, 8, 4282.	3.3	102
54	PatSearch: a program for the detection of patterns and structural motifs in nucleotide sequences. <i>Nucleic Acids Research</i> , 2003, 31, 3608-3612.	14.5	101

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55	Structural and compositional features of untranslated regions of eukaryotic mRNAs. <i>Gene</i> , 1997, 205, 95-102.	2.2	99
56	Massive transcriptome sequencing of human spinal cord tissues provides new insights into motor neuron degeneration in ALS. <i>Scientific Reports</i> , 2017, 7, 10046.	3.3	99
57	Internet resources for the functional analysis of 5' and 3' untranslated regions of eukaryotic mRNAs. <i>Trends in Genetics</i> , 1999, 15, 378.	6.7	97
58	Mitochondrial DNA in metazoa: degree of freedom in a frozen event. <i>Gene</i> , 2002, 286, 3-12.	2.2	97
59	Changes in <i>Escherichia coli</i> transcriptome during acclimatization at low temperature. <i>Research in Microbiology</i> , 2003, 154, 573-580.	2.1	94
60	Investigating RNA editing in deep transcriptome datasets with REDIttools and REDIportal. <i>Nature Protocols</i> , 2020, 15, 1098-1131.	12.0	94
61	T Follicular Helper Cells Promote a Beneficial Gut Ecosystem for Host Metabolic Homeostasis by Sensing Microbiota-Derived Extracellular ATP. <i>Cell Reports</i> , 2017, 18, 2566-2575.	6.4	87
62	Complete mitochondrial DNA sequence of the fat dormouse, <i>Glis glis</i> : further evidence of rodent paraphyly. <i>Molecular Biology and Evolution</i> , 1998, 15, 499-505.	8.9	86
63	REDIportal: millions of novel A-to-I RNA editing events from thousands of RNAseq experiments. <i>Nucleic Acids Research</i> , 2021, 49, D1012-D1019.	14.5	86
64	Reference databases for taxonomic assignment in metagenomics. <i>Briefings in Bioinformatics</i> , 2012, 13, 682-695.	6.5	82
65	PscanChIP: finding over-represented transcription factor-binding site motifs and their correlations in sequences from ChIP-Seq experiments. <i>Nucleic Acids Research</i> , 2013, 41, W535-W543.	14.5	80
66	RAP: RNA-Seq Analysis Pipeline, a new cloud-based NGS web application. <i>BMC Genomics</i> , 2015, 16, S3.	2.8	79
67	Phylogenetic Comparison of Huntingtin Homologues Reveals the Appearance of a Primitive polyQ in <i>Sea Urchin</i> . <i>Molecular Biology and Evolution</i> , 2008, 25, 330-338.	8.9	78
68	TRIM8 modulates p53 activity to dictate cell cycle arrest. <i>Cell Cycle</i> , 2012, 11, 511-523.	2.6	78
69	PatSearch: a pattern matcher software that finds functional elements in nucleotide and protein sequences and assesses their statistical significance. <i>Bioinformatics</i> , 2000, 16, 439-450.	4.1	76
70	In silico representation and discovery of transcription factor binding sites. <i>Briefings in Bioinformatics</i> , 2004, 5, 217-236.	6.5	74
71	Mitogenomics reveals two cryptic species in <i>Ciona intestinalis</i> . <i>Trends in Genetics</i> , 2007, 23, 419-422.	6.7	73
72	TRIM8 restores p53 tumour suppressor function by blunting N-MYC activity in chemo-resistant tumours. <i>Molecular Cancer</i> , 2017, 16, 67.	19.2	73

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73	Analysis of oligonucleotide AUG start codon context in eukariotic mRNAs. <i>Gene</i> , 2000, 261, 85-91.	2.2	70
74	WORDUP: an efficient algorithm for discovering statistically significant patterns in DNA sequences. <i>Nucleic Acids Research</i> , 1992, 20, 2871-2875.	14.5	67
75	MoD Tools: regulatory motif discovery in nucleotide sequences from co-regulated or homologous genes. <i>Nucleic Acids Research</i> , 2006, 34, W566-W570.	14.5	67
76	Single-cell transcriptomics reveals specific RNA editing signatures in the human brain. <i>Rna</i> , 2017, 23, 860-865.	3.5	65
77	DNA microenvironments and the molecular clock. <i>Journal of Molecular Evolution</i> , 1989, 29, 407-411.	1.8	63
78	Elucidating the editome: bioinformatics approaches for RNA editing detection. <i>Briefings in Bioinformatics</i> , 2019, 20, 436-447.	6.5	63
79	High throughput approaches reveal splicing of primary microRNA transcripts and tissue specific expression of mature microRNAs in <i>Vitis vinifera</i> . <i>BMC Genomics</i> , 2009, 10, 558.	2.8	62
80	Intestinal microbiota sustains inflammation and autoimmunity induced by hypomorphic <i>RAG</i> defects. <i>Journal of Experimental Medicine</i> , 2016, 213, 355-375.	8.5	61
81	Complexity and Dynamics of the Winemaking Bacterial Communities in Berries, Musts, and Wines from Apulian Grape Cultivars through Time and Space. <i>PLoS ONE</i> , 2016, 11, e0157383.	2.5	60
82	The untranslated regions of eukaryotic mRNAs: Structure, function, evolution and bioinformatic tools for their analysis. <i>Briefings in Bioinformatics</i> , 2000, 1, 236-249.	6.5	59
83	Correlated substitution analysis and the prediction of amino acid structural contacts. <i>Briefings in Bioinformatics</i> , 2007, 9, 46-56.	6.5	58
84	The influence of invasive jellyfish blooms on the aquatic microbiome in a coastal lagoon (Varano, SE Tj ETQqO 0 0 rgBT /Overlock 10 Tf 5	2.4	58
85	p53FamTaG: a database resource of human p53, p63 and p73 direct target genes combining in silico prediction and microarray data. <i>BMC Bioinformatics</i> , 2007, 8, S20.	2.6	57
86	On the statistical assessment of classifiers using DNA microarray data. <i>BMC Bioinformatics</i> , 2006, 7, 387.	2.6	56
87	Evolutionary origin of nonuniversal CUGSer codon in some <i>Candida</i> species as inferred from a molecular phylogeny.. <i>Genetics</i> , 1995, 141, 903-907.	2.9	56
88	TRIM8 anti-proliferative action against chemo-resistant renal cell carcinoma. <i>Oncotarget</i> , 2014, 5, 7446-7457.	1.8	55
89	The Members of the RH Gene Family (RH50 and RH30) Followed Different Evolutionary Pathways. <i>Journal of Molecular Evolution</i> , 1999, 48, 151-159.	1.8	53
90	Differences in Gene Expression and Cytokine Release Profiles Highlight the Heterogeneity of Distinct Subsets of Adipose Tissue-Derived Stem Cells in the Subcutaneous and Visceral Adipose Tissue in Humans. <i>PLoS ONE</i> , 2013, 8, e57892.	2.5	51

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91	Gene expression profile of endothelial cells during perturbation of the gut vascular barrier. <i>Gut Microbes</i> , 2016, 7, 540-548.	9.8	51
92	The evolution of the mitochondrial D-loop region and the origin of modern man.. <i>Molecular Biology and Evolution</i> , 1992, 9, 587-98.	8.9	49
93	CLEANUP: a fast computer program for removing redundancies from nucleotide sequence databases. <i>Bioinformatics</i> , 1996, 12, 1-8.	4.1	49
94	MitoZoa 2.0: a database resource and search tools for comparative and evolutionary analyses of mitochondrial genomes in Metazoa. <i>Nucleic Acids Research</i> , 2012, 40, D1168-D1172.	14.5	49
95	BioMaS: a modular pipeline for Bioinformatic analysis of Metagenomic AmpliconS. <i>BMC Bioinformatics</i> , 2015, 16, 203.	2.6	49
96	Targeting Chemoresistant Tumors: Could TRIM Proteins-p53 Axis Be a Possible Answer?. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1776.	4.1	49
97	Dynamic inosinome profiles reveal novel patient stratification and gender-specific differences in glioblastoma. <i>Genome Biology</i> , 2019, 20, 33.	8.8	49
98	RNAProfile: an algorithm for finding conserved secondary structure motifs in unaligned RNA sequences. <i>Nucleic Acids Research</i> , 2004, 32, 3258-3269.	14.5	48
99	Transcriptional Analysis of <i>Acinetobacter</i> sp. neg1 Capable of Degrading Ochratoxin A. <i>Frontiers in Microbiology</i> , 2016, 7, 2162.	3.5	48
100	MitoZoa: A curated mitochondrial genome database of metazoans for comparative genomics studies. <i>Mitochondrion</i> , 2010, 10, 192-199.	3.4	47
101	Comparative Genomics of <i>Listeria</i> Sensu Lato: Genus-Wide Differences in Evolutionary Dynamics and the Progressive Gain of Complex, Potentially Pathogenicity-Related Traits through Lateral Gene Transfer. <i>Genome Biology and Evolution</i> , 2015, 7, 2154-2172.	2.5	47
102	Profile of microbial communities on carbonate stones of the medieval church of San Leonardo di Siponto (Italy) by Illumina-based deep sequencing. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 8537-8548.	3.6	47
103	Long-branch attraction phenomenon and the impact of among-site rate variation on rodent phylogeny. <i>Gene</i> , 2000, 259, 177-187.	2.2	45
104	Complete mtDNA of <i>Ciona intestinalis</i> Reveals Extensive Gene Rearrangement and the Presence of an <i>atp8</i> and an Extra <i>trnM</i> Gene in Ascidians. <i>Journal of Molecular Evolution</i> , 2004, 58, 376-389.	1.8	45
105	Phylogenetic analyses of complete mitochondrial genome sequences suggest a basal divergence of the enigmatic rodent <i>Anomalurus</i> . <i>BMC Evolutionary Biology</i> , 2007, 7, 16.	3.2	45
106	Computational Methods for Ab Initio and Comparative Gene Finding. <i>Methods in Molecular Biology</i> , 2010, 609, 269-284.	0.9	45
107	BioVeL: a virtual laboratory for data analysis and modelling in biodiversity science and ecology. <i>BMC Ecology</i> , 2016, 16, 49.	3.0	45
108	UTRdb: a specialized database of 5' and 3' untranslated regions of eukaryotic mRNAs. <i>Nucleic Acids Research</i> , 1999, 27, 188-191.	14.5	44

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109	Epstein-Barr virus genetic variants are associated with multiple sclerosis. <i>Neurology</i> , 2015, 84, 1362-1368.	1.1	44
110	WEP: a high-performance analysis pipeline for whole-exome data. <i>BMC Bioinformatics</i> , 2013, 14, S11.	2.6	43
111	What is a gene? An updated operational definition. <i>Gene</i> , 2008, 417, 1-4.	2.2	42
112	The metagenomic data life-cycle: standards and best practices. <i>GigaScience</i> , 2017, 6, 1-11.	6.4	42
113	The neglected genome. <i>EMBO Reports</i> , 2012, 13, 473-474.	4.5	41
114	Uncovering RNA Editing Sites in Long Non-Coding RNAs. <i>Frontiers in Bioengineering and Biotechnology</i> , 2014, 2, 64.	4.1	41
115	A Novel Method for Estimating Substitution Rate Variation Among Sites in a Large Dataset of Homologous DNA Sequences. <i>Genetics</i> , 2001, 157, 859-865.	2.9	41
116	Glutamine synthetase gene evolution in bacteria.. <i>Molecular Biology and Evolution</i> , 1995, 12, 189-97.	8.9	40
117	Lineage Specificity of the Evolutionary Dynamics of the mtDNA D-Loop Region in Rodents. <i>Journal of Molecular Evolution</i> , 2002, 54, 145-155.	1.8	40
118	Mitochondrial phylogeny of Anura (Amphibia): A case study of congruent phylogenetic reconstruction using amino acid and nucleotide characters. <i>Gene</i> , 2006, 366, 228-237.	2.2	40
119	ASPicDB: A database resource for alternative splicing analysis. <i>Bioinformatics</i> , 2008, 24, 1300-1304.	4.1	40
120	The nuclear OXPPOS genes in insecta: a common evolutionary origin, a common cis-regulatory motif, a common destiny for gene duplicates. <i>BMC Evolutionary Biology</i> , 2007, 7, 215.	3.2	39
121	Ascidian Mitogenomics: Comparison of Evolutionary Rates in Closely Related Taxa Provides Evidence of Ongoing Speciation Events. <i>Genome Biology and Evolution</i> , 2014, 6, 591-605.	2.5	39
122	Hypervariability of Ascidian Mitochondrial Gene Order: Exposing the Myth of Deuterostome Organelle Genome Stability. <i>Molecular Biology and Evolution</i> , 2010, 27, 211-215.	8.9	38
123	ASPicDB: a database of annotated transcript and protein variants generated by alternative splicing. <i>Nucleic Acids Research</i> , 2011, 39, D80-D85.	14.5	38
124	Towards global interoperability for supporting biodiversity research on essential biodiversity variables (EBVs). <i>Biodiversity</i> , 2015, 16, 99-107.	1.1	38
125	Human Endometrial Microbiota at Term of Normal Pregnancies. <i>Genes</i> , 2019, 10, 971.	2.4	38
126	CSTminer: a web tool for the identification of coding and noncoding conserved sequence tags through cross-species genome comparison. <i>Nucleic Acids Research</i> , 2004, 32, W624-W627.	14.5	37

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127	Energy biogenesis: one key for coordinating two genomes. <i>Trends in Genetics</i> , 2005, 21, 12-16.	6.7	37
128	WeederH: an algorithm for finding conserved regulatory motifs and regions in homologous sequences. <i>BMC Bioinformatics</i> , 2007, 8, 46.	2.6	37
129	Assessment of orthologous splicing isoforms in human and mouse orthologous genes. <i>BMC Genomics</i> , 2010, 11, 534.	2.8	37
130	Genomic organization and recombinational unit duplication-driven evolution of ovine and bovine T cell receptor gamma loci. <i>BMC Genomics</i> , 2008, 9, 81.	2.8	36
131	VDR primary targets by genome-wide transcriptional profiling. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2014, 143, 348-356.	2.5	36
132	Genome Sequencing of Multiple Isolates Highlights Subtelomeric Genomic Diversity within <i>Fusarium fujikuroi</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 3062-3069.	2.5	36
133	Diversity of hydrolases from hydrothermal vent sediments of the Levante Bay, Vulcano Island (Aeolian) Tj ETQq1 1 0.784314 rgBT /Overl esterases and an arabinopyranosidase. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 10031-10046.	3.6	36
134	Seasonal rather than spatial variability drives planktonic and benthic bacterial diversity in a microtidal lagoon and the adjacent open sea. <i>Molecular Ecology</i> , 2017, 26, 5961-5973.	3.9	35
135	Characterization of <i>Bacillus cereus</i> Group Isolates From Human Bacteremia by Whole-Genome Sequencing. <i>Frontiers in Microbiology</i> , 2020, 11, 599524.	3.5	35
136	Stochastic models of molecular evolution and the estimation of phylogeny and rates of nucleotide substitution in the hominoid primates. <i>Journal of Human Evolution</i> , 1989, 18, 775-794.	2.6	34
137	Inclusion of Cetaceans Within the Order Artiodactyla Based on Phylogenetic Analysis of Pancreatic Ribonuclease Genes. <i>Journal of Molecular Evolution</i> , 1999, 48, 360-368.	1.8	34
138	Cscan: finding common regulators of a set of genes by using a collection of genome-wide ChIP-seq datasets. <i>Nucleic Acids Research</i> , 2012, 40, W510-W515.	14.5	34
139	Using Weeder, Pscan, and PscanChIP for the Discovery of Enriched Transcription Factor Binding Site Motifs in Nucleotide Sequences. <i>Current Protocols in Bioinformatics</i> , 2014, 47, 2.11.1-31.	25.8	34
140	EphB2 stem-related and EphA2 progression-related miRNA-based networks in progressive stages of CRC evolution: clinical significance and potential miRNA drivers. <i>Molecular Cancer</i> , 2018, 17, 169.	19.2	34
141	RNA editing in plants: A comprehensive survey of bioinformatics tools and databases. <i>Plant Physiology and Biochemistry</i> , 2019, 137, 53-61.	5.8	33
142	Evolutionary analysis of the nucleus-encoded subunits of mammalian cytochrome c oxidase. <i>FEBS Journal</i> , 1991, 195, 151-156.	0.2	32
143	Gypsy/Ty3-like elements in the genome of the terrestrial salamander <i>Hydromantes</i> (Amphibia, Urodela). <i>Journal of Molecular Evolution</i> , 1996, 43, 584-593.	1.8	32
144	Transcript Mapping and Genome Annotation of Ascidian mtDNA Using EST Data. <i>Genome Research</i> , 2003, 13, 2203-2212.	5.5	32

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145	ASPIC: a novel method to predict the exon-intron structure of a gene that is optimally compatible to a set of transcript sequences. <i>BMC Bioinformatics</i> , 2005, 6, 244.	2.6	32
146	Selection of relevant genes in cancer diagnosis based on their prediction accuracy. <i>Artificial Intelligence in Medicine</i> , 2007, 40, 29-44.	6.5	32
147	Using REDIttools to Detect RNA Editing Events in NGS Datasets. <i>Current Protocols in Bioinformatics</i> , 2015, 49, 12.12.1-12.12.15.	25.8	32
148	UTRdb: a specialized database of 5'- and 3'-untranslated regions of eukaryotic mRNAs. <i>Nucleic Acids Research</i> , 1998, 26, 192-195.	14.5	31
149	Molecular Clock and Gene Function. <i>Journal of Molecular Evolution</i> , 2003, 57, S277-S285.	1.8	31
150	ITSoneDB: a comprehensive collection of eukaryotic ribosomal RNA Internal Transcribed Spacer 1 (ITS1) sequences. <i>Nucleic Acids Research</i> , 2018, 46, D127-D132.	14.5	31
151	Comparative Genomics Reveals Early Emergence and Biased Spatiotemporal Distribution of SARS-CoV-2. <i>Molecular Biology and Evolution</i> , 2021, 38, 2547-2565.	8.9	31
152	A backtranslation method based on codon usage strategy. <i>Nucleic Acids Research</i> , 1988, 16, 1715-1728.	14.5	30
153	Computational identification of protein coding potential of conserved sequence tags through cross-species evolutionary analysis. <i>Nucleic Acids Research</i> , 2003, 31, 4639-4645.	14.5	30
154	RNentropy: an entropy-based tool for the detection of significant variation of gene expression across multiple RNA-Seq experiments. <i>Nucleic Acids Research</i> , 2018, 46, e46-e46.	14.5	30
155	Regularized Least Squares Cancer Classifiers from DNA microarray data. <i>BMC Bioinformatics</i> , 2005, 6, S2.	2.6	29
156	ExpEdit: a webserver to explore human RNA editing in RNA-Seq experiments. <i>Bioinformatics</i> , 2011, 27, 1311-1312.	4.1	29
157	Geographic Population Structure in Epstein-Barr Virus Revealed by Comparative Genomics. <i>Genome Biology and Evolution</i> , 2016, 8, 3284-3291.	2.5	29
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