

Graziano Pesole

List of Publications by Year in descending order

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Version: 2024-02-01

330
papers

30,582
citations

14124

69
h-index

6177

164
g-index

355
all docs

355
docs citations

355
times ranked

43574
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of an Amylomaltase from the Halophilic Archaeon <i>Haloquadratum walsbyi</i> by Functional Metagenomics: Structural and Functional Insights. <i>Life</i> , 2022, 12, 85.	1.1	2
2	MetaCOXI: an integrated collection of metazoan mitochondrial cytochrome oxidase subunit-I DNA sequences. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	1.4	7
3	Microbiome composition indicate dysbiosis and lower richness in tumor breast tissues compared to healthy adjacent paired tissue, within the same women. <i>BMC Cancer</i> , 2022, 22, 30.	1.1	23
4	Morphological, molecular, and biochemical study of cyanobacteria from a eutrophic Algerian reservoir (Cheffia). <i>Environmental Science and Pollution Research</i> , 2022, 29, 27624.	2.7	1
5	Detection of A-to-I RNA Editing in SARS-COV-2. <i>Genes</i> , 2022, 13, 41.	1.0	24
6	A Machine Learning Approach to Parkinson's Disease Blood Transcriptomics. <i>Genes</i> , 2022, 13, 727.	1.0	10
7	Platelets from patients with visceral obesity promote colon cancer growth. <i>Communications Biology</i> , 2022, 5, .	2.0	5
8	High-Throughput Sequencing to Detect DNA-RNA Changes. <i>Methods in Molecular Biology</i> , 2021, 2181, 193-212.	0.4	10
9	YAP contributes to DNA methylation remodeling upon mouse embryonic stem cell differentiation. <i>Journal of Biological Chemistry</i> , 2021, 296, 100138.	1.6	25
10	Next generation sequencing of SARS-CoV-2 genomes: challenges, applications and opportunities. <i>Briefings in Bioinformatics</i> , 2021, 22, 616-630.	3.2	143
11	REDIportal: millions of novel A-to-I RNA editing events from thousands of RNAseq experiments. <i>Nucleic Acids Research</i> , 2021, 49, D1012-D1019.	6.5	86
12	RAP: A Web Tool for RNA-Seq Data Analysis. <i>Methods in Molecular Biology</i> , 2021, 2284, 393-415.	0.4	0
13	Databases for RNA Editing Collections. <i>Methods in Molecular Biology</i> , 2021, 2284, 467-480.	0.4	1
14	A primer on machine learning techniques for genomic applications. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 4345-4359.	1.9	8
15	RNA Editing Detection in HPC Infrastructures. <i>Methods in Molecular Biology</i> , 2021, 2284, 253-270.	0.4	2
16	Stem Cell Impairment at the Host-Microbiota Interface in Colorectal Cancer. <i>Cancers</i> , 2021, 13, 996.	1.7	22
17	Comparative Genomics Suggests a Taxonomic Revision of the <i>Staphylococcus cohnii</i> Species Complex. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	6
18	TRIM Proteins in Colorectal Cancer: TRIM8 as a Promising Therapeutic Target in Chemo Resistance. <i>Biomedicines</i> , 2021, 9, 241.	1.4	12

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19	Comparative Genomics Reveals Early Emergence and Biased Spatiotemporal Distribution of SARS-CoV-2. <i>Molecular Biology and Evolution</i> , 2021, 38, 2547-2565.	3.5	31
20	Emerging Roles of TRIM8 in Health and Disease. <i>Cells</i> , 2021, 10, 561.	1.8	16
21	Genomic Surveillance of Circulating SARS-CoV-2 in South East Italy: A One-Year Retrospective Genetic Study. <i>Viruses</i> , 2021, 13, 731.	1.5	8
22	aScan: A Novel Method for the Study of Allele Specific Expression in Single Individuals. <i>Journal of Molecular Biology</i> , 2021, 433, 166829.	2.0	1
23	ITSoneWB: profiling global taxonomic diversity of eukaryotic communities on Galaxy. <i>Bioinformatics</i> , 2021, 37, 4253-4254.	1.8	1
24	Amylomaltases in Extremophilic Microorganisms. <i>Biomolecules</i> , 2021, 11, 1335.	1.8	10
25	Evaluating the Efficiency of DNA Metabarcoding to Analyze the Diet of <i>Hippocampus guttulatus</i> (Teleostea: Syngnathidae). <i>Life</i> , 2021, 11, 998.	1.1	9
26	Gene electrotransfer of IL-2 and IL-12 plasmids effectively eradicated murine B16.F10 melanoma. <i>Bioelectrochemistry</i> , 2021, 141, 107843.	2.4	16
27	Bioinformatics Resources for RNA Editing. <i>Methods in Molecular Biology</i> , 2021, 2181, 177-191.	0.4	2
28	CorGAT: a tool for the functional annotation of SARS-CoV-2 genomes. <i>Bioinformatics</i> , 2021, 36, 5522-5523.	1.8	12
29	Accurate detection and quantification of SARS-CoV-2 genomic and subgenomic mRNAs by ddPCR and meta-transcriptomics analysis. <i>Communications Biology</i> , 2021, 4, 1215.	2.0	10
30	VINYL: Variant prioritization by survival analysis. <i>Bioinformatics</i> , 2021, 36, 5590-5599.	1.8	4
31	Laniakea@ReCaS: exploring the potential of customisable Galaxy on-demand instances as a cloud-based service. <i>BMC Bioinformatics</i> , 2021, 22, 544.	1.2	4
32	<i>VID22</i> counteracts G-quadruplex-induced genome instability. <i>Nucleic Acids Research</i> , 2021, 49, 12785-12804.	6.5	5
33	Evaluating DNA metabarcoding to analyze diet composition of wild long-snouted seahorse <i>Hippocampus guttulatus</i> . , 2021, , .		1
34	Critical assessment of bioinformatics methods for the characterization of pathological repeat expansions with single-molecule sequencing data. <i>Briefings in Bioinformatics</i> , 2020, 21, 1971-1986.	3.2	5
35	Laniakea: an open solution to provide Galaxy "on-demand" instances over heterogeneous cloud infrastructures. <i>GigaScience</i> , 2020, 9, .	3.3	10
36	The Microbial Community Associated with <i>Rhizostoma pulmo</i> : Ecological Significance and Potential Consequences for Marine Organisms and Human Health. <i>Marine Drugs</i> , 2020, 18, 437.	2.2	16

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37	ELIXIR-IT HPC@CINECA: high performance computing resources for the bioinformatics community. BMC Bioinformatics, 2020, 21, 352.	1.2	25
38	HPC-REDIttools: a novel HPC-aware tool for improved large scale RNA-editing analysis. BMC Bioinformatics, 2020, 21, 353.	1.2	28
39	Plant Health and Rhizosphere Microbiome: Effects of the Bionematicide Aphanocladium album in Tomato Plants Infested by Meloidogyne javanica. Microorganisms, 2020, 8, 1922.	1.6	18
40	Investigating Human Mitochondrial Genomes in Single Cells. Genes, 2020, 11, 534.	1.0	8
41	Quantifying RNA Editing in Deep Transcriptome Datasets. Frontiers in Genetics, 2020, 11, 194.	1.1	27
42	Genetic structure of the long-snouted seahorse, <i>Hippocampus guttulatus</i> , in the Central-Western Mediterranean Sea. Biological Journal of the Linnean Society, 2020, 130, 771-782.	0.7	5
43	A Differential Metabarcoding Approach to Describe Taxonomy Profiles of Bacteria and Archaea in the Saltern of Margherita di Savoia (Italy). Microorganisms, 2020, 8, 936.	1.6	21
44	Endogenous murine microbiota member Faecalibaculum rodentium and its human homologue protect from intestinal tumour growth. Nature Microbiology, 2020, 5, 511-524.	5.9	248
45	Investigating RNA editing in deep transcriptome datasets with REDIttools and REDlportal. Nature Protocols, 2020, 15, 1098-1131.	5.5	94
46	Human access impacts biodiversity of microscopic animals in sandy beaches. Communications Biology, 2020, 3, 175.	2.0	28
47	Characterization of Bacillus cereus Group Isolates From Human Bacteremia by Whole-Genome Sequencing. Frontiers in Microbiology, 2020, 11, 599524.	1.5	35
48	Accurate quantification of bacterial abundance in metagenomic DNAs accounting for variable DNA integrity levels. Microbial Genomics, 2020, 6, .	1.0	8
49	Jellyfish summer outbreaks as bacterial vectors and potential hazards for marine animals and humans health? The case of Rhizostoma pulmo (Scyphozoa, Cnidaria). Science of the Total Environment, 2019, 692, 305-318.	3.9	27
50	Enrichment of intestinal Lactobacillus by enhanced secretory IgA coating alters glucose homeostasis in P2rx7 ^{-/-} mice. Scientific Reports, 2019, 9, 9315.	1.6	18
51	Changes in gene expression and metabolic profile of drupes of Olea europaea L. cv Carolea in relation to maturation stage and cultivation area. BMC Plant Biology, 2019, 19, 428.	1.6	21
52	Targeting Chemoresistant Tumors: Could TRIM Proteins-p53 Axis Be a Possible Answer?. International Journal of Molecular Sciences, 2019, 20, 1776.	1.8	49
53	RNA editing in plants: A comprehensive survey of bioinformatics tools and databases. Plant Physiology and Biochemistry, 2019, 137, 53-61.	2.8	33
54	Dynamic inosinome profiles reveal novel patient stratification and gender-specific differences in glioblastoma. Genome Biology, 2019, 20, 33.	3.8	49

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55	Human Endometrial Microbiota at Term of Normal Pregnancies. <i>Genes</i> , 2019, 10, 971.	1.0	38
56	<i>Staphylococcus arlettae</i> Genomics: Novel Insights on Candidate Antibiotic Resistance and Virulence Genes in an Emerging Opportunistic Pathogen. <i>Microorganisms</i> , 2019, 7, 580.	1.6	10
57	TRIM8 Blunts the Pro-proliferative Action of $\hat{1}^{\text{Np63}}\hat{1}^{\pm}$ in a p53 Wild-Type Background. <i>Frontiers in Oncology</i> , 2019, 9, 1154.	1.3	8
58	Elucidating the editome: bioinformatics approaches for RNA editing detection. <i>Briefings in Bioinformatics</i> , 2019, 20, 436-447.	3.2	63
59	Genome Sequencing and Comparative Analysis of Three <i>Hanseniaspora uvarum</i> Indigenous Wine Strains Reveal Remarkable Biotechnological Potential. <i>Frontiers in Microbiology</i> , 2019, 10, 3133.	1.5	12
60	DNA Multiple Sequence Alignment Guided by Protein Domains: The MSA-PAD 2.0 Method. <i>Methods in Molecular Biology</i> , 2018, 1746, 173-180.	0.4	0
61	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.	6.5	30
62	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.	1.6	102
63	ITSoneDB: a comprehensive collection of eukaryotic ribosomal RNA Internal Transcribed Spacer 1 (ITS1) sequences. <i>Nucleic Acids Research</i> , 2018, 46, D127-D132.	6.5	31
64	Unbiased Taxonomic Annotation of Metagenomic Samples. <i>Journal of Computational Biology</i> , 2018, 25, 348-360.	0.8	12
65	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.	4.7	218
66	Draft Genome Sequences of Three Novel <i>Staphylococcus arlettae</i> Strains Isolated from a Disused Biological Safety Cabinet. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	5
67	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.	7.9	34
68	A-GAME: improving the assembly of pooled functional metagenomics sequence data. <i>BMC Genomics</i> , 2018, 19, 44.	1.2	7
69	CoVaCS: a consensus variant calling system. <i>BMC Genomics</i> , 2018, 19, 120.	1.2	29
70	REDIdb 3.0: A Comprehensive Collection of RNA Editing Events in Plant Organellar Genomes. <i>Frontiers in Plant Science</i> , 2018, 9, 482.	1.7	28
71	Single-cell transcriptomics reveals specific RNA editing signatures in the human brain. <i>Rna</i> , 2017, 23, 860-865.	1.6	65
72	RNA editing signature during myeloid leukemia cell differentiation. <i>Leukemia</i> , 2017, 31, 2824-2832.	3.3	29

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73	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.	2.9	87
74	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.	2.0	35
75	Transcriptomic analysis of nickel exposure in <i>Sphingobium</i> sp. ba1 cells using RNA-seq. <i>Scientific Reports</i> , 2017, 7, 8262.	1.6	11
76	Massive transcriptome sequencing of human spinal cord tissues provides new insights into motor neuron degeneration in ALS. <i>Scientific Reports</i> , 2017, 7, 10046.	1.6	99
77	The metagenomic data life-cycle: standards and best practices. <i>GigaScience</i> , 2017, 6, 1-11.	3.3	42
78	TRIM8 restores p53 tumour suppressor function by blunting N-MYC activity in chemo-resistant tumours. <i>Molecular Cancer</i> , 2017, 16, 67.	7.9	73
79	REDIportal: a comprehensive database of A-to-I RNA editing events in humans. <i>Nucleic Acids Research</i> , 2017, 45, D750-D757.	6.5	256
80	Diversity and temporal patterns of planktonic protist assemblages at a Mediterranean Long Term Ecological Research site. <i>FEMS Microbiology Ecology</i> , 2017, 93, fiw200.	1.3	173
81	MetaShot: an accurate workflow for taxon classification of host-associated microbiome from shotgun metagenomic data. <i>Bioinformatics</i> , 2017, 33, 1730-1732.	1.8	21
82	Targeted next-generation sequencing detects novel gene-phenotype associations and expands the mutational spectrum in cardiomyopathies. <i>PLoS ONE</i> , 2017, 12, e0181842.	1.1	28
83	Unbiased Taxonomic Annotation of Metagenomic Samples. <i>Lecture Notes in Computer Science</i> , 2017, , 162-173.	1.0	0
84	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.	0.2	128
85	Gene expression profile of endothelial cells during perturbation of the gut vascular barrier. <i>Gut Microbes</i> , 2016, 7, 540-548.	4.3	51
86	BioVeL: a virtual laboratory for data analysis and modelling in biodiversity science and ecology. <i>BMC Ecology</i> , 2016, 16, 49.	3.0	45
87	Geographic Population Structure in Epstein-Barr Virus Revealed by Comparative Genomics. <i>Genome Biology and Evolution</i> , 2016, 8, 3284-3291.	1.1	29
88	No Change in the Mucosal Gut Microbiome is Associated With Celiac Disease-Specific Microbiome Alteration in Adult Patients. <i>American Journal of Gastroenterology</i> , 2016, 111, 1659-1661.	0.2	18
89	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.	1.7	47
90	Intestinal microbiota sustains inflammation and autoimmunity induced by hypomorphic <i>RAG</i> defects. <i>Journal of Experimental Medicine</i> , 2016, 213, 355-375.	4.2	61

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91	Transcriptional Analysis of <i>Acinetobacter</i> sp. neg1 Capable of Degrading Ochratoxin A. <i>Frontiers in Microbiology</i> , 2016, 7, 2162.	1.5	48
92	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.	1.1	60
93	Profiling RNA editing in human tissues: towards the inosinome Atlas. <i>Scientific Reports</i> , 2015, 5, 14941.	1.6	194
94	RAP: RNA-Seq Analysis Pipeline, a new cloud-based NGS web application. <i>BMC Genomics</i> , 2015, 16, S3.	1.2	79
95	Functional Integration of mRNA Translational Control Programs. <i>Biomolecules</i> , 2015, 5, 1580-1599.	1.8	9
96	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.	1.1	47
97	Towards global interoperability for supporting biodiversity research on essential biodiversity variables (EBVs). <i>Biodiversity</i> , 2015, 16, 99-107.	0.5	38
98	The influence of invasive jellyfish blooms on the aquatic microbiome in a coastal lagoon (Varano, SE) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.2	58
99	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
100	MSA-PAD: DNA multiple sequence alignment framework based on PFAM accessed domain information: Fig. 1.. <i>Bioinformatics</i> , 2015, 31, 2571-2573.	1.8	6
101	Epstein-Barr virus genetic variants are associated with multiple sclerosis. <i>Neurology</i> , 2015, 84, 1362-1368.	1.5	44
102	Draft genome sequence of <i>Acinetobacter</i> sp. neg1 capable of degrading ochratoxin A. <i>FEMS Microbiology Letters</i> , 2015, 362, .	0.7	12
103	BioMaS: a modular pipeline for Bioinformatic analysis of Metagenomic AmpliconS. <i>BMC Bioinformatics</i> , 2015, 16, 203.	1.2	49
104	Genome Sequencing of Multiple Isolates Highlights Subtelomeric Genomic Diversity within <i>Fusarium fujikuroi</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 3062-3069.	1.1	36
105	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.	1.7	36
106	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.	6.6	247
107	Tissue-specific mtDNA abundance from exome data and its correlation with mitochondrial transcription, mass and respiratory activity. <i>Mitochondrion</i> , 2015, 20, 13-21.	1.6	146
108	Transcriptome Assembly and Alternative Splicing Analysis. <i>Methods in Molecular Biology</i> , 2015, 1269, 173-188.	0.4	1

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109	Detection of Post-Transcriptional RNA Editing Events. <i>Methods in Molecular Biology</i> , 2015, 1269, 189-205.	0.4	10
110	Exploring the RNA Editing Potential of RNA-Seq Data by ExpEdit. <i>Methods in Molecular Biology</i> , 2015, 1269, 327-338.	0.4	5
111	A Guideline for the Annotation of UTR Regulatory Elements in the UTRsite Collection. <i>Methods in Molecular Biology</i> , 2015, 1269, 339-348.	0.4	1
112	ASPicDB: A Database Web Tool for Alternative Splicing Analysis. <i>Methods in Molecular Biology</i> , 2015, 1269, 365-378.	0.4	5
113	Uncovering RNA Editing Sites in Long Non-Coding RNAs. <i>Frontiers in Bioengineering and Biotechnology</i> , 2014, 2, 64.	2.0	41
114	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.	1.1	39
115	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
116	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.	1.8	166
117	Draft Genome Sequences of Six <i>Listeria monocytogenes</i> Strains Isolated from Dairy Products from a Processing Plant in Southern Italy. <i>Genome Announcements</i> , 2014, 2, .	0.8	11
118	Draft genome sequence of <i>Sphingobium</i> sp. strain ba1, resistant to kanamycin and nickel ions. <i>FEMS Microbiology Letters</i> , 2014, 361, 8-9.	0.7	14
119	Ascidian Mitogenomics: Comparison of Evolutionary Rates in Closely Related Taxa Provides Evidence of Ongoing Speciation Events. <i>Genome Biology and Evolution</i> , 2014, 6, 931-931.	1.1	1
120	ODESSA: A high performance analysis pipeline for Ultra Deep targeted Exome Sequencing data. , 2014, , .		1
121	VDR primary targets by genome-wide transcriptional profiling. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2014, 143, 348-356.	1.2	36
122	EasyCluster2: an improved tool for clustering and assembling long transcriptome reads. <i>BMC Bioinformatics</i> , 2014, 15, S7.	1.2	3
123	TRIM8 anti-proliferative action against chemo-resistant renal cell carcinoma. <i>Oncotarget</i> , 2014, 5, 7446-7457.	0.8	55
124	NGS-Trex: Next Generation Sequencing Transcriptome profile explorer. <i>BMC Bioinformatics</i> , 2013, 14, S10.	1.2	14
125	WEP: a high-performance analysis pipeline for whole-exome data. <i>BMC Bioinformatics</i> , 2013, 14, S11.	1.2	43
126	REDIttools: high-throughput RNA editing detection made easy. <i>Bioinformatics</i> , 2013, 29, 1813-1814.	1.8	243

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127	A platform independent RNA-Seq protocol for the detection of transcriptome complexity. BMC Genomics, 2013, 14, 855.	1.2	7
128	Motif discovery and transcription factor binding sites before and after the next-generation sequencing era. Briefings in Bioinformatics, 2013, 14, 225-237.	3.2	129
129	ASPic-GenelD: A Lightweight Pipeline for Gene Prediction and Alternative Isoforms Detection. BioMed Research International, 2013, 2013, 1-11.	0.9	8
130	PscanChIP: finding over-represented transcription factor-binding site motifs and their correlations in sequences from ChIP-Seq experiments. Nucleic Acids Research, 2013, 41, W535-W543.	6.5	80
131	SpliceAid-F: a database of human splicing factors and their RNA-binding sites. Nucleic Acids Research, 2013, 41, D125-D131.	6.5	148
132	Regulation of the expression of CLU isoforms in endometrial proliferative diseases. International Journal of Oncology, 2013, 42, 1929-1944.	1.4	11
133	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. PLoS ONE, 2013, 8, e57892.	1.1	51
134	Genome-Wide Analysis of Differentially Expressed Genes and Splicing Isoforms in Clear Cell Renal Cell Carcinoma. PLoS ONE, 2013, 8, e78452.	1.1	19
135	Clustering and Assembling Large Transcriptome Datasets by EasyCluster2. Communications in Computer and Information Science, 2013, , 231-236.	0.4	1
136	MitoZoa 2.0: a database resource and search tools for comparative and evolutionary analyses of mitochondrial genomes in Metazoa. Nucleic Acids Research, 2012, 40, D1168-D1172.	6.5	49
137	SVM 2 : an improved paired-end-based tool for the detection of small genomic structural variations using high-throughput single-genome resequencing data. Nucleic Acids Research, 2012, 40, e145-e145.	6.5	21
138	Cscan: finding common regulators of a set of genes by using a collection of genome-wide ChIP-seq datasets. Nucleic Acids Research, 2012, 40, W510-W515.	6.5	34
139	A Novel Computational Strategy to Identify A-to-I RNA Editing Sites by RNA-Seq Data: De Novo Detection in Human Spinal Cord Tissue. PLoS ONE, 2012, 7, e44184.	1.1	19
140	BCR/ABL1 Fusion Transcripts Generated from Alternative Splicing: Implications for Future Targeted Therapies in Ph+ Leukaemias. Current Molecular Medicine, 2012, 12, 547-565.	0.6	6
141	The neglected genome. EMBO Reports, 2012, 13, 473-474.	2.0	41
142	Reference databases for taxonomic assignment in metagenomics. Briefings in Bioinformatics, 2012, 13, 682-695.	3.2	82
143	Mitochondrial genomes gleaned from human whole-exome sequencing. Nature Methods, 2012, 9, 523-524.	9.0	102
144	D.P.12 Whole exome sequencing and RNAseq in a Duchenne-like female with no dystrophin mutations: Search for dystrophin gene modifiers. Neuromuscular Disorders, 2012, 22, 811.	0.3	0

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145	Editorial. Briefings in Bioinformatics, 2012, 13, 645-645.	3.2	3
146	TRIM8 modulates p53 activity to dictate cell cycle arrest. Cell Cycle, 2012, 11, 511-523.	1.3	78
147	Plntron: a fast method for detecting the gene structure due to alternative splicing via maximal pairings of a pattern and a text. BMC Bioinformatics, 2012, 13, S2.	1.2	8
148	An improved procedure for clustering and assembly of large transcriptome data. EMBnet Journal, 2012, 18, 134.	0.2	2
149	Developmental factor IRF6 exhibits tumor suppressor activity in squamous cell carcinomas. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 13710-13715.	3.3	141
150	Expression and genomic analyses of Camelus dromedarius T cell receptor delta (TRD) genes reveal a variable domain repertoire enlargement due to CDR3 diversification and somatic mutation. Molecular Immunology, 2011, 48, 1384-1396.	1.0	26
151	ExpEdit: a webserver to explore human RNA editing in RNA-Seq experiments. Bioinformatics, 2011, 27, 1311-1312.	1.8	29
152	ASPicDB: a database of annotated transcript and protein variants generated by alternative splicing. Nucleic Acids Research, 2011, 39, D80-D85.	6.5	38
153	Assessment of orthologous splicing isoforms in human and mouse orthologous genes. BMC Genomics, 2010, 11, 534.	1.2	37
154	Large-scale detection and analysis of RNA editing in grape mtDNA by RNA deep-sequencing. Nucleic Acids Research, 2010, 38, 4755-4767.	6.5	135
155	UTRdb and UTRsite (RELEASE 2010): a collection of sequences and regulatory motifs of the untranslated regions of eukaryotic mRNAs. Nucleic Acids Research, 2010, 38, D75-D80.	6.5	285
156	Hypervariability of Ascidian Mitochondrial Gene Order: Exposing the Myth of Deuterostome Organelle Genome Stability. Molecular Biology and Evolution, 2010, 27, 211-215.	3.5	38
157	Identification of tumor-associated cassette exons in human cancer through EST-based computational prediction and experimental validation. Molecular Cancer, 2010, 9, 230.	7.9	5
158	MitoZoa: A curated mitochondrial genome database of metazoans for comparative genomics studies. Mitochondrion, 2010, 10, 192-199.	1.6	47
159	Bioinformatics approaches for genomics and post genomics applications of next-generation sequencing. Briefings in Bioinformatics, 2010, 11, 181-197.	3.2	141
160	Computational Methods for Ab Initio and Comparative Gene Finding. Methods in Molecular Biology, 2010, 609, 269-284.	0.4	45
161	New Tools for Expression Alternative Splicing Validation. Communications in Computer and Information Science, 2010, , 222-231.	0.4	0
162	A Unique, Consistent Identifier for Alternatively Spliced Transcript Variants. PLoS ONE, 2009, 4, e7631.	1.1	8

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