

# Graziano Pesole

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

322  
papers

24,506  
citations

64  
h-index

152  
g-index

355  
ext. papers

28,182  
ext. citations

8.4  
avg. IF

6.45  
L-index

#	Paper	IF	Citations
322	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> , <b>2022</b> , 22, 30	4.8	3
321	Morphological, molecular, and biochemical study of cyanobacteria from a eutrophic Algerian reservoir (Cheffia).. <i>Environmental Science and Pollution Research</i> , <b>2022</b> , 29, 27624	5.1	
320	A Machine Learning Approach to Parkinson Disease Blood Transcriptomics. <i>Genes</i> , <b>2022</b> , 13, 727	4.2	3
319	Laniakea@ReCaS: exploring the potential of customisable Galaxy on-demand instances as a cloud-based service. <i>BMC Bioinformatics</i> , <b>2021</b> , 22, 544	3.6	2
318	<b>2021</b> ,		1
317	Accurate detection and quantification of SARS-CoV-2 genomic and subgenomic mRNAs by ddPCR and meta-transcriptomics analysis. <i>Communications Biology</i> , <b>2021</b> , 4, 1215	6.7	2
316	Emerging Roles of TRIM8 in Health and Disease. <i>Cells</i> , <b>2021</b> , 10,	7.9	4
315	Genomic Surveillance of Circulating SARS-CoV-2 in South East Italy: A One-Year Retrospective Genetic Study. <i>Viruses</i> , <b>2021</b> , 13,	6.2	3
314	aScan: A Novel Method for the Study of Allele Specific Expression in Single Individuals. <i>Journal of Molecular Biology</i> , <b>2021</b> , 433, 166829	6.5	0
313	High-Throughput Sequencing to Detect DNA-RNA Changes. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2181, 193-212	1.4	3
312	YAP contributes to DNA methylation remodeling upon mouse embryonic stem cell differentiation. <i>Journal of Biological Chemistry</i> , <b>2021</b> , 296, 100138	5.4	11
311	REDIportal: millions of novel A-to-I RNA editing events from thousands of RNAseq experiments. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, D1012-D1019	20.1	19
310	RAP: A Web Tool for RNA-Seq Data Analysis. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2284, 393-415	1.4	
309	Databases for RNA Editing Collections. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2284, 467-480	1.4	1
308	A primer on machine learning techniques for genomic applications. <i>Computational and Structural Biotechnology Journal</i> , <b>2021</b> , 19, 4345-4359	6.8	1
307	RNA Editing Detection in HPC Infrastructures. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2284, 253-270	1.4	1
306	Stem Cell Impairment at the Host-Microbiota Interface in Colorectal Cancer. <i>Cancers</i> , <b>2021</b> , 13,	6.6	5

305	Comparative Genomics Suggests a Taxonomic Revision of the <i>Staphylococcus cohnii</i> Species Complex. <i>Genome Biology and Evolution</i> , <b>2021</b> , 13,	3.9	3
304	TRIM Proteins in Colorectal Cancer: TRIM8 as a Promising Therapeutic Target in Chemo Resistance. <i>Biomedicines</i> , <b>2021</b> , 9,	4.8	2
303	Comparative Genomics Reveals Early Emergence and Biased Spatiotemporal Distribution of SARS-CoV-2. <i>Molecular Biology and Evolution</i> , <b>2021</b> , 38, 2547-2565	8.3	10
302	Amylomaltases in Extremophilic Microorganisms. <i>Biomolecules</i> , <b>2021</b> , 11,	5.9	3
301	Evaluating the Efficiency of DNA Metabarcoding to Analyze the Diet of (Teleostea: Syngnathidae). <i>Life</i> , <b>2021</b> , 11,	3	2
300	Gene electrotransfer of IL-2 and IL-12 plasmids effectively eradicated murine B16.F10 melanoma. <i>Bioelectrochemistry</i> , <b>2021</b> , 141, 107843	5.6	1
299	Bioinformatics Resources for RNA Editing. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2181, 177-191	1.4	1
298	Detection of A-to-I RNA Editing in SARS-COV-2.. <i>Genes</i> , <b>2021</b> , 13,	4.2	11
297	Plant Health and Rhizosphere Microbiome: Effects of the Bionematicide in Tomato Plants Infested by. <i>Microorganisms</i> , <b>2020</b> , 8,	4.9	7
296	Investigating Human Mitochondrial Genomes in Single Cells. <i>Genes</i> , <b>2020</b> , 11,	4.2	6
295	Quantifying RNA Editing in Deep Transcriptome Datasets. <i>Frontiers in Genetics</i> , <b>2020</b> , 11, 194	4.5	11
294	Genetic structure of the long-snouted seahorse, <i>Hippocampus guttulatus</i> , in the CentralWestern Mediterranean Sea. <i>Biological Journal of the Linnean Society</i> , <b>2020</b> , 130, 771-782	1.9	4
293	A Differential Metabarcoding Approach to Describe Taxonomy Profiles of and in the Saltern of Margherita di Savoia (Italy). <i>Microorganisms</i> , <b>2020</b> , 8,	4.9	8
292	Endogenous murine microbiota member <i>Faecalibaculum rodentium</i> and its human homologue protect from intestinal tumour growth. <i>Nature Microbiology</i> , <b>2020</b> , 5, 511-524	26.6	104
291	Investigating RNA editing in deep transcriptome datasets with REDIttools and REDIportal. <i>Nature Protocols</i> , <b>2020</b> , 15, 1098-1131	18.8	35
290	Human access impacts biodiversity of microscopic animals in sandy beaches. <i>Communications Biology</i> , <b>2020</b> , 3, 175	6.7	14
289	VINYL: Variant prioritization by survival analysis. <i>Bioinformatics</i> , <b>2020</b> ,	7.2	3
288	CorGAT: a tool for the functional annotation of SARS-CoV-2 genomes. <i>Bioinformatics</i> , <b>2020</b> ,	7.2	6

287	Accurate quantification of bacterial abundance in metagenomic DNAs accounting for variable DNA integrity levels. <i>Microbial Genomics</i> , <b>2020</b> , 6,	4.4	3
286	Critical assessment of bioinformatics methods for the characterization of pathological repeat expansions with single-molecule sequencing data. <i>Briefings in Bioinformatics</i> , <b>2020</b> , 21, 1971-1986	13.4	4
285	Laniakea: an open solution to provide Galaxy "on-demand" instances over heterogeneous cloud infrastructures. <i>GigaScience</i> , <b>2020</b> , 9,	7.6	8
284	The Microbial Community Associated with : Ecological Significance and Potential Consequences for Marine Organisms and Human Health. <i>Marine Drugs</i> , <b>2020</b> , 18,	6	7
283	ELIXIR-IT HPC@CINECA: high performance computing resources for the bioinformatics community. <i>BMC Bioinformatics</i> , <b>2020</b> , 21, 352	3.6	6
282	HPC-REDIttools: a novel HPC-aware tool for improved large scale RNA-editing analysis. <i>BMC Bioinformatics</i> , <b>2020</b> , 21, 353	3.6	8
281	Characterization of Group Isolates From Human Bacteremia by Whole-Genome Sequencing. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 599524	5.7	8
280	Targeting Chemoresistant Tumors: Could TRIM Proteins-p53 Axis Be a Possible Answer?. <i>International Journal of Molecular Sciences</i> , <b>2019</b> , 20,	6.3	19
279	RNA editing in plants: A comprehensive survey of bioinformatics tools and databases. <i>Plant Physiology and Biochemistry</i> , <b>2019</b> , 137, 53-61	5.4	18
278	Dynamic inosinome profiles reveal novel patient stratification and gender-specific differences in glioblastoma. <i>Genome Biology</i> , <b>2019</b> , 20, 33	18.3	32
277	Genome Sequencing and Comparative Analysis of Three Indigenous Wine Strains Reveal Remarkable Biotechnological Potential. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 3133	5.7	5
276	Jellyfish summer outbreaks as bacterial vectors and potential hazards for marine animals and humans health? The case of <i>Rhizostoma pulmo</i> (Scyphozoa, Cnidaria). <i>Science of the Total Environment</i> , <b>2019</b> , 692, 305-318	10.2	17
275	Enrichment of intestinal <i>Lactobacillus</i> by enhanced secretory IgA coating alters glucose homeostasis in P2rx7 mice. <i>Scientific Reports</i> , <b>2019</b> , 9, 9315	4.9	14
274	Changes in gene expression and metabolic profile of drupes of <i>Olea europaea</i> L. cv <i>Carolea</i> in relation to maturation stage and cultivation area. <i>BMC Plant Biology</i> , <b>2019</b> , 19, 428	5.3	12
273	Human Endometrial Microbiota at Term of Normal Pregnancies. <i>Genes</i> , <b>2019</b> , 10,	4.2	22
272	Genomics: Novel Insights on Candidate Antibiotic Resistance and Virulence Genes in an Emerging Opportunistic Pathogen. <i>Microorganisms</i> , <b>2019</b> , 7,	4.9	4
271	TRIM8 Blunts the Pro-proliferative Action of $\text{Np63}\beta$ in a p53 Wild-Type Background. <i>Frontiers in Oncology</i> , <b>2019</b> , 9, 1154	5.3	4
270	Elucidating the editome: bioinformatics approaches for RNA editing detection. <i>Briefings in Bioinformatics</i> , <b>2019</b> , 20, 436-447	13.4	43

269	DNA Multiple Sequence Alignment Guided by Protein Domains: The MSA-PAD 2.0 Method. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1746, 173-180	1.4	
268	RNEntropy: an entropy-based tool for the detection of significant variation of gene expression across multiple RNA-Seq experiments. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, e46	20.1	23
267	Whole transcriptome profiling of Late-Onset Alzheimer's Disease patients provides insights into the molecular changes involved in the disease. <i>Scientific Reports</i> , <b>2018</b> , 8, 4282	4.9	46
266	ITSoneDB: a comprehensive collection of eukaryotic ribosomal RNA Internal Transcribed Spacer 1 (ITS1) sequences. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, D127-D132	20.1	15
265	Unbiased Taxonomic Annotation of Metagenomic Samples. <i>Journal of Computational Biology</i> , <b>2018</b> , 25, 348-360	1.7	8
264	REDIdb 3.0: A Comprehensive Collection of RNA Editing Events in Plant Organellar Genomes. <i>Frontiers in Plant Science</i> , <b>2018</b> , 9, 482	6.2	16
263	Building essential biodiversity variables (EBVs) of species distribution and abundance at a global scale. <i>Biological Reviews</i> , <b>2018</b> , 93, 600-625	13.5	145
262	Draft Genome Sequences of Three Novel Staphylococcus arlettae Strains Isolated from a Disused Biological Safety Cabinet. <i>Microbiology Resource Announcements</i> , <b>2018</b> , 7,	1.3	3
261	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> , <b>2018</b> , 17, 169	42.1	24
260	A-GAME: improving the assembly of pooled functional metagenomics sequence data. <i>BMC Genomics</i> , <b>2018</b> , 19, 44	4.5	6
259	CoVaCS: a consensus variant calling system. <i>BMC Genomics</i> , <b>2018</b> , 19, 120	4.5	14
258	Single-cell transcriptomics reveals specific RNA editing signatures in the human brain. <i>Rna</i> , <b>2017</b> , 23, 860-865	5.8	45
257	RNA editing signature during myeloid leukemia cell differentiation. <i>Leukemia</i> , <b>2017</b> , 31, 2824-2832	10.7	16
256	T Follicular Helper Cells Promote a Beneficial Gut Ecosystem for Host Metabolic Homeostasis by Sensing Microbiota-Derived Extracellular ATP. <i>Cell Reports</i> , <b>2017</b> , 18, 2566-2575	10.6	51
255	Seasonal rather than spatial variability drives planktonic and benthic bacterial diversity in a microtidal lagoon and the adjacent open sea. <i>Molecular Ecology</i> , <b>2017</b> , 26, 5961-5973	5.7	22
254	Transcriptomic analysis of nickel exposure in Sphingobium sp. ba1 cells using RNA-seq. <i>Scientific Reports</i> , <b>2017</b> , 7, 8262	4.9	7
253	Massive transcriptome sequencing of human spinal cord tissues provides new insights into motor neuron degeneration in ALS. <i>Scientific Reports</i> , <b>2017</b> , 7, 10046	4.9	59
252	The metagenomic data life-cycle: standards and best practices. <i>GigaScience</i> , <b>2017</b> , 6, 1-11	7.6	29

251	TRIM8 restores p53 tumour suppressor function by blunting N-MYC activity in chemo-resistant tumours. <i>Molecular Cancer</i> , <b>2017</b> , 16, 67	42.1	38
250	REDportal: a comprehensive database of A-to-I RNA editing events in humans. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D750-D757	20.1	166
249	Diversity and temporal patterns of planktonic protist assemblages at a Mediterranean Long Term Ecological Research site. <i>FEMS Microbiology Ecology</i> , <b>2017</b> , 93,	4.3	78
248	MetaShot: an accurate workflow for taxon classification of host-associated microbiome from shotgun metagenomic data. <i>Bioinformatics</i> , <b>2017</b> , 33, 1730-1732	7.2	9
247	Targeted next-generation sequencing detects novel gene-phenotype associations and expands the mutational spectrum in cardiomyopathies. <i>PLoS ONE</i> , <b>2017</b> , 12, e0181842	3.7	15
246	Unbiased Taxonomic Annotation of Metagenomic Samples. <i>Lecture Notes in Computer Science</i> , <b>2017</b> , 162-173	0.9	
245	BioVeL: a virtual laboratory for data analysis and modelling in biodiversity science and ecology. <i>BMC Ecology</i> , <b>2016</b> , 16, 49	2.7	26
244	Geographic Population Structure in Epstein-Barr Virus Revealed by Comparative Genomics. <i>Genome Biology and Evolution</i> , <b>2016</b> , 8, 3284-3291	3.9	23
243	No Change in the Mucosal Gut Mycobioma Is Associated with Celiac Disease-Specific Microbiome Alteration in Adult Patients. <i>American Journal of Gastroenterology</i> , <b>2016</b> , 111, 1659-1661	0.7	15
242	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> , <b>2016</b> , 100, 8537-48	5.7	36
241	Intestinal microbiota sustains inflammation and autoimmunity induced by hypomorphic RAG defects. <i>Journal of Experimental Medicine</i> , <b>2016</b> , 213, 355-75	16.6	45
240	Transcriptional Analysis of sp. Capable of Degrading Ochratoxin A. <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 2162	5.7	21
239	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> , <b>2016</b> , 11, e0157383	3.7	34
238	Metagenomics Reveals Dysbiosis and a Potentially Pathogenic <i>N. flavescens</i> Strain in Duodenum of Adult Celiac Patients. <i>American Journal of Gastroenterology</i> , <b>2016</b> , 111, 879-90	0.7	94
237	Gene expression profile of endothelial cells during perturbation of the gut vascular barrier. <i>Gut Microbes</i> , <b>2016</b> , 7, 540-548	8.8	26
236	The influence of invasive jellyfish blooms on the aquatic microbiome in a coastal lagoon (Varano, SE Italy) detected by an Illumina-based deep sequencing strategy. <i>Biological Invasions</i> , <b>2015</b> , 17, 923-940	2.7	43
235	Using REDIttools to Detect RNA Editing Events in NGS Datasets. <i>Current Protocols in Bioinformatics</i> , <b>2015</b> , 49, 12.12.1-12.12.15	24.2	23
234	MSA-PAD: DNA multiple sequence alignment framework based on PFAM accessed domain information. <i>Bioinformatics</i> , <b>2015</b> , 31, 2571-3	7.2	6

233	Epstein-Barr virus genetic variants are associated with multiple sclerosis. <i>Neurology</i> , <b>2015</b> , 84, 1362-8	6.5	29
232	Draft genome sequence of <i>Acinetobacter</i> sp. neg1 capable of degrading ochratoxin A. <i>FEMS Microbiology Letters</i> , <b>2015</b> , 362,	2.9	6
231	BioMaS: a modular pipeline for Bioinformatic analysis of Metagenomic AmpliconS. <i>BMC Bioinformatics</i> , <b>2015</b> , 16, 203	3.6	34
230	Genome Sequencing of Multiple Isolates Highlights Subtelomeric Genomic Diversity within <i>Fusarium fujikuroi</i> . <i>Genome Biology and Evolution</i> , <b>2015</b> , 7, 3062-9	3.9	32
229	Diversity of hydrolases from hydrothermal vent sediments of the Levante Bay, Vulcano Island (Aeolian archipelago) identified by activity-based metagenomics and biochemical characterization of new esterases and an arabinopyranosidase. <i>Applied Microbiology and Biotechnology</i> , <b>2015</b> , 99, 10031-46	5.7	25
228	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> , <b>2015</b> , 43, 527-40	32.3	188
227	Tissue-specific mtDNA abundance from exome data and its correlation with mitochondrial transcription, mass and respiratory activity. <i>Mitochondrion</i> , <b>2015</b> , 20, 13-21	4.9	94
226	Profiling RNA editing in human tissues: towards the inosinome Atlas. <i>Scientific Reports</i> , <b>2015</b> , 5, 14941	4.9	137
225	RAP: RNA-Seq Analysis Pipeline, a new cloud-based NGS web application. <i>BMC Genomics</i> , <b>2015</b> , 16, S3	4.5	58
224	Functional Integration of mRNA Translational Control Programs. <i>Biomolecules</i> , <b>2015</b> , 5, 1580-99	5.9	7
223	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> , <b>2015</b> , 7, 2154-72	3.9	31
222	Towards global interoperability for supporting biodiversity research on essential biodiversity variables (EBVs). <i>Biodiversity</i> , <b>2015</b> , 16, 99-107	0.7	35
221	Transcriptome assembly and alternative splicing analysis. <i>Methods in Molecular Biology</i> , <b>2015</b> , 1269, 173-88	1.4	1
220	Detection of post-transcriptional RNA editing events. <i>Methods in Molecular Biology</i> , <b>2015</b> , 1269, 189-205	1.4	7
219	Exploring the RNA editing potential of RNA-Seq data by ExpEdit. <i>Methods in Molecular Biology</i> , <b>2015</b> , 1269, 327-38	1.4	3
218	A guideline for the annotation of UTR regulatory elements in the UTRsite collection. <i>Methods in Molecular Biology</i> , <b>2015</b> , 1269, 339-48	1.4	1
217	ASPicDB: a database web tool for alternative splicing analysis. <i>Methods in Molecular Biology</i> , <b>2015</b> , 1269, 365-78	1.4	3
216	ODESSA: A high performance analysis pipeline for Ultra Deep targeted Exome Sequencing data <b>2014</b> ,		1

215	VDR primary targets by genome-wide transcriptional profiling. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , <b>2014</b> , 143, 348-56	5.1	32
214	EasyCluster2: an improved tool for clustering and assembling long transcriptome reads. <i>BMC Bioinformatics</i> , <b>2014</b> , 15 Suppl 15, S7	3.6	3
213	Uncovering RNA Editing Sites in Long Non-Coding RNAs. <i>Frontiers in Bioengineering and Biotechnology</i> , <b>2014</b> , 2, 64	5.8	34
212	Ascidian mitogenomics: comparison of evolutionary rates in closely related taxa provides evidence of ongoing speciation events. <i>Genome Biology and Evolution</i> , <b>2014</b> , 6, 591-605	3.9	35
211	Using Weeder, Pscan, and PscanChIP for the Discovery of Enriched Transcription Factor Binding Site Motifs in Nucleotide Sequences. <i>Current Protocols in Bioinformatics</i> , <b>2014</b> , 47, 2.11.1-31	24.2	20
210	MToolBox: a highly automated pipeline for heteroplasmy annotation and prioritization analysis of human mitochondrial variants in high-throughput sequencing. <i>Bioinformatics</i> , <b>2014</b> , 30, 3115-7	7.2	132
209	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> , <b>2014</b> , 2,		9
208	TRIM8 anti-proliferative action against chemo-resistant renal cell carcinoma. <i>Oncotarget</i> , <b>2014</b> , 5, 7446-573	5.3	31
207	NGS-Trex: Next Generation Sequencing Transcriptome profile explorer. <i>BMC Bioinformatics</i> , <b>2013</b> , 14 Suppl 7, S10	3.6	14
206	WEP: a high-performance analysis pipeline for whole-exome data. <i>BMC Bioinformatics</i> , <b>2013</b> , 14 Suppl 7, S11	3.6	38
205	REDitools: high-throughput RNA editing detection made easy. <i>Bioinformatics</i> , <b>2013</b> , 29, 1813-4	7.2	157
204	A platform independent RNA-Seq protocol for the detection of transcriptome complexity. <i>BMC Genomics</i> , <b>2013</b> , 14, 855	4.5	4
203	Motif discovery and transcription factor binding sites before and after the next-generation sequencing era. <i>Briefings in Bioinformatics</i> , <b>2013</b> , 14, 225-37	13.4	89
202	ASPic-GeneID: a lightweight pipeline for gene prediction and alternative isoforms detection. <i>BioMed Research International</i> , <b>2013</b> , 2013, 502827	3	6
201	PscanChIP: Finding over-represented transcription factor-binding site motifs and their correlations in sequences from ChIP-Seq experiments. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, W535-43	20.1	56
200	SpliceAid-F: a database of human splicing factors and their RNA-binding sites. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D125-31	20.1	87
199	Regulation of the expression of CLU isoforms in endometrial proliferative diseases. <i>International Journal of Oncology</i> , <b>2013</b> , 42, 1929-44	4.4	11
198	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> , <b>2013</b> , 8, e57892	3.7	46

197	Genome-wide analysis of differentially expressed genes and splicing isoforms in clear cell renal cell carcinoma. <i>PLoS ONE</i> , <b>2013</b> , 8, e78452	3.7	14
196	Clustering and Assembling Large Transcriptome Datasets by EasyCluster2. <i>Communications in Computer and Information Science</i> , <b>2013</b> , 231-236	0.3	1
195	Pintron: a fast method for detecting the gene structure due to alternative splicing via maximal pairings of a pattern and a text. <i>BMC Bioinformatics</i> , <b>2012</b> , 13 Suppl 5, S2	3.6	8
194	Reference databases for taxonomic assignment in metagenomics. <i>Briefings in Bioinformatics</i> , <b>2012</b> , 13, 682-95	13.4	68
193	Mitochondrial genomes gleaned from human whole-exome sequencing. <i>Nature Methods</i> , <b>2012</b> , 9, 523-4	21.6	87
192	TRIM8 modulates p53 activity to dictate cell cycle arrest. <i>Cell Cycle</i> , <b>2012</b> , 11, 511-23	4.7	44
191	MitoZoa 2.0: a database resource and search tools for comparative and evolutionary analyses of mitochondrial genomes in Metazoa. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D1168-72	20.1	41
190	SVM $\square$ an improved paired-end-based tool for the detection of small genomic structural variations using high-throughput single-genome resequencing data. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, e145	20.1	16
189	Cscan: finding common regulators of a set of genes by using a collection of genome-wide ChIP-seq datasets. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, W510-5	20.1	28
188	A novel computational strategy to identify A-to-I RNA editing sites by RNA-Seq data: de novo detection in human spinal cord tissue. <i>PLoS ONE</i> , <b>2012</b> , 7, e44184	3.7	15
187	BCR/ABL1 fusion transcripts generated from alternative splicing: implications for future targeted therapies in Ph+ leukaemias. <i>Current Molecular Medicine</i> , <b>2012</b> , 12, 547-65	2.5	6
186	The neglected genome. <i>EMBO Reports</i> , <b>2012</b> , 13, 473-4	6.5	33
185	An improved procedure for clustering and assembly of large transcriptome data. <i>EMBnet Journal</i> , <b>2012</b> , 18, 134	2.3	2
184	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> , <b>2011</b> , 108, 13710-5	11.5	109
183	mRNA Untranslated Regions (UTRs) <b>2011</b> ,		3
182	Expression and genomic analyses of <i>Camelus dromedarius</i> T cell receptor delta (TRD) genes reveal a variable domain repertoire enlargement due to CDR3 diversification and somatic mutation. <i>Molecular Immunology</i> , <b>2011</b> , 48, 1384-96	4.3	20
181	ExpEdit: a webserver to explore human RNA editing in RNA-Seq experiments. <i>Bioinformatics</i> , <b>2011</b> , 27, 1311-2	7.2	24
180	ASPicDB: a database of annotated transcript and protein variants generated by alternative splicing. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D80-5	20.1	35

179	Large-scale detection and analysis of RNA editing in grape mtDNA by RNA deep-sequencing. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, 4755-67	20.1	117
178	UTRdb and UTRsite (RELEASE 2010): a collection of sequences and regulatory motifs of the untranslated regions of eukaryotic mRNAs. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, D75-80	20.1	247
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