Graziano Pesole

List of Publications by Citations

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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	The transcriptional landscape of the mammalian genome. *Science*, **2005**, 309, 1559-63	33.3	2807
321	The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla. *Nature*, **2007**, 449, 463-7	50.4	2675
320	Evolution of genes and genomes on the Drosophila phylogeny. *Nature*, **2007**, 450, 203-18	50.4	1586
319	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. *Nature*, **2002**, 420, 563-73	50.4	1350
318	Assessing computational tools for the discovery of transcription factor binding sites. *Nature Biotechnology*, **2005**, 23, 137-44	44.5	950
317	Genome sequence of the metazoan plant-parasitic nematode Meloidogyne incognita. *Nature Biotechnology*, **2008**, 26, 909-15	44.5	790
316	Untranslated regions of mRNAs. *Genome Biology*, **2002**, 3, REVIEWS0004	18.3	637
315	Functional annotation of a full-length mouse cDNA collection. *Nature*, **2001**, 409, 685-90	50.4	560
314	Evolution of the mitochondrial genome of Metazoa as exemplified by comparison of congeneric species. *Heredity*, **2008**, 101, 301-20	3.6	399
313	Mammalian mitochondrial D-loop region structural analysis: identification of new conserved sequences and their functional and evolutionary implications. *Gene*, **1997**, 205, 125-40	3.8	383
312	Weeder Web: discovery of transcription factor binding sites in a set of sequences from co-regulated genes. *Nucleic Acids Research*, **2004**, 32, W199-203	20.1	363
311	Evolutionary genomics in Metazoa: the mitochondrial DNA as a model system. *Gene*, **1999**, 238, 195-209	3.8	329
310	Nucleotide substitution rate of mammalian mitochondrial genomes. *Journal of Molecular Evolution*, **1999**, 48, 427-34	3.1	327
309	Structural and functional features of eukaryotic mRNA untranslated regions. *Gene*, **2001**, 276, 73-81	3.8	320
308	Pscan: finding over-represented transcription factor binding site motifs in sequences from co-regulated or co-expressed genes. *Nucleic Acids Research*, **2009**, 37, W247-52	20.1	295
307	Asymmetrical directional mutation pressure in the mitochondrial genome of mammals. *Molecular Biology and Evolution*, **1998**, 15, 957-66	8.3	291
306	The guinea-pig is not a rodent. *Nature*, **1996**, 381, 597-600	50.4	291

305	The main regulatory region of mammalian mitochondrial DNA: structure-function model and evolutionary pattern. *Journal of Molecular Evolution*, **1991**, 33, 83-91	3.1	278
304	UTRdb and UTRsite (RELEASE 2010): a collection of sequences and regulatory motifs of the untranslated regions of eukaryotic mRNAs. *Nucleic Acids Research*, **2010**, 38, D75-80	20.1	247
303	An algorithm for finding signals of unknown length in DNA sequences. *Bioinformatics*, **2001**, 17 Suppl 1, S207-14	7.2	242
302	uAUG and uORFs in human and rodent 5'untranslated mRNAs. *Gene*, **2005**, 349, 97-105	3.8	196
301	A transcriptional sketch of a primary human breast cancer by 454 deep sequencing. *BMC Genomics*, **2009**, 10, 163	4.5	191
300	Evolutionary analysis of cytochrome b sequences in some Perciformes: evidence for a slower rate of evolution than in mammals. *Journal of Molecular Evolution*, **1994**, 39, 589-97	3.1	190
299	BALB/c and C57BL/6 Mice Differ in Polyreactive IgA Abundance, which Impacts the Generation of Antigen-Specific IgA and Microbiota Diversity. *Immunity*, **2015**, 43, 527-40	32.3	188
298	REDIportal: a comprehensive database of A-to-I RNA editing events in humans. *Nucleic Acids Research*, **2017**, 45, D750-D757	20.1	166
297	UTRdb and UTRsite: specialized databases of sequences and functional elements of 5' and 3' untranslated regions of eukaryotic mRNAs. Update 2002. *Nucleic Acids Research*, **2002**, 30, 335-40	20.1	164
296	REDItools: high-throughput RNA editing detection made easy. *Bioinformatics*, **2013**, 29, 1813-4	7.2	157
295	Building essential biodiversity variables (EBVs) of species distribution and abundance at a global scale. *Biological Reviews*, **2018**, 93, 600-625	13.5	145
294	Profiling RNA editing in human tissues: towards the inosinome Atlas. *Scientific Reports*, **2015**, 5, 14941	4.9	137
293	MToolBox: a highly automated pipeline for heteroplasmy annotation and prioritization analysis of human mitochondrial variants in high-throughput sequencing. *Bioinformatics*, **2014**, 30, 3115-7	7.2	132
292	UTRdb and UTRsite: a collection of sequences and regulatory motifs of the untranslated regions of eukaryotic mRNAs. *Nucleic Acids Research*, **2005**, 33, D141-6	20.1	122
291	Bioinformatics approaches for genomics and post genomics applications of next-generation sequencing. *Briefings in Bioinformatics*, **2010**, 11, 181-97	13.4	120
290	Large-scale detection and analysis of RNA editing in grape mtDNA by RNA deep-sequencing. *Nucleic Acids Research*, **2010**, 38, 4755-67	20.1	117
289	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, 13710-5	11.5	109
288	The 67-kDa laminin receptor originated from a ribosomal protein that acquired a dual function during evolution. *Molecular Biology and Evolution*, **1998**, 15, 1017-25	8.3	109

287	Glutamine synthetase gene evolution: a good molecular clock. *Proceedings of the National Academy of Sciences of the United States of America*, **1991**, 88, 522-6	11.5	106
286	Endogenous murine microbiota member Faecalibaculum rodentium and its human homologue protect from intestinal tumour growth. *Nature Microbiology*, **2020**, 5, 511-524	26.6	104
285	Congruent mammalian trees from mitochondrial and nuclear genes using Bayesian methods. *Molecular Biology and Evolution*, **2004**, 21, 397-403	8.3	100
284	Lineage-specific evolutionary rate in mammalian mtDNA. *Molecular Biology and Evolution*, **2000**, 17, 1022-31	8.3	98
283	Where do rodents fit? Evidence from the complete mitochondrial genome of Sciurus vulgaris. *Molecular Biology and Evolution*, **2000**, 17, 979-83	8.3	97
282	Evolution of the mitochondrial genetic system: an overview. *Gene*, **2000**, 261, 153-9	3.8	97
281	Identification and functional characterization of two new transcriptional variants of the human p63 gene. *Nucleic Acids Research*, **2009**, 37, 6092-104	20.1	96
280	Tissue-specific mtDNA abundance from exome data and its correlation with mitochondrial transcription, mass and respiratory activity. *Mitochondrion*, **2015**, 20, 13-21	4.9	94
279	Metagenomics Reveals Dysbiosis and a Potentially Pathogenic N. flavescens Strain in Duodenum of Adult Celiac Patients. *American Journal of Gastroenterology*, **2016**, 111, 879-90	0.7	94
278	Influence of base composition on quantitative estimates of gene evolution. *Methods in Enzymology*, **1990**, 183, 570-83	1.7	93
277	Structural and compositional features of untranslated regions of eukaryotic mRNAs. *Gene*, **1997**, 205, 95-102	3.8	92
276	Discrimination of non-protein-coding transcripts from protein-coding mRNA. *RNA Biology*, **2006**, 3, 40-8	4.8	90
275	Motif discovery and transcription factor binding sites before and after the next-generation sequencing era. *Briefings in Bioinformatics*, **2013**, 14, 225-37	13.4	89
274	Changes in Escherichia coli transcriptome during acclimatization at low temperature. *Research in Microbiology*, **2003**, 154, 573-80	4	88
273	Mitochondrial genomes gleaned from human whole-exome sequencing. *Nature Methods*, **2012**, 9, 523-4	21.6	87
272	SpliceAid-F: a database of human splicing factors and their RNA-binding sites. *Nucleic Acids Research*, **2013**, 41, D125-31	20.1	87
271	PatSearch: A program for the detection of patterns and structural motifs in nucleotide sequences. *Nucleic Acids Research*, **2003**, 31, 3608-12	20.1	87
270	Mitochondrial DNA in metazoa: degree of freedom in a frozen event. *Gene*, **2002**, 286, 3-12	3.8	83

269	Internet resources for the functional analysis of 5’ and 3’ untranslated regions of eukaryotic mRNAs. *Trends in Genetics*, **1999**, 15, 378	8.5	81
268	Diversity and temporal patterns of planktonic protist assemblages at a Mediterranean Long Term Ecological Research site. *FEMS Microbiology Ecology*, **2017**, 93,	4.3	78
267	Bioinformatics in Italy: BITS2007, the fourth annual meeting of the Italian Society of Bioinformatics. *BMC Bioinformatics*, **2008**, 9,	3.6	78
266	Bioinformatics in Italy: BITS2006, the third annual meeting of the Italian Society of Bioinformatics. *BMC Bioinformatics*, **2007**, 8,	3.6	78
265	Complete mitochondrial DNA sequence of the fat dormouse, Glis glis: further evidence of rodent paraphyly. *Molecular Biology and Evolution*, **1998**, 15, 499-505	8.3	73
264	Reference databases for taxonomic assignment in metagenomics. *Briefings in Bioinformatics*, **2012**, 13, 682-95	13.4	68
263	UTRdb and UTRsite: specialized databases of sequences and functional elements of 5’ and 3’ untranslated regions of eukaryotic mRNAs. *Nucleic Acids Research*, **2000**, 28, 193-6	20.1	67
262	PatSearch: a pattern matcher software that finds functional elements in nucleotide and protein sequences and assesses their statistical significance. *Bioinformatics*, **2000**, 16, 439-50	7.2	66
261	Phylogenetic comparison of huntingtin homologues reveals the appearance of a primitive polyQ in sea urchin. *Molecular Biology and Evolution*, **2008**, 25, 330-8	8.3	65
260	Mitogenomics reveals two cryptic species in Ciona intestinalis. *Trends in Genetics*, **2007**, 23, 419-22	8.5	65
259	Analysis of oligonucleotide AUG start codon context in eukariotic mRNAs. *Gene*, **2000**, 261, 85-91	3.8	64
258	In silico representation and discovery of transcription factor binding sites. *Briefings in Bioinformatics*, **2004**, 5, 217-36	13.4	63
257	Massive transcriptome sequencing of human spinal cord tissues provides new insights into motor neuron degeneration in ALS. *Scientific Reports*, **2017**, 7, 10046	4.9	59
256	MoD Tools: regulatory motif discovery in nucleotide sequences from co-regulated or homologous genes. *Nucleic Acids Research*, **2006**, 34, W566-70	20.1	59
255	RAP: RNA-Seq Analysis Pipeline, a new cloud-based NGS web application. *BMC Genomics*, **2015**, 16, S3	4.5	58
254	WORDUP: an efficient algorithm for discovering statistically significant patterns in DNA sequences. *Nucleic Acids Research*, **1992**, 20, 2871-5	20.1	58
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252	PscanChIP: Finding over-represented transcription factor-binding site motifs and their correlations in sequences from ChIP-Seq experiments. *Nucleic Acids Research*, **2013**, 41, W535-43	20.1	56

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250	Correlated substitution analysis and the prediction of amino acid structural contacts. *Briefings in Bioinformatics*, **2008**, 9, 46-56	13.4	54
249	High throughput approaches reveal splicing of primary microRNA transcripts and tissue specific expression of mature microRNAs in Vitis vinifera. *BMC Genomics*, **2009**, 10, 558	4.5	52
248	T Follicular Helper Cells Promote a Beneficial Gut Ecosystem for Host Metabolic Homeostasis by Sensing Microbiota-Derived Extracellular ATP. *Cell Reports*, **2017**, 18, 2566-2575	10.6	51
247	p53FamTaG: a database resource of human p53, p63 and p73 direct target genes combining in silico prediction and microarray data. *BMC Bioinformatics*, **2007**, 8 Suppl 1, S20	3.6	48
246	On the statistical assessment of classifiers using DNA microarray data. *BMC Bioinformatics*, **2006**, 7, 387	3.6	48
245	Evolutionary origin of nonuniversal CUGSer codon in some Candida species as inferred from a molecular phylogeny. *Genetics*, **1995**, 141, 903-7	4	47
244	Whole transcriptome profiling of Late-Onset Alzheimer's Disease patients provides insights into the molecular changes involved in the disease. *Scientific Reports*, **2018**, 8, 4282	4.9	46
243	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	3.7	46
242	Single-cell transcriptomics reveals specific RNA editing signatures in the human brain. *Rna*, **2017**, 23, 860-865	5.8	45
241	Intestinal microbiota sustains inflammation and autoimmunity induced by hypomorphic RAG defects. *Journal of Experimental Medicine*, **2016**, 213, 355-75	16.6	45
240	RNAProfile: an algorithm for finding conserved secondary structure motifs in unaligned RNA sequences. *Nucleic Acids Research*, **2004**, 32, 3258-69	20.1	45
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238	Correction: High throughput approaches reveal splicing of primary microRNA transcripts and tissue specific expression of mature microRNAs in Vitis vinifera. *BMC Genomics*, **2010**, 11, 109	4.5	44
237	The members of the RH gene family (RH50 and RH30) followed different evolutionary pathways. *Journal of Molecular Evolution*, **1999**, 48, 151-9	3.1	44
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. *Biological Invasions*, **2015**, 17, 923-940	2.7	43
235	Complete mtDNA of Ciona intestinalis reveals extensive gene rearrangement and the presence of an atp8 and an extra trnM gene in ascidians. *Journal of Molecular Evolution*, **2004**, 58, 376-89	3.1	43
234	Long-branch attraction phenomenon and the impact of among-site rate variation on rodent phylogeny. *Gene*, **2000**, 259, 177-87	3.8	43

233	Elucidating the editome: bioinformatics approaches for RNA editing detection. *Briefings in Bioinformatics*, **2019**, 20, 436-447	13.4	43
232	MitoZoa: a curated mitochondrial genome database of metazoans for comparative genomics studies. *Mitochondrion*, **2010**, 10, 192-9	4.9	41
231	MitoZoa 2.0: a database resource and search tools for comparative and evolutionary analyses of mitochondrial genomes in Metazoa. *Nucleic Acids Research*, **2012**, 40, D1168-72	20.1	41
230	Phylogenetic analyses of complete mitochondrial genome sequences suggest a basal divergence of the enigmatic rodent Anomalurus. *BMC Evolutionary Biology*, **2007**, 7, 16	3	40
229	UTRdb: a specialized database of 5’ and 3’ untranslated regions of eukaryotic mRNAs. *Nucleic Acids Research*, **1999**, 27, 188-91	20.1	40
228	WEP: a high-performance analysis pipeline for whole-exome data. *BMC Bioinformatics*, **2013**, 14 Suppl 7, S11	3.6	38
227	TRIM8 restores p53 tumour suppressor function by blunting N-MYC activity in chemo-resistant tumours. *Molecular Cancer*, **2017**, 16, 67	42.1	38
226	Mitochondrial phylogeny of Anura (Amphibia): a case study of congruent phylogenetic reconstruction using amino acid and nucleotide characters. *Gene*, **2006**, 366, 228-37	3.8	38
225	Lineage specificity of the evolutionary dynamics of the mtDNA D-loop region in rodents. *Journal of Molecular Evolution*, **2002**, 54, 145-55	3.1	38
224	What is a gene? An updated operational definition. *Gene*, **2008**, 417, 1-4	3.8	37
223	Profile of microbial communities on carbonate stones of the medieval church of San Leonardo di Siponto (Italy) by Illumina-based deep sequencing. *Applied Microbiology and Biotechnology*, **2016**, 100, 8537-48	5.7	36
222	CLEANUP: a fast computer program for removing redundancies from nucleotide sequence databases. *Bioinformatics*, **1996**, 12, 1-8	7.2	36
221	ASPicDB: a database resource for alternative splicing analysis. *Bioinformatics*, **2008**, 24, 1300-4	7.2	36
220	Investigating RNA editing in deep transcriptome datasets with REDItools and REDIportal. *Nature Protocols*, **2020**, 15, 1098-1131	18.8	35
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215	BioMaS: a modular pipeline for Bioinformatic analysis of Metagenomic AmpliconS. *BMC Bioinformatics*, **2015**, 16, 203	3.6	34
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210	Energy biogenesis: one key for coordinating two genomes. *Trends in Genetics*, **2005**, 21, 12-6	8.5	33
209	Dynamic inosinome profiles reveal novel patient stratification and gender-specific differences in glioblastoma. *Genome Biology*, **2019**, 20, 33	18.3	32
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207	VDR primary targets by genome-wide transcriptional profiling. *Journal of Steroid Biochemistry and Molecular Biology*, **2014**, 143, 348-56	5.1	32
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205	A novel method for estimating substitution rate variation among sites in a large dataset of homologous DNA sequences. *Genetics*, **2001**, 157, 859-65	4	32
204	Comparative Genomics of Listeria Sensu Lato: Genus-Wide Differences in Evolutionary Dynamics and the Progressive Gain of Complex, Potentially Pathogenicity-Related Traits through Lateral Gene Transfer. *Genome Biology and Evolution*, **2015**, 7, 2154-72	3.9	31
203	Genomic organization and recombinational unit duplication-driven evolution of ovine and bovine T cell receptor gamma loci. *BMC Genomics*, **2008**, 9, 81	4.5	31
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199	Stochastic models of molecular evolution and the estimation of phylogeny and rates of nucleotide substitution in the hominoid primates. *Journal of Human Evolution*, **1989**, 18, 775-794	3.1	31
198	TRIM8 anti-proliferative action against chemo-resistant renal cell carcinoma. *Oncotarget*, **2014**, 5, 7446-57	3.3	31

197	Molecular clock and gene function. *Journal of Molecular Evolution*, **2003**, 57 Suppl 1, S277-85	3.1	30
196	Epstein-Barr virus genetic variants are associated with multiple sclerosis. *Neurology*, **2015**, 84, 1362-8	6.5	29
195	The metagenomic data life-cycle: standards and best practices. *GigaScience*, **2017**, 6, 1-11	7.6	29
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193	Computational identification of protein coding potential of conserved sequence tags through cross-species evolutionary analysis. *Nucleic Acids Research*, **2003**, 31, 4639-45	20.1	29
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190	Cscan: finding common regulators of a set of genes by using a collection of genome-wide ChIP-seq datasets. *Nucleic Acids Research*, **2012**, 40, W510-5	20.1	28
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186	A backtranslation method based on codon usage strategy. *Nucleic Acids Research*, **1988**, 16, 1715-28	20.1	27
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184	GenoMiner: a tool for genome-wide search of coding and non-coding conserved sequence tags. *Bioinformatics*, **2006**, 22, 497-9	7.2	26
183	Evolutionary analysis of the nucleus-encoded subunits of mammalian cytochrome c oxidase. *FEBS Journal*, **1991**, 195, 151-6		26
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173	Geographic Population Structure in Epstein-Barr Virus Revealed by Comparative Genomics. *Genome Biology and Evolution*, **2016**, 8, 3284-3291	3.9	23
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162	Human Endometrial Microbiota at Term of Normal Pregnancies. *Genes*, **2019**, 10,	4.2	22

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