

Graziano Pesole CV

Graziano Pesole is full professor of Molecular Biology in the University of Bari "A. Moro" and Director of the Institute of Biomembranes, Bioenergetics and Molecular Biotechnologies (IBIOM) of the National Research Council (Bari).

Bibliometric facts:

h-index: 66 (Google scholar), 55 (Scopus)

peer-reviewed publications: >280

Sum of Times Cited without self-citations:
>25,000

Graziano Pesole has since long carried out research activity in the fields of bioinformatics, comparative genomics and molecular evolution. His current research interests are focused on bioinformatics application for the management and analysis of next generation sequencing data, obtained also at single-cell resolution, including: i) genome assembly and annotation; ii) transcriptome profiling of the protein coding and non-coding portion of the genomes (e.g. miRNAs and lncRNAs), including the characterization of novel splicing isoforms, to investigate gene expression in healthy and disease conditions and identify diagnostic and prognostic molecular biomarkers; iii) Detection and functional assessment of disease-causative mutations; iv) ChIP-Seq analysis for the characterization of epigenetic signatures in healthy and disease conditions; v) RNA editing studies; v) Metagenomics analysis to investigate the microbial composition of clinical and environmental samples and their functional role.

He has developed several specialized databases including **UTRdb/UTRsite** collecting mRNA untranslated sequences and related regulatory motifs involved in the post-transcriptional regulation of gene expression, **ASPicDB** and **SpliceAID-F**, information resources for alternative splicing analysis, **ITSoneDB** for DNA metabarcoding analysis of eukaryal microbiome, and **REDiportal**, a comprehensive database of A-to-I RNA editing events in human.

He has also developed widely used analysis software and algorithms which are available as standalone software or through the web including: 1) **PatSearch**, for the detection of regular expression patterns and structural motifs in nucleotide sequences; 2) **CSTminer/GenoMiner**, for the blind identification of coding and non coding conserved sequence tags through the pairwise comparison of genome sequences; 3) **Weeder**, for the discovery of transcription factor binding sites and other regulatory elements, by detecting over-represented nucleotide patterns in nucleotide sequences; 4) **RNAprofile**, for the discovery of conserved sequence/structural motifs in unaligned RNA sequences; 5) **Exalign**, for comparative analysis of exon-intron gene structures; 6) **ExpEdit and REDITOOLS**: for exploring RNA editing from NGS data; 7) **WEP** and **CoVaCS**, for the characterization of nucleotide sequence variations through the analysis of whole-exome sequence data; 8) **RAP and NGS-Trex**, for transcriptome profiling and differential expression analysis from RNA-Seq data; 9) **BioMaS**, a modular pipeline for Bioinformatic analysis of Metagenomic AmpliconS; 10) **MetaShot**, an accurate workflow for taxon classification of host-associated microbiome from shotgun metagenomic data; 11) **A-Game**, for functional metagenomics analyses.

He leads an interdisciplinary research group including molecular biologists, computer scientists and mathematicians.

He coordinated research units in several research projects funded by national (MIUR, CNR, Telethon, AIRC, AISIM, ARISLA) and international (EU, NIH) agencies, and has filed several international patents.

He is Section Editor for the journal BMC Bioinformatics and member of the editorial Board of other international journals (Nature Scientific Reports, Nucleic Acids Research – Genomics and Bioinformatics, BMC Genomics, Computational Biology and Chemistry, Briefings in Bioinformatics; Comparative and Functional Genomics), co-author of books on Bioinformatics, Genomics and Molecular Biology published by Italian (Zanichelli, Ambrosiana, Gnocchi) and international (Wiley) editors.

He has been one of the founders and past-president of the Italian Society of Bioinformatics and is currently the head of the Italian node of ELIXIR infrastructure for Bioinformatics.

Bibliometric links

WoS ResearcherID: <http://www.researcherid.com/rid/E-9051-2014>

Google Scholar: <https://scholar.google.it/citations?user=KXj1IFAAAAAJ&hl=it>

ORCID ID: <http://orcid.org/0000-0003-3663-0859>

Research Gate: https://www.researchgate.net/profile/Graziano_Pesole2

Scopus Author ID: <http://www.scopus.com/authid/detail.url?authorId=7005831630>

10 Relevant publication in the past five years

1: Silvestris DA, Picardi E, Cesarini V, Fosso B, Mangraviti N, Massimi L, Martini M, Pesole G, Locatelli F, Gallo A. Dynamic inosinome profiles reveal novel patient stratification and gender-specific differences in glioblastoma. *Genome Biol.* 2019 Feb 13;20(1):33.

2: De Robertis M, Mazza T, Fusilli C, Loiacono L, Poeta ML, Sanchez M, Massi E, Lamorte G, Diodoro MG, Pescarmona E, Signori E, Pesole G, Vescovi AL, Garcia-Foncillas J, Fazio VM. EphB2 stem-related and EphA2 progression-related miRNA-based networks in progressive stages of CRC evolution: clinical significance and potential miRNA drivers. *Mol Cancer.* 2018 Nov 30;17(1):169.

3: Marzano F, Faienza MF, Caratozzolo MF, Brunetti G, Chiara M, Horner DS, Annese A, D'Erchia AM, Consiglio A, Pesole G, Sbisà E, Inzaghi E, Cianfarani S, Tullo A. Pilot study on circulating miRNA signature in children with obesity born small for gestational age and appropriate for gestational age. *Pediatr Obes.* 2018 Dec;13(12):803-811.

4: Annese A, Manzari C, Lionetti C, Picardi E, Horner DS, Chiara M, Caratozzolo MF, Tullo A, Fosso B, Pesole G, D'Erchia AM. Whole transcriptome profiling of Late-Onset Alzheimer's Disease patients provides insights into the molecular changes involved in the disease. *Sci Rep.* 2018 Mar 9;8(1):4282.

5: Chiara M, Gioiosa S, Chillemi G, D'Antonio M, Flati T, Picardi E, Zambelli F, Horner DS, Pesole G, Castrignanò T. CoVaCS: a consensus variant calling system. *BMC Genomics.* 2018 Feb 5;19(1):120.

6: Zambelli F, Mastropasqua F, Picardi E, D'Erchia AM, Pesole G, Pavesi G. RNentropy: an entropy-based tool for the detection of significant variation of gene expression across multiple RNA-Seq experiments. *Nucleic Acids Res.* 2018 May 4;46(8):e46.

7: Diroma MA, Ciaccia L, Pesole G, Picardi E. Elucidating the editome: bioinformatics approaches for RNA editing detection. *Brief Bioinform.* 2017 Oct 11. doi: 10.1093/bib/bbx129. PubMed PMID: 29040360.

8: Santamaria M, Fosso B, Licciulli F, Balech B, Larini I, Grillo G, De Caro G, Liuni S, Pesole G. ITSoneDB: a comprehensive collection of eukaryotic ribosomal RNA Internal Transcribed Spacer 1 (ITS1) sequences. *Nucleic Acids Res.* 2018 Jan 4;46(D1):D127-D132.

9: D'Erchia AM, Gallo A, Manzari C, Raho S, Horner DS, Chiara M, Valletti A, Aiello I, Mastropasqua F, Ciaccia L, Locatelli F, Pisani F, Nicchia GP, Svelto M, Pesole G, Picardi E. Massive transcriptome sequencing of human spinal cord tissues provides new insights into motor neuron degeneration in ALS. *Sci Rep.* 2017 Aug 30;7(1):10046.

10: Rossetti C, Picardi E, Ye M, Camilli G, D'Erchia AM, Cucina L, Locatelli F, Fianchi L, Teofili L, Pesole G, Gallo A, Sorrentino R. RNA editing signature during myeloid leukemia cell differentiation. *Leukemia.* 2017 Dec;31(12):2824-2832.