Graziano Pesole
Curriculum Vitae

Affiliation: National Research Council, Institute of Biomembranes and Bioenergetics, and University of Bari "A. Moro", Department of Biosciences, Biotechnology and Biopharmaceutics, Campus "E. Quagliariello", via Orabona 4, 70125 Bari, Italy**.**

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Position: Director of the Institute of Biomembranes, Bioenergetics and Molecular Biotechnologies, Full Professor of Molecular Biology,

Personal Data

Date of birth:	02/01/1959
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Sex:	Male
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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

Education

I received a degree in Chemistry, Summa cum Laude, at the University of Bari in April 1983, after completing a special internship at the Institute of Biological Chemistry at the same University, discussing a thesis on: "The concentration of the mitochondrial transcripts in rat liver", supervised by the professors Palmiro Cantatore and Cecilia Saccone.

Professional experience

Feb 2010 – present	Director of the Institute of Biomembranes, Bioenergetics and Molecular Biotechnologies, National Research Council, Bari, Italy
Dec. 2005 – present:	Full Professor of Molecular Biology at the Department of Biochemistry and Molecular Biology (University of Bari, Italy)
Dec. 2002 – Nov. 2005:	Full Professor of Molecular Biology at the Department of Biomolecular science and Biotechnology (University of Milan, Italy)

Nov. 1998 – Nov. 2002:   Associate Professor of Molecular Biology at the Department of General Physiology and Biochemistry (University of Milan, Italy)

March 1996 – October 1998:   Research Associate (Ricercatore) in Biochemistry at the Department of Biology D.B.A.F. (University of Basilicata, Italy)

Jan. 1989 - Feb. 1996 :   Research Assistant (Tecnico Laureato) at the Department of Biochemistry and Molecular Biology (University of Bari, Italy)

Sept.1986 - January 1989 :   full teacher of Chemistry in the high school.

May 1986 - September 1986:   researcher at the ENICHEM VALBASENTO labs (Pisticci - MT) for a research project on carbon fibers.

January 1985 - May 1986 :   Scholarship at the Centro Ricerche Bonomo (Bari - Italy) for a research project in food science.

October 1983 - January 1985 : National Service as chemist officer at the Stabilimento Militare Nucleare - Fisico - Chimico in Civitavecchia (Rome).

Research activity

Bioinformatics, comparative genomics and molecular evolution are the major topics of the research activity carried out within my interdisciplinary research team including molecular biologists, computer scientists and statisticians.

In particular, my interests include: i) molecular evolution and computational approaches for the structural and functional analysis of nucleotide sequences, particularly focused on the identification of regulatory elements in non-coding genome regions; ii) epigenomics; iii) transcriptome profiling, including the study of alternative splicing and RNA editing; iv) functional analysis of untranslated regions of eukaryotic mRNAs; v) assessment and functional characterization of the microbiome in clinical and environmental samples.

Within my studies on molecular evolution, I carried out several studies on the evolution of mitochondrial genome at the intra-species level, in order to clarify some aspects of the origin of modern man, and at the inter-species level to reconstruct mammal phylogeny and to study the evolutionary dynamics of the mitochondrial genome of Tunicata.

More recently, I am currently focusing on bioinformatics application for the management and analysis of next generation sequencing data, including:
   i)   genome assembly and annotation;

ii) transcriptome profiling of the protein coding and non-coding portion of the genomes (e.g. miRNAs, lincRNAs, circRNAs), 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

vi) Metagenomics to investigate the microbial composition of clinical and environmental samples and their functional role.

Finally, in order to study the nucleo-mitochondrial cross-talk I proposed an innovative methodology to reconstruct complete mitochondrial genomes and quantify their relative abundance through the analysis of whole genome (WGS) or exome (WES) sequence data.

Within my research activity in the field of Bioinformatics, I developed several specialised databases, including:

D1) **UTRdb/UTRsite** (http://utrdb.ba.itb.cnr.it/), collecting mRNA untranslated sequences and related regulatory motifs involved in the post-transcriptional regulation of gene expression.

D2) **ASPicDB** ([http:// srv00.recas.ba.infn.it/ASPicDB/](http://srv00.recas.ba.infn.it/ASPicDB/)), collecting alternative splicing full-length variants of genes from human and other species.

D3) **SpliceAid-F** (http://srv00.recas.ba.infn.it/SpliceAidF/), collecting information on splicing factors and their binding sites.

D4) **ITSoneDB** (http://itsonedb.cloud.ba.infn.it/), a curated collection of eukaryotic ribosomal RNA Internal Transcribed Spacer 1 (ITS1) sequences aimed at supporting metagenomic surveys of environmental communities.

D5) **REDIportal** (http://srv00.recas.ba.infn.it/atlas/), a comprehensive collection of A-to-I RNA editing events in human and other organisms.

I also developed several algorithms and software for sequence analysis, devoted to the identification and characterization of regulatory elements in non coding genome regions and to the analysis of next-generation sequencing data (NGS), including:

S1) **PatSearch**, for the detection or regular expression patterns and structural motifs in nucleotide sequences;

S2) **CSTminer/GenoMiner**, for the blind identification of coding and non coding conserved sequence tags through the pairwise comparison of genome sequences;

S3) **Weeder,** for the discovery of promoter and other regulatory elements, by detecting over-represented nucleotide patterns in nucleotide sequences;

S4) **RNAprofile**, for the discovery of conserved sequence/structural motifs in unaligned RNA sequences;

S5) **Exalign**, for comparative analysis of exon-intron gene structures;

S6) **ExpEdit and REDITOOLS**: for exploring RNA editing from NGS data;

S7) **WEP/CoVaCS**: for the characterization of nucleotide sequence variations through the analysis of whole-exome sequence data

S8) **RAP and NGS-Trex**: for transcriptome profiling and differential expression analysis from RNA-Seq data

S9) **BioMaS**: a modular pipeline for Bioinformatic analysis of Metagenomic AmpliconS

All tools above are available as standalone software or through web browsers (see the relevant publications in the list below).

S10) **Metashot**: a modular pipeline for Bioinformatic analysis of shotgun Metagenomic data, specifically designed for human clinical samples

S11) **A-GAME**: a Galaxy-based web service for Bioinformatic analysis of functional metahgenomics data.

Bibliometric scores (ISI)

I authored over 270 publications on peer-reviewed International Journals (h-index=66 (Google Scholar) or 54 (Scopus), average citations per item>90, total cites ≥20,000.

Books

- Principi di Bioinformatica. Gnocchi editore (Napoli, 1997)

- Introduzione alla Bioinformatica. Zanichelli editore (Bologna, 2003)

- Handbook of Comparative and Evolutionary Genomics. Wiley Ed. (New York, 2003)

- Biologia Molecolare, Ambrosiana & Zanichelli Ed. (I edizione Milano, 2010; II edizione Milano, 2014, III edizione Milano, 2018))

- Fondamenti di Bioinformatica, Zanichelli Ed. (Milano, 2018)

Patents

1. GeneUP algorithm to search optimal primers for RNA fingerprinting (Pat. No. 08/925,816/Sep 5th 1997 entitled to Michael McClelland and Graziano Pesole).

2. Method for the preparation and amplification of representative and strand- specific libraries of cDNA for high throughput sequencing, use thereof, kit and cartridges for automation kit - Application Numbers & Dates: EP11738288 2011-05-30 [2011EP-0738288] A1 (Brevetto italiano n. RM2010A000293/2010) -Applicant/Assignee: CONSIGLIO NAZIONALE DELLE RICERCHE [IT]

Editorial Activity

- Section Editor of "BMC Bioinformatics"
- Member of the Editorial Board of "Briefings in Bioinformatics"
- Member of the Editorial Board of "BMC Genomics"
- Member of the Editorial Board of "Computational Biology and Chemistry"
- Member of the Editorial Board of "Comparative and Functional Genomics"
- Member of the Editorial Board of "International Journal of Evolutionary Biology"
- Member of the Editorial Board of "Frontiers in Genetics"

Research projects (2010 – 2018)

I coordinated several research programs funded by national (MIUR, CNR, Telethon, AIRC, AISM, ARISLA) and international (EU, NIH) agencies. Below the list of the research projects in the last five years (total budget > 5M €):

- H2020-INFRAEOSC-2018-2020 EOSC-Life (2019-2023)- Providing an open collaborative space for digital biology in Europe (Project Research Unit coordinator)
- FISM 2017 (2019-2020) - Epstein-Barr virus genotypes in multiple sclerosis and their functional relevance in the disease etiology (Project Research Unit coordinator)
- Cluster Tecnologici Regione Puglia (2015-2017) - "DICLIMAX: Strumentazione per diagnostica clinica basata su next generation sequencing di acidi nucleici" (Project Research Unit coordinator)
- H2020-INFRASUPP-2014-2 GLOBIS-B (2015-2018)- GLOBal Infrastructures for Supporting Biodiversity research (Project Research Unit coordinator)
- H2020-INFRADEV-1-2015-1 ELIXIR-EXCELERATE (2015-2019) - Fast-track ELIXIR implementation and drive early user exploitation across the life sciences (Project Research Unit coordinator)
- H2020-BG-2014-2 INMARE (2015-2019) - Industrial Applications of Marine Enzymes: Innovative screening and expression platforms to discover and use the functional protein diversity from the sea (Project Research Unit coordinator)
- H2020-INFRADEV-1-2014-1 EMBRIC (2015-2019)- European Marine Biological Research Infrastructure Cluster to promote the Blue Bioeconomy (Project Research Unit coordinator)
- H2020-EINFRA-2014-2 INDIGO (2015-2017) - INtegrating Distributed data Infrastructures for Global ExplOitation (Project Research Unit coordinator)
- ERC HomeoGUT (2014-2019) - Immune mechanisms that control the homeostasis of the gut and that are deregulated in intestinal pathologies (G.A: 615735) (Project research unit coordinator)

- FP7 INFRASTRUCTURES-2011-2 - BioVel (2011-2014) - Biodiversity Virtual e-laboratory - (GRANT AGREEMENT FP7 N. 283359) (Project research unit coordinator)
- FP7 INFRASTRUCTURES-2011-2 - CReATIVE-B (2011-2014) - Coordination of Research e-Infrastructures Activities Toward an International Virtual Environment for Biodiversity (GRANT AGREEMENT FP7 N. 284441) (Project research unit coordinator)
- FISM (2011-2014) - High-throughput investigation of Multiple Sclerosis associated infectious agents by unbiased cDNA deep sequencing (Project coordinator)
- FISM (2010-2013) - Characterization of Epstein-Barr virus genotypes in multiple sclerosis through next generation sequencing approaches (FISM 2011/R/31) (Project research unit coordinator)
- PO FESR 2007-2013 - PON02_00186_34147512 (2012-2015) - Strumenti Innovativi per il Miglioramento della Sicurezza Alimentare (S.I.Mi.S.A.) (Project research unit coordinator)
- ARISLA - REDISALS - RNA editing landscape of motor neurons in sporadic ALS by massive transcriptome sequencing (Project coordinator)
- PO FESR 2007-2013 - VIRTUALAB PON 01_01297 (2011-2015) - Sistemi avanzati di Meccatronica Biomedicale di Diagnosi di Terapia Medica basati su Realtà Virtuale e Aumentata, Microelettronica, e su Laboratori robotizzati ad elevato throughput (Project research unit coordinator)
- PO FESR 2007-2013 - MICROMAP PON 01_02589 (2011-2015) - Sviluppo di una piattaforma tecnologica multiplex per diagnostica molecolare, portatile ed automatizzata, basata sulla logica strumentale del lab-on-chip, in grado di consentire applicazioni multiparametriche in campo infettivologico. (Project research unit coordinator)
- PO FESR 2007-2013 - BIOforIU PONa3_00025 (2012-2015) - Infrastruttura multidisciplinare per lo studio e la valorizzazione della Biodiversità marina e terrestre nella prospettiva della "Innovation Union" (Project coordinator)
- Progetto bandiera CNR – EPIGEN (2012-2018) (Project research unit coordinator)
- Progetto ESFRI ELIXIR (2012-2023) - European infrastructure for biological data (Project coordinator)
- Progetto ESFRI Lifewatch (2012-2023) - European infrastructure for Molecular Biodiversity (Project research unit coordinator)
- Eu-JPI ENPADASI (2015-2016) - the European Nutrition Phenotype Assessment and Data Sharing Initiative (Project research unit coordinator)

Management Activities

- Director of the Institute of Biomembranes, Bioenergetics and Molecular Biotechnologies, CNR, Bari (2010-present)
- Head of the Italian node of ELIXIR, the ESFRI infrastructure for biological data (2012-present)
- President of the Scientific Board (Comitato Tecnico Scientifico) of the Technological District for Health Biotechnology in the Apulia Region (2013-present)
- Chair of MoBiLab (Molecular Biodiversity Laboratory) of the ESFRI infrastructure for Biodiversity "LifeWatch" (2013-present).
- CIB (Consorzio Italiano Biotecnologie) – Coordinator for the University of Bari

Awards

Associazione "G. Quagliariello" Award (1999)

Membership of Scientific Societies and Consortia (2009-present)

- Italian Bioinformatics Society (Founder and Past-President)
- Italian Society for Molecular Biology and Biophysics (SIBBM)
- ISCB (International Society of Computational Biology)
- INBB (Istituto Nazionale di Biostrutture e Biosistemi)
- CEGBA (Centro di Eccellenza in Genomica Comparata), Bari, Italy

Event Chair and Panelist (2010-present)

2nd Next Generation Sequencing Workshop, Bari, Italy   2010
3rd Next Generation Sequencing Workshop, Bari, Italy   2011
4th Next Generation Sequencing Workshop, Bari, Italy   2012
FISV Conference, Rome, Italy   2012

External PhD Thesis Examiner (2010- present)

PhD	University of Adelaide, Australia	Michael Tran	2010
PhD	University of Udine, Italy	Francesco Vezzi	2011
PhD	University of Rome, Italy	Guido Leoni	2012
PhD	University of Milan-Bicocca, Italy	Stefano Beretta	2012
PhD	University of Rome, Italy	Silvia Gioiosa	2013
PhD	University of Rome, Tor Vergata, Italy	Alessio Colantoni	2014
PhD	National University of Singapore	Lakshmi Narayanan Lakshmanan	2014
PhD	Università di Milano	Vittoria Bocchi	2019

PC Member/Reviewer

AlCoB 2019
BITS 2011, 2012, 2013, 2014
CCGRID 2014
ECCB 2010, 2016, 2018
IWBBIO 2016
NETTAB 2015, 2018
NGS 2017

Reviewer of over 200 manuscript (2010-2019).

Invited Presentations (2010-present, selected)

Pesole G. Metagenomics: High-Throughput profiling of Microbiome-Host interactions, Globis-B, Fourth International Workshop on Essential Biodiversity Variables, Bari, 26 February, 2018

Pesole G. Single cell transcriptomics reveals specific RNA editing signatures in the human brain. 9th Annual Next Generation Sequencing Congress, 5th Annual Single Cell Analysis Congress and 3rd Annual Genome Editing Congress. 9-10 November 2017, Novotel London West Hotel, London, UK

Pesole G. Computational investigation of epigenetic regulation mechanisms by simultaneous analysis of genome and transcriptome data. SMBE satellite meeting on RNA modifications and its implications on adaption and evolution. Valencia (Spain) May 17-20 2016

Pesole G. BioMas: a cloud-based web service for the analysis of DNA meta-barcoding amplicons – The case study of harmful microalgae. Open bridges for life science data. Metagenomics: bridging between environment and life. 18 November 2015, Hinxton (UK)

Pesole G. Elixir: an european infrastructure for biological data. Workshop on Italian-German Cooperation in Biological and Medical Research Infrastructures. Berlin, 16-17. December 2014 Italian Embassy, Tiergartenstrasse 22.

Pesole G. BioMas: a cloud-based service facility for the analysis of DNA meta-barcoding amplicons. Joint 2014 Annual Meeting British Ecological Society and Société Française d'Ecologie. 9 – 12 December 2014, Grand Palais, Lille, France

Pesole G. High-throughput investigation of RNA editing in Amiotrophic Lateral Sclerosis. NGS and non-coding RNA data analysis. SeqAhead COST Action Workshop. Bari (Italy), 17-18 April 2013

Pesole G. Experimental and computational strategies for large scale investigation of human mutations involved in genetic diseases through whole exome sequencing: implications for early diagnosis and personalized therapies. 6th Foresight Training Course, Biotech and Innovative Science to meet patient needs. Bari (Italy), 30th September 2013

Pesole G. Identification of tumor-associated cassette exons in human cancer through exon array and RNA-Seq data analysis. Post-GWAS Horizons in Molecular Epdemiology: Digging deeper into the environment. 11-14 November 2012, Westin Diplomat Resort, Holywood, FL, USA.

Pesole G, ASPicDB a database of annotated transcript and protein variants generated by alternative splicing. First Post-EURASNET Symposium, Regulation of Gene Expression through RNA splicing, Trieste (Italy), 24-27 March 2012

Pesole G. High-throughput sequencing for transcriptome profiling and alternative splicing pattern analysis. 12th Bologna Winter School. Deep Sequencing Analysis Data: a challenge for personalized medicine. Bologna, 7-11 February 2011

Pesole G. De novo detection of RNA editing changes by RNA deep-sequencing. 12th Bologna Winter School. Deep Sequencing Analysis Data: a challenge for personalized medicine. Bologna, 7-11 February 2011

Pesole G. De novo detection of RNA editing changes by RNA deep-sequencing. Structural and functional diversity of the eukaryotic genome IUBS International Workshop. Brno, Czech Republic, October 14-16 2010

Pesole G. Computational detection and experimental validation of cancer-specific alternative splicing isoforms. Workshop on "Current Trends in Biomedicine: RNA-protein interactions in development and cancer". October 1-3, 2009, Baeza, Spain

Pavesi G, Zambelli F and **Pesole G.** Gene Complexity And Alternative Splicing. System Biology: Integrative, Comparative and Multiscale Modeling, 11-14 June 2009 – Iowa State University (Usa)

List of publications in peer-reviewed journals (2010-present)

Lavecchia A, Chiara M, Manzari C, Trotta M, Marzano M, Horner D, **Pesole G**, Placido A. Draft Genome Sequences of Three Novel Staphylococcus arlettae Strains Isolated from a Disused Biological Safety Cabinet. Microbiol Resour Announc. 2018 Oct 4;7(13). pii: e01012-18. doi: 10.1128/MRA.01012-18. eCollection 2018 Oct. PubMed PMID: 30533690; PubMed Central PMCID: PMC6256559.

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. doi: 10.1186/s12943-018-0912-z. PubMed PMID: 30501625; PubMed Central PMCID: PMC6271583.

Oliva M, Monno R, Addabbo P, **Pesole G**, Scrascia M, Calia C, Dionisi AM, Chiara M, Horner DS, Manzari C, Pazzani C. IS26 mediated antimicrobial resistance gene shuffling from the chromosome to a mosaic conjugative FII plasmid. Plasmid. 2018 Oct 16;100:22-30. doi: 10.1016/j.plasmid.2018.10.001.

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 Aug 29. doi: 10.1111/ijpo.12439.

Lo Giudice C, **Pesole G**, Picardi E. REDIdb 3.0: A Comprehensive Collection of RNA Editing Events in Plant Organellar Genomes. Front Plant Sci. 2018 Apr 11;9:482. doi: 10.3389/fpls.2018.00482. eCollection 2018. PubMed PMID: 29696033

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. doi: 10.1038/s41598-018-22701-2. PubMed PMID: 29523845

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. doi: 10.1186/s12864-018-4508-1. PubMed PMID: 29402227.

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 Jan 30. doi: 10.1093/nar/gky055. [Epub ahead of print] PubMed PMID: 29390085.

Chiara M, Placido A, Picardi E, Ceci LR, Horner DS, **Pesole G**. A-GAME: improving the assembly of pooled functional metagenomics sequence data. *BMC Genomics.* 2018 Jan 12;19(1):44. doi: 10.1186/s12864-017-4369-z. PubMed PMID: 29329522; PubMed Central PMCID: PMC5767027.

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. [Epub ahead of print] PubMed PMID: 29040360.

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. doi: 10.1093/nar/gkx855. PubMed PMID: 29036529; PubMed Central PMCID: PMC5753230.

Fosso B, **Pesole G**, Rosselló F, Valiente G. Unbiased Taxonomic Annotation of Metagenomic Samples. *J Comput Biol*. 2017 Oct 13. doi: 10.1089/cmb.2017.0144. [Epub ahead of print] PubMed PMID: 29028181.

Quero GM, Perini L, **Pesole G**, Manzari C, Lionetti C, Bastianini M, Marini M, Luna GM. Seasonal rather than spatial variability drives planktonic and benthic bacterial diversity in a microtidal lagoon and the adjacent open sea. *Mol Ecol.* 2017 Nov;26(21):5961-5973. doi: 10.1111/mec.14363. Epub 2017 Oct 9 PubMed PMID: 28926207.

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. doi: 10.1038/s41598-017-10488-7. PubMed PMID: 28855684; PubMed Central PMCID: PMC5577269.

Volpicella M, Leoni C, Manzari C, Chiara M, Picardi E, Piancone E, Italiano F, D'Erchia A, Trotta M, Horner DS, **Pesole G**, Ceci LR. Transcriptomic analysis of nickel exposure in Sphingobium sp. ba1 cells using RNA-seq. *Sci Rep.* 2017 Aug 15;7(1):8262. doi: 10.1038/s41598-017-08934-7. PubMed PMID: 28811613; PubMed Central PMCID: PMC5557971.

Kissling WD, Ahumada JA, Bowser A, Fernandez M, Fernández N, García EA, Guralnick RP, Isaac NJB, Kelling S, Los W, McRae L, Mihoub JB, Obst M, Santamaria M, Skidmore AK, Williams KJ, Agosti D, Amariles D, Arvanitidis C, Bastin L, De Leo F, Egloff W, Elith J, Hobern D, Martin D, Pereira HM, **Pesole G**, Peterseil J, Saarenmaa H, Schigel D, Schmeller DS, Segata N, Turak E, Uhlir PF, Wee B, Hardisty AR. Building essential biodiversity variables (EBVs) of species distribution and abundance at a global scale. *Biol Rev Camb Philos Soc.* 2018 Feb;93(1):600-625. doi: 10.1111/brv.12359. Epub 2017 Aug 2. PubMed PMID: 28766908.

Forleo C, D'Erchia AM, Sorrentino S, Manzari C, Chiara M, Iacoviello M, Guaricci AI, De Santis D, Musci RL, La Spada A, Marangelli V, **Pesole G**, Favale S. Targeted next-generation sequencing detects novel gene-phenotype associations and expands the mutational spectrum in cardiomyopathies. PLoS One. 2017 Jul 27;12(7):e0181842. doi: 10.1371/journal.pone.0181842. eCollection 2017. PubMed PMID: 28750076; PubMed Central PMCID: PMC5531468.

Ten Hoopen P, Finn RD, Bongo LA, Corre E, Fosso B, Meyer F, Mitchell A,Pelletier E, **Pesole G**, Santamaria M, Willassen NP, Cochrane G. The metagenomics data life-cycle: standards and best practices. *Gigascience*. 2017 Aug 1;6(8):1-11. doi: 10.1093/gigascience/gix047. PubMed PMID: 28637310; PubMed Central PMCID:PMC5737865.

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. doi: 10.1038/leu.2017.134. Epub 2017 May 9. PubMed PMID: 28484266; PubMed Central PMCID: PMC5729351.

Mastropasqua F, Marzano F, Valletti A, Aiello I, Di Tullio G, Morgano A, Liuni S, Ranieri E, Guerrini L, Gasparre G, Sbisà E, **Pesole G**, Moschetta A, Caratozzolo MF, Tullo A. TRIM8 restores p53 tumour suppressor function by blunting N-MYC activity in chemo-resistant tumours. *Mol Cancer*. 2017 Mar 21;16(1):67. doi:10.1186/s12943-017-0634-7. PubMed PMID: 28327152; PubMed Central PMCID:PMC5359838.

Perruzza L, Gargari G, Proietti M, Fosso B, D'Erchia AM, Faliti CE, Rezzonico-Jost T, Scribano D, Mauri L, Colombo D, Pellegrini G, Moregola A, Mooser C, **Pesole G**, Nicoletti M, Norata GD, Geuking MB, McCoy KD, Guglielmetti S, Grassi F. T Follicular Helper Cells Promote a Beneficial Gut Ecosystem for Host Metabolic Homeostasis by Sensing Microbiota-Derived Extracellular ATP. *Cell Rep.* 2017 Mar 14;18(11):2566-2575. doi: 10.1016/j.celrep.2017.02.061. PubMed PMID:28297661; PubMed Central PMCID: PMC5368345.

Picardi E, Horner DS, **Pesole G**. Single cell transcriptomics reveals specific RNA editing signatures in the human brain. *RNA*. 2017 Mar 3. pii: rna.058271.116. doi: 10.1261/rna.058271.116. [Epub ahead of print] PubMed PMID: 28258159.

Fosso B, Santamaria M, D'Antonio M, Lovero D, Corrado G, Vizza E, Passaro N, Garbuglia AR, Capobianchi MR, Crescenzi M, Valiente G, **Pesole G**. MetaShot: an accurate workflow for taxon classification of host-associated microbiome from shotgun metagenomic data. *Bioinformatics*. 2017 Jan 27. pii: btx036. doi: 10.1093/bioinformatics/btx036. [Epub ahead of print] PubMed PMID: 28130230.

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