

Pubblicazioni su riviste nazionali ed internazionali

- Enhancing nutritional and sensory properties of plant-based beverages: a study on chickpea and Kamut® flours fermentation using *Lactococcus lactic*.
Mefleh M, Omri G, Limongelli R, Minervini F, Santamaria M, Faccia M.
Front Nutr. 2024 Jan 24; 11:1269154. doi: 10.3389/fnut.2024.1269154.
- Establishing the ELIXIR Microbiome Community. Finn RD, Balech B, Burgin J, Chua P, Corre E, Cox CJ, Donati C, Martins dos Santos V, Fosso B, Hancock J, Heil, Ishaque N, Kale V, Kunath BJ, Médigue C, Pafilis E, Pesole, Richardson L, Santamaria M, Van Den Bossche T, Vizcaíno JA, Zafeiropoulos H, Willassen NP, Pelletier E, Batut B. [version 1; peer review: awaiting peer review]. F1000Research 2024, 13(ELIXIR):50
- Hippocampus guttulatus diet based on DNA metabarcoding.
Lazic T, Fosso B, Balech B, Corriero G, Gristina M, Marzano M, Pesole G, Santamaria M and Pierri C.
Original Research, Frontiers in Marine Science, Electronic ISSN 2296-7745, IF = 5.247. 2023 Mar 17.
- The future of food and nutrition in ELIXIR. Balech B, Brennan L, Carrillo de Santa Pau E, Cavalieri D, Coort S, D'Elia D, Ove Dragsted L, Eftimov T, Evelo CT, Ferk P, Finglas P, Gori A, Hancock J, Kalaš M, Koroušić Seljak B, Lachat C, Leskošek B, Pasolli E, Pesole G, Presser K, Sandionigi A, Santamaria M, Dede Şener D, Traka M, Vergères G, Zimmermann K L, Bouwman J. F1000Research 2022, 11(ELIXIR):978
(<https://doi.org/10.12688/f1000research.51747.1>). ISSN 20461402, IF = 2.297
Submitted [version 1; peer review: 1 approved with reservations]
- Recommendations for connecting molecular sequence and biodiversity research infrastructures through ELIXIR.
Waterhouse RM, Adam-Blondon AF, Agosti D, Baldrian P, Balech B, Corre E, Davey RP, Lantz H, Pesole G, Quast C, Glöckner FO, Raes N, Sandionigi A, Santamaria M, Addink W, Vohradsky J, Nunes-Jorge A, Willassen NP, Lanfear J. F1000Research 2022, 10(ELIXIR):1238 (<https://doi.org/10.12688/f1000research.73825.2>). IF = 2.297
- MetaCOXI: an integrated collection of metazoan mitochondrial cytochrome oxidase subunit-I DNA sequences.
Balech B, Sandionigi A, Marzano M, Pesole G, Santamaria M. Database (Oxford). 2022 Feb 3; 2022:baab084. doi: 10.1093/database/baab084.
- Evaluating the Efficiency of DNA Metabarcoding to Analyze the Diet of Hippocampus Guttulatus (Teleostea: Syngnathidae).
Lazic T, Pierri C, Corriero G, Balech B, Cardone F, Deflorio M, Fosso B, Gissi C, Marzano M, Nonnis Marzano F, Pesole G, Santamaria M, Gristina M.
Life, 2021 Sept 22, 11, 998. <https://doi.org/10.3390/life11100998>
- ITSoneWB: profiling global taxonomic diversity of eukaryotic communities on Galaxy.
Tangaro M, Defazio G, Fosso B, Licciulli VF, Grillo G, Donvito G, Lavezzi E, Baruzzo G, Pesole G, Santamaria M. Bioinformatics, 2021 Jun 12:btab431. doi: 10.1093/bioinformatics/btab431. PMID: 34117876.
- Genetic structure of the long-snouted seahorse, *Hippocampus guttulatus*, in the Central–Western Mediterranean Sea.
Lazic T, Pierri C, Cardone F, Cariani A, Colangelo P, Corriero G, Ferrari A, Marzano M, Messinetti S, Pesole G, Senczuk G, Santamaria M, Tinti F, Gristina M. Biological Journal of the Linnean Society, Volume 130, Issue 4, August 2020, Pages 771–782.
- Building essential biodiversity variables (EBVs) of species distribution and abundance at a global scale.
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, Hobson 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. Biol Rev Camb Philos Soc. 2018 Feb;93(1):600-625.

- Molecular identification of Tomato spotted wilt virus on pepper and tobacco in Republic of Srpska (Bosnia and Herzegovina).
Delic D, Balech B, Radulovic M, Duric Z, Lolic B, Santamaria M, Duric G (2018) EUROPEAN JOURNAL OF PLANT PATHOLOGY, ISSN: 0929-1873.
- ITSoneDB: a comprehensive collection of eukaryotic ribosomal RNA Internal Transcribed Spacer 1 (ITS1) sequences.
Santamaria M, Fosso B, Licciulli F, Balech B, Larini I, Grillo G, De Caro G, Liuni S, Pesole G. Nucleic Acids Res. 2018 Jan 4;46(D1):D127-D132.
- Characterization of surface layer microbial communities of *Anopheles gambiae* complex larval habitats in Burkina Faso
Pombi M, Totino V, Fosso B, Santamaria M, Guerrieri F, Bassole I, Guelbeogo WM, Sagnon N, Iebba V, Pesole G, della Torre A, Schippa S, Costantini C. AMERICAN JOURNAL OF TROPICAL MEDICINE AND HYGIENE, nov 2017, Vol 95 Issue5: 251-251 SupplementS - Meeting Abstract.
- The metagenomic data life-cycle: standards and best practices.
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. Gigascience. 2017 Aug 1;6(8):1-11.
- MetaShot: an accurate workflow for taxon classification of host-associated microbiome from shotgun metagenomic data.
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. Bioinformatics. 2017 Jan 27. pii: btx036.
- BioVeL: a virtual laboratory for data analysis and modelling in biodiversity science and ecology.
Hardisty AR, Bacall F, Beard N, Balcázar-Vargas MP, Balech B, Barcza Z, Bourlat SJ, De Giovanni R, de Jong Y, De Leo F, Dobor L, Donvito G, Fellows D, Guerra AF, Ferreira N, Fetyukova Y, Fosso B, Giddy J, Goble C, Güntsch A, Haines R, Ernst VH, Hettling H, Hidy D, Horváth F, Ittzés D, Ittzés P, Jones A, Kottmann R, Kulawik R, Leidenberger S, Lyytikäinen-Saarenmaa P, Mathew C, Morrison N, Nenadic A, de la Hidalga AN, Obst M, Oostermeijer G, Paymal E, Pesole G, Pinto S, Poigné A, Fernandez FQ, Santamaria M, Saarenmaa H, Sipos G, Sylla KH, Tähtinen M, Vicario S, Vos RA, Williams AR, Yilmaz P. BMC Ecol. 2016 Oct 20;16(1):49.
- Complexity and Dynamics of the Winemaking Bacterial Communities in Berries, Musts, and Wines from Apulian Grape Cultivars through Time and Space.
Marzano M, Fosso B, Manzari C, Grieco F, Intrantuovo M, Cozzi G, Mulè G, Scioscia G, Valiente G, Tullo A, Sbisà E, Pesole G, Santamaria M. PLoS One. 2016 Jun 14;11(6):e0157383.
- Towards global interoperability for supporting biodiversity research on essential biodiversity variables (EBVs).
Kissling WD, Hardisty A, García EA, Santamaria M, De Leo F, Pesole G, Freyhof J, Manset D, Wissel S, Konijn J & Los W. Biodiversity. 2015;1-9.
- BioMaS: a modular pipeline for Bioinformatic analysis of Metagenomic AmpliconS. Fosso B, Santamaria M, Marzano M, Alonso-Alemany D, Valiente G, Donvito G, Monaco A, Notarangelo P, Pesole. BMC Bioinformatics. 2015;16:203.
- The influence of invasive jellyfish blooms on the aquatic microbiome detected by an Illumina-based deep sequencing strategy.
Manzari C, Fosso B, Marzano M, Annese A, Caprioli R, D'Erchia AM, Gissi C, Intrantuovo M, Picardi E, Santamaria M, Scorrano S, Sgaramella G, Stabili L, Piraino S, Pesole G. Biological Invasions 2015, Volume 17 (3), pp 923-940.
- Reference databases for taxonomic assignment in metagenomics.
Santamaria M, Fosso B, Consiglio A, De Caro G, Grillo G, Licciulli F, Liuni S, Marzano M, Alonso-Alemany D, Valiente G, Pesole G. Brief Bioinform. 2012 13(6):682-95.
(Santamaria M. and Fosso B. contributed equally to this work).
- ITSoneDB: a specialized ITS1 database for amplicon-based metagenomic characterization of environmental fungal communities. Fosso B, Santamaria M, Consiglio A, De Caro G, Grillo G, Licciulli F, Liuni S, Marzano M, G Pesole. EMBnet.journal April 29, 2012. Meeting Abstract.
- Searching for a needle in the haystack: Comparing six methods to evaluate heteroplasmy in difficult sequence context.

Kurelac I, Lang M, Zuntini R, Calabrese C, Simone D, Vicario S, Santamaria M, Attimonelli M, Romeo G, Gasparre G. Biotechnol Adv. 2011 Jun 13.

- Analysis of pineapple [Ananas comosus (L.) Merr.] fruit proteinases by 2-D zymography and direct identification of the major zymographic spots by mass spectrometry.
Larocca M, Rossano R, Santamaria M, Riccio P. Food Chem., 2010. doi: 10.1016/j.foodchem.2010.06.016.
- Pathogenicity phenotypes of Fusarium spp. associated to citrus dry root rot: primary results.
Hussien A, Yaseen T, Vicario S, Santamaria M, Saccone C, D'Onghia AM. (2009) JOURNAL OF PLANT PATHOLOGY, ISSN: 1125-4653.
- Towards barcode markers in Fungi: an intron map of Ascomycota mitochondria. Santamaria M, Vicario S, Pappadà G, Scioscia G, Scazzocchio C, Saccone C.BMC Bioinformatics, 2009, 10 Suppl 6:S15.
- Variability of the mitochondrial genome in mammals at the inter-species/intra-species boundary.
Santamaria M., Lanave C., Vicario S., Saccone C.Biological Chemistry, 2007, 388, Pages 943–946, Review.
- Human mtDNA Site-Specific Variability Values Can Act as Haplogroup Markers. Accetturo M., Santamaria M., Lascaro D., Rubino F., Achilli A., Torroni A., Tommaseo-Ponzetta M. and Attimonelli M.Human Mutation, 2006, 27 Issue 9, Pages 965 – 974. (Matteo Accetturo, Monica Santamaria, and Daniela Lascaro contributed equally to this work).
- HmtDB, a Human Mitochondrial Genomic Resource Based on Variability Studies Supporting Population Genetics and Biomedical Research.
Attimonelli M., Accetturo M., Santamaria M., Lascaro D., Scioscia G., Pappadà G., Russo L., Zanchetta L. and Tommaseo-Ponzetta M. BMC Bioinformatics, 2005, 6 (Suppl 4):S4.
- Comparative genomics: the evolutionary history of the Bcl-2 family.
Lanave C., Santamaria M., Saccone C. Gene, 2004, Volume 333, 71-79.
- The evolution of the adenine nucleotide translocase family.
Santamaria M., Lanave C., Saccone C. Gene, 2004, 333, 51-59.
- MitoNuc: a database of nuclear genes coding for mitochondrial proteins. Update 2002. Attimonelli M., Catalano D., Gissi C., Grillo G., Licciulli F., Liuni S., Santamaria M., Pesole G. and Saccone C. Nucleic Acids Research, 2002, 30(1), 172-173.

Contributi in volumi/libri

- Variant Calling Algorithms Benchmark Using High Performance Computing. Balech B, Chiara M, Santamaria M, Pesole G (2020) Gangemi Editore spa, Roma (Italia) in Atti dell'incontro con gli utenti DATA CENTER ReCaS-BARI, 2020
- DNA Multiple Sequence Alignment Guided by Protein Domains: The MSA-PAD 2.0 Method. Balech B, Monaco A, Perniola M, Santamaria M, Donvito G, Vicario S, Maggi G, Pesole G. Methods Mol Biol. 2018;1746:173-180.
- e-DNA Meta-Barcoding: From NGS Raw Data to Taxonomic Profiling. Fosso B; Marzano M; Santamaria, M. (2015) RNA Bioinformatics
- Protocolli di laboratorio e strumenti bioinformatici innovativi per l'analisi composizionale dei microbiomi ambientali. Cacucci Editore, Bari (Italia). Santamaria M, De Leo F, Pesole G. (2014)
- Determining mycotoxins and mycotoxicogenic fungi in food and feed. Maestroni B, Cannavan A, Razzazi-Fazeli E Reiter E V, Shephard G S, Spanjer M C, Goryacheva I Y, Senyuva H Z, Gilbert J, De Beer J O, Routledge M N, Gong Y Y, Riley R T and A Voss K, Frisvad J C, Munaut F, Van Hove F, Santamaria M, Tothill I E, Di Mavungu J D, De Saeger S, Singh C B, Jayas D S. Edited by S De Saeger, Ghent University, Belgium. Woodhead Publishing Series in Food Science, Technology and Nutrition No. 203

- The LIBI Grid Platform for Bioinformatics. Book chapter in “Handbook of Research on Computational Grid Technologies for Life Sciences, Biomedicine and Healthcare”. Mirto M, Epicoco I, Fiore S, Cafaro M, Negro A, Tartarini D, Lezzi D, Marra O, Turi A, Ferramosca A, Zara V, Aloisio G, Donvito G, Carota L, Cuscela G, Maggi GP, La Rocca G, Mazzucato M, My S, Selvaggi G, Scioscia G, Leo P, Di Pace L, Pappada' G, Quinto V, Berardi M, Falciano F, Emerson A, Rossi E, Lavorgna G, Vanni A, Bartoli L, Di Lena P, Fariselli P, Fronza R, Margara L, Montanucci L, Martelli PL, Rossi I, Vassura M, and Casadio R, Castrignanò T, D'Elia D, Grillo G, Licciulli F, Liuni S, Gisel A, Santamaria M, Vicario S, Saccone C, Anselmo A, Horner D, Mignone F, Pavesi G, Picardi E, Piccolo V, Re M, Zambelli F, Pesole G. IGI Global , 2009. Edited By: Mario Cannataro, University Magna Graecia of Catanzaro, Italy