Alessio Colantoni

Nationality: Italian **Gender:** Male

WORK EXPERIENCE

UniCamillus - Saint Camillus International University of Health and Medical Sciences – Rome, Italy

City: Rome | **Country:** Italy

Fixed-term tenure track researcher (RTT)

[01/09/2025 – Current]

- Research activities.
- Teacher of the "Biologia Molecolare" module (4 ECTS) of the "BIOCHIMICA" integrated course.
- Teacher of the "Biologia Molecolare" module (3 ECTS) of the "BIOLOGIA CELLULARE, MOLECOLARE E GENETICA" integrated course.

Sapienza University of Rome – Rome, Italy

City: Rome | **Country:** Italy

Fixed-term researcher, type A (RTDA)

[03/01/2022 – 31/08/2025]

- Research activities.
- Teacher of the "Computational Methods in Biology" course (6 ECTS).
- Teacher of the "R programming - basics of statistical data analysis" course in the Corso di Alta Formazione in Bioinformatica for the academic years 2022/2023 and 2023/2024.
- Visit to Rockefeller University from April 28th, 2025 to May 5fth, 2025 to carry out the research project “Manual curation of H9 genome assembly” at the Vertebrate Genome Lab, Rockefeller University, under the supervision of Dr. Giulio Formenti and Dr. Erich Jarvis.

Sapienza University of Rome – Rome, Italy

City: Rome | **Country:** Italy

Adjunct professor for the academic year 2020-2021

[2020 – 2021]

Teacher of the "Computational Methods in Biology" course (6 ECTS).

Center for Life Nano- & Neuro-Science, Fondazione Istituto Italiano di Tecnologia (IIT) – Rome, Italy

City: Rome | **Country:** Italy

Collaborator

[01/04/2020 – 31/12/2021]

Postdoc with a Collaborator contract in the RNA Systems Biology laboratory of Professor Gian Gaetano Tartaglia at the Fondazione Istituto Italiano di Tecnologia, within the ASTRA project, awarded under the H2020 Synergy Grants program.

Sapienza University of Rome – Rome, Italy

City: Rome | **Country:** Italy

Research fellow

[30/11/2014 – 31/03/2020]

Postdoc as a bioinformatician in the laboratory of Professor Irene Bozzoni, Department of Biology and Biotechnology “Charles Darwin”, Sapienza University of Rome.

EDUCATION AND TRAINING

PhD in Cellular and Molecular Biology (Bioinformatic Curriculum)

University of Rome "Tor Vergata" [2011 – 2015]

City: Rome | **Country:** Italy

Master's Degree in Bioinformatics with a grade of 110/110 cum laude

University of Rome "Tor Vergata" [2009 – 2011]

City: Rome | **Country:** Italy

Bachelor's Degree in Cellular and Molecular Biology with a grade of 110/110 cum laude

University of Rome "Tor Vergata" [2006 – 2009]

City: Rome | **Country:** Italy

High School Diploma with a grade of 100/100

Liceo Scientifico “Isacco Newton” [2000 – 2006]

City: Rome | **Country:** Italy

LANGUAGE SKILLS

Mother tongue(s): Italian

Other language(s):

English

LISTENING C1 **READING** C1 **WRITING** C1

SPOKEN PRODUCTION C1 **SPOKEN INTERACTION** C1

Spanish

LISTENING A2 **READING** A2 **WRITING** A2

SPOKEN PRODUCTION A2 **SPOKEN INTERACTION** A2

Levels: A1 and A2: Basic user; B1 and B2: Independent user; C1 and C2: Proficient user

SKILLS

Excellent knowledge of the C, C++, Python, R and Ruby programming languages. / Excellent knowledge of the software for the analysis of Next Generation Sequencing data. / Excellent knowledge of the software for the analysis of macromolecular sequence and structure. / Ability to create and manage relational databases. / Ability to create and manage static (HTML) and dynamic (PHP, Python CGI) web pages. / Excellent knowledge of Linux/Unix environments. Ability to handle and administer Linux servers. / Containerization (Docker, Singularity, Kubernetes) / HPC cluster usage

SCIENTIFIC INTERESTS

Main areas of expertise

• Analysis of Second Generation (short-read) and Third Generation (long-read) high-throughput sequencing data (Bulk and Single-Cell): RNA-Seq and its variants (RIP-Seq, CLIP-Seq, RNA pull-down sequencing), ChIP-Seq, ChIRP-Seq, ATAC-Seq, and Whole Genome Sequencing.

• Study of gene regulation mechanisms, including how transcription factor binding and epigenetic modifications influence transcriptional activity, using integrative analyses of omics data.

• Systematic study of non-coding RNAs (lncRNAs, miRNAs, circRNAs), focusing on their regulatory functions, interaction networks, and implications in developmental processes, neurodegenerative diseases, muscular dystrophies, and cancer. Application of computational and experimental methods to identify new classes of functional RNAs and diagnostic/prognostic biomarkers.

• Prediction and characterization of RNA interactions with proteins or other RNAs using computational approaches based on thermodynamics, co-expression models, and machine learning. Development and application of bioinformatic pipelines for the inference of RNP complexes and their role in post-transcriptional regulation.

• In-depth study of alternative splicing, with particular attention to the mechanisms regulating splice site selection and the impact of alternative splicing events on protein function and disease onset. Use of RNA-Seq data for profiling alternative transcriptomes and discovering new functional isoforms.

• Investigation of the effects of RNA modifications on RNA biogenesis, function, and structure.

• Telomere-to-telomere genome assembly.

QUALIFICATIONS

[07/03/2025 – Current]

National scientific qualification for full professorship in the Academic Discipline 05/E2 – Molecular Biology

PARTICIPATION IN EDITORIAL BOARDS OF SCIENTIFIC JOURNALS.

[17/04/2024 – Current]

Guest Editor of the "Protein–RNA Interactions: Function, Mechanism, and Identification" special issue of the "International Journal of Molecular Sciences" journal

As an Associate Editor, I curated the editing of eleven scientific articles, of which seven were published. The profile is accessible at the following link: https://loop.frontiersin.org/people/1262607/overview.

[10/05/2023 – Current]

Associate Editor in the "RNA Networks and Biology" section of the "Frontiers in Molecular Biosciences" journal

As a Review Editor, I curated the revision of twelve scientific articles, of which five were published.

[10/03/2021 – Current]

Review Editor in the "RNA Networks and Biology" section of the "Frontiers in Molecular Biosciences" journal

CONFERENCES AND SEMINARS

[02/06/2025 – 06/06/2025] CIBIO, Trento

EMBO Practical Course: Embo gROUNDbreaking approaches for advancing circRNA research: Detection, function, therapeutics

Participation as a Trainer for the Data Analysis section.

[06/05/2025 – 10/05/2025] Cold Spring Harbor Laboratory, Laurel Hollow

Cold Spring Harbor Biology of Genomes Conference 2025

Presentation of a poster titled "Reference-quality genomes of human cell lines for precision omics".

[18/05/2024] Polo di San Lorenzo, Sapienza University of Rome, Rome

Invited speaker for a seminar at Sapienza University of Rome

Seminar titled "Prediction of protein-RNA interactions from single-cell transcriptomic data".

[07/10/2024 – 09/10/2024] Memox Basel Main Station, Basel

Non-coding RNA World 2024: Exploring Mechanisms, Designing Medicines

Oral talk titled "Prediction of protein-RNA interactions from single-cell transcriptomic data".

[15/05/2023 – 18/05/2023] Collegium Iuridicum Novum, Poznan

EMBO Workshop: Non-coding RNA medicine

Oral talk titled “FUS Alters circRNA Metabolism in Human Motor Neurons Carrying the ALS-Linked P525L Mutation”.

[15/11/2022 – 18/11/2022] EMBL Heidelberg

EMBO Workshop: From functional genomics to systems biology

Presentation of a poster titled “Multi-omics analysis reveals a crucial role for Retinoic Acid in promoting epigenetic and transcriptional competence of an in vitro model of human Pharyngeal Endoderm”.

[23/04/2022 – 29/04/2022] EMBL Heidelberg

EMBO Practical Course: Methods for analysis of circRNAs: From discovery to function

Participation as a Trainer for the Data Analysis section.

[10/2019] EMBL Heidelberg

EMBO Practical Course: Methods for Analysis of Circular RNAs: No Tautology

Participation as a Trainer for the Data Analysis section.

[01/2014] Sapienza University of Rome

Annual meeting of the Bioinformatics Italian Society

Presentation of a poster titled "Global characterization of alternative splicing events in long non coding RNAs".

[06/2013] Berlin

ISMB/ECCB

Presentation of a poster titled "Global characterization of alternative splicing events in long non coding RNAs".

[04/2012] University of Catania

Annual meeting of the Bioinformatics Italian Society

Oral talk titled "Alternative splicing as regulator of protein-protein interactions".

BIBLIOMETRIC INDICATORS

Scopus metrics 03/09/2025

number of citations: 2151

h-index: 18

Google Scholar metrics 03/09/2025

number of citations: 2689

h-index: 18

PUBLICATIONS

Marocco F, Garbo S, Montaldo C, Colantoni A, Quattrocchi L, Gaboardi G, Sabarese G, Cicchini C, Lecce M, Carnevale A, Paolini R, Tartaglia GG, Battistelli C, Tripodi M. Negative regulation of miRNA sorting into EVs is mediated by the capacity of RBP PCBP2 to impair the SYNCRIP-dependent miRNA loading. Elife. 2025 Jul 2;14:RP105017.

Scatolini L, Graziadio L, Guerrini D, Maccallini P, Marino C, di Vito R, Hassan A, Grimaldi M, Fidaleo M, Dehghannasiri R, Proietti G, Piergentili R, Salvati E, Cacchione S, De Pittà C, Doksani Y, D'Ursi AM, Wakefield J, Chen L, Gatti M, Colantoni A, Usiello A, Raffa GD. RNase H1 counteracts DNA damage and ameliorates SMN-dependent phenotypes in a Drosophila model of Spinal Muscular Atrophy. BioRxiv 2025.04.17.649348.

Fiorentino F, Armaos A, Montrone C, Colantoni A, Tartaglia GG. scRAPID-web: a web server for predicting protein-RNA interactions from single-cell transcriptomics. BioRxiv 2025.03.12.642785.

Setti A, Bini G, Maiorca V, Pellegrini F, Proietti G, Miltiadis-Vrachnos D, Armaos A, Martone J, Monti M, Ruocco G, Rodolà E, Bozzoni I, Colantoni A, Tartaglia GG. Decoding RNA-RNA Interactions: The Role of Low-Complexity Repeats and a Deep Learning Framework for Sequence-Based Prediction. BioRxiv 2025.02.16.638500.

Silvestri B, Mochi M, Mawrie D, de Turris V, Colantoni A, Borhy B, Medici M, Anderson EN, Garone MG, Zammerilla CP, Simula M, Ballarino M, Pandey UB, Rosa A. HuD impairs neuromuscular junctions and induces apoptosis in human iPSC and Drosophila ALS models. Nat Commun. 2024 Nov 7;15(1):9618.

Cipriano A, Colantoni A, Calicchio A, Fiorentino J, Gomes D, Moqri M, Parker A, Rasouli S, Caldwell M, Briganti F, Roncarolo MG, Baldini A, Weinacht KG, Tartaglia GG, Sebastiano V. Transcriptional and epigenetic characterization of a new in vitro platform to model the formation of human pharyngeal endoderm. Genome Biol. 2024 Aug 8;25(1):211.

Garbo S, D'Andrea D, Colantoni A, Fiorentino F, Mai A, Ramos A, Tartaglia GG, Tancredi A, Tripodi M, Battistelli C. m6A modification inhibits miRNAs' intracellular function, favoring their extracellular export for intercellular communication. Cell Rep. 2024 Jun 25;43(6):114369.

Desideri F, Grazzi A, Lisi M, Setti A, Santini T, Colantoni A, Proietti G, Carvelli A, Tartaglia GG, Ballarino M, Bozzoni I. CyCoNP lncRNA establishes cis and trans RNA-RNA interactions to supervise neuron physiology. Nucleic Acids Res. 2024 Jul 11:gkae590.

Fiorentino J, Armaos A, Colantoni A, Tartaglia GG. Prediction of protein-RNA interactions from single-cell transcriptomic data. Nucleic Acids Res. 2024 Apr 12;52(6):e31.

Benedetti MC, D'andrea T, Colantoni A, Silachev D, de Turris V, Boussadia Z, Babenko VA, Volovikov EA, Belikova L, Bogomazova AN, Pepponi R, Whye D, Buttermore ED, Tartaglia GG, Lagarkova MA, Katanaev VL,

Musayev I, Martinelli S, Fucile S, Rosa A. Cortical neurons obtained from patient-derived iPSCs with GNAO1 p.G203R variant show altered differentiation and functional properties. Heliyon. 2024 Feb 21;10(5):e26656.

Centrón-Broco A, Rossi F, Grelloni C, Garraffo R, Dattilo D, Giuliani A, Di Timoteo G, Colantoni A, Bozzoni I, Beltran Nebot M. CircAFF1 Is a Circular RNA with a Role in Alveolar Rhabdomyosarcoma Cell Migration. Biomedicines. 2023 Jul 4;11(7):1893.

Colantoni A, Capauto D, Alfano V, D'Ambra E, D'Uva S, Tartaglia GG, Morlando M. FUS Alters circRNA Metabolism in Human Motor Neurons Carrying the ALS-Linked P525L Mutation. Int J Mol Sci. 2023 Feb 6;24(4):3181.

Vandelli A, Arnal Segura M, Monti M, Fiorentino J, Broglia L, Colantoni A, Sanchez de Groot N, Torrent Burgas M, Armaos A, Tartaglia GG. The PRALINE database: protein and Rna humAn singLe nucleotIde variaNts in condEnsates. Bioinformatics. 2023 Jan 1;39(1):btac847.

Chen L, Roake CM, Maccallini P, Bavasso F, Dehghannasiri R, Santonicola P, Mendoza-Ferreira N, Scatolini L, Rizzuti L, Esposito A, Gallotta I, Francia S, Cacchione S, Galati A, Palumbo V, Kobin MA, Tartaglia GG, Colantoni A, et al. TGS1 impacts snRNA 3'-end processing, ameliorates survival motor neuron-dependent neurological phenotypes in vivo and prevents neurodegeneration. Nucleic Acids Res. 2022 Nov 28;50(21):12400-12424.

Carvelli A, Setti A, Desideri F, Galfrè SG, Biscarini S, Santini T, Colantoni A, Peruzzi G, Marzi MJ, Capauto D, Di Angelantonio S, Ballarino M, Nicassio F, Laneve P, Bozzoni I. A multifunctional locus controls motor neuron differentiation through short and long noncoding RNAs. EMBO J. 2022 Jul 4;41(13):e108918.

Fiorillo C, Yen PS, Colantoni A, Mariconti M, Azevedo N, Lombardo F, Failloux AB, Arcà B. MicroRNAs and other small RNAs in Aedes aegypti saliva and salivary glands following chikungunya virus infection. Sci Rep. 2022 Jun 9;12(1):9536.

Scalzitti S, Mariani D, Setti A, Colantoni A, Lisi M, Bozzoni I, Martone J. Lnc-SMaRT Translational Regulation of Spire1, A New Player in Muscle Differentiation. J Mol Biol. 2022 Jan 30;434(2):167384.

Rossi F, Beltran M, Damizia M, Grelloni C, Colantoni A, Setti A, Di Timoteo G, Dattilo D, Centrón-Broco A, Nicoletti C, Fanciulli M, Lavia P, Bozzoni I. Circular RNA ZNF609/CKAP5 mRNA interaction regulates microtubule dynamics and tumorigenicity. Mol Cell. 2022 Jan 6;82(1):75-89.e9.

Rossi F, Centrón-Broco A, Dattilo D, Di Timoteo G, Guarnacci M, Colantoni A, Beltran Nebot M, Bozzoni I. CircVAMP3: A circRNA with a Role in Alveolar Rhabdomyosarcoma Cell Cycle Progression. Genes (Basel). 2021 Jun 28;12(7):985.

Armaos A, Colantoni A, Proietti G, Rupert J, Tartaglia GG. catRAPID omics v2.0: going deeper and wider in the prediction of protein-RNA interactions. Nucleic Acids Res. 2021 Jun 4:gkab393.

Cipriano A, Macino M, Buonaiuto G, Santini T, Biferali B, Peruzzi G, Colantoni A, Mozzetta C, Ballarino M. Epigenetic regulation of Wnt7b expression by the cis-acting long noncoding RNA Lnc-Rewind in muscle stem cells. Elife. 2021 Jan 12;10:e54782.

Dobrowolny G, Martone J, Lepore E, Casola I, Petrucci A, Inghilleri M, Morlando M, Colantoni A, Scicchitano BM, Calvo A, Bisogni G, Chiò A, Sabatelli M, Bozzoni I, Musarò A. A longitudinal study defined circulating microRNAs as reliable biomarkers for disease prognosis and progression in ALS human patients. Cell Death Discov. 2021 Jan 11;7(1):4.

Desideri F, Cipriano A, Petrezselyova S, Buonaiuto G, Santini T, Kasparek P, Prochazka J, Janson G, Paiardini A, Calicchio A, Colantoni A, Sedlacek R, Bozzoni I, Ballarino M. Intronic Determinants Coordinate Charme lncRNA Nuclear Activity through the Interaction with MATR3 and PTBP1. Cell Rep. 2020 Dec 22;33(12):108548.

Colantoni A, Rupert J, Vandelli A, Tartaglia GG, Zacco E. Zooming in on protein-RNA interactions: a multi-level workflow to identify interaction partners. Biochem Soc Trans. 2020 Aug 28;48(4):1529-1543.

Martone J, Lisi M, Castagnetti F, Rosa A, Di Carlo V, Blanco E, Setti A, Mariani D, Colantoni A, Santini T, Perone L, Di Croce L, Bozzoni I. Trans-generational epigenetic regulation associated with the amelioration of Duchenne Muscular Dystrophy. EMBO Mol Med. 2020 Aug 7;12(8):e12063.

Martone J, Mariani D, Santini T, Setti A, Shamloo S, Colantoni A, Capparelli F, Paiardini A, Dimartino D, Morlando M, Bozzoni I. SMaRT lncRNA controls translation of a G-quadruplex-containing mRNA antagonizing the DHX36 helicase. EMBO Rep. 2020 Jun 4;21(6):e49942.

Garone MG, Alfano V, Salvatori B, Braccia C, Peruzzi G, Colantoni A, Bozzoni I, Armirotti A, Rosa A. Proteomics analysis of FUS mutant human motoneurons reveals altered regulation of cytoskeleton and other ALS-linked proteins via 3'UTR binding. Sci Rep. 2020 Jul 16;10(1):11827.

Di Timoteo G, Dattilo D, Centrón-Broco A, Colantoni A, Guarnacci M, Rossi F, Incarnato D, Oliviero S, Fatica A, Morlando M, Bozzoni I. Modulation of circRNA Metabolism by m6A Modification. Cell Rep. 2020 May 12;31(6): 107641.

De Santis R, Alfano V, de Turris V, Colantoni A, Santini L, Garone M G, Antonacci G, Peruzzi G, Sudria-Lopez E, Wyler E. Anink J J, Aronica E, Landthaler M, Pasterkamp R J, Bozzoni I, Rosa A. Mutant FUS and ELAVL4 (HuD) Aberrant Crosstalk in Amyotrophic Lateral Sclerosis. Cell Rep. 2019 Jun 25:27(13):3818–3831.e5.

Arcà B, Colantoni A, Fiorillo C, Severini F, Benes V, Di Luca M, Calogero R A, Lombardo, F. MicroRNAs from saliva of anopheline mosquitoes mimic human endogenous miRNAs and may contribute to vector-host-pathogen interactions. Sci Rep. 2019 Feb 27;9(1):2955.

Rossi F, Legnini I, Megiorni F, Colantoni A, Santini T, Morlando M, Di Timoteo G, Dattilo D, Dominici C, Bozzoni I. Circ-ZNF609 regulates G1-S progression in rhabdomyosarcoma. Oncogene. 2019 Jan 22.

Capauto D, Colantoni A, Lu L, Santini T, Peruzzi G, Biscarini S, Morlando M, Shneider NA, Caffarelli E, Laneve P, Bozzoni I. A Regulatory Circuitry Between Gria2, miR-409, and miR-495 Is Affected by ALS FUS Mutation in ESC-Derived Motor Neurons. Mol Neurobiol. 2018 Oct;55(10):7635-7651.

Ballarino M, Cipriano A, Tita R, Santini T, Desideri F, Morlando M, Colantoni A, Carrieri C, Nicoletti C, Musarò A, Carroll DO, Bozzoni I. Deficiency in the nuclear long noncoding RNA Charme causes myogenic defects and heart remodeling in mice. EMBO J. 2018 Sep 14;37(18).

Dimartino D, Colantoni A, Ballarino M, Martone J, Mariani D, Danner, J, Bruckmann, A, Meister G, Morlando M, Bozzoni I. The Long Non-coding RNA lnc-31 Interacts with Rock1 mRNA and Mediates Its YB-1-Dependent Translation. Cell Rep. 2018 Apr 17;23(3):733-740.

Biscarini S, Capauto D, Peruzzi G, Lu L, Colantoni A, Santini T, Shneider NA, Caffarelli E, Laneve P, Bozzoni I. Characterization of the lncRNA transcriptome in mESC-derived motor neurons: Implications for FUS-ALS. Stem Cell Res. 2018 Mar;27:172-179.

De Santis R, Santini L, Colantoni A, Peruzzi G, de Turris V, Alfano V, Bozzoni I, Rosa A. FUS Mutant Human Motoneurons Display Altered Transcriptome and microRNA Pathways with Implications for ALS Pathogenesis. Stem Cell Reports. 2017 Nov 14;9(5):1450-1462.

Errichelli L, Dini Modigliani S, Laneve P, Colantoni A, Legnini I, Capauto D, Rosa A, De Santis R, Scarfò R, Peruzzi G, Lu L, Caffarelli E, Shneider NA, Morlando M, Bozzoni I. FUS affects circular RNA expression in murine embryonic stem cell-derived motor neurons. Nat Commun. 2017 Mar 30;8:14741.

Ferrè F, Colantoni A, Helmer-Citterich M. Revealing protein-lncRNA interaction. Brief Bioinform. 2016 Jan; 17(1):106-16.

Bianchi V, Colantoni A, Calderone A, Ausiello G, Ferrè F, Helmer-Citterich M. DBATE: database of alternative transcripts expression. Database (Oxford). 2013 Jul 9;2013:bat050.

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I hereby authorize the processing of my personal data contained in my CV pursuant to art. 13 d. lgs. 30 giugno 2003 n. 196 - "Codice in materia di protezione dei dati personali" and art. 13 GDPR 679/16 - "Regolamento europeo sulla protezione dei dati personali".

Rome, 03/09/2025