

Toma Tebaldi

ABOUT ME

My research aims at understanding the RNA molecular mechanisms underlying dysregulation in human diseases, by combining high-resolution experimental and computational approaches and with focus on mutant RNA binding proteins, RNA modifications (the epitranscriptome), non-coding RNAs, alternative splicing, translation dynamics, single cell and spatial expression data.

WORK EXPERIENCE

Associate Research Scientist

Yale School of Medicine [8/2017 – Current]

City: New Haven

Country: United States

Research on RNA dysregulation in hematologic malignancies: high resolution single cell and spatial expression profiling, RNA modifications (epitranscriptomics), aberrant splicing, altered RNA-protein interactions.

Visiting Professor

Department of Information Engineering and Computer Science, University of Trento [9/2020 – 12/2021]

City: Trento

Country: Italy

Visiting Professor

Department of Information Engineering and Computer Science, University of Trento [2/2019 – 5/2019]

City: Trento

Country: Italy

Postdoctoral Fellowship

Department CIBIO - University of Trento [8/2013 – 8/2017]

City: Trento

Country: Italy

RNA and translation dysregulation in motor neuron diseases (ALS, SMA). Development of software for the analysis and integration of multi-omics (Ribo-Seq, CLIP-Seq, RNA-Seq).

EMBO Short Fellowship

School of Informatics, University of Edinburgh [1/2015 – 3/2015]

City: Edinburgh

Country: United Kingdom

Computational methods to detect RNA-protein interactions in CLIP-Seq data.

International Internship

School of Informatics, University of Edinburgh [5/2013 – 12/2013]

City: Edinburgh

Country: United Kingdom

"Statistical methods to detect RNA-protein interactions from CLIP-Seq data". Research collaboration with Prof. Guido Sanguinetti

Postdoctoral Fellowship

Department CIBIO - University of Trento [5/2012 – 5/2013]

City: Trento

Country: Italy

Post-transcriptional regulation in cancer: melanoma, neuroblastoma. Software development and RNA omics analysis.

Postdoctoral Fellowship

Department CIBIO - University of Trento [4/2010 – 4/2012]

City: Trento

Country: Italy

Gene expression dynamics in eukaryotic cells, focusing on uncoupling between transcription and translation.

International Internship

Center for Biomedical Informatics, Harvard Medical School [6/2009 – 9/2009]

City: Boston

Country: United States

"Integration of heterogeneous biological datasets". Research collaboration with Prof. Peter J. Park.

International internship

University of Sheffield [2/2009 – 3/2009]

City: Sheffield

Country: United Kingdom

"Application of Bayesian networks to post-transcriptional regulation dynamics". Research collaboration with Prof. Guido Sanguinetti.

TEACHING ACTIVITIES

Teacher: PhD course in Artificial Intelligence for Bioinformatics

[3/2019 – Current]

University of Trento, Department CIBIO and DISI

Doctoral School in Information and Communication Technology (ICT)

Doctoral Programme in Biomolecular Sciences

Teaching Assistant: Bioinformatics

[3/2019 – Current]

University of Trento, Department CIBIO and DISI

Master degree in Quantitative Biology and Master degree in Informatics

Teacher: Bioinformatics Resources

[2/2017 – 2/2019]

University of Trento, Department CIBIO and DISI

Master degree in Quantitative Biology

Teaching Assistant: Scientific Programming

[9/2016 – 7/2017]

University of Trento, Department CIBIO and DISI

Master degree in Quantitative Biology

Teaching Assistant: Introduction to Cell Biology

[9/2013 – 2/2016]

University of Trento, Department of Mathematics and DISI

BIO/13 - 05/F1

Teaching Assistant: Molecular Basis of Disease

[9/2012 – 2/2013]

University of Trento, Department CIBIO

BIO/13 - 05/F1

Teaching Assistant: Systems Biology

[9/2012 – 2/2013]

University of Trento, Department CIBIO

BIO/13 - 05/F1

Teaching Assistant: Biology

[9/2008 – 12/2010]

University of Trento, Department CIBIO and DISI

BIO/13 - 05/F1

EDUCATION AND TRAINING

PhD in Information and Communication Technology

ICT International Doctoral School, University of Trento [11/2006 – 3/2010]

Address: Trento (Italy)

Level in EQF: EQF level 8

Thesis: Computational and experimental detection of uncoupling between translome and transcriptome

Master Degree in Biotechnologies - Bioinformatics

University of Milano Bicocca [9/2003 – 6/2006]

Address: Milan (Italy)

Final grade : 110/110 with honours – Level in EQF: EQF level 7

Student at Collegio di Milano

Collegio di Milano (inter-university campus of excellence) [3/2003 – 7/2006]

Address: Milan (Italy)

Honour school offering a Cultural Program complementary to academic career, aimed at interdisciplinary interaction and multiculturalism.

Bachelor Degree in Biotechnologies

University of Milano Bicocca [9/2000 – 7/2003]

Address: Milan (Italy)

Final grade : 110/110 with honours – Level in EQF: EQF level 6

PUBLICATIONS

Complete Bibliography:

<https://www.ncbi.nlm.nih.gov/myncbi/toma.tebaldi.1/bibliography/public/>

Transcriptome-wide quantification of double-stranded RNAs in live mouse tissues by dsRIP-Seq

[2021]

<https://doi.org/10.1016/j.xpro.2021.100366>

Gao et al. STAR Protoc. 2021 Mar 18;2(1):100366.

Role: **co-corresponding author**

Combined liver-cytokine humanization comes to the rescue of circulating human red blood cells

[2021]

<https://doi.org/10.1126/science.abe2485>

Song et al.. Science. 2021 Mar 5;371(6533):1019-1025

Role: **co-author** (IF 41.8)

Influence of the microenvironment on the modulation of the host response by the typhoid toxin

[2021]

<https://doi.org/10.1016/j.celrep.2021.108931>

Martin et al. Cell Rep. 2021 Apr 6;35(1):108931

Role: **co-author** (IF 8.1)

m6A Modification Prevents Formation of Endogenous Double-Stranded RNAs ...

[2020]

<https://doi.org/10.1016/j.immuni.2020.05.003>

Gao et al. Immunity. 2020;52(6):1007-1021.e8.

Role: **co-corresponding author** (IF 22.6)

SMN-primed ribosomes modulate the translation of transcripts related to spinal muscular atrophy

[2020]

<https://doi.org/10.1038/s41556-020-00577-7>

Lauria et al. Nat Cell Biol. 2020 Oct;22(10):1239-1251

Role: **co-first author** (IF 20.0)

High-Spatial-Resolution Multi-Omics Atlas Sequencing of Mouse Embryos via Deterministic ...

[2020]

<https://doi.org/10.1016/j.cell.2020.10.026>

Liu et al. Cell. 2020

Role: **co-author** (IF 38.6)

Regulation of cellular sterol homeostasis by the oxygen responsive noncoding RNA lincNORS

[2020]

<https://doi.org/10.1038/s41467-020-18411-x>

Wu et al. Nat Commun. 2020 Sep 21;11(1):4755.

Role: **co-author** (IF 12.1)

The altered transcriptome of pediatric myelodysplastic syndrome revealed by RNA sequencing

[2020]

<https://doi.org/10.1186/s13045-020-00974-3>

Zubovic et al. J Hematol Oncol. 2020 Oct 12;13(1):135.

Role: **co-author** (IF 11.1)

A Computing System for Discovering Causal Relationships among Human Genes to Improve Drug ...

[2020]

<https://doi.org/10.1109/TETC.2020.3031024>

Blanzieri et al. IEEE Transactions on Emerging Topics In Computing

Role: **co-author** (IF 6.0)

Low Iron Promotes Megakaryocytic Commitment of Megakaryocytic-Erythroid Progenitors in Humans ...

[2019]

<https://doi.org/10.1182/blood.2019002039>

Xavier-Ferrucio et al. Blood. 2019;134(18):1547-1557.

Role: **co-author** (IF 17.5)

Hypomorphic mutation of the mouse Huntington's disease gene orthologue

[2019]

<https://doi.org/10.1371/journal.pgen.1007765>

Murthy et al. PLoS Genet. 2019;15(3):e1007765

Role: **co-first author** (IF 5.2)

A highly efficient and faithful MDS patient-derived xenotransplantation model ...

[2019]

<https://doi.org/10.1038/s41467-018-08166-x>

Song et al. Nat Commun. 2019;10(1):366.

Role: **co-author** (IF 12.1)

SRSF2 mutations drive oncogenesis by activating a global program of aberrant alternative splicing

[2018]

<https://doi.org/10.1038/s41375-018-0152-7>

Liang Y et al. Leukemia. 2018;32(12):2659-2671

Role: **co-first author** (IF 8.7) Recommended In F1000Prime as being of special significance in its field

Active Ribosome Profiling with RiboLace

[2018]

<https://doi.org/10.1016/j.celrep.2018.09.084>

Clamer M et al. Cell Rep. 2018;25(4):1097-1108.e5.

Role: **co-author** (IF 8.1) Journal cover award

riboWaltz: Optimization of ribosome P-site positioning in ribosome profiling data

[2018]

<https://doi.org/10.1371/journal.pcbi.1006169>

Lauria et al. PLoS Comput Biol. 2018;14(8):e1006169.

Role: **co-first author** (IF 4.7)

HuD Is a Neural Translation Enhancer Acting on mTORC1-Responsive Genes and Counteracted by ...

[2018]

<https://doi.org/10.1016/j.molcel.2018.06.032>

Tebaldi et al. Mol Cell. 2018;71(2):256-270.e10

Role: **co-first author** (IF 15.6)

Hydrogen peroxide is a neuronal alarmin that triggers specific RNAs, local translation ...

[2018]

<https://doi.org/10.1261/rna.064816.117>

Negro et al. RNA. 2018;24(7):915-925.

Role: **co-first author** (IF 4.3)

Cancer cell metabolic plasticity allows resistance to NAMPT inhibition but invariably induces ...

[2018]

<https://doi.org/10.1186/s40170-018-0174-7>

Thongon et al. Cancer Metab. 2018;6:1.

Role: **co-author** (IF 5.0)

The hnRNP RALY regulates transcription and cell proliferation by modulating the expression ...

[2017]

<https://doi.org/10.1074/jbc.M117.795591>

Cornella et al. J Biol Chem. 2017;292(48):19674-19692.

Role: **co-author** (IF 4.2)

The Unexpected Tuners: Are LncRNAs Regulating Host Translation during Infections?

[2017]

<https://doi.org/10.3390/toxins9110357>

Knap et al. Toxins (Basel). 2017;9(11):357.

Role: **co-author** (IF 3.5)

In Vivo Translatome Profiling in Spinal Muscular Atrophy Reveals a Role for SMN Protein ...

[2017]

<https://doi.org/10.1016/j.celrep.2017.10.010>

Bernabò et al. Cell Rep. 2017;21(4):953-965.

Role: **co-first author** (IF 8.1) Journal cover award

Identification and dynamic changes of RNAs isolated from RALY-containing ribonucleoprotein ...

[2017]

<https://doi.org/10.1093/nar/gkx235>

Rossi et al. Nucleic Acids Res. 2017;45(11):6775-6792.

Role: **co-author** (IF 11.5)

RNAcommender: genome-wide recommendation of RNA-protein interactions

[2016]

<https://doi.org/10.1093/bioinformatics/btw517>

Corrado et al. Bioinformatics. 2016;32(23):3627-3634.

Role: **co-author** (IF 5.6)

The Typhoid Toxin Promotes Host Survival and the Establishment of a Persistent Asymptomatic ...

[2016]

<https://doi.org/10.1371/journal.ppat.1005528>

Del Bel Belluz et al. PLoS Pathog. 2016;12(4):e1005528.

Role: **co-author** (IF 6.2) Research highlight in Nature: "Microbiology: Salmonella live on thanks to toxin"

RiboAbacus: a model trained on polyribosome images predicts ribosome density ...

[2015]

<https://doi.org/10.1093/nar/gkv781>

Lauria et al. Nucleic Acids Res. 2015;43(22):e153

Role: **co-author** (IF 11.5)

Global translation variations in host cells upon attack of lytic and sublytic Staphylococcus ...

[2015]

<https://doi.org/10.1042/BJ20150284>

Clamer et al. Biochem J. 2015;472(1):83-95.

Role: **co-first author** (IF 4.1)

TrkA is amplified in malignant melanoma patients and induces an anti-proliferative response ...

[2015]

<https://doi.org/10.1186/s12885-015-1791-y>

Pasini et al. BMC Cancer. 2015;15:777

Role: **co-author** (IF 3.2)

eIF6 coordinates insulin sensitivity and lipid metabolism by coupling translation to transcription

[2015]

<https://doi.org/10.1038/ncomms9261>

Brina et al. Nat Commun. 2015;6:8261.

Role: **co-author** (IF 12.1)

Whole-genome cartography of p53 response elements ranked on transactivation potential

[2015]

<https://doi.org/10.1186/s12864-015-1643-9>

Tebaldi et al. BMC Genomics. 2015;16(1):464.

Role: **co-first and co-corresponding author** (IF 3.6)

Three distinct ribosome assemblies modulated by translation are the building blocks of polysomes

[2015]

<https://doi.org/10.1083/jcb.201406040>

Viero et al. J Cell Biol. 2015;208(5):581-596

Role: **co-author** (IF 8.8)

Translational downregulation of HSP90 expression by iron chelators in neuroblastoma cells

[2015]

<https://doi.org/10.1124/mol.114.095729>

Sidarovich et al. Mol Pharmacol. 2015;87(3):513-524.

Role: **co-author** (IF 3.7)

Cooperative interactions between p53 and NFkB enhance cell plasticity

[2014]

<https://doi.org/10.18632/oncotarget.2545>

Bisio et al. Oncotarget. 2014;5(23):12111-12125

Role: **co-author**

p53-directed translational control can shape and expand the universe of p53 target genes

[2014]

<https://doi.org/10.1038/cdd.2014.79>

Zaccara et al. Cell Death Differ. 2014;21(10):1522-1534.

Role: **co-author** (IF 10.7)

Increased frequency of minimal homozygous deletions is associated with poor prognosis ...

[2014]

<https://doi.org/10.1002/gcc.22160>

Boi et al. Genes Chromosomes Cancer. 2014;53(6):487-496.

Role: **co-author** (IF 3.4)

PTRcombiner: mining combinatorial regulation of gene expression from post-transcriptional ...

[2014]

<https://doi.org/10.1186/1471-2164-15-304>

Corrado et al. BMC Genomics. 2014;15:304.

Role: **co-first author** (IF 3.6)

AURA 2: Empowering discovery of post-transcriptional networks

[2014]

<https://doi.org/10.4161/trla.27738>

Dassi et al. Translation (Austin). 2014;2(1):e27738.

Role: **co-author**

tRanslatome: an R/Bioconductor package to portray translational control

[2014]

<https://doi.org/10.1093/bioinformatics/btt634>

Tebaldi et al. Bioinformatics. 2014;30(2):289-291.

Role: **co-first and corresponding author** (IF 5.6)

Interaction between p53 and estradiol pathways in transcriptional responses to chemotherapeutics

[2013]

<https://doi.org/10.4161/cc.24309>

Lion et al. Cell Cycle. 2013;12(8):1211-1224.

Role: **co-author** (IF 3.7)

Widespread uncoupling between transcriptome and translome variations after a stimulus ...

[2012]

<https://doi.org/10.1186/1471-2164-13-220>

Tebaldi et al. BMC Genomics. 2012;13:220.

Role: **co-first author** (IF 3.6)

Downregulation of HuR as a new mechanism of doxorubicin resistance in breast cancer cells

[2012]

<https://doi.org/10.1186/1476-4598-11-13>

Latorre et al. Mol Cancer. 2012;11:13.

Role: **co-author** (IF 15.3)

AURA: Atlas of UTR Regulatory Activity

[2012]

<https://doi.org/10.1093/bioinformatics/btr608>

Dassl et al. Bioinformatics. 2012;28(1):142-144.

Role: **co-author** (IF 5.6)

Integration of heterogeneous expression data sets extends the role of the retinol pathway ...

[2009]

<https://doi.org/10.1093/bioinformatics/btp559>

Park et al. Bioinformatics. 2009;25(23):3121-3127.

Role: **co-author** (IF 5.6)

BOOK CHAPTERS

Regulation of Gene Expression in Hematology

[2021]

Book: **Hoffman, Hematology, 8th Edition (Elsevier) *In press***

Role: **co-author**

Active ribosome profiling with RiboLace: from bench to data analysis

[3/2021]

Book: **Ribosome Profiling (Springer)**

Clamer et al. Methods Mol Biol. 2021;2252:201-220.

https://doi.org/10.1007/978-1-0716-1150-0_9

Role: **co-author**

FUNDING

Multimodal single-cell analysis of hematologic malignancies

[2021 – 2026]

AIRC - MFAG

Understanding how RNA methylation shapes hematopoiesis

[10/2018 – Current]

Pilot Project Award from the Yale Cooperative Center of Excellence In Hematology (YCCEH)

Identification of post-transcriptional interactions (RNA-proteins and RNA-RNA) from CLIP-seq data

[1/2015 – 3/2015]

EMBO Short Fellowship Award from the European Molecular Biology Organization

HONOURS AND AWARDS

Italian National Scientific Qualification as Associate Professor in Molecular Biology (05/E2)

Ministry of Education, University and Research (Italy) [2020]

Yale YCCEH Pilot and Feasibility Program Award

Yale Cooperative Center of Excellence In Hematology [2018]

Cell Reports Cover Award (Vol. 25, Issue 4)

[2018]

Cell Reports Cover Award (Vol. 21, Issue 4)

[2017]

RNA Society Travel Award: RNA2016, Kyoto

RNA society [2016]

EMBO Short Fellowship Award

European Molecular Biology Organization [2015]

EMBO Travel Grant Award: Protein synthesis and translational control

EMBO, Heidelberg [2015]

EMBO Travel Grant Award: The complex life of mRNA

EMBO/EMBL, Heidelberg [2014]

EMBL Corporate Partnership Registration Fee Fellowship: Protein synthesis and translational control

EMBL/EMBO Heidelberg [2013]

EMBL Registration Fee and Travel Fellowship: The complex life of mRNA

EMBO/EMBL, Heidelberg [2012]

Residence Scholarship

Fondazione Collegio delle Università Milanesi [2003]

Master Degree Scholarship

University of Milano Bicocca [2003]

Study Scholarship

Collegio Vescovile Sant' Alessandro, Bergamo [2000]

SEMINARS AND INVITED TALKS

A comparison of computational methods for single cell RNA sequencing

[4/2019]

Invited talk

Reproducibility for AI In Predictive Medicine - 3rd Annual MAQC Society Conference, Riva Del Garda, Italy

Mapping post-transcriptional regulation by positional analysis of RNA sequencing data

[1/2019]

Invited talk

SISSA - Scuola Internazionale Superiore di Studi Avanzati, Trieste, Italy

Mining combinatorial regulation of gene expression from post-transcriptional interaction maps

[6/2014]

Selected talk

Biodays, University of Trento, Italy

Visual, mathematical and computational analysis of translation

[6/2013]

Invited talk

Ph.D. in Biosciences and Biotechnologies, University of Padua, Italy

Computational analysis of translational regulation

[3/2013]

Invited talk

Ph.D. in Complex Systems in Life Science, University of Torino, Italy

Widespread uncoupling between transcriptional and translational control of gene expression

[9/2011]

Selected talk

13th AIBG Congress (AIBG11), AIBG - Italian Society of Applied Biology and Genetics, Padova, Italy

MEMBERSHIPS AND ACTIVITIES

Research Member of the Yale Cancer Center

[1/2020 - Current]

Genomics, Genetics & Epigenetics Research Group

Member of the Yale Center for Biomedical Data Science

[2/2018 - Current]

Editor and board member of the Italian Society of Yale Students and Affiliates

[8/2017 – Current]

Organizer of the Yale Hematology Scientific Coding Club

[4/2020 – Current]

Associate Editor for Computational Genomics - Frontiers in Genetics

[2/2021 – Current]

Review editor for Frontiers academic publisher

[6/2015 – Current]

Scientific Expert reviewer for the French National Research Agency (ANR)

[2/2019 – Current]

Project reviewer for the National Science Center, Poland

[3/2017 – Current]

Member of The RNA Society

[5/2016 – Current]

Session Chair

[5/2019]

Workshop on Splicing Factor Mutations and RNA Biology in Cancer

New Haven, United States

Member of The International Society for Computational Biology

[1/2010 – 12/2014]

Tutoring for PhD and master degree students

[4/2010 – 8/2017]

University of Trento

Scientific organizer of the 3S Biology Summer School

[1/2008 – 9/2008]

University of Trento

LANGUAGE SKILLS

Mother tongue(s):

Italian

Other language(s):

English

LISTENING C2 READING C2 WRITING C2

SPOKEN PRODUCTION C2 SPOKEN INTERACTION C2

DIGITAL SKILLS

R and R Studio / Pandas Numpy Scikit-learn PyTorch Matplotlib Tidyverse / Scripting in Python and/or Bash / computational biology

OTHER SKILLS

Job-related skills

Computational biology: data mining of sequencing data (single-cell, spatial RNA-seq, ribosome profiling, CLIP-seq, RIP-seq, Cut&Run, DNA-seq) and MS proteomics. Sequence, structure and interaction network analysis of DNA, RNA and proteins. Extensive use of biological databases. Development of software packages in R and Python.

Experimental biology: detailed knowledge of experimental techniques currently employed in cellular and molecular biology.

Communication and interpersonal skills

Teaching skills acquired as a PhD and Master Degree teacher. **Scientific presentation and dissemination** skill acquired by participating to multiple international conferences. **Scientific writing** skills acquired upon contribution to project grants and publication of multiple research papers and book chapters.

Organisational skills

Coordination and team building skills acquired while working in multidisciplinary research projects, mediating participants with different backgrounds, and coordinating Post-Doctoral fellows, PhD and undergraduate students.