

Gian Gaetano Tartaglia
Gene Function and Evolution
Bioinformatics and Genomics CRG/ICREA

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Short biography

I graduated at the University La Sapienza in the academic year 1999-2000 with a thesis on **mathematical modeling of neurons** (Physics department). Between 2001 and 2005, I carried out my doctoral studies at the University of Zurich CH (Biochemistry department) focusing on the **folding and misfolding of proteins** associated with neurodegenerative disorders. As an associate researcher, I worked at the University of Cambridge UK (Chemistry and Genetics departments) under the supervision of Chris Dobson and Michele Vendruscolo. In the period 2005-2010, I participated in several computational and experimental studies on **amyloidosis**. I am life member of the Clare Hall College in Cambridge UK since 2011.

At present, I am a junior PI at the **Centre for Genomic Regulation** (CRG) in Barcelona. My group is composed of 5 post-doctoral researchers, 6 doctoral students and 2 technicians. The doctoral and post-doctoral researches hold competitive fellowships from Marie Curie, Ministry of Science and La Caixa bank. In 2013, I have been awarded an ERC starting grant for the studies on the role of coding and non-coding transcripts in regulation of amyloid genes. Since 2014, I am tenured in Catalonia as **ICREA professor of Life and Medical Sciences**.

My main scientific goal is to achieve a better understanding of cellular phenomena and produce science in service of human health. I am highly motivated to consolidate my academic profile at ICREA where I actively promote multidisciplinary collaborations and international competitiveness.

Positions and Education

- Since 2014 **ICREA Professor** (permanent position)
Life and Medical Sciences, Catalan Institution for Advanced Research
Highly competitive position: maximum of 2 professorships are awarded every 2 years in *Life and Medical Sciences* since 2014 (<https://goo.gl/F21Ulf>).
- Since 2014 Affiliated with the BSC - CRG - IRB Program in Computational Biology
<https://goo.gl/QpfZbg>
- Since 2010 Group Leader
Bioinformatics and Genomics, Centre for Genomic Regulation, Spain
In my group, *Gene Function and Evolution*, the research is highly interdisciplinary, involves a number of international collaborators and focuses on structural biology and the uncharted territory of non-coding RNAs involved in transcriptional and translational regulation (e.g., X-chromosome inactivation) as

well as human disorders (e.g., Parkinson's disease). We aim to identify regulatory mechanisms controlling protein production and contributing to cell homeostasis.

2007 – 2010 **Clare Hall Research Fellow**
Genetics, University of Cambridge, United Kingdom
Supervisors: Prof. C. Dobson and Prof. M. Vendruscolo

2005 – 2010 **Assistant researcher**
Chemistry, University of Cambridge, United Kingdom
Supervisors: Prof. C. Dobson and Prof. M. Vendruscolo

During my post-doctoral studies, I developed a series of models to predict aspects of protein folding, chaperone interactions and aggregation under a variety of environmental conditions and I directly participated in their experimental validation. From 2008 to 2010, I was associated with the Department of Genetics, where I worked on projects that involved the rational design and the *in vivo* testing of neurotoxins in a *D. melanogaster* model of Alzheimer's disease.

2001 – 2006 PhD – *top score*
Structural Biology, **Biochemistry**, University of Zurich, Switzerland
Supervisor: Prof. A. Caflisch (Biochemistry Department)

Motivated by the interaction with Prof. A. Tramontano (Biochemistry Department, Rome, Sapienza, Italy), I moved to the field of structural biology. During my PhD studies, I worked on folding, misfolding and aggregation of proteins involved in Alzheimer's, Parkinson's and Prion diseases. As part of my formal training, I attended courses of Organic Chemistry, Biology, NMR spectroscopy and X-ray crystallography.

1996 – 2000 MSc – *top score*
Statistical Mechanics, **Physics**, University of Rome La Sapienza, Italy
Supervisor: Prof. B. Tirozzi (Mathematics Department)

In my undergraduate studies I developed models to predict the firing patterns of single neurons. I proposed a formula for the optimal control of signals, trajectories and velocities of eye movements.

During these years, I started to be strongly interested in protein folding and structural biology topics.

Scientific production

- I received **4000** citations (**3000** in the last 5 years; total of **80** papers). With respect to the productivity and impact factor of my published work, my h-index is **33** (my i10-index is **52**). Since May 2010, my group published > **40** articles with the CRG affiliation (**I am the corresponding author in 80% of all my publications**). Only in 2017, my group published 5 papers with IF>10.
- I am recipient of a **H2020 grant on personalized medicine** (awarded in **2017**) and **Wellcome Trust** (the UK agency made an exception to allow my participation as non-UK researcher).
- Since 2011 I secured >**3 millions of euros** for my research. In 2013, I was awarded an **ERC** starting grant to study amyloid diseases (RIBOMYLOME), which led to >**30** publications in highly influential journals such as **Nature Methods, Genome Biology, Cell Reports, Nucleic Acids Research, Bioinformatics** and **RNA** to cite some.
- All our results and press-releases are publicly available in our webpages at the CRG as well as <http://www.tartaglialab.com/>. At the time of writing, all our algorithms are publicly available through **webservers** that were run by **116275** users since 2012.

Translational research and technology transfer

- In 2017, my group received a Proof of Concept Commercialization Gap Fund grant on the design of RNA aptamers.
- In 2016, I built a section of *Frontiers in Biomolecular Science* called **Ribonucleoprotein Networks** (<https://goo.gl/Ri7GNP>) to interface two rapidly growing fields: transcriptomics and proteomics.
- In 2015 I started a collaboration with Dr MJ Marti' at the Hospital Clinic (Barcelona) on projects related to the discovery of biomarkers for Parkinson's disease and Multiple System Atrophy.
- My work is being exploited by the CRG tech-transfer office: The **catRAPID** algorithm developed in my group (2011-2017) for prediction of protein-RNA interactions has been licensed in 2016 (<https://goo.gl/y7Bn7q>). New tools will be licensed in the next year.

Patents The *Zygggregator* method for protein aggregation was patented by University of Cambridge (No PCT/GB2008/051055; post-doctoral work) and a related algorithm, *PAGE* was licensed under academic and commercial licenses (University of Zurich, Technology Opportunity Ref. No. UZ-08/314; doctoral work).

Training, mentoring and science communication

- Since 2011 I supervised **7 Post-docs**, **9 PhD students** and **5 MSc** supported by Marie Curie Program, Leonardo da Vinci program, La Caixa, Interpod EU co-fund, Women in Science fellowships, Severo Ochoa and Ministry of Economy and Competitiveness. Six of my students already have received the doctoral degree with top marks: Federico Agostini (2014), Davide Cirillo (**best UPF thesis of 2016**), Domenica Marchese (2016) and Petr Klus (2016) in the Department of Bioinformatics and Genomics (CRG, ES). Previously, I co-supervised Sebastian Pechmann in the Department of Chemistry (2014, University of Cambridge, UK) and Prajwal Ciriam in the Department of Genetics (2015, University of Cambridge, UK). Federico Agostini and Davide Cirillo (best thesis of the UPF) are now post-docs respectively at the Cancer Research UK (<http://www.luscombelab.org/agostini/>) and Barcelona Supercomputing Centre (<https://www.bsc.es/cirillo-davide>). Domenica Marchese has been contacted for a prestigious post-doctoral position at University of Rome, Sapienza and Petr Klus is scientific director of a SME. Benedetta Bolognesi and Sebastian Pechmann are now PI at IBEC (Barcelona) and Montreal Canada (<http://pechmannlab.org/>), respectively.
- I do support equal opportunities: the current gender balance in my group is 54% females and there have been 9 pregnancies in the lab since 2011.
- In 2017, the articles and video clips mentioning my science at the CRG have reached an audience of **12 millions of people**, resulting in an economic value of more than 64 thousand euros.
- In 2016, I wrote a book on Biotechnology for the layman (<https://goo.gl/ayAlhn> now available in 5 countries).

Lab Composition

Postdoctoral Fellows:

Dr. Benedetta Bolognesi (leaving in 2018)
Dr. Teresa Botta-Orfila
Dr. Natalia Sanchez
Dr. Stefanie Marti
Dr. Ricardo Graña Montes

Technicians:

Dr. Elias Bechara
Dr. Iona Gelabert

Doctoral Students:

Fernando Cid
Riccardo delli Ponti
Alexandros Armaos

Alessandro Dasti
Nieves de Lorenzo (previously technician)
Maria Carla Antonelli

Collaborations

I am collaborating with a number of PIs at the CRG (an article has been recently published with B. Lehner), recently established collaborations are listed below:

- **Peter Hyslop**, Medicine University of Cambridge, UK. **Phase transitions and Amyotrophic Lateral Sclerosis (ALS)**. I am a recipient of a **Wellcome trust (2017)** grant together with Prof. P. Hyslop. *ALS/FTD Mutation-Induced Phase Transition of FUS Liquid Droplets and Reversible Hydrogels into Irreversible Hydrogels Impairs RNP Granule Function*. Murakami T, Qamar S, Lin JQ, Schierle GS, Rees E, Miyashita A, Costa AR, Dodd RB, Chan FT, Michel CH, Kronenberg-Versteeg D, Li Y, Yang SP, Wakutani Y, Meadows W, Ferry RR, Dong L, Tartaglia GG, Favrin G, Lin WL, Dickson DW, Zhen M, Ron D, Schmitt-Ulms G, Fraser PE, Shneider NA, Holt C, Vendruscolo M, Kaminski CF, St George-Hyslop P. *Neuron*. 2015 Nov 18;88(4):678-90. doi: 10.1016/j.neuron.2015.10.030. Epub 2015 Oct 29. **A new manuscript has been submitted (June 2017) on the effect of FUS methylation on ALS/FTD and has been accepted in December 2017.**
- **Ellen Gelpi**, Brain Bank Vienna Austria (previously in Barcelona) **Granules and pathophysiology. Neuronal intranuclear (hyaline) inclusion disease and Fragile X-Associated Tremor/Ataxia Syndrome: a morphological and molecular dilemma**. Gelpi E*, **Botta-Orfila T***, Bodi L, Marti S, Kovacs B, Grau-Rivera O, Lozano M, Sanchez Vale R, Munoz E, Vallderoriola F, Pagonabarraga J, Tartaglia GG and Mila' Montse. *Brain* 10.1093/brain/awx156 in press (IF=11, *co-first authors).
- **Mitchell Guttman**, Caltech, US. **Long non-coding RNAs and protein interactions. Quantitative predictions of protein interactions with long non-coding RNAs**. Cirillo D, Blanco M, Armaos A, Buness A, Avner P, Guttman M, Cerase A and **Tartaglia GG**. *Nat Methods*. 2017 Jan 1;14(1):5-6. doi: 10.1038/nmeth.4100. **We are now working together on the large-scale in silico / in vivo characterization of non-coding RNA interactions.**
- **Maria Jose Marti**, Hospital Clinic and IDIBAPS, Barcelona. **Synucleinopathies**. I am a recipient of a Marato' TV3 with Dr. MJ. Marti. *Cerebrospinal fluid levels of coenzyme Q10 are reduced in multiple system atrophy*. Compta Y, Giraldo DM, Muñoz E, Antonelli G, Fernandez M, Bravo P, Soto M, Cámara A, Botta-Orfila T, Marchese M, Tartaglia GG and Martí **published in Parkinsonism and related disorders**. A second paper, in which I am in the corresponding author has been recently accepted: *Marchese M, Botta-Orfila T, Cirillo D, Rodriguez JA, Livi CA, Fernández-Santiago R, Ezquerra M, Martí MJ Bechara E and Tartaglia GG. Discovering the 3' UTR-Mediated Regulation of Alpha-Synuclein*. 2017. *Nucleic Acids Research* 10.1093/nar/gkx1048 (in press).
- **Renate Hukema**, Erasmus University Netherland, **FMRI granules and Fragile X Mental Retardation (FXTAS)**. In my group, we have predicted *in silico* and validated *in vivo* interactions of CGG repeats with proteins and Renate confirmed them in a mouse model as well as human patients, showing implications for FXTAS. **A paper with Teresa Botta-Orfila (first author) and myself (last author) is being written.**
- **Eleonora Candi**, University Tor Vergata, Rome, Italy, **long non-coding RNA regulation**. We have predicted *in silico* and validated *in vivo* interactions of TUC-291 long non-coding RNA with proteins. In particular, we discovered the binding of TUC-291 chromatin-associated ACTL6A (among other proteins) using *catRAPID* and protein-arrays, which has strong implications for cancer. **The paper is currently under review at PNAS.**

- **George Paliouras**, Demokritos Institute, Greece. *Personalized medicine*. Together with George I have a *H2020 project (2017)* on personalized medicine (“IASIS” the first grant of this kind given to my institute). We integrate information from disparate sources, including genomics, electronic health records and bibliography, and applying advanced analytics methods to discover useful patterns. Our goal is to turn these large amounts of data into actionable information to authorities for planning public health activities and policies. The aggregation and analysis of these heterogeneous sources will enable the best decisions to be made, allowing for diagnosis and treatment to be personalised to each individual. The project offers a common representation schema for the heterogeneous data sources. The infrastructure will be converting clinical notes into usable data, combine them with genomic data, related bibliography, image data and more, and create a global knowledge base.
- **Christine Brun**, INSERM Marseille. France. *Protein networks. Protein complex scaffolding as a prevalent function of human long non-coding RNAs*. Diogo M. Ribeiro, Andreas Zanzoni, Lionel Spinelli, Riccardo Delli Ponti, Gian Gaetano Tartaglia*, Christine Brun* (*corresponding authors, accepted paper). Using an original computational approach coupling protein-RNA interaction predictions with our in-house *catRAPID* algorithm) and statistical analyses, we generated the largest protein-RNA interaction network ever proposed, and identified scaffolding lncRNAs. We propose that the mechanism of action of several known lncRNA associated to disease involves the scaffolding of protein complexes and modules.
- **Andrea Cavalli**, IRB Bellinzona, Switzerland. *protein simulations (molecular dynamics). ALMOST: an all atom molecular simulation toolkit for protein structure determination*. Fu B, Sahakyan AB, Camilloni C, Tartaglia GG, Paci E, Caflisch A, Vendruscolo M, Cavalli A. J Comput Chem. 2014 May 30;35(14):1101-5. doi: 10.1002/jcc.23588. Epub 2014 Mar 27.

Community Activities

- Committees.** Member of the CRG Doctoral, Postdoctoral, Tech transfer, HR excellence committees.
- Teaching.** Lectures for University Pompeu Fabra (UPF) and practical courses including doctoral classes at Scuola Normale Superiore (Italy). I am the main organizer of the Structural Biology Seminars at the Parc de Recerca Biomèdica de Barcelona
- Diffusion.** I wrote a book on Biotechnology for the layman (published by international press). Press releases and commentaries on our work can be found at <http://s.tartaglialab.com/page/contact>.

Tech-transfer

Algorithms from my lab are licensed by the CRG Technology Transfer office and my institute is currently considering the opportunity of creating a spin-off on RNA aptamers generation.

Commissions of trust

- Since 2017 **Faculty of 1000 member**, section *Structural Biology Modelling and Simulation*
- Since 2016 **Chief editor** of the section *Ribonucleoprotein Networks for Frontiers in Molecular Biosciences*
- Since 2014 **Editorial board** member of *Frontiers in Molecular Biosciences; PeerJ; Translational Genetics and Genomics; Current Updates in Bioinformatics*
- Since 2011 Clare Hall Life Member (University of Cambridge, UK)
- Since 2010 **Reviewer** for *Nature, Nature Methods, Cell Reports, Trends in Biochemical Sciences, PLoS Computational Biology, Bioinformatics, Nucleic Acids Research, JACS, Molecular Biosystems, Gene, Molecular Biology and Evolution, FEBS and Proteins*.

- Since 2010 I reviewed > 10 grants for ERC and national agencies in Spain, Austria, France, Switzerland, Belgium, Israel, Sweden, Slovakia and Argentina.
- 2005- 2010 Consultant for the companies Zyentia and Lonza Biologics.

Participation to meetings (selected)

2017. Speaker at the Phase Transitions in Biology and Disease Symposium (VIB, Leuven, Belgium), Personalized Medicine Meeting (Madrid, Spain), Aggregation Workshop (Porto, Portugal) and keynote at Nano Innovation Conference (Rome, Italy).
2016. Speaker at Gordon Conference (Diableret, Switzerland), Max Planck Institute, MPI Genetics (U. Orom's lab; Berlin, Germany), German Centrum for Neurodegenerative diseases DZNE (I. Vorberg's lab; Bonn, Germany) and EMBL (P. Avner's lab; Monterotondo, Italy)
2015. Speaker at Tel Aviv University (Tel Aviv, Israel), Centre for Integrative Biology (Trento, Italy) and RNA society meeting (Madison, US).
2014. Visitor/speaker at INSERM (C. Brun's lab; Marseille, France)
2013. Speaker at Institute of Neurosciences (R. Melki's lab; Paris, France), RNA society meeting (Davos, Switzerland) and Max Perutz Laboratories (Zagovic's lab, Vienna; Austria)
2012. Visitor at the University of Pavia (V. Bellotti's lab; Italy); Speaker at the Institute for Protein Research, Osaka University (Japan)
2011. Speaker at the International Centre for Theoretical Physics, (Trieste, Italy), Frankfurt Institute for Molecular Life Sciences (Frankfurt, Germany) and keynote at the Hellenic Society for Computational Biology and Bioinformatics (Greece)

Publications (** most relevant articles)

Last five years

Recent submissions.

- Physiological and Pathological Phase Transition of FUS is Modulated by its Methylation and Interaction with TNPO1 (*Cell* accepted)
- Ultra-conserved non-coding transcript uc.291 controls somatic epithelial differentiation by interfering with the ACTL6A/BAF complex (*PNAS* under review)
- An active role of free RNA assemble machinery using proteostatic stress (submitted to *Nature*).

Published. Group members are written in italics

- *Marchese M, Botta-Orfila T, Cirillo D, Rodriguez JA, Livi CA, Fernández-Santiago R, Ezquerra M, Martí MJ Bechara E and Tartaglia GG.* Discovering the 3' UTR-Mediated Regulation of Alpha-Synuclein. 2017. *Nucleic Acids Research* 10.1093/nar/gkx1048 (*in press*) [impact factor: 10] **
- *Ribeiro DM, Zanzoni A, Cipriano A, Ballarino M, Spinelli L, Delli Ponti R, Bozzoni I, Tartaglia GG (corresponding author), Brun C,* Protein complex scaffolding as a prevalent function of human long non-coding RNAs. 2018. *Nucleic Acids Research* doi: 10.1093/nar/gkx1169 (*in press*) [impact factor: 10] **
- *Gelpi E, Botta-Orfila T, Bodi L, Marti S, Kovacs G, Grau-Rivera O, Lozano M, Sánchez-Valle R, Muñoz E, Valdeoriola F, Pagonabarraga J, Tartaglia GG, Milà M.* Neuronal intranuclear (hyaline) inclusion disease and fragile X-associated tremor/ataxia syndrome: a morphological and molecular dilemma. *Brain*. 2017 Aug 1;140(8):e51. doi: 10.1093/brain/awx156 [impact factor: 10] **
- *Armaos A, Cirillo D, Tartaglia GG.* omiXcore: a web server for prediction of protein interactions with large RNA. *Bioinformatics*. 2017 Oct 1;33(19):3104-3106. doi: 10.1093/bioinformatics/btx361 [impact factor: 7.5]
- *Compta Y, Giraldo DM, Muñoz E, Antonelli F, Fernández M, Bravo P, Soto M, Cámara A, Torres F, Martí MJ; Catalan MSA Registry (CMSAR including Botta T, Marchese D and Tartaglia GG).* Cerebrospinal fluid levels of coenzyme Q10 are reduced in multiple system atrophy. *Parkinsonism Relat Disord*. 2017 Oct 20. pii: S1353-8020(17)30381-4. doi: 10.1016/j.parkreldis.2017.10.010
- *Ciryam P, Lambert-Smith IA, Bean DM, Freer R, Cid F, Tartaglia GG et al.* Spinal motor neuron protein supersaturation patterns are associated with inclusion body formation in ALS. *Proc Natl Acad Sci U S A*. 2017 Apr 10. pii: 201613854. doi: 10.1073/pnas.1613854114
- *Cirillo D, Blanco M, Armaos A, Bunes A, Avner P, Guttman M, Cerase A and Tartaglia GG.* Quantitative predictions of protein interactions with long non-coding RNAs. *Nat Methods*. 2017 Jan 1;14(1):5-6. doi: 10.1038/nmeth.4100 [impact factor: 25]. **
- *Riccardo Delli Ponti, Stefanie Marti, Alexandros Armaos, Tartaglia GG.* A High-throughput approach to profile RNA structure, *Nucleic Acids Res*. 2017 March 28. pii: gkw1094 [impact factor: 10]. **
- *Botta Orfila T, Tartaglia GG, Michalon A.* Molecular pathophysiology of fragile X-associated tremor/ataxia syndrome and perspectives for drug development. *Cerebellum* 2016 Oct;15(5):599-610. doi: 10.1007/s12311-016-0800-2
- **Tartaglia GG.** The Grand Challenge of Characterizing Ribonucleoprotein Networks. *Frontiers in Molecular Biosciences Front. Mol. Biosci.*, 09 June 2016 *Front Mol Biosci*. 2016 Jun 9;3:24. doi: 10.3389/fmolb.2016.00024.
- *Bolognesi B, Lorenzo Gotor N, Dhar Riddhiman Cirillo D, Baldrighi M, Tartaglia GG (corresponding author), Lehner B.* Dosage sensitivity caused by increased protein concentration triggering a liquid phase separation. *Cell Reports* 16, 1–10, June 28, 2016 [impact factor: 8.5] **
- *Lobanov MY, Klus P, Sokolovsky IV, Tartaglia GG (corresponding author), Galzitskaya OV.* Non-random distribution of homo-repeats: links with biological functions and human diseases. *Sci Rep*. 2016 Jun 3;6:26941.

- doi: 10.1038/srep26941 [impact factor: 5.5]
- *Marchese D, Sanchez de Groot N, Lorenzo Gotor N, Livi CM, Tartaglia GG.* Advances in the characterization of RNA-binding proteins. *RNA Wiley* 2016 Nov;7(6):793-810. doi: 10.1002/wrna.1378. Epub 2016 Aug 8
 - *Klus P, Ponti RD, Livi CM, Tartaglia GG.* Protein aggregation, structural disorder and RNA-binding ability: a new approach for physico-chemical and gene ontology classification of multiple datasets. *BMC Genomics.* 2015 Dec 16;16:1071. doi: 10.1186/s12864-015-2280-z. [impact factor: 4.0]
 - *Murakami T, Qamar S, Lin JQ, Schierle GS, Rees E, Michel CH, [...] Tartaglia GG [...], St George-Hyslop P.* ALS/FTD Mutation-Induced Phase Transition of FUS Liquid Droplets and Reversible Hydrogels into Irreversible Hydrogels Impairs RNP Granule Function. *Neuron.* 2015 Nov 18;88(4):678-90. doi: 10.1016/j.neuron.2015.10.030
 - *Livi CM, Klus P, Delli Ponti R, Tartaglia GG.* catRAPID signature: identification of ribonucleoproteins and RNA-binding regions. *Bioinformatics.* 2016 Mar 1;32(5):773-5. doi: 10.1093/bioinformatics/btv629. [5-years impact factor:8]
 - *Klus P, Cirillo D, Botta Orfila T, Tartaglia GG.* Neurodegeneration and Cancer: Where the Disorder Prevails. *Sci Rep.* 2015 Oct 23;5:15390. doi: 10.1038/srep15390. [impact factor: 5.5]
 - *Marchese D, Livi CM, Tartaglia GG.* A Computational Approach for the Discovery of Protein-RNA Networks. *Methods Mol Biol.* 2016;1358:29-39. doi: 10.1007/978-1-4939-3067-8_2.
 - *Cirillo D, Botta-Orfila T, Tartaglia GG.* By the company they keep: interaction networks define the binding ability of transcription factors. *Nucleic Acids Res.* 2015 Jun 18. pii: gkv607. [impact factor: 9.0]
 - *Porcari R, Proukakis C, Waudby CA, Bolognesi B, Mangione PP, Paton JF, Mullin S, Cabrita LD, Penco A, Relini A, Verona G, Vendruscolo M, Stoppini M, Tartaglia GG, Camilloni C, Christodoulou J, Schapira AH, Bellotti V.* The H50Q mutation induces a 10-fold decrease in the solubility of α -synuclein. *J Biol Chem.* 2015 Jan 23;290(4):2395-404. doi: 10.1074/jbc.M114.610527. Epub 2014 Dec 10.
 - *Agostini F, Cirillo D, Ponti RD, Tartaglia GG.* SeAMotE: a method for high-throughput motif discovery in nucleic acid sequences. *BMC Genomics.* 2014 Oct 23;15:925. doi: 10.1186/1471-2164-15-925. [impact factor: 4.0]
 - *Agostini F, Cirillo D, Livi CM, Delli Ponti R, Tartaglia GG.* ccSOL omics: a webserver for solubility prediction of endogenous and heterologous expression in *Escherichia coli*. *Bioinformatics.* 2014 Oct 15;30(20):2975-7. doi: 10.1093/bioinformatics/btu420 [5-years impact factor:8]
 - *Ciryam P, Tartaglia GG, Morimoto R, Dobson C, Vendruscolo M.* Widespread aggregation and neurodegenerative diseases are associated with supersaturated proteins. *Cell Reports* 2013 Nov 14;5(3):781-90. doi: 10.1016/j.celrep.2013.09.043. Epub 2013 Oct 31 [I have been supervising the PhD project of Ciryam]
 - *Cirillo D, Marchese D, Agostini F, Livi CM, Botta-Orfila T, Tartaglia GG.* Constitutive patterns of gene expression regulated by RNA-binding proteins. *Genome Biol.* 2014 Jan 2;15(1):R13. [impact factor: 10.288] **
 - *Fu B, Sahakyan A, Camilloni C, Tartaglia GG, Paci E, Caflisch A, Vendruscolo M and Cavalli A.* ALMOST: An all atom molecular simulation toolkit for protein structure determination. *J Comput Chem.* 2014 Mar 27. doi: 10.1002/jcc.23588.
 - *Cirillo D, Agostini F, Livi CM and Tartaglia GG.* Discovery of Protein-RNA Networks. *Molecular Biosystems* 2014 in *Mol Biosyst.* 2014 Jul;10(7):1632-42. doi: 10.1039/c4mb00099d. [we obtained the cover of the journal]
 - *Klus P, Agostini F, Bolognesi B, Zanzoni A, Tartaglia GG.* The cleverSuite Approach for Protein Characterization: Predictions of Structural Properties, Solubility, Chaperone Requirements and RNA-Binding Abilities. *Bioinformatics.* 2014 Jun 1;30(11):1601-8. PMID: 24493033 [5-years impact factor:8]
 - *Zanzoni A, Marchese D, Agostini F, Bolognesi B, Tartaglia GG.* Principles of self-organization in biological pathways. *Nucleic Acids Res.* 2013 Dec;41(22):9987-98. [impact factor: 9] **
 - *Agostini F, Zanzoni A, Klus P, Marchese D, Cirillo D, Tartaglia GG.* catRAPID omics: a web server for large-scale predictions of protein-RNA interactions; *Bioinformatics.* 2013 Nov 15;29(22):2928-30. doi: 10.1093/bioinformatics/btt495. [5-years impact factor:8] **
 - *Cirillo D, Agostini F, Klus P, Marchese D, Rodriguez S, Bolognesi B, Tartaglia GG.* Neurodegenerative diseases: quantitative predictions of protein-RNA interactions. *RNA.* 2013 Feb; 19(2): 129-40. [impact factor: 5.088]
 - *Agostini F, Cirillo D, Bolognesi B, Tartaglia GG.* X-inactivation: quantitative predictions of protein interactions in the Xist network. *Nucleic Acids Res.* 2013 Jan 7;41(1):e31 doi: 10.1093/nar/gks968 [impact

factor: 8.278]

- *Cirillo D, Agostini F, Tartaglia GG*, Prediction of RNA-Protein interactions WIREs Computational Molecular Science 2013. 3 (2) , 161-175. [impact factor 11]
- Johnson R, Noble W, **Tartaglia GG**, Buckley NJ. Neurodegeneration as an RNA disorder. Prog Neurobiol. 2012 Dec; 99(3):293-315. [impact factor: 9.035]
- Roodveldt C, Andersson A, De Genst EJ, Labrador-Garrido A, Buell AK, Dobson CM, **Tartaglia GG**, Vendruscolo M. A rationally designed six-residue swap generates comparability in the aggregation behavior of α -synuclein and β -synuclein. Biochemistry. 2012 Nov 6;51(44):8771-8.

Publications after joining the CRG (until 2012)

The following articles arise from my PI work (2010-2012). Group members are written in italics:

- Iglesias-Platas I, Martin-Trujillo A, *Cirillo D*, Court F, Guillaumet-Adkins A, Camprubi C, Burchis D, Hata K, Feil R, **Tartaglia GG**, Arnaud P, Monk D, Characterization of Novel Paternal ncRNAs at the Plagl1 Locus, Including Hymai, Predicted to Interact with Regulators of Active Chromatin. PLoS One. 2012;7(6):e38907. Epub 2012 Jun 19.
- Calloni G, Chen T, Schermann SM, Chang H, Genevax P, *Agostini F*, **Tartaglia GG**, Hayer-Hartl M and Hartl FU. DnaK Functions as a Central Hub in the E. coli Chaperone Network. Cell Reports, March 8, 2012.
- *Agostini F*, Vendruscolo M, **Tartaglia GG**. Sequence-based prediction of protein solubility. J Mol Biol. 2012 Aug 10;421(2-3):237-41. doi: 10.1016/j.jmb.2011.12.005. Epub 2011 Dec 9 [Joined project involving one PhD student in my group] (corresponding author) [impact factor: 3.905]
- Mossuto MF, *Bolognesi B*, Guixer B, Dhulesia A, *Agostini F*, Kumita JR, **Tartaglia GG**, Dumoulin M, Dobson CM, Salvatella X. Disulfide bonds reduce the toxicity of the amyloid fibrils formed by an extracellular protein. Angew Chem Int Ed Engl. 2011 Jul 25;50(31):7048-51 [Part of calculations and experiments were performed by members of my group].
- *Bellucci M, Agostini F, Masin M*, **Tartaglia GG**. Predicting protein associations with long noncoding RNAs. Nature Methods. 2011 Jun;8(6):444-5. [impact factor: 19.276] **
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