

## Part A. PERSONAL INFORMATION

Date	9/02/2021
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First and Family name	Marco Mariotti		
Researcher codes	WoS Researcher ID	AAB-7136-2019	
	ORCID	0000-0002-7411-4161	

### A1. Position starting in May 2021

Name of University/Institution	Universitat de Barcelona Institut de Biomedicina de la Universitat de Barcelona		
Department	Department of Genetics, Microbiology and Statistics		
Address and Country	Diagonal, 643, 08028, Barcelona, Spain		
Position	Ramon y Cajal Fellow / Group Leader	From	May 2021
Key words	Comparative genomics, Evolution, Bioinformatics, Recoding, Selenium		

### A2. Education, postdoctoral training, and current position

B.Sc. in Biotechnologies	Università di Bologna (Italy)	07/06
M.Sc. in Bioinformatics	Università di Bologna (Italy)	10/08
Ph.D. in Biomedicine	Centre de Regulació Genòmica (Barcelona)	11/08-12/13
EMBO short-term postdoc	University College Cork (Ireland)	07/14-11/14
Postdoctoral fellow	Centre de Regulació Genòmica (Barcelona)	12/14-08/15
Research fellow (postdoc)	Brigham and Women's Hospital, Harvard Med School, USA	09/15-01/19
Instructor (junior faculty)	Brigham and Women's Hospital, Harvard Med School, USA	02/19-03/21

### A3. Summary of scientific production

H-index: 18      i10-index: 23

- 32 research papers published in top quartile (Q1) journals; of which:
  - 10 as first or co-first author
  - 5 as corresponding or co-corresponding author
  - 5 featured on the journal cover with my own custom artwork
  - 7 research papers within consortia (>30 authors)
- 4 invited book chapters

Total citations: 12,794

Average citations after Ph.D. defense (2014-2019): 1,130 per year

All data obtained from Google Scholar: <https://scholar.google.com/citations?user=Ea2ysyYAAAAJ>

## Part B. CV SUMMARY

My scientific path crosses the intersection of computational, evolutionary, and molecular genomics. My research is centered on a *comparative genomics* perspective: I consider genetic biodiversity, in form of rapidly increasing nucleotide sequences, as the central asset of present-day biology. My research leverages molecular data from diverse lineages, which I interrogate through the lens of evolution to understand biological functions and mechanisms. I use bioinformatics as main method of discovery, often followed up by targeted molecular biology experiments.

I typically work on “omics” data, mostly consisting of sequences derived from genome assemblies, transcriptomics and proteomics. During my PhD, I learned about computational genomics and transcriptomics with Roderic Guigó. As postdoc, I received training in large scale phylogenetics and gene evolution with Toni Gabaldón. I then worked on protein synthesis with John F. Atkins and Pavel V. Baranov, learning to design and perform wet-lab experiments. Today I work in the lab of Vadim N. Gladyshev, world-renowned for redox biology and aging research, where I was promoted to Instructor (junior faculty at Harvard Medical School). In this role, I advise on all projects in the lab, I handle the computational infrastructure, I manage a lab technician hired through my own funds, and I co-supervise a PhD student that recently joined our group.

In 2020, I secured three options to transition to an independent group leader position in Europe (see Research Projects and Grants), and I ultimately chose to join the Universitat de Barcelona as “Ramón y Cajal” researcher, starting in May 2021.



I dedicated the majority of my research so far to the biology of selenium. This trace element plays diverse essential roles for human health as part of selenocysteine (Sec), the 21st amino acid found in selenoproteins. Notably, translation deviates from the genetic code for selenoproteins: the UGA codon, normally a stop, is *recoded* for Sec insertion. Due to recoding, annotation of selenoproteins in genomes is challenging and typically involved meticulous case-by-case curation.

Throughout my career, I built automated bioinformatics tools that became gold standards of selenium genomics, and I characterized the distribution, evolution and function of selenoproteins. Today, I am well established in this field, as testified by a conspicuous list of publications, two awards at the most prestigious selenium conference, invitations to teach workshop participants, frequent requests for peer-review work, and four invited contributions to book chapters.

My research plan builds upon my earlier work on Sec, and expands to additional forms of recoding. In particular, I focus on stop codon readthrough, where Sec constitutes one example among many other types. My plan is motivated by the recent discovery that readthrough occurs in thousands of genes (particularly in insects), and yet its mechanisms and functions are mostly unknown. I will combine bioinformatics and experiments to delve into this unexplored diversity, and discover and characterize this process at unprecedented scale.

My career has been characterized by ability and motivation to independently lead research studies, to establish successful collaborations, and to attract funding at each stage. Now that I have built a prestigious reputation and formed a wide network of international collaborators, I look forward to transition to a role of independent group leader.

## Part C. RELEVANT MERITS

### C1. Selected publications (including books)

*Note: below, \* indicates equal contributions as first author; † indicates the corresponding author(s). The impact factor (IF) listed refers to the year of publication. Citations are from Google Scholar*

#### Research papers

2019 Baclaocos J\*, Santesmasses D\*, Mariotti M<sup>†</sup>, Bierła K, et al. (incl. Atkins JF) [3<sup>\*†</sup>/14]  
Processive recoding and metazoan evolution of Selenoprotein P: up to 132 UGAs in molluscs.  
*J Mol Bio.* 10.1016/j.jmb.2019.08.0074:759-765

Journal rank: Q1      IF: 5.1      Cited: 5      ★ Featured on journal cover with my own artwork

2019 Mariotti M<sup>†</sup>, Salinas G, Gabaldón T, Gladyshev VN<sup>†</sup>  
Utilization of selenocysteine in early-branching fungal phyla.  
*Nature Microbiology.* 4:759-765

Journal rank: Q1      IF: 14.3      Cited: 12

2018 Yordanova MM\*, Loughran G\*, Zhdanov AV, Mariotti M, et al. (incl. Baranov PV<sup>†</sup>) [4/14]  
AMD1 mRNA employs ribosome stalling as a mechanism for molecular memory formation.  
*Nature.* 553(7688):356-360.

Journal rank: Q1      IF: 43.1      Cited: 37

2017 Mariotti M, Shetty S, Baird L, Wu S, Loughran G, Copeland PR, Atkins JF, Howard MT<sup>†</sup>  
Multiple RNA structures affect translation initiation and UGA redefinition efficiency during synthesis of selenoprotein P.

*Nucleic Acids Res.* 45:13004-13015.

Journal rank: Q1      IF: 11.6      Cited: 19

2016 Mariotti M, Lobanov AV, Manta B, Santesmasses D, Bofill A, Guigó R, Gabaldón T, Gladyshev VN<sup>†</sup>  
Lokiarchaeota marks the transition between the archaeal and eukaryotic selenocysteine encoding systems.

*Mol Biol Evol.* Sep;33(9):2441-53.

Journal rank: Q1      IF: 6.2      Cited: 25      ★ Featured on journal cover with my own artwork

2015 Mariotti M<sup>†</sup>, Santesmasses D, Capella-Gutierrez S, Mateo A, et al. (incl. Guigó R<sup>†</sup>) [1<sup>†</sup>/13]



Evolution of selenophosphate synthetases: emergence and relocation of function through independent duplications and recurrent subfunctionalization.

*Genome Res.* 25(9):1256-67.

Journal rank: Q1      IF: 11.4      Cited: 35 ★ Featured on journal cover with my own artwork

2013 Mariotti M, Lobanov AV, Guigó R<sup>†</sup>, Gladyshev VN<sup>†</sup>

SECIsearch3 and Seblastian: new tools for prediction of SECIS elements and selenoproteins.

*Nucleic Acids Res.* 41(15):e149.

Journal rank: Q1      IF: 8.8      Cited: 68

2012 Mariotti M<sup>\*</sup>, Ridge PG<sup>\*</sup>, Zhang Y<sup>\*</sup>, Lobanov AV, Pringle TH, Guigó R, Hatfield DL, Gladyshev VN<sup>†</sup>

Composition and evolution of the vertebrate and mammalian selenoproteomes.

*PLoS ONE.* 7(3).

Journal rank: Q1      IF: 3.7      Cited: 186

- Omitting 17 additional Q1 research papers published in *Nat Commun*, *Mol Biol Evol*, *Proc Natl Acad Sci U S A*, *Nucleic Acids Res*, and other journals.

### Research papers within genome consortia

2012 The ENCODE Project Consortium (including Mariotti M) [not ordered / 460 authors]

An integrated encyclopedia of DNA elements in the human genome.

*Nature.* 489, 57–74.

Journal rank: Q1      IF: 38.6      Cited: 9401

- Omitting 6 additional consortia research papers (>30 authors) published in *Nature*, *PLoS Biology*, *Proc Natl Acad Sci U S A*, and *Genome Biol*.

### Book chapters

2016 Mariotti M<sup>†</sup>, Santesmasses D, Guigó R

Evolution of Selenophosphate Synthetase.

In: *Selenium. Its Molecular Biology and Role in Human Health*. p85-99.

Springer International Publishing.

- Omitting 3 additional book chapters papers published by *Springer International Publishing* and *Humana Press*.

## C2. Research projects and grants

### Grant: Ayudas Ramón y Cajal - RYC2019-027746-I

Institution: Spanish Ministry of Science, Innovation and Universities

Title: “Comparative genomics of selenocysteine, the 21st amino acid, and other forms of stop codon readthrough”

Amount: €308,000 (40k for research, 168k for salary 5 years, 100k for later permanence)

Start, end date: 01/05/2021 – 30/04/2026 [projected]

My role: Principal investigator

### Grant: ATIP/Avenir Program 2020

Institution: Inserm / CNRS, France

Title: “Diversity of stop codon readthrough in insects and other metazoa”

Amount: €425,000 (180k for research, 245k for salaries of PI and a postdoc)

My role: Principal investigator

Note: I renounced this award since incompatible with RYC2019-027746-I

### Grant: Ayudas Beatriz Galindo - BG20/00115 “Genomics and proteomics”

Institution: Spanish Ministry of Science, Innovation and Universities

Amount: €140,000 (Salary for 4 years)

Applicant: Department of Genetics, Microbiology and Statistics – Universitat de Barcelona

My role: Writer of program proposal; Top selected candidate by national committee



Note: I renounced this award since incompatible with RYC2019-027746-I

#### **Grant: Hearst Young Investigator Award 2020 - HEARST**

Institution: Department of Medicine, Brigham and Women's Hospital, Harvard Medical School

Title: "Targeting clinical nonsense mutations through translational recoding"

Amount: \$50,000

Start, end date: 01/01/2020 – 31/12/2020

My role: Principal investigator

#### **Grant: Research Project R01 - 1R01DK117149-01**

Institution: National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK)

Title: "Systems level understanding of selenoprotein biosynthesis"

Principal investigator: Vadim N. Gladyshev (Brigham and Women's Hospital, Boston, MA, USA)

Funding amount: \$263,773

Start, end date: 01/04/2018 - 31/03/2023

My role: key research personnel; contributor to project design and writing of proposal.

#### **Grant: Research Program Project Grant - P01 AG047200**

Institution: National Institute on Aging (NIA)

Grant title: "Comparative genomics of longevity"

Principal investigator: Vera Gorbunova (University of Rochester, Rochester, NY, USA)

Project 4 title: "Comparative genomics and epigenomics of aging"

Project 4 leader: Vadim N. Gladyshev (Brigham and Women's Hospital, Boston, MA, USA)

Funding amount: \$300,000 (Project 4 only)

Start, end date: 01/05/2019 – 30/04/2024

My role: key research personnel (Project 4); contributor to writing of proposal (Project 4).

### **C5. Doctoral and Postdoctoral Fellowships**

2020 Beatriu de Pinos 2019 postdoctoral fellowship. Renounced in favor of grant RYC2019

2014 EMBO short term postdoctoral fellowship ASTF 289 - 2014

2008-12 FPU doctoral grant AP2008-04334 by the Spanish ministry of education

### **C6. Scientific Awards**

2017 Young Investigator Award at "200 Years of Selenium Research" conference, Stockholm.

2013 Best Poster / Young Investigator at "10th International Conference on Selenium", Berlin.

### **C7. Other merits and activities**

- Invited peer-reviewer for the journals *Nucleic Acids Research*, *Molecular Biology and Evolution*, *PLoS One*, and many others.
- Invited reviewer of Master thesis for the MSc in Bioinformatics for Health Sciences, Universitat Pompeu Fabra, Barcelona, Spain (years 2018-2019 and 2019-2020).
- Contributor to the Bioinformatics Course for Biology undergraduates at Universitat Pompeu Fabra, Barcelona, from 2008 to 2013. Tasks: design of the research project, preparation of resources, tutoring activity to students and to the other tutors, evaluation of student work, occasional lecturing.
- Informal supervision of ~10 undergraduate and master students during short term stays (voluntary summer internships and master thesis projects) at the Guigó Lab.
- Invited speaker at RNA summer school at Boston College, 2016.
- In the media: I feature on the episode "Unravel the Evolution of Life and Universe by Element" of the documentary show "Cosmic Front", produced by NHK (Japan's national television), aired in Sept 2014. I was interviewed as expert on selenium and its role on the evolution of life.
- Art and science: I often teamed up with my friends and family to design artistic renditions of my scientific discoveries. This resulted in five artwork covers published in *Genome Research* (Sept 2015), *Molecular Biology and Evolution* (Sept 2016, Nov 2016, and Feb 2020), and *Journal of Molecular Biology* (Nov 2019).