

EVA MARIA NOVOA

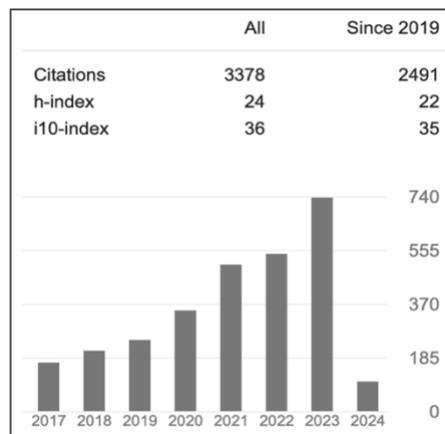
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Place and date of birth: June 25th, 1983, Barcelona, Spain

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SUMMARY

In the last twelve years, I have conducted research in the fields of protein translation, RNA epitranscriptomics and bioinformatics. During this period, I have published **43 peer-reviewed publications**, which include **15 publications as corresponding and last author**, and have filed **3 patents**. Since September 2018, I lead the “Epitranscriptomics and RNA Dynamics” laboratory at the Centre for Genomic Regulation (CRG). In our laboratory, we want to understand how gene expression is regulated with surgical precision, in a tissue-dependent, spatial and temporal dimension. In these years, we have established ourselves as internationally-recognized leaders in the use and development of direct RNA nanopore sequencing technologies to study RNA modifications. Specifically, we have pioneered the development of novel algorithms to map and quantify RNA modifications (Liu et al., *Nat Comm* 2019, Begik et al., *Nat Biotech* 2021), we have optimized the library preparations to make the technology applicable to low-input samples (Smith et al., *Genome Res* 2020) and we have expanded its applicability beyond coding mRNAs (Begik et al., *Nature Methods* 2022; Lucas et al., *Nature Biotech* 2023). We are now applying this technology to: i) decipher the role that RNA modifications play in sperm formation, maturation and intergenerational inheritance (project funded by ERC Starting Grant); ii) dissect how RNA modification dysregulation leads to human disease to then develop novel antitumoral targets (project funded by MERCK Innovation Grant); and iii) bring this technology to the next level to apply it for rapid diagnosis of cancer, and classification of cancer types (project funded by AECC, LAB AECC Grant).



Google Scholar citations, accessed 15/Feb/2024

EDUCATION

- 2008 - 2012 **Ph.D. in Biomedicine**, IRB Barcelona - University of Barcelona, Spain
Extraordinary PhD prize (top 1%), given by University of Barcelona
Young Researcher prize for PhD thesis, given by Catalan Society of Biology
- 2007 - 2009 **M.Sc in Bioinformatics**, University Pompeu Fabra - University of Barcelona, Spain
- 2004 - 2007 **B.Sc in Biochemistry**, University of Barcelona, Spain
Extraordinary BSc prize, given by University of Barcelona
- 2001 - 2004 **B.Sc in Biology**, University of Barcelona, Spain (first cycle)

RESEARCH EXPERIENCE

- Sep 2018 - present **Group Leader** – Epitranscriptomics and RNA Dynamics
Center for Genomic Regulation (CRG) – Spain
- 2017 - 2018 **Senior Postdoctoral Researcher / Early-career research fellow (DECRA)**
Garvan Institute of Medical Research & University of New South Wales – Australia
Supervisor: Prof. John S. Mattick
- 2013 - 2016 **Postdoctoral fellow (EMBO & HFSP)**
Massachusetts Institute of Technology (MIT) & Broad Institute of Harvard and MIT – USA
Supervisor: Prof. Manolis Kellis
- Jan-May 2013 **Postdoctoral researcher** - Institute for Research in Biomedicine (IRB) – Spain
Supervisor: Prof. Lluís Ribas de Pouplana
- 2008- 2012 **PhD student** - Institute for Research in Biomedicine (IRB) – Spain
Supervisor: Prof. Lluís Ribas de Pouplana
- 2008- 2010 **MSc student** - Barcelona Supercomputing Center & IRB Barcelona – Spain
Supervisor: Prof. Modesto Orozco

CAREER BREAKS

Aug - Jan 2023	Full-time maternity leave (6 months)
Jun - Nov 2021	Full-time maternity leave (6 months)
Jan. - Jun 2018	Full-time maternity leave (6 months)

GRANTS, FELLOWSHIPS and AWARDS

* Project grants:

- Ongoing:

2024-2024	AGAUR LLAVOR Grant – <u>20,000€</u> (Role: PI) Project: “Simple and cost-effective cancer diagnosis in liquid biopsy through native tRNA sequencing”. Translational grant to bring a product idea towards market.
2023-2026	AGAUR SGR Emerging Grant (GRE) – <u>36,000€</u> (Role: PI) Flexible funds recognizing excellence in research, not associated to a specific project.
2022-2027	European Research Council (ERC) Starting Grant – <u>1,500,000€</u> (Role: PI) Project: “Dissecting the role of sperm transcriptome dynamics in intergenerational inheritance through native RNA nanopore sequencing”
2022-2025	Spanish MICINN National Funding - <u>230,000€</u> (Role: PI) Project: “Systematic analysis of RNA modification dynamics upon neuronal activation and differentiation using native RNA nanopore sequencing”
2022-2026	Horizon 2020 MSCA-DN – <u>2,700,000€</u> (Role: co-PI; 251,000€ for our group) Project: “LongTREC: Long-reads Transcriptome European Consortium: The next generation transcriptome biology revealed by single molecule sequencing technologies”
2021-2024	LAB AECC 2021 - Spanish Association against Cancer - <u>300,000€</u> (Role: PI) Project: “Native RNA nanopore sequencing as a novel technology for rapid cancer screening and monitoring”
2021-2024	Merck Innovation Grant 2020 - <u>900,000€</u> (Role: co-PI; 227,500€ for our group) Project: “A drug discovery programme targeting cancer-specific RNA modifying enzymes”
2020-2024	Horizon 2020 MSCA-ITN – <u>3,000,000€</u> (Role: co-PI; 251,000€ for our group) Project: “ROPES: Roles of epitranscriptomics in diseases”

- Completed:

2019-2021	Spanish MICINN National Funding - <u>116,000€</u> (Role: PI) Project: “Characterization of the role of 3-methylcytosine RNA modifications in myogenic differentiation”
2018-2019	Australian Research Council (ARC) Discovery Project Grant - <u>AUD \$398,000</u> (Role: PI) Project: “Charting the unknown human epitranscriptome”
2017-2018	Garvan-Weizmann Collaborative Research Project Grant - <u>AUD \$100,000</u> (Role: co-PI) Project: “Establishing nanopore sequencing for quantitative transcriptome-wide mapping of RNA modifications at single nucleotide resolution”

* Fellowships:

2016-2018	ARC Discovery Early Career Research Award (DECRA) - <u>AUD \$372,000</u>
2014-2016	Human Frontier Science Program (HFSP) Postdoctoral Fellowship - <u>USD \$165,000</u>
2013-2014	EMBO Long Term Postdoctoral Fellowship - <u>USD \$90,000</u>
2008-2012	LaCaixa-IRB International PhD Program Fellowship - <u>100,000€</u>
2006-2007	Undergraduate Research Collaboration Fellowship, given by AGAUR - <u>3,000€</u>

*** Collaborations with industry:**

2023-2024 **Research Collaboration Agreement** with IMMAGINA Biotech - 130,000€ (Role: PI)
2023-2024 **Research Collaboration Agreement** with Servier - 15,000€ (Role: PI)

AWARDS AND PRIZES

2024 **EMBO Young Investigator Programme (EMBO YIP) Award**, awarded by EMBO
2023 **R3 Certification**, awarded by Spanish Ministry of Science and Innovation
2023 **IBUB-SEBBM Young Investigator Award**, awarded by Institute of Biomedicine of the University of Barcelona (IBUB) and the Spanish Society of Molecular Biology and Biochemistry (SEBBM)
2020 **Eppendorf IRB Alumni Excellence Award**, awarded by Institute for Research in Biomedicine
2017 **Rising Star Prize**, awarded by St Vincent's Research Organization
2016 **Young Researcher Prize (Premi Jove Investigador)**, awarded by the Catalan Society of Biology
2013 **Fisher Scientific Prize for Young Spanish Researchers**, awarded by Spanish Society of Molecular Biology and Biochemistry
2013 **Extraordinary PhD Prize (Premi Extraordinari de Doctorat)**, awarded by University of Barcelona
2012 **PhD Cum Laude**
2012 **Article of the month**, given by Spanish Society of Molecular Biology and Biochemistry
2007 **Extraordinary BSc Prize (Premi Extraordinari de Llicenciatura)**, awarded by University of Barcelona

* From lab members :

2023 **RNA Society Eclipse Innovation Award** (to Ms. Morghan Lucas)
2023 **MSCA-DN PhD fellowship** (to Ms. Xanthi-Lida Katopodi)
2023 **FPI-MICINN PhD fellowship** (to Ms. Maria Cristina Petrella)
2022 **FPI-Severo Ochoa PhD fellowship** (to Mr. Nikola Todorov)
2021 **Cells Journal PhD prize** (to Mr. Oguzhan Begik)
2021 **RNA Society Eclipse Innovation Award** (to Mr. Oguzhan Begik)
2021 **MSCA-ITN PhD fellowship** (to Mr. Gregor Dientshuber)
2019 **laCaixa INPHINIT PhD fellowship** (to Ms. Sonia Cruciani)
2019 **FPI-Severo Ochoa PhD fellowship** (to Ms. Anna Delgado-Tejedor)
2018 **laCaixa International PhD fellowship** (to Mr. Ivan Milenkovic)
2018 **FPI-Severo Ochoa PhD fellowship** (to Ms. Morghan Lucas)
2018 **Marie Curie INTREPID Postdoctoral fellowship** (to Dr. Leszek Prysycz)
2017 **UNSW International PhD fellowship** (to Mr. Oguzhan Begik)

PATENTS

2023 **'A method of detecting non-canonical bases in sequencing data'**
Inventors: Leszek Prysycz, Sonia Cruciani, Anna Delgado Tejedor, Eva Maria Novoa.
EU Patent Application No.: EP23383128.8
2022 **'Method to analyze tRNA using direct sequencing' -- Licensed.**
Inventors: Morghan Lucas, Leszek Prysycz, Eva Maria Novoa.
EU Patent Application No.: EP22382917.7
2019 **'High-throughput Untranslated Region Engineering and Screening'**
Inventors: Jicong Cao, Eva Maria Novoa, Zhizhuo Zhang, Manolis Kellis, Tim Lu.
US Patent Application No.: 16/441,647 ; Patent publication: US20200066375A1

TOP HIGHLIGHTED PUBLICATIONS

1. Lucas MC*, Prysycz LP*, Medina R, Milenkovic I, Camacho N, Marchand V, Motorin Y, Ribas de Pouplana L and **Novoa EM**#. Quantitative analysis of native tRNAs using direct RNA nanopore sequencing ***Nature Biotech*** 2023. doi: /10.1038/s41587-023-01743-6

*** Patent filed (and licensed) associated to this work*

*** Broad coverage of the publication in media, including radio, television, written press, twitter, blogs, in autonomic, national and international press:*

- o - *The Telegraph (international): <https://www.telegraph.co.uk/global-health/science-and-disease/cancer-test-breakthrough-scientists-spain/>*
- o - *RTVE (national): <https://www.rtve.es/noticias/20230406/metodo-para-diagnosticar-diferentes-tipos-cancere-menos-tres-horas/2436706.shtml>*
- o - *TV3 (autonomic): <https://www.ccma.cat/324/desenvolupen-a-barcelona-un-metode-per-detectar-el-cancer-en-menys-de-3-hores-amb-arn/noticia/3222416/>*

2. Begik O, Diensthuber G, Liu H, Delgado-Tejedor A, Kontur C, Niazi AM, Valen E, Giraldez AJ, Beaudoin JD, Mattick JS and **Novoa EM**#. Nano3P-seq: transcriptome-wide analysis of gene expression and tail dynamics using end-capture nanopore sequencing. ***Nature Methods*** 2022 20:75-83. doi: 10.1038/s41592-022-01714-w

3. Milenkovic I, Vieira HGS, Lucas MC, Ruiz-Orera J, Patone G, Kesteven S, Wu J, Feneley M, Espadas G, Sabidó E, Hubner N, van Heesch S, Voelkers M and **Novoa EM**#. Dynamic interplay between RPL3- and RPL3L-containing ribosomes modulates mitochondrial activity in the mammalian heart. ***Nucl Acids Res.*** 2023, doi: /10.1093/nar/gkad121

*** Selected as 'Breakthrough' by Nucleic Acids Res Editors*

4. Begik O*, Lucas MC*, Prysycz LP, Ramirez JM, Medina R, Milenkovic I, Cruciani C, Vieira HGS, Liu H, Sas-Chen A, Mattick JS, Schwartz S and **Novoa EM**#. Quantitative profiling of native RNA modifications and their dynamics using nanopore sequencing. ***Nature Biotech*** 2021. doi: 10.1038/s41587-021-00915-6

*** Publication highlighted by Nature Methods as Research Highlight: (<https://www.nature.com/articles/s41592-021-01211-6>)*

*** Publication highlighted by GenomeWeb: (<https://www.genomeweb.com/sequencing/new-algorithms-enable-direct-nanopore-based-detection-additional-rna-modifications#.YPKPdC0Rq1t>)*

5. Begik O, Lucas MC, Ramirez JM, Liu H, Mattick JS and **Novoa EM**#. Integrative analyses of the RNA modification machinery reveal tissue- and cancer-specific signatures. ***Genome Biology*** 2020, 21:97. doi: 10.1186/s13059-020-02009-z

*** Publication highlighted by national spanish press: (https://www.eldiario.es/sociedad/Descubren-pueden-dianas-terapeuticas-infertilidad_0_1024698012.html)*

6. Liu H*, Begik O*, Lucas MC, Ramirez JM, Mason CE, Wiener D, Schwartz S, Mattick JS, Smith MA and **Novoa EM**#. Accurate detection of m6A RNA modifications in native RNA sequences. ***Nature Comm*** 2019, 10:4079. doi:10.1038/s41467-019-11713-9

*** Highlighted among top breakthroughs of the year using Nanopore sequencing: (<https://nanoporetech.com/about-us/news/7-breakthroughs-rna-research-nanopore-community>)*

*** Publication highlighted in Science magazine news: (<https://www.sciencemag.org/features/2019/05/epitranscriptomics-rna-revisited>)*

FULL LIST OF PUBLICATIONS

a) As INDEPENDENT GROUP LEADER

- Preprints/under review:

1. Diensthuber G*, Prysycz LP*, Llovera L, Lucas MC, Delgado-Tejedor A, Cruciani C, Roignant JY, Begik O[#] and **Novoa EM[#]**. Enhanced detection of RNA modifications and mappability with high-accuracy nanopore RNA basecalling models. *bioRxiv* 2023, doi: 10.1101/2023.11.28.568965v1 (under review in Genome Res, 2nd revision)
2. Spectral libraries from nucleobases and deoxyribonucleosides facilitate the identification of ribonucleosides by nLC-MSMS. Espadas G, Ollivier A, Llovera L, Tuorto F, **Novoa EM** and Sabidó E (under review in Rapid Comm Mass Spec, 1st revision).
3. Cruciani S*, Delgado-Tejedor A*, Prysycz LP*[#], Medina R, Llovera L and **Novoa EM[#]**. De novo basecalling of m6A modifications at single molecule and single nucleotide resolution. *bioRxiv* 2023, doi: 10.1101/2023.11.13.566801 (under revision in Nat Biotech, 2nd revision)
4. Delgado-Tejedor A, Medina M, Begik O, Cozzuto L, Ponomarenko J, **Novoa EM[#]**. Native RNA nanopore sequencing reveals antibiotic-induced loss of rRNA modifications in the A- and P-sites. *bioRxiv* 2023, doi: doi.org/10.1101/2023.03.21.533606 (under review in Nat Comm, 2nd revision)
5. Pauli C, Kienhöfer M, Blank MF, Begik O, Rohde C, Heid D, Xu F, Zimmermann S, Weidenauer K, Delaunay S, Krall N, Trunk K, Zhao D, Zhou F, Broberg C, Aznar-Benitah S, Krijgsveld J, **Novoa EM**, Müller-Tidow C, Frye M. Unbiased functional genetic screens reveal essential RNA modifications in human cancer and drug resistance (under review).

- Peer-reviewed publications:

6. Baquero-Perez B*, Yonchev I*, Delgado-Tejedor A*, Medina R, Puig-Torrents M, Sudbery I, Begik O, Wilson S[#], **Novoa EM[#]**, Diez J[#]. N6-methyladenosine modification is not a general trait of viral RNA genomes. *Nat Comm* 2024 (accepted). Preprint available at doi: 10.1101/2023.10.13.561839.
7. Sierra C, Sabariego M, Fernandez-Blanco A, Cruciani S, Zamora-Moratalla A, **Novoa EM** and Dierssen M. The lncRNA Sngh11, a new candidate contributing to neurogenesis, plasticity and memory deficits in Down syndrome. *Mol Psychiatry* 2024. doi: https://doi.org/10.1038/s41380-024-02440-9
8. Sklias A, Cruciani C, Marchand V, Spagnuolo M, Lavergne G, Dreos R, **Novoa EM**, Motorin Y and Roignant J-Y. Comprehensive map of ribosomal 2'-O-methylation and C/D box snoRNAs in Drosophila melanogaster. *Nucl Acids Res* 2024 doi: https://doi.org/10.1093/nar/gkae139
9. Lucas MC*, Prysycz LP*, Medina R, Milenkovic I, Camacho N, Marchand V, Motorin Y, Ribas de Pouplana L and **Novoa EM[#]**. Quantitative analysis of native tRNAs using direct RNA nanopore sequencing *Nature Biotech* 2023. doi: /10.1038/s41587-023-01743-6
10. Milenkovic I, Vieira HGS, Lucas MC, Ruiz-Orera J, Patone G, Kesteven S, Wu J, Feneley M, Espadas G, Sabidó E, Hubner N, van Heesch S, Voelkers M and **Novoa EM[#]**. Dynamic interplay between RPL3- and RPL3L-containing ribosomes modulates mitochondrial activity in the mammalian heart. *Nucl Acids Res*, 2023, doi: /10.1093/nar/gkad121
11. Begik O, Diensthuber G, Liu H, Delgado-Tejedor A, Kontur C, Niazi AM, Valen E, Giraldez AJ, Beaudoin JD, Mattick JS and **Novoa EM[#]**. Nano3P-seq: transcriptome-wide analysis of gene expression and tail dynamics using end-capture nanopore sequencing. *Nat Methods* 2023. 2023, 20:75-85. doi: 10.1038/s41592-022-01714-w

12. Jungfleisch J, Böttcher, R, Talló-Parra M, Corral C, Merits A, **Novoa EM** and Diez J. CHIKV infection reprograms codon optimality to favor viral RNA translation by altering the tRNA epitranscriptome. *Nature Comm* 2022, 13(1):1-12. doi: 10.1038/s41467-022-31835-x
13. Espadas G, Morales-Sanfrutos J, Medina R, Lucas MC, **Novoa EM** and Sabidó E. High performance nano-flow liquid chromatography column combined with high- and low-collision energy data-independent acquisition enables targeted and discovery identification of modified ribonucleotides by mass spectrometry. *J Chrom Anal* 2022, 1665, 452803.
14. Begik O*, Lucas MC*, Prysycz LP, Ramirez JM, Medina R, Milenkovic I, Cruciani C, Vieira HGS, Liu H, Sas-Chen A, Mattick JS, Schwartz S and **Novoa EM**#. Quantitative profiling of pseudouridylation dynamics in native RNAs with nanopore sequencing. *Nature Biotech* 2021. doi: 10.1038/s41587-021-00915-6
15. Jonkhout N*, Cruciani C*, Vieira HGS, Tran J, Liu H, Liu G, Camacho N, Pickford R, Kaczorowski D, Vauti F, Ribas de Pouplana L, Christ D, Schonrock N, Mattick JS# and **Novoa EM**#. Subcellular relocalization and nuclear redistribution of the RNA methyltransferases TRMT1 and TRMT1L upon neuronal activation. *RNA Biol* 2021. doi: 10.1080/15476286.2021.1881291.
16. Prysycz LP# and **Novoa EM**#. ModPhred: an integrative toolkit for the analysis and storage of nanopore sequencing DNA and RNA modification data. *Bioinformatics* 2021. doi:https://doi.org/10.1093/bioinformatics/btab539
17. Torres AG, Rodriguez-Escriba M, Marcet-Houben M, Vieira HGS, Camacho N, Catena H, Murillo M, Torres FM, Pardo-Saganta A, Gabaldon T, **Novoa EM** and Ribas de Pouplana L. Human tRNAs with inosine 34 are essential to efficiently translate eukarya-specific low-complexity proteins. *Nucl Acids Res* 2021, doi: 10.1093/nar/gkab461
18. Smith MA*., Ersavas T*, Ferguson JM*, Liu J, Lucas MC, Begik O, Bojarski L, Barton K and **Novoa EM**#. Molecular barcoding of native RNAs using nanopore sequencing and deep learning. *Genome Research* 2020 30(9): 1345-1353.
19. Begik O, Lucas MC, Ramirez JM, Liu H, Mattick JS and **Novoa EM**#. Integrative analyses of the RNA modification machinery reveal tissue- and cancer-specific signatures. *Genome Biology* 2020, 21,97. doi: 10.1186/s13059-020-02009-z
20. Cozzuto L, Liu H, Prysycz LP, Hermoso Pulido T, Delgado-Tejedor A, Ponomarenko J and **Novoa EM**#. MasterOfPores: a workflow for the analysis of Oxford Nanopore direct RNA sequencing datasets. *Front in Genet* 2020, 11:211.
21. Liu H*, Begik O*, Lucas MC, Ramirez JM, Mason CE, Wiener D, Schwartz S, Mattick JS, Smith MA and **Novoa EM**#. Accurate detection of m6A RNA modifications in native RNA sequences. *Nature Comm* 2019, 10:4079. doi:10.1038/s41467-019-11713-9

b) As POSTDOCTORAL RESEARCHER

22. Cao J*, **Novoa EM***, Zhang Z*, Chen WCW, Liu D, Choi GCG, Wong ASL, Wehrspaun C, Kellis K# and Lu TK#. High-throughput 5'UTR engineering for enhanced protein production in non-viral gene therapies. *Nature Comm* 2021 12:4138, doi: 10.1038/s41467-021-24436-7
23. Moore et al., **Novoa EM**, et al. The ENCODE Project Consortium. Expanded encyclopedias of DNA elements in the human and mouse genomes. *Nature* 2020 583:699-710.
24. **Novoa EM**#, Jungreis I, Jaillon O and Kellis M#. Elucidation of codon usage signatures across the domains of life. *Mol Biol Evol* 2019, doi: https://doi.org/10.1093/molbev/msz124
25. Wu MR, Nissim L, Stupp D, Pery E, Binder-Nissim A, Weisinger K, Enghuus C, Palacios SR, Humphrey M, Zhang Z, **Novoa EM**, Kellis M, Weiss R, Rabkin SD, Tabach Y and Lu TK. A high-throughput screening and

computation platform for identifying synthetic promoters with enhanced cell-state specificity (SPECS). *Nature Comm* 2019,10 (1):1-10

26. Picchioni D, Antolin-Fontes A, Camacho N, Schmitz C, Pons-Pons A, Rodriguez-Escribà M, Machallekidou A, Güler MN, Panagiota S, Carretero-Junquera M, Serrano A, Hovde SL, Knobel PA, **Novoa EM**, Solà-Vilarrubias, Kaguni SK, Stracker TH and Ribas de Pouplana L. Mitochondrial protein synthesis and mtDNA levels coordinated through an aminoacyl-tRNA synthetase subunit. *Cell Reports* 2019, 27(1):40-47.
27. Beaudoin JD*, **Novoa EM***, Vejnar CE, Yartseva V, Takacs CM, Kellis M and Giraldez AJ. Analyses of mRNA structure dynamics identify the embryonic gene regulatory programs. *Nat Struct Mol Biol* 2018, 25, 677-686.
28. **Novoa EM***, Beaudoin JD*, Giraldez AJ, Mattick JS#, Kellis M#. Best practices for genome-wide RNA structure analysis: combination of mutational profiles and drop-off information. *bioRxiv*, 2017 176883
29. Barsacchi M, **Novoa EM**, Kellis M and Bechini A. SwiSpot: Modelling riboswitches by spotting out switching sequences. *Bioinformatics* 2016, 32(21): 3252-3259.
30. The Anopheles consortium. Neafsey D, et al, **Novoa EM**, et al., Boransky N. Highly evolvable malaria vectors: the genomes of 16 Anopheles mosquitoes. *Science* 2015, 347(6217):1258522.

c) As PhD STUDENT:

31. Saint-Leger A, Bello C, Dans PD, Torres AG, **Novoa EM**, Camacho N, Orozco M, Kondrashov FA and Ribas de Pouplana L. Saturation of recognition elements blocks evolution of new tRNA identities. *Science Advances* 2016, 2(4):e1501860.
32. **Novoa EM**, Vargas-Rodriguez O, Lange S, Goto Y, Suga H, Musier-Forsyth K and Ribas de Pouplana, L. Ancestral AlaX editing enzymes for control of genetic code fidelity are not tRNA specific. *J Biol Chem* 2015, 290:10495-10503.
33. **Novoa EM** and Ribas de Pouplana L. Cooperation for better inhibiting. *Chem & Biol* 2015, 22: 685-686.
34. Liu Z, Vargas-Rodriguez O, Goto Y, **Novoa EM**, Ribas de Pouplana L, Suga H and Musier-Forsyth K. Homologous trans-editing factors with broad tRNA specificity prevent mistranslation caused by serine/threonine misactivation. *Proc. Natl. Acad. Sci. USA* 2015, 112(19):6027-6032.
35. **Novoa EM**, Camacho N, Tor A, Wilkinson B, Moss S, Marín-García P, Azcárate IG, Bautista JM, Mirando AC, Fracklyn CS, Varon S, Royo M, Cortés A and Ribas de Pouplana L. Analogs of natural aminoacyl-tRNA synthetase inhibitors clear malaria in vivo. *Proc. Natl. Acad. Sci. USA* 2014, 111(51):5508-17.

** Publication highlighted in TV, in "TV3 news": (<http://www.ccma.cat/tv3/alacarta/Telenoticies-Migdia/Malaria-es-redueixen-a-la-meitat-les-morts/video/5395391/>)

** Publication highlighted in radio "Cadena Ser" (http://play.cadenaser.com/audio/cadenaser_hoyporhoy_20141211_070000_080000/hoy-hoy-11-12-2014-tramo-de-07-00-08-00/)

36. Hoen R*, **Novoa EM***, Lopez A, Camacho N, Cubells L, Vieira P, Santos M, Marin-Garcia P, Bautista JM, Cortés A and Ribas de Pouplana L. Selective inhibition of the apicoplast lysyl-tRNA synthetase of Plasmodium falciparum. *ChemBioChem* 2013, 14: 499-509.

37. **Novoa EM**, Pavon-Eternod M, Pan T and Ribas de Pouplana L. A role for tRNA modifications in genome structure and codon usage. *Cell* 2012, 149: 202-213.

** Publication highlighted in F1000Prime Article Recommendations as "Exceptional" (<https://facultyopinions.com/prime/717964007>)

** Publication in national press "La Vanguardia" describing the outcome of the work: (http://www.irbbarcelona.org/files/File/2012_03_30_LaVanguardia_cast_LRibas.pdf)

38. **Novoa EM**, Ribas de Pouplana L, Barril X, and Orozco M. Ensemble docking in homology models. *J. Chem. Theory Comput.*, 2010, 6 (8): 2547-2557.
39. **Novoa EM**, Castro de Moura M, Orozco M and Ribas de Pouplana L. A genomics method to identify pathogenicity-related proteins. Application to aminoacyl-tRNA synthetase-like proteins. *FEBS Lett* 2010, 584(2): 460-6.
- d) REVIEWS and BOOK CHAPTERS:**
40. Lucas MC and **Novoa EM**[#]. Long-read sequencing in the era of epigenomics and epitranscriptomics. *Nat Methods* 2023, 20:25-29. Doi: <https://doi.org/10.1038/s41592-022-01724-8>
41. Cozzuto L*, Delgado-Tejedor A*, Hermoso T, **Novoa EM**[#]. and Ponomarenko J[#]. Nanopore direct RNA sequencing data processing and analysis using MasterOfPores. *Methods Mol Biol* 2022. Oliveira P (eds). (accepted)
42. Begik O, Mattick JS[#] and **Novoa EM**[#]. Exploring the epitranscriptome by native RNA sequencing. *RNA* 2022 28:1430-1439.
43. Liu H, Begik O and **Novoa EM**[#]. EpiNano: Detection of m6A RNA modifications using Oxford Nanopore direct RNA sequencing. *Methods Mol Biol* 2021, Vol 2298 In: McMahon M. (eds) RNA Modifications. Humana, New York, NY. https://doi.org/10.1007/978-1-0716-1374-0_3.
44. Furlan M, Delgado-Tejedor A, Mulroney L, Pelizzola M[#], **Novoa EM**[#] and Leonardi T[#]. Computational methods for RNA modification detection from nanopore direct RNA sequencing data. *RNA Biol* 2021. <https://doi.org/10.1080/15476286.2021.1978215>
45. Jonkhout N, Tran J, Smith MA, Schonrock N, Mattick JS[#] and **Novoa EM**[#]. The RNA modification landscape in human disease. *RNA* 2017, 12:1754-1769.
46. **Novoa EM**[#], Mason CE, Mattick JS. Charting the unknown epitranscriptome. *Nat Rev Mol Cell Biol* 2017, 18:339-340.
47. **Novoa EM** and Ribas de Pouplana L. Speeding with control: codon usage, tRNAs and ribosomes. *Trends Genet.* 2012, 28(11):574-581.
48. **Novoa EM**, Ribas de Pouplana L and Orozco M. Small molecule docking from theoretical structural models. In: "*Computational Modeling of Biological Systems: From Molecules to Pathways*". 2012. Ed. Springer, New York (USA); Vol 4, pp 75-96.

TEACHING & MENTORING

- 2019-present **Guest Lecturer** at Bachelor in Bioinformatics (ESCI-UPF)
- 2017-present **Supervisor of PhD students, MSc students and Undergraduates**
 Current: Main supervisor of 5PhD students, 1BSc student
 Finished: co-supervision of 1PhD thesis, 4MSc thesis, 1BSc thesis
- 2016-2018 **High School student supervisor** at Garvan Institute.
 Weekly experiences of highly talented 10th grade students, first contact with research.
- 2013-2015 **Guest Lecturer** at Massachusetts Institute of Technology.
 Courses 6.047 (undergraduate) & 6.878 (graduates): "Computational Biology: Genomes, Networks, Evolution".
- 2013-2015 **Student project supervisor**, Massachusetts Institute of Technology.
 Course 6.047: "Computational Biology: Genomes, Networks, Evolution".

REVIEWING ACTIVITIES

Invited Scientific Advisory Board member (academia):

RMaP: RNA modification and processing (DFG multi-institutional collaborative project) (2021-present).

Scientific Advisory Board / Expert Consultant for Companies:

Scientific Advisory Board – MadeOfGenes (2015 – present) -- <https://madeofgenes.com>

Scientific Advisory Board – IMMAGINA Biotech (2022 – present) -- <https://immaginabiotech.com>

Ad hoc Peer Reviewer:

Journals: Nature Methods, Nature Biotech, Nucleic Acids Res, Bioinformatics, Nature Comm, Life Science Alliance, RNA, RNA Biology, Science Advances

Invited Ad hoc Grant Reviewer:

Expert Reviewer for National grants: Spanish Research Grants (2018-present).

Expert Reviewer for International grants: Wellcome Trust (2019-present); Australian Research Council (2016-2018); European Research Council (2019-present)

MEMBERSHIPS

2022 - 2026 COST Action "TRANSLACORE" member (<https://www.cost.eu/actions/CA21154/>)

2018 - 2021 COST Action "EPITRAN" member (<https://epitran.eu>)

2015 - present RNA Society member

2012 - present Spanish Society for Molecular Biology and Biochemistry (SEBBM) Member

CONTRIBUTIONS TO CONFERENCES and INVITED TALKS (Selection)

Invited Speaker to International Conferences: **more than 50 invited talks** in renamed Conferences and Meetings around the world including USA, Canada, Australia, UK, Israel, Norway, Italy, Austria, Switzerland, Germany, Singapore, Poland, Croatia, France and Spain. Average of 10 invited talks per year since becoming independent group leader (Sep 2018).

Selection of contributions:

- 2024 **Invited Keynote Speaker** – Conference: IUBMB tRNA conference - Japan (to take place in Nov)
- 2024 **Invited Speaker** – Conference: Precision Medicine in RNA modifications - Belgium (to take place Nov)
- 2024 **Invited Speaker** – Conference: Nucleic Acids Symposium - Germany (to take place in Sep)
- 2024 **Invited Keynote Speaker** – Conference: Nanopore Day Barcelona – Spain
- 2023 **Conference Chair** – Conference: Keystone RNA Modifications – USA
- 2023 **Invited Speaker** – Seminar: IMMAGINA Biotechnology Retreat – Italy
- 2023 **Invited Speaker** – Conference: Royal Society of London 'Specialized Ribosomes' – UK
- 2023 **Invited Speaker** – Conference: SEBBM Conference (Premi IBUB-SEBBM talk) – Spain
- 2023 **Invited Speaker** – Conference: NIH Epitranscriptomics Symposium – USA (*virtual*)
- 2023 **Invited Speaker** – Conference: NIA RNA Metabolism and Aging Meeting – USA (*virtual*)
- 2023 **Invited Speaker** – Seminar: RNADeco Austrian Consortium – Austria (*virtual*)
- 2023 **Invited Speaker** – Seminar: Emory University – USA (*virtual*)
- 2023 **Invited Session Chair & Speaker** – Conference: RNA Society meeting– Singapore
- 2023 **Invited Speaker** – Workshop: National Academy of Sciences "Mapping RNA modifications" – USA
- 2023 **Invited Speaker** – Symposium: lncRNAs, non-canonical ORFs and cancer – France
- 2023 **Invited Speaker** – Seminar: Center for Integrative Biology (CBI) – France
- 2022 **Invited Speaker** – Seminar: Barcelona Supercomputing Center (BSC)– Spain
- 2022 **Invited Speaker** – Seminar: NIH/NCI invited– USA (*virtual*)
- 2022 **Invited Speaker** – Seminar: University of Laussane/CIG– Switzerland
- 2022 **Invited Speaker** – Conference: Nature Conference: RNA at the Bench and Bedside III – USA
- 2022 **Invited Speaker** – Conference: EMBO 'The Complex Life of RNA' – Germany
- 2022 **Invited Speaker** – Conference: EMBO 'Epigenome Inheritance and Reprogramming' – Croatia
- 2022 **Invited Speaker** – Conference: Nanopore Sequencing of Biopolymers – USA (*virtual*)
- 2022 **Invited Speaker** – Conference: RNA: beyond its genetic code – Germany (*virtual*)
- 2022 **Invited Speaker** – Symposium: 3rd symposium on Nucleic Acid Modifications – Germany

- 2022 **Invited Speaker** – Symposium: RNA regulation and Disease symposium – France
- 2022 **Invited Speaker** – Seminar: IIMCB invited seminar – Poland (*virtual*)
- 2021 **Invited Speaker** – Conference: London Calling Nanopore Conference – UK (*virtual*)
- 2021 **Invited Speaker** – Seminar: NIH/NIEHS Invited seminar – USA (*virtual*)
- 2021 **Invited Speaker** – Seminar: Center for Cancer Investigation (CIC) – Spain (*virtual*)
- 2021 **Invited Speaker** – Seminar: RiboClub, Montreal Clinical Research Institute (IRCM) – Canada (*virtual*)
- 2021 **Invited Speaker** – Symposium: UB-CIBERER MiniSymposium in Rare Diseases – Spain (*virtual*)
- 2020 **Invited Speaker** – Symposium: IberION meeting - Spain (*virtual*)
- 2020 **Invited Speaker** – Seminar: QMUL Epigenetics EpiHub Seminar, MRC)– UK (*virtual*)
- 2020 **Session Chair** – Conference: SCB Covid-19 Bioinformatics and Genomics symposium - Spain (*virtual*)
- 2020 **Invited Speaker & Session Chair** – Conference: Keystone Meeting in RNA editing and Modifications - USA (*virtual*)
- 2020 **Invited Speaker** – Conference: NCI Epitranscriptomics Conference - USA (*virtual*)
- 2019 **Plenary Speaker** – Conference: London Calling Nanopore Conference – UK
- 2019 **Invited Speaker** – Conference: 2nd Symposium Nucleic Acid Modifications – Israel
- 2019 **Invited Speaker** – Seminar: Josep Carreras Institute - Spain
- 2019 **Invited Speaker** – Conference: EMBL Translational Medicine meeting - Spain
- 2019 **Selected abstract (oral presentation)** – Conference: Gordon Research Conference in RNA Editing – Italy
- 2018 **Invited Speaker** – Seminar: Sven Furberg Seminars - Norway
- 2018 **Invited Speaker** – EPITRAN Cost Action meeting – Spain

DISSEMINATION OF RESULTS TO SOCIETY

1. Regular maintenance of digital resources:

- - Creation of Lab website: <http://novoalab.com>
- - Lab Github account (code availability): <https://github.com/novoalab>
- - Lab Instagram account: [@secuenciasdeciencia](https://www.instagram.com/secuenciasdeciencia) (>6000 followers, 100K accounts/month reached)
- - Twitter accounts: [@NovoaLab](https://twitter.com/NovoaLab) (Novoa Lab twitter account) (>900 followers)

2. **Participation in seminars and conferences:** The PI has been an invited speaker to **more than 50 invited talks** in renamed international Conferences and Meetings around the world including USA, Canada, Australia, UK, Israel, Norway, Italy, France and Spain. Average of 10 invited talks per year since becoming independent group leader (Sep 2018).
3. **Participation in #100cientifiques, which focuses on the dissemination** of science in high schools
4. **Participation in OpenPRBB days**, which aims to increase accessibility/visibility of the wider public to the academic research environment.
5. **Strategies related to open science:** All publications from the lab are either open access or have been made publicly available (e.g. UPF database). Our code is publicly available in GitHub, and our data is publicly available in appropriate resources (e.g. European National Archive for sequencing data).

INTERNATIONAL ACTIVITIES

A) Member of International PhD training networks:

- 2020-2024 **Horizon 2020 MSCA-ITN** – 3,000,000€
Project: “ROPES: Roles of epitranscriptomics in diseases”
- 2022-2026 **Horizon 2020 MSCA-DN** – 2,700,000€
Project: “LongTREC: Long-reads Transcriptome European Consortium: The next generation transcriptome biology revealed by single molecule sequencing technologies”

B) Participation in international networks:

- 2024 - 2028 EMBO Young Investigator Program (EMBO YIP) member
- 2022 – 2026 COST Action “TRANSLACORE” member
- 2018 – 2021 COST Action “EPITRAN” member

C) International Scientific Advisory Board membership:

RMaP: RNA modification and processing (DFG multi-institutional collaborative project) (2021-present).

D) Organization of international seminars and congresses

- 2023 **Keystone Symposia Organizer** – “RNA modifications” (with Eric Miska and Ramesh Pillai)
- 2023 **RNA Society Meeting Session Chair** – “Session: RNA modifications” (Singapore)
- 2019 **Committee Member** of conference in “Advances in Computational Biology”, Barcelona, Spain
- 2017 **GRS Conference Chair**, for "Translation Machinery in Health and Disease" in Texas, USA

E) International grants schemes with international collaborators (excluding PhD training networks):

- 2021-2024 **Merck Innovation Grant 2020** - 900,000€ (Role: co-PI)
Project: “A drug discovery programme targeting cancer-specific RNA modifying enzymes” (with Michaela Frye and Carsten Muller-Tidow, Germany)
- 2018-2019 **Australian Research Council** - AUD \$398,000 (Role: lead PI).
Project: “Charting the unknown human epitranscriptome” (with Schraga Schwartz, Israel; Christopher Mason, USA; Martin Smith, Australia)
- 2017-2018 **Garvan-Weizmann Collaborative Project Grant** - AUD \$100,000 (co-PI).
Project: “Establishing nanopore sequencing for quantitative transcriptome-wide mapping of RNA modifications at single nucleotide resolution” (with Schraga Schwartz, Israel)

F) Collaborations with international scientists (highlights):

- **Prof. Schraga Schwartz** (Weizmann Institute, Israel). Co-PI in ARC grant and Weizmann-Garvan grants, development of nanopore-based algorithms to detect m6A and pseudo modifications.
- **Prof. Jean-Yves Roignant** (University of Lausanne, Switzerland). Co-PI in MSCA-ITN grant, development of nanopore-based methods for the detection of Nm modifications.
- **Prof. Michaela Frye** (DKFZ, Germany). Co-PI in Merck Innovation grant, identification of novel epitranscriptome drug targets for cancer treatment.
- **Prof. Carsten Muller-Tidow** (Uni Heidelberg, Germany). Co-PI in Merck Innovation grant and collaborator on independent project to reveal novel biomarkers in plasma samples for early cancer diagnosis
- **A/Prof. Ana Raquel Soares** (University of Aveiro, Portugal). Study of the dysregulation of tRNA modifications in host human tRNAs upon viral infection using nanopore sequencing.
- **Prof. Denis LaFontaine** (Université de Bruxelles, Belgium). Study of RNA modification dysregulation in Diamond-Blackfan anemia patients.
- **Prof. Timothy Bredy** (University of Queensland, Australia). Study of dysregulation of m6A in neuronal phenotypes.
- **Prof. Davide Ruggiero** (UCSF, USA). Study of rRNA modification dynamics in aging.
- **Prof. Antonio Giraldez** (Yale University, USA). Study of the interplay between m6A and deadenylation during the maternal-to-zygotic transition in zebrafish embryos.
- **Prof. Francesca Tuorto** (University Mannheim, Germany). Study of the role of queuosine in sperm RNA and the transmission of dietary information across generations.
- **Prof. Ya Ming** (Jefferson University, USA). Co-PI in NIH grant to develop novel machine learning algorithms and basecalling models to map RNA modifications with single molecule resolution.
- **Prof. Panagiotis Ntziachristos** (Ghent University, Belgium). Analysis of m6A modifications and its dysregulation in leukemia.
- **Prof. Ralf Gilsbach** (University of Heidelberg, Germany). Characterization of the m6A modification dynamics upon induced heart disease conditions in vivo.
- **Prof. Tim Mercer** (University of Brisbane, Australia). Development of m1Y-modification aware-basecalling algorithm to enhance mRNA/vaccine(in vitro transcript quality control mechanisms.