

Curriculum Vitae – Mar Albà

Current Position

ICREA Research Professor
 Head of the Research Programme on Biomedical Informatics (GRIB-HMRI)
 Group Leader Evolutionary Genomics Group
 Hospital del Mar Research Institute (HMRI)
 Barcelona 08003, Spain
 evolutionarygenomics.imim.es

Personal details

Born on 20th June 1969
 DNI: 52216154J
 Phone: +34 662558544
 E-mail: malba@researchmar.net

Group webpage: evolutionarygenomics.imim.es

GoogleScholar: http://scholar.google.com/citations?user=K3Y_DHkAAAAJ&hl=es
 H-index: 48

ORCID: 0000-0002-7963-7375

RESEARCH LINES

Computational Genomics
 Evolution of genes and proteins
 Transcriptomics

EDUCATION

| | |
|----------|--|
| Sep 1999 | MSc in Molecular Modelling and Bioinformatics (Distinction) Crystallography Department, Birkbeck College, University of London. |
| Mar 1997 | PhD in Biological Sciences (Cum laude Premio Extraordinario) Supervisor: Montserrat Pagès (CID/CSIC) Faculty of Biology, Universitat de Barcelona, Spain. |
| Jun 1992 | BSc in Biological Sciences (Grade: 3.15) Faculty of Biology, Universitat de Barcelona, Spain. |

EMPLOYMENT

| | |
|---------------------|---|
| July 2021 – to date | Director Research Programme on Biomedical Informatics Hospital del Mar Research Institute |
| Oct 2005 - to date | ICREA Research Professor Hospital del Mar Research Institute |
| Oct 2005 – Sep 2022 | Coordinator/Lecturer “Principles in Genome bioinformatics” MSc bioinformatics for Health Sciences Department of Health and Experimental Sciences Universitat Pompeu Fabra, Barcelona, Spain |
| Jan 2002 – Sep 2005 | Scientist Ramón y Cajal Programme Department of Health and Experimental Sciences Universitat Pompeu Fabra, Barcelona, Spain |
| Oct 2001- Dec 2001 | Lecturer Assistant (profesor ayudante) Department of Health and Experimental Sciences |

Universitat Pompeu Fabra, Barcelona, Spain

Apr 1999 – Sep 2001

Postdoctoral Research Assistant

Windeyer Institute for Medical Sciences
University College London, UK.

Apr 1998 - Mar 1999

Postdoctoral Fellow

(funded by Ministerio de Educación y Cultura, Spanish Gov.)
Medical Research Council Clinical Sciences Centre
Imperial College School for Medicine, London, UK.

Apr 1997 - Mar 1998

Postdoctoral fellow

(funded by Ministerio de Educación y Cultura, Spanish Gov.)
Medical Research Council Laboratory for Molecular Cell Biology University
College London, UK.

Aug 1996 - Oct 1996

Short visit fellowship FI

(funded by Generalitat de Catalunya)
John Innes Centre, Norwich, UK.

Oct 1994 – Dec 1994

Short visit fellowship FI

(funded by Generalitat de Catalunya)
University of Pennsylvania, Philadelphia, USA.

Jan 1993 - Dec 1996

Predocctoral fellow FI

(funded by Generalitat de Catalunya)
Consejo Superior de Investigaciones Científicas (CID/CSIC) Barcelona, Spain.

Jul 1992 - Dec 1992

Postgraduate fellow CSIC

(funded by CSIC)
Consejo Superior de Investigaciones Científicas (CID/CSIC) Barcelona, Spain.

TEACHING

2005-2022

Coordinator and Lecturer of Principles of Genome Bioinformatics, MSc Bioinformatics for the Health Sciences, Universitat Pompeu Fabra, Barcelona.

Nov 2018

Seminar on New Genes and Evolutionary Innovation, in MSc in Genetics and Genomics, Universitat de Barcelona. 09/11/2018.

Dec 2015

Seminar on Pervasive transcription and the evolution of new genes, in MSc in Biodiversity, Universitat de Barcelona. 01/12/2015.

May 2015

Frontiers in Genomics Series: the continuous birth of new genes revealed by deep RNA sequencing, Centro de Ciencias Genómicas Universidad Autónoma de México (México). 4-5/05/2015.

Feb 2009

Seminar on Evolutionary Patterns of Recently-formed Genes, in MSc in Biodiversity, Universitat de Barcelona. 16/02/2009.

Jun 2008

Seminar in the course Temporal Aspects in Genetic Analysis, PROUST project (EU), Tartu (Estonia).

Feb 2008

Seminar on Identification of Gene Expression Regulatory Sequences, in MSc in Comparative Genomics, Universitat de Barcelona. 28/02/2008.

May 2007

Minicourse in Evolutionary Genomics, Università degli Studi di Milano (Italy). 24-25/05/2007.

Apr 2007

Lecturer in EMBO World Practical Course on Comparative Genomics, Fiocruz, Rio de Janeiro (Brasil). 8-13/04/2007.

Sep 2005

Seminar on Introduction to Bioinformatics – Alignment and Evolution of Sequences, Genome Projects, Universitat de Vic. 19-23/09/2005.

Dec 2004

Seminar on Evolution of microsatellite-type sequences in genes and proteins, in Master Europeen de Genomique, Université Paris V – Paris VII (France). 07/12/2004.

Jul 2004

Seminar on DNA sequencing and the Human Genome Project, in Summer School, Universitat de Tarragona. 17/07/2004.

2002-2005 Lecturer in Bioinformatics (~60 hours/year), BSc Human Biology, Universitat Pompeu Fabra, Barcelona.
 Feb 2000 Virus Bioinformatics. MRes Complexity. University College London (UK).

RESEARCH GRANTS

2023-2024 Adaptation Genomics Network (AdaptNet). Agencial Estatal de Investigación (AEI), Ministerio de Ciencia e Innovación, Spanish Government.
 P.I.: Carles Vila Arbonés. Amount: 18,300 Euros.

2023-2025 Identification of novel mechanisms of response to immunotherapy in advanced bladder cancer. Instituto de Salud Carlos III, Spanish Government.
 P.I.: Joaquim Bellmunt/Júlia Perera. Amount: 171,820 Euros.

2022-2025 Evolution of non-canonical peptides and their role as neoantigens in cancer (PID2021- 122726NB-I00). Agencial Estatal de Investigación (AEI), Ministerio de Ciencia e Innovación, Spanish Government.
 P.I.: M.Mar Albà. Amount: 217,800.00 Euros.

2022-2024 Unitat de Genòmica Computacional (GENCOMP). Grups Reconeguts de Recerca, SGR-Cat 2021. Generalitat de Catalunya.
 P.I.: M.Mar Albà. Amount: 60,000 Euros.

2022-2024 Development of novel transcriptome-informed methods to predict the response to immunotherapy in cancer. Fundación BBVA.
 P.I.: Mar Albà. Amount: 146,497 Euros.

2022-2027 Deciphering de novo gene birth in populations (NovoGenePop). ERC Advanced Grant, European Research Council.
 P.I.: Mar Albà. Amount: 2,453,751.00 euros.

2021-2024 Desarrollo de antitumorales basados en microproteínas (DATUM). Government of Navarra (Spain).
 P.I.: Puri Fortes/Pablo Sarobe. Amount: 342,776.37 Euros.

2022-2024 IMPaCT-Datos. Carlos III Institute of Health, Spanish Government. P.I.: Ferran Sanz. Amount: 120,000 euros.

2019-2022 The evolution of new coding and non-coding genes (PGC2018-094091-B-I00), Ministerio de Ciencia, Innovación y Universidades, Spanish Government.
 P.I.: M.Mar Albà. Amount: 190,575.00 euros.

2017-2019 Computational Genomics Unit (GENCOMP). Suport a les activitats del Grups de Recerca (SGR) Generalitat de Catalunya
 P.I.: Eduardo Eyrales/Robert Castelo

2017-2019 Grant PT17/0009/0014, Plataformas de Apoyo a la Investigación en Ciencias y Tecnologías de la Salud. Instituto de Salud Carlos III, Spanish Government.
 P.I.: Ferran Sanz

2016-2018 Mechanisms of formation of new genes (BFU2015-65235-P). Ministerio de Economía y Competitividad, Spanish Government.
 P.I.: M.Mar Albà

2008-2014 Integrating bioinformatics and cheminformatics approaches for the development of expert systems allowing the in silico prediction of toxicities (eTOX-ENSO). Innovative Medicines Initiative (IMI), EC.
 P.I.: Ferran Sanz

2013-2015 Evolution of novel gene functions in mammalian genomes (BFU2012-36820) Ministerio de Economía y Competitividad, Spanish Government.
 P.I.: M.Mar Albà

| | |
|-----------|--|
| 2008-2013 | Red Española de Esclerosis Múltiple (RETICS). Ministerio de Sanidad y Consumo, Spanish Government. P.I.: M.Mar Albà |
| 2009-2012 | Genome-wide analysis of the patterns of natural selection in mammalian genes (BIO2009-08160) Ministerio de Innovación y Ciencia, Spanish Government. P.I.: M.Mar Albà |
| 2006-2009 | Study of the relationship between gene mutation rate, gene age and gene function in metazoan genomes (BFU2006-07120). Ministerio de Educación y Ciencia, Spanish Government. P.I.: M.Mar Albà. |
| 2004-2007 | Bioinformática y Genómica (Instituto Nacional de Bioinformática). Fundación Genoma España. P.I.: Dr. Roderic Guigó. |
| 2004-2007 | Virtual Institute of Bioinformatics Education (Instituto Nacional de Bioinformática). Fundación Genoma España. P.I.: Ferran Sanz. |
| 2004-2007 | INFOBIOMED – Structuring European Biomedical Informatics to Support Individualised Healthcare (Network of Excellence). European Commission. P.I.: Ferran Sanz. |
| 2006 | Jornadas de Bioinformática 2006 (Acciones Complementarias). Ministerio de Educación y Ciencia, Spanish Government. P.I.: M.Mar Albà. |
| 2002-2005 | Predicción de función en genomas virales e interacción con el genoma del huésped mamífero. (BIO2002-04426-C02-01). Ministerio de Ciencia y Tecnología, Spanish Government. P.I.: M.Mar Albà. |
| 2003-2006 | Data mining of virus-host systems to understand regulatory interactions. Fundación Banco Bilbao Vizcaya Argentaria. P.I.: M.Mar Albà. |

SUPERVISION OF GRADUATE AND POSTGRADUATE STUDENTS

Director of PhD theses

| | |
|-------------|---|
| Ongoing | Marta Espinosa Camarena. Tentative title: Microproteins as cancer testis-antigens. Universitat Pompeu Fabra. |
| Ongoing | Lilian Boll (La Caixa InPHINIT PhD fellowship). Tentative title: Prediction of the response to immunotherapy in bladder cancer. Universitat Pompeu Fabra. |
| Ongoing | José Carlos Montañés (FPI fellowship). Tentative title: Genome-wide analysis of emerging microproteins. Universitat Pompeu Fabra. |
| 17 Jan 2020 | William Robert Blevins (FI fellowship), Evolutionary dynamics of transcriptional and translational I regulation in yeast. |
| 19 Jan 2017 | Jorge Ruiz Orera (FPI fellowship), Understanding the mechanisms of de novo gene evolution using transcriptomics data (Excel.lent cum laude, <u>Premio Extraordinario</u>), Universitat Pompeu Fabra. |
| 20 Nov 2015 | José Luis Villanueva Cañas (FPI fellowship), Insights into Mammalian Adaptive Evolution through Genomics Data (Excel.lent cum laude, <u>Premio Extraordinario</u>), Universitat Pompeu Fabra. |

- 25 Jul 2013 Steve Laurie (FI fellowship), Evolutionary Patterns of Nucleotide Insertions and Deletions in Mammalian Genes (Excel.lent cum laude), Universitat Pompeu Fabra
- 3 May 2013 Núria Radó Trilla (IMIM PhD fellowship), Low-complexity regions in proteins as a source of evolutionary innovation (Excel.lent cum laude), Universitat Pompeu Fabra
- 28 Mar 2012 Macarena Toll Riera (FPU fellowship), Mechanisms of Evolutionary Innovation in Mammalian Genes (Excel.lent cum laude), Universitat Pompeu Fabra
- 7 Nov 2011 Medya Shikhagaie, Characterization of UL1, a member of the human cytomegalovirus RL11 gene family (co-directed with Miguel López-Botet) (Excel.lent cum laude), Universitat Pompeu Fabra.
- 6 May 2011 Alice Ledda (Government of Sardinia PhD fellowship), Structure and Evolution of DNA Tandem Repeats in Eukaryotic Genomes (Excel.lent cum laude), Universitat Pompeu Fabra
- 26 Feb 2010 Nicolás Bellora, In silico analysis of regulatory motifs in gene promoters (Excel.lent cum laude), Universitat Pompeu Fabra.
- 28 Jul 2008 Loris Mularoni. Comparative Genomics of Amino Acid Tandem Repeats (Excel.lent cum laude), Universitat Pompeu Fabra.
- 15 Jul 2008 Domènec Farré Marimón. Bioinformatics Analysis of Gene Expression Regulatory Sequences in Eukaryotes (co-directed with Xavier Messeguer) (Excel.lent cum laude), Universitat de Barcelona.

Director of Master/Engineering projects

- Ongoing Sara Razquin, MSc in Bioinformatics, Universitat Autònoma de Barcelona.
- July 2022 Lillian Boll, MSc in Bioinformatics for the Health Sciences, Universitat Pompeu Fabra/Universitat de Barcelona.
- July 2022 Marta Espinosa Camarena, MSc in Bioinformatics for the Health Sciences, Universitat Pompeu Fabra/Universitat de Barcelona. Co-supervised with Júlia Perera.
- July 2022 Xavier Martí Pérez, MSc in Bioinformatics, Universitat Autònoma de Barcelona. Co-supervised with Gabriel Santpere.
- Sep 2018 Audald Lloret Villas, MSc Omics Data Analysis, Universitat de Vic.
- Jul 2017 Teresa Tavella, International Bologna Master in Bioinformatics, Università di Bologna.
- Jul 2016 Isabel Agea Lorente, MSc Bioinformatics, Universitat Autònoma de Barcelona.
- Jul 2015 Willam R. Blevins, MSc Bioinformatics for Health Sciences, Universitat Pompeu Fabra.
- Sep 2014 Antonio Agraz Doblas, MSc Omics Data Analysis, Universitat de Vic.
- Jun 2013 Jorge Ruiz Orera, MSc Bioinformatics for Health Sciences, Universitat Pompeu Fabra.
- Jun 2012 Magda Gayà Vidal, MSc Bioinformatics for Health Sciences, Universitat Pompeu Fabra.
- Jun 2012 José Luis Villanueva Cañas, Msc Bioinformatics for Health Sciences, Universitat Pompeu Fabra.
- Sep 2009 Nuria Radó Trilla, MSc Genetics and Developmental Biology, Universitat de Barcelona.
- Jun 2009 Steve Laurie, MSc Bioinformatics for the Health Sciences, Universitat Pompeu Fabra.
- Jun 2008 Macarena Toll Riera, MSc Human Biology, Universitat de Barcelona.
- Jun 2007 Angel Carreño, Informatics Engineering, Universitat Politècnica de Catalunya.

Sep 2004 Rachid Kara. Project Master Functional Genomics, Université Paris VII, France.
Jul 2004 David García. Informatics Engineering, Universitat Politècnica de Catalunya.
Apr 2001 Ruth Escudero. Informatics Engineering, Universitat Politècnica de Catalunya.
Jul 2001 Oscar Núñez. Informatics Engineering, Universitat Politècnica de Catalunya.
Jul 2001 Javier Martínez. Informatics Engineering, Universitat Politècnica de Catalunya.
Jun 2000 Rhiju Das. MRes Biocomplexity, University College London, UK
Jun 2000 Michael Michael. MRes Biocomplexity, University College London, UK

Student Internships

Mar-May 2024 Sophia Huspek, Internship, University of Applied Sciences Upper Austria (Austria)
Sep 2020 -Sep 2021 Marta Huertas, Practicum BSc Genetics, Universitat Autònoma de Barcelona.
Apr-Jun 2019 Cedric Hermans, Internship, Howest University of Applied Sciences (Belgium)
Jun-Sep 2018 Beatriz Calvo, Final Project BSc in Human Biology, Universitat Pompeu Fabra.
Jun-Sep 2016 Alejandro Valenzuela, Practicum BSc Genetics, Universitat Autònoma de Barcelona (UAB).
Jun-Sep 2012 Joana Carlevaro, Final Project BSc in Human Biology, Universitat Pompeu Fabra.
Apr-Dec 2007 Macarena Toll Riera, Final Project BSc in Human Biology, Universitat Pompeu Fabra.
Feb-Apr 2011 Florian Martys, Bioinformatics Internship, University of Vienna.

PhD external advisor

Jan 2024- Stefanie Kau, PhD University of Regensburg, Germany.

AWARDS

Feb 2023 Distinció Mujeres en Ciencia e Innovación FECYT (ERC Adv Grant 2021)
Mar 2011 Acreditació de Recerca Avançada (AGAUR, Generalitat de Catalunya)
Jul 2004 Acreditació de Recerca (AGAUR, Generalitat de Catalunya)
Jun 1999 Distinction MSc in Bioinformatics University of London (UK)
Jun 1998 Premio Extraordinario de Doctorado 1996/97. Faculty of Biology, Universitat de Barcelona, Spain.

EDITORIAL BOARDS

Editorial Board Bioinformatics Advances (Sep 2021-)
Associate Editor Genome Biology and Evolution (Jan 2014-2023)
Associate Editor Journal of Experimental Zoology-B (Dec 2012-2021)

MEMBER OF SOCIETES/CONSORTIA

| | |
|-------|--|
| 2020- | Member of the Ribo-Seq Consortium Ensembl/GENCODE. |
| 2018- | Institut Estudis Catalans (IEC) |
| 2008- | International Society of Molecular Evolution (SMBE) |
| 2006 | International Tandem Repeat Consortium (ITRC) |
| 1999- | International Society for Computational Biology (ISCB) |
| 1996- | Federation of European Biochemical Societies (FEBS) |

SCIENTIFIC COMMITTEES

| | |
|----------------|--|
| 2024 | Member Evaluation Panel Agence Nationale de la Recherche (ANR). Panel Genetics, Genomics and RNA. Jan-Jun 2024. |
| 2023 | Jury Prevosti Prize XXII Jornada de Biologia Evolutiva, IEC, Barcelona. Jul 5 2023. |
| 2023 | Organizing Committee "Proteomics 2023" (Elsinore, Denmark). Funded by Novo Nordisk Foundation. May 31 – Jun 2 2023. |
| 2021/2022 | Member Evaluation Panel IGNITE-BIST projects. May 10 2021 & Dec 20 2022, Barcelona. |
| 2020 | Member Evaluation Panel Swiss Science Prize Marcel Benoist 2020 (online). |
| 2020 | Member Evaluation Committee COV20 - Proyectos de investigación sobre el virus SARS-CoV-2 y la enfermedad CoVid-19, Convocatoria 2020, Instituto de Salud Carlos III. |
| 2020 | Chair of the Nomination Committee for new Council Members 2020-2023 Society for Molecular Biology and Evolution (SMBE)(online) |
| 2020 | Member of Jury Premi Ciutat de Barcelona 2019 Ciències de la Vida. Barcelona. |
| 2019 | Organizing Committee Advances in Computational Biology conference (AdCompBio, 28-29 Nov 2019), Barcelona. |
| 2019 | Member of the Fitch Prize Jury at the Annual Meeting Society for Molecular Biology and Evolution (SMBE), 23 July 2019. Manchester, UK. |
| 2019 | Scientific Committee X Meeting of the Argentinian Society of Bioinformatics and Computational Biology (A2B2C). |
| 2019 | Member of Jury Premi Ciutat de Barcelona 2018 Ciències de la Vida. Barcelona. |
| 2018 | Evaluation Committee SMBE Career Awards 2018. |
| 2016,2018 | Evaluation Committee Master in Bioinformatics for the Health Sciences (UPF/UB), Barcelona. |
| 2016 | Chair of the NGS Technologies: Genomics & Transcriptomics session, XIII Symposium on Bioinformatics (10-13 May), Valencia. |
| 2015 | Scientific Committee European Conference on Computational Biology (July 10-15, ECCB'15), Dublin, Ireland. |
| 2015,2018 | Evaluation Committee INTREPID CRG International Postdoctoral Programme, Barcelona. |
| 2015 | Comisión de Expertos (Proyectos BFU), Dirección General de Proyectos de Investigación MINECO (Madrid 9-11 Feb) |
| 2015,2016,2017 | Evaluation Committee Master in Bioinformatics and Computational Biology ISCIII-ENS, Madrid. |

| | |
|-----------|---|
| 2014 | Chair of the Phylogenetics and Evolution session, XII Symposium on Bioinformatics (Sevilla 21-24 Sep) |
| 2013 | Scientific Committee BIOINFORMATICS 2014 5th International Conference on Bioinformatics Models, Methods and Algorithms (Angers, France) |
| 2013 | Chair of the Genomics session in the biannual meeting of the Spanish Genetics Society (SEG'13, Girona 18-20 Sep) |
| 2013 | Committee for the Prize to the Best Talk, XIII Jornada de Biología Evolutiva (Jul 2), Societat Catalana de Biologia, Barcelona. |
| 2011-2014 | Access Committee Barcelona Supercomputing Centre (BSc)-Centro Nacional de Supercomputación (CNS) |
| 2008-2012 | Research Committee (Commissió de Recerca), Institut Municipal d'Investigació Mèdica (IMIM), Barcelona. |
| 2011 | Comisión de Expertos Proyectos BFU Ministerio de Ciencia y Tecnología (MICINN), Madrid. |
| 2008 | Area Chair VIII Spanish Bioinformatics Symposium (13-15 Feb), Valencia. |
| 2007 | CRG Group Leader Selection Committee (15-16 Jan). Centre for Regulatory Genomics, Barcelona Biomedical Research Park, Barcelona. |
| 2007 | Programme Committee 1st International Conference on Research and Development (BIRD, 12-14 March), Berlin. |
| 2006 | Co-organizer VII Spanish Bioinformatics Symposium (JdB'06, 20-22 Nov), Zaragoza. |
| 2005-2006 | Co-coordinator Spanish Bioinformatics Network. |
| 2005 | Program Committee CompBioNets 2005 (5-7 Dec), Lyon, France. |
| 2005 | Area Chair European Conference on Computational Biology (ECCB 2005, Sep 28- Oct1), Madrid. |
| 2004 | Co-organizer V Spanish Bioinformatics Symposium (JBI'04, 29 Nov-2 Dec), Barcelona. |
| 2002 | Area Chair III Spanish Bioinformatics Symposium (JBI'02, 18-20 Sep), Málaga. |

EXTERNAL REVIEWER GRANT AGENCIES

Instituto de Salud Carlos III, Proyectos de Investigación en Salud: 2021

Instituto de Salud Carlos III, Proyectos COV20: 2020

European Research Council (ERC) external reviewer: 2020

French National Research Agency (ANR): 2015, 2016, 2017, 2022

Research Foundation Flanders: 2016, 2019

EU Cost Actions: 2017

Portuguese Foundation for Science and Technology: 2010, 2011

AGAUR Generalitat de Catalunya: 2007, 2008, 2009

Agencia Nacional de Evaluación y Prospectiva (ANEP, Spain): 2006, 2007, 2008, 2009, 2010, 2014, 2017, 2021, 2022, 2024

Ministerio de Educación, Ciencia y Tecnología (FONCYT, Gobierno de Argentina): 2006

OUTREACH

- 2023 Interviewed by TV3 as part of a report on the 75th Anniversary of IMIM. June 15 2023. Aired in TV3 Telenotícies.
- 2023 Organization of activities for the Open Day PRBB. Oct 7 2023. Members of the research group involved: Chris Papadopoulos, Covadonga Vara, Marta Espinosa, Lillian Boll.
- 2023 Interviewed by Elizabeth Pennisi for a News piece in Science. Jan 5 2023.
- 2022 Interview at El.lipse PRBB. Community, Scientific Life 24.05.2022. <https://ellipse.prbb.org/mar-alba-new-director-of-the-grib-receives-an-erc-of-2-5-million-euros/>
- 2021 Interview at the Institute of Evolutionary Biology (IBE, CSIC-UPF) web page, https://www.ibe.upf-csic.es/home/-/asset_publisher/T2caeLMECPvW/content/id/248995638/maximized#.YUifJB1S_BV
- 2021 Publication of a Behind the Paper blogpost "Identification of recently evolved genes in yeast" in the Nature Ecology and Evolution Community Blog, explaining the research underlying the paper "Uncovering de novo gene birth in yeast using deep transcriptomics" (Blevins et al., 2021, Nature Com)(Jan 27 2021)
- 2019 Interviewed by Adam Levy in "How evolution builds genes from scratch", Nature News Feature 16 Oct 2019.
- 2018 Invited to participate in the Seminar Series "Descobert a Girona", organized by the Universitat de Girona. Talk: Com ens afecta la genòmica i com ha canviat la recerca científica?. Girona (Nov 13)
- 2018 Interviewed for the University of Pittsburgh School of Medicine Summer 2018 Magazine (July Issue)
- 2018 Publication of "New proteins on the test track" in the Nature Ecology and Evolution Community Blog, explaining the research underlying the paper "Translation of neutrally evolving peptides provides a basis for *de novo* gene evolution" (Ruiz-Orera et al., 2018, Nature Ecol. and Evol.)(Mar 19)
- 2017 Coverage in TV3 Telenotícies of our work "New genes and functional innovation in mammals" (Villanueva-Cañas et al., 2017, Genome Biol.Evol.)(Dec 15)
- 2017 Invited to participate in the Ada Lovelace Day at the PRBB, talk on my experience as a woman scientist (Oct 10)
- 2016 Article in El Periódico "¿Hibernación humana? El secreto esté en los genes de este lemur" by Michele Catanzaro, about our work "Gene expression profiling in the hibernating primate, Cheirogaleus Medius" (Villanueva-Cañas, 2016, Genome Biol. and Evol.) (Sep 12)
- 2016 Article in Quo magazine on our publication "Origin of de novo genes in human and chimpanzee" (Ruiz-Orera et al., 2015, Plos Genetics)(Jan 28)
- 2016 Interviewed in El Punt Avui Televisió (Jan 20)
- 2016 Article in Diario Médico on our publication "Origin of de novo genes in human and chimpanzee" (Ruiz-Orera et al., 2015, Plos Genetics) (Jan 13)
- 2014 Article in La Vanguardia on our publication "Uncovering adaptive evolution in the human lineage" (Gayà-Vidal and Albà, 2014, BMC Genomics) (Jul 22)
- 2013 Participation in the production of the video "Evolution of orphan genes"
IP Workshop Inform Animation, 13-30 June
EU Life Long Learning Programme, Programme Erasmus, University of Alghero

- 2013 Interviewed by journalist Helen Pilcher, followed by article “All alone” covering research on orphan genes (New Scientist, Jan 19 2013).
- 2013 Invited to participate in “La ciència en primera persona”, Dia de la Ciència a les Escoles (Nov 27), Institut Federica Montseny, Badia del Vallés.
- 2012 Interviewed by Diario Médico on “Sequence shortening in the rodent ancestor” (Laurie et al., 2012, Genome Res.)(Jan 24 2012)
- 2010 Coverage of the publication “Natural selection drives the accumulation of amino acid tandem repeats in proteins” (Mularoni et al., 2010, Genome Res.) by GenomeWeb “This week in Genome Research” (March 31 2010)
- 2010 Commentary on the publication “Natural selection drives the accumulation of amino acid tandem repeats in proteins” in bulletins-electronique.com (Ministère des Affaires Étrangères et Européennes, Govern de França) “Répétitions en tandem et sélection naturelle” (May 7 2010)
- 2010 Article by M.Mar Albà in El.lipse (Parc Recerca Biomèdica Barcelona) “Les pistes de la selecció natural” (July/August 2010)
- 2010 Interviewed by Diario Médico on “Natural selection drives the accumulation of amino acid tandem repeats in proteins” (June 4 2010)
- 2004 Extensive press coverage of the paper “Genome sequence of the brown norway rat yields insights into mammalian evolution” (Gibbs et al., Nature 428: 493-521, 2004) (April 1 2004). La Vanguardia “Hermana rata: el genoma del roedor revela nuevos datos sobre el funcionamiento del cuerpo humano”. El País “Descifrado el genoma de la rata, más próximo al humano que el del ratón”. El Periodico de Catalunya “Rates i humans comparteixen el 40% del genoma”
Avui “Un equip científic català participa en la seqüenciació del genoma de la rata”.
Diario Médico “El IMIM vuelve a aportar el trabajo bioinformático”.

INVITED/SELECTED TALKS

- Mar 2024 Albà, M.M. Microproteins contribute to evolutionary innovation and cancer. Boulder Peptide Foundation Seminars, USA (Webinar). March 12 2024. (Invited)
- Feb 2024 Albà, M.M. Harnessing omics data for personalized medicine. Feb 21 2024. 1st VHIO Computational Oncology Award, Casa de la Convalescència UAB, Barcelona. (Keynote).
- Nov 2023 Albà, M.M. Omics data for personalized medicine. Nov 8 2023. 75 Anniversary IMIM Scientific Retreat, PRBB, Barcelona. (Invited)
- Nov 2023 Papadopoulos, C., Montañés, J.C., Albà, M.M. De novo gene intra-species diversity in *Saccharomyces cerevisiae*. Nov 7 2023. SMBE Satellite Meeting on de novo gene birth. Texas A&M University - College Station, TX, USA. (Selected)
- Nov 2023 Vara, C., Montañés, J.C., Papadopoulos, C., Szegedi, A., Wange, L, Albà, M.M. Investigating de novo gene formation in human populations. Nov 6 2023. SMBE Satellite Meeting on de novo gene birth. Texas A&M University - College Station, TX, USA. (Selected)
- Oct 2023 Albà, M.M. De novo gene birth in yeast. Oct 20 2023. Université Strasbourg, France. (Invited)
- Sep 2023 Albà, M.M. Non-canonical ORFs translated from tumor-specific transcripts as a source of cancer neoantigens. Sep 8 2023. Institute Curie. Paris, France. (Invited)
- June 2023 Montañés, J.C., Huertas, M., Messeguer, X., Albà, M.M. Evolutionary trajectories of new duplicated and putative de novo genes. June 2 2023. Microproteins 2023. Helsingor, Denmark. (Selected)

May 2023 [Albà, M.M.](#) The hidden world of evolutionary novel genes. May 26 2023. Distinguished Speaker Seminar Series at the Max Planck Institute for Biology, Tübingen, Germany. (Invited)(online)

Mar 2023 [Albà, M.M.](#) Nature inventing new genes. Mar 29 2023. University College London Genetics Institute, London (UK). (Invited)

Feb 2023 [Albà, M.M.](#) Uncovering the small proteome. Feb 3 2023. Workshop of the Interuniversity PhD Program in Bioinformatics, Universitat de Vic, Spain. (Invited)

Sep 2022 [Albà, M.M.](#) The emerging small proteome. Sep 21 2022. European Conference on Computational Biology (ECCB 2022). Melià Hotel Conference Center, Sitges. (Keynote).

June 2022 [Albà, M.M.](#) Neoantigens as predictors of response to IO. June 17 2022. Optimizing Immunotherapy - New Approaches, Biomarkers, Sequences and Combinations. IMIM/Hospital del Mar, Barcelona Biomedical Research Park Auditorium (Invited).

Apr 2022 [Albà, M.M.](#) Evolution of new proteins from translated sORFs in lncRNAs. April 7 2022. Keystone Symposia Micropeptides: Biogenesis and Function. Snowbird, Utah, USA. (Invited).

Sep 2021 [Albà, M.M.](#) Evolutionary innovation by *de novo* gene birth. 16 Sep 2021. Evolutionary Biology Institute (IBE, UPF-CSIC, Barcelona). (Invited)(online)

July 2021 [Albà, M.M.](#) The birth of new proteins from scratch. 20 Jul 2021. 43rd Meeting Sociedad Española de Bioquímica y Biología Molecular (Invited)(online)

July 2021 [Albà, M.M.](#) Pervasive translation of lncRNAs and the birth of new proteins. 5 Jul 2021. Annual Meeting of the Society for Molecular Biology and Evolution (SMBE'21), Symposium "Evolution and regulation of gene expression at the translational level". (Invited)(online)

May 2021 [Albà, M.M.](#) Formation of new genes: *de novo* or duplicated?. 18 May 2021. ETH Zürich, Switzerland (Invited)(online)

April 2021 [Albà, M.M.](#) New Trends to personalize immunotherapy in cancer. 9 Apr 2021. Optimizing Immunotherapy - New Approaches, Biomarkers, Sequences and Combinations. IMIM/Hospital del Mar, Barcelona Biomedical Research Park Auditorium (Invited)

Mar 2021 [Albà, M.M.](#) Evolutionary innovation by *de novo* gene birth. 22 Mar 2021. LeedsOmics Institute, Leeds University, UK (Invited)(online)

Nov 2020 [de la Rubia, I.](#), [Indi, J.A.](#), [Carbonell-Sala, S.](#), [Lagarde, J.](#), [Albà, M.M.](#), [Eyras, E.](#) Reference-free reconstruction and quantification of transcriptomes from Nanopore long-read sequencing. ABACBS 2020 Conference, Australia (Selected)(online)

Sep 2020 [Albà, M.M.](#) *De novo* gene birth. Presentation to Nature journals editors. 29 Sep 2020. (Invited)(online)

June 2020 [Albà, M.M.](#) *De novo* gene evolution in yeast. 10 June 2020. Group Leader Seminars Series Barcelona Biomedical Research Park. (Contributed)(online)

Nov 2019 [Albà, M.M.](#) The hidden world of micropeptides. 5 Nov 2019. CRG Annual Proteomics Symposium, Barcelona. (Invited)

June 2019 [Albà, M.M.](#) 6 June 2019. Models of Evolution, a CONTRA Innovative Training Network Workshop, Barcelona. (Invited)

May 2019 [Albà, M.M.](#) Omics approaches to identify gene expression alterations in disease. 29 May 2019. IMIM Symposium, Barcelona. (Contributed)

Mar 2019 [Albà, M.M.](#) Building from scratch: *de novo* gene birth. 26 Mar 2019. Barcelona Supercomputing Center, Barcelona. (Invited)

- Nov 2018 Albà, M.M. Pervasive translation and *de novo* gene birth. 9 Congreso Argentino de Bioinformática y Biología Computacional. 19-22 Nov 2018. Mar del Plata, Argentina. (Keynote invited)
- Oct 2018 Albà, M.M. Functionalization of recently evolved transcripts. Genomic parasites and non-coding RNA in evolution and disease, Workshop Current Trends in Biomedicine, Universidad Internacional de Andalucía, 28-30 Oct 2018. Baeza, Spain. (Invited)
- Jul 2018 Villanueva-Cañas, J-L., Faherty, S., Albà, M.M., Yoder, A. Transcriptomics in the wild: hibernation physiology in free-ranging dwarf lemurs. Meeting of the Society for Molecular Biology and Evolution (SMBE), July 8-12 2018. Yokohama, Japan. (Selected)
- Jul 2018 Reixachs, M., Ruiz-Orera, J., Albà, M.M., Eyra, E. Measuring ribosome profiling at isoform level: towards unveiling the functional impact of alternative splicing. International Society for Computational Biology Meeting, July 6-10 2018. Chicago, United States. (Selected).
- Jun 2018 Albà, M.M. *De novo* gene evolution, fact or fiction? XVIII Jornada de Biología Evolutiva, June 25 2018. Barcelona, Spain. (Invited)
- May 2018 Bosch, E./Albà, M.M. How can we read the genome to understand past adaptations? Parc de Recerca Biomèdica de Barcelona (PRBB), May 23 2018. (Group Leader Seminars)
- Jul 2017 Ruiz-Orera, J., Villanueva-Cañas, J-L., Blevins, W.R., Albà, M.M. How do we transition from non-coding to coding? Meeting of the Society for Molecular Biology and Evolution (SMBE), Jul 21-25. Austin, United States. (Selected)
- Jun 2017 Villanueva-Cañas, J-L., Albà, M.M., Ruiz-Orera, J. New genes and functional innovation in mammals. 5th Quest for Orthologs Meeting, June 8-10 2017. Los Angeles, United States. (Selected)
- Oct 2016 Ruiz-Orera, J., Verdaguer-Grau, P., Villanueva-Cañas, J-L., Messeguer, X., Albà, M.M. Nucleotide variation patterns of translated ORFs in lncRNAs support widespread translation of non-functional proteins. XXI Seminario de Genética de Poblaciones y Evolución, Oct 3 2016. Sitges, Spain. (Selected)
- Aug 2016 Albà, M.M. Identification of novel peptides using ribosome profiling. Copenhagen University, Aug 25 2016. Copenhagen, Denmark. (Invited)
- Sep 2015 Albà, M.M. A quest for recently evolved genes in human and chimpanzee. German Genetics Society Meeting, Sep 29 2015. Kiel, Germany. (Plenary Invited)
- Jul 2015 Albà, M.M. The link between pervasive transcription and *de novo* gene evolution. Meeting of the Society for Molecular Biology and Evolution (SMBE), Jul 13 2015. Vienna, Austria. (Invited)
- Jul 2015 Albà, M.M. Long non-coding RNAs as a source of new peptides. Integrative RNA Biology, Meeting of the International Society for Computational Biology (IRB-ISMB), Jul 10 2015. Dublin, Ireland. (Invited)
- Jul 2015 Albà, M.M. LncRNAs as a source of new peptides. Parc de Recerca Biomèdica de Barcelona (PRBB), Jul 8 2015. Barcelona, Spain. (Group Leader seminars)
- May 2015 Albà, M.M. Evolution in action: how do new genes originate in genomes? Facultad Ciencias, Universidad Autónoma de México, May 7 2015. Mexico City, Mexico. (Invited)
- Apr 2015 Albà, M.M. Long non-coding RNAs as a source of new peptides. Ghent University, Apr 9 2015. Ghent, Belgium. (Invited)
- Jan 2015 Albà, M.M. Deep transcriptomics reveals continuous emergence of new genes. Instituto de Biomedicina de Valencia (IBV-CSIC), Jan 28 2015. Valencia, Spain. (Invited)

- Jun 2014 Ruiz-Orera, J., Villanueva-Cañas, J-L., Albà, M.M. Using transcriptomics to improve the classification of genes into evolutionary age classes. Meeting of the Society for Molecular Biology and Evolution (SMBE), June 8-12. Puerto Rico, United States. (Selected)
- Apr 2014 Albà, M.M. How are new genes born? Insights from deep sequencing of mammalian transcriptomes. Barcelona Supercomputing Center (BSC), Apr 25 2014. Barcelona, Spain. (Invited)
- Dec 2013 Albà, M.M. How are new genes born? 9th Workshop Genomics and Proteomics, Societat Catalana de Biologia, Dec 17 2013. Institut d'Estudis Catalans, Barcelona. (Selected)
- Nov 2013 Santpere, G., Darre, F., Alcami, A., Villoslada, P., Albà, M.M., Navarro, A. Genome-wide analysis of wild-type Epstein-Barr virus genomes derived from healthy individuals of the 1000 Genomes Project. 4th Meeting of the Spanish Society of Evolutionary Biology (SESBE), Nov 27-29 2013. CosmoCaixa, Barcelona. (Selected)
- Nov 2013 Ruiz-Orera, J., Albà, M.M. De novo gene emergence in eukaryotic genomes. GDRE Comparative Genomics Meeting, Nov 25-26 2013. PRBB, Barcelona. (Selected)
- Nov 2013 Ruiz-Orera, J., Albà, M.M. Identification of recently evolved genes in human and chimpanzee using next generation sequencing technologies. I Jornada de Bioinformàtica i Biologia Computacional, Nov 22 2013, Barcelona. (Selected)
- Oct 2013 Villanueva-Cañas, J.J. Albà, M.M. Functional characterization of Iberian lynx genes. Iberian lynx consortium third meeting, Oct 24-25. 2013. Sevilla. (Consortium Meeting)
- Sep 2013 Albà, M.M. Recently emerged genes and functional innovation. Sep 23. Basel, Biozentrum. (Invited)
- July 2013 Villanueva-Cañas, J.L., Albà, M.M. Incorporating protein isoform information into genome-wide studies. July 2. XIII Jornada de Biologia Evolutiva, Societat Catalana de Biologia, Barcelona. (Selected)
- April 2013 Albà, M.M. Evolution of novel protein coding sequences from scratch. April 16. University of Zurich. (Invited)
- Mar 2013 Albà, M.M. Birth of novel protein coding sequences and their role in lineage-specific evolutionary innovations. March 21. Max Planck Institute Ploen. Ploen, Germany. (Invited)
- July 2012 Albà, M.M. The formation of novel protein-coding genes from scratch in eukaryotic genomes. Workshop on Protein Evolution. Westfalian Wilhelms-University Muenster (WWU) and Ludwig-Maximilians-University Munich (LMU). Munich, Germany. (Invited)
- May 2012 Albà, M.M. Orphan genes and novel functions. University of Lausanne. (Invited)
- July 2012 Pegueroles, C., Laurie, S., Albà, M.M. Evolution of recent rodent gene duplicates. Global Questions on Advanced Biology. Societat Catalana de Biologia. Barcelona, Spain. (Selected)
- June 2012 Toll-Riera, M., Bostick, D., Albà, M.M., Plotkin, J.B. Age and structural characteristics as determinants of protien evolutionary rate. Meeting of the Society for Molecular Biology and Evolution (SMBE). Dublin, Ireland. (Selected)
- Mar 2012 Toll-Riera, M., Bostick, D., Albà, M.M., Plotkin, J.B. Age and structural properties as determinants of protien evolutionary rate. French-Spanish meeting on bioinformatics and evolutionary genomics, Banyuls-sur-mer, France. (Selected)
- Mar 2012 Gayà-Vidal, M., Albà, M.M. Adaptive gene evolution in the human lineage. French-Spanish meeting on bioinformatics and evolutionary genomics, Banyuls-sur-mer, France. (Selected)
- Jan 2012 Radó-Trilla, N., Albà, M.M. Low-complexity regions as a mechanism of protein

- diversification, Jornadas de Bioinformática 2012, Barcelona. (Selected)
- Nov 2011 Radó-Trilla, N., Albà, M.M. Evolution of low-complexity regions in chordate proteins. SESBE meeting 2011, Madrid. (Selected)
- Sep 2011 Albà, M.M. The effect of sequence age on protein evolutionary rate
15th Evolutionary Biology Meeting, Marseilles, France. (Selected)
- Jul 2010 Albà, M.M. Non-clock evolution of mammalian proteins
Meeting of the Society for Molecular Biology and Evolution 2010, Lyon, France. (Selected)
- Jan 2009 Toll-Riera, M. Castelo, R., Bellora, N. and Albà, M.M. Evolution of primate orphan genes.
Protein Evolution - sequences, structures and systems, Hinxton, Cambridge, UK. (Selected)
- June 2008 Albà, M.M. Relationship between gene age and evolutionary rate
Temporal Aspects of Genetic Analysis (PROUST), Tartu, Estonia. (Invited)
- March 2008 Albà, M.M. Learning about gene expression regulation using comparative genomics.
Barcelona Supercomputer Centre Seminar Series, Spain. (Invited)
- Feb 2008 Bellora, N., Farré, D., Albà, M.M. Identification of regulatory motifs on mammalian promoters
by positional bias. VIII Spanish Bioinformatics Symposium, Valencia, Spain. (Selected)
- Sep 2007 Castresana, J., Toll-Riera, M. Albà, M.M. Genes of recent origin show accelerated evolution.
11th Evolutionary Biology Meeting, Marseilles, France. (Selected)
- April 2007 Albà, M.M. Gene evolutionary rate variation in metazoans
EMBO World Practical Course on Comparative Genomics, Rio de Janeiro, Brasil. (Invited)
- Sep 2006 Albà, M.M. Coding microsatellites and the evolution of protein function.
Microsat 2006. Budapest, Hungary. (Invited)
- May 2005 Albà, M.M. Variability and Conservation in Vertebrate Promoters.
European Science Foundation Workshop on Transcription Networks,
Madrid, Spain. (Invited)
- Jun 2003 Albà, M.M. Simple sequences in proteins: evolution and functional associations. Relating
molecular evolution and protein function, Valencia, Spain. (Invited)
- Nov 2002 Albà, M.M. Virus bioinformatics. EC High Level Scientific Conference on Computational
Biology 2002. Dagstuhl, Germany. (Invited)
- Sep 2002 Albà, M.M. Virus Bioinformatics. EMBnet AGM2002. Oeiras, Portugal. (Invited)
- Aug 2002 Albà, M.M., Holzerlandt, R., Orengo, A., Kellam, P. The Virus Database VIDA. The World of
Microbes 2002. Paris, France. (Selected)
- Jun 2001 Farré, D., Messeguer, X., Albà, M.M. PROMO: a bioinformatics tool to predict transcription
factor binding sites. II Spanish Bioinformatics Symposium. Málaga, Spain. (Selected)
- Feb 2001 Albà, M.M., Holzerlandt, R., Orengo, A., Kellam, P. The Virus Database VIDA (Talk). 5th
Bioinformatics BBSRC Grantholders' Workshop. Hinxton, UK. (Grant Holders Meeting)
- Jun 2000 Albà, M.M. Low complexity sequences in proteins. I Spanish Bioinformatics Symposium.
Cartagena, Spain. (Selected)
- Feb 2000 Albà, M.M., Holzerlandt, R., Orengo, A., Kellam, P. The Virus Database VIDA (Talk). 4th
Bioinformatics BBSRC Grantholders' Workshop. Hinxton, UK. (Grant Holders Meeting)

PUBLICATIONS

Peer-reviewed articles:

Gröger, A., Martínez-Albo, I., [Albà, M.M.](#), Ayté, J., Vega, M., Hidalgo, E. (2023) Comparing Mitochondrial Activity, Oxidative Stress Tolerance, and Longevity of Thirteen Ascomycota Yeast Species. **Antioxidants** 12 (10), 1810.

Boll, L.#, Perera-Bel, J.#, Rodríguez-Vida, A., Arpí, O., Rovira, A., Juanpere, N., Vázquez, S., Hernández-Llodrà, S., Lloreta, J., [Albà, M.M.](#)*, Bellmunt, J.*. (2023) The impact of mutational clonality in predicting the response to immune checkpoint inhibitors in advanced urothelial cancer. **Scientific Reports** 13:15287. #co-first, *co-corresponding

Montañés, J.C., Huertas, M., Messeguer, X. & [Albà, M.M.](#) (2023). Evolutionary trajectories of new duplicated and putative de novo genes. **Molecular Biology and Evolution**, 40(5):msad098.

Boix, O., Martinez, M., Vidal, S., Giménez-Alejandre, M., Palenzuela, L., Lorenzo-Sanz, L., Quevedo, L., Moscoso, O., Ruiz-Orera, J., Ximénez-Embún, P., Ciriaco, N., Nuciforo, P., Stephan-Otto Attolini, C., [Albà, M.M.](#), Muñoz, J., Tian, T.V., Varela, I., Vivancos, A., Ramón Y Cajal, S., Muñoz, P., Rivas, C., Abad, M. (2022) pTINCR microprotein promotes epithelial differentiation and suppresses tumor growth through CDC42 SUMOylation and activation. **Nature Communications** 13(1):6840.

Mudge, J.M., Ruiz-Orera, J., Prensner, J.R., Brunet, M.A., Calvet Riera, F., Jungreis, I., Gonzalez, J.M., Magrane, M., Martinez, T.F., Schulz, J.F., Yang, Y.T., [Albà, M.M.](#), Aspden, J.L., Baranov, P.V., Bazzini, A., Bruford, E., Martin, M.J., Calviello, L., Carvunis, A-R., Chen, J., Couso, J.P., Deutsch, E.W., Flicek, P., Frankish, A., Gerstein, M., Hubner, N., Ingolia, N.T., Kellis, M., Menschaert, G., Moritz, R.L., Ohler, U, Roucou, X., Saghatelian, A., Weissman, J., van Heesch, S.(2022). Standarized annotation of translated open reading frames. **Nature Biotechnology**, 40(7):994-999.

de la Rubia, I., Srivastava1, A., Xue, W., Indi, J.A., Carbonell-Sala, S., Lagarde, J., [Albà, M.M.](#)*, Eyraes, E.*(2022). RATTLE: reference-free reconstruction and quantification of transcriptomes from Nanopore sequencing. **Genome Biology**, 23:153. *co-corresponding

Montañés, J.C., Huertas, M., Moro, S.G., Blevins, W.R., Carmona, M., Ayté, J., Hidalgo, E., [Albà, M.M.](#) (2022) Native RNA sequencing in fission yeast reveals frequent alternative splicing isoforms. **Genome Research**, 32: 1215-1227.

de Jong, J.J., Valderrama, B.P., Perera-Bel, J., Juanpere, N., Cejas, P., Long, H., [Albà, M.M.](#), Gibb, E.A., Bellmunt, J. (2022). Non-muscle-invasive micropapillary bladder cancer has a distinct lncRNA profile associated with unfavorable prognosis. **British Journal of Cancer**, 127(2):313-320.

Pérez-Núñez, I., Rozalén, C., Palomeque, J.A., Sangrador, I, Dalmau, M., Comerma, L, Hernández-Prat, A., Casadevall, D., Menéndez, S., Liu, D.D., Shen, M., Berenguer, J., Rius Ruiz, I., Peña, R., Montañés, J.C., [Albà, M.M.](#), Bonnin, S., Ponomarenko, J., Gomis, R.R., Cejalvo, J.M., Servitja, S., Marzese, D.M., Morey, Ll., Woorwerk, L., Arribas, J., Bermejo, B., Kok, M., Puzstai, L., Kang, Y., Albanell, J., Celià-Terrassa, T. (2022). LCOR mediates interferon-independent tumor immunity and responsiveness to immune-checkpoint blockade in triple-negative breast cancer. **Nature Cancer** 3:355-370.

Senís, E., Esgleas, M., Najas, S., Jiménez, V., Bertani, C., Giménez-Alejandre, M., Ruiz-Orera, J., Hergueta, M., Jiménez, M., Giralt, A., Nuciforo, P., [Albà, M.M.](#), Del Toro, D., Peinado, H., Hove-Madsen, J., Götz, M. Abad, M. (2021). TUNAR lncRNA encodes a microprotein that regulates neural differentiation and neurite formation by modulating calcium dynamics. **Frontiers in Cell and Developmental Biology** 9:747667.

Hernández-Fernández, J., Pinzón Velasco A.M., López Barrera, E.A., Rodríguez Becerra, M., Villanueva-Cañas, J.L., [Albà, M.M.](#), Mariño Ramírez, L. (2021). De novo assembly and functional annotation of blood transcriptome of loggerhead turtle, and in silico characterization of peroxiredoxins and thioredoxins. **PeerJ** 9: e12395.

Moro, S.G., Hermans, C., Ruiz-Orera, J., [Albà, M.M.](#) (2021) Impact of uORFs in mediating regulation of translation in stress conditions. **BMC Molecular Cell Biology** 22: 29.

Blevins, W.R., Ruiz-Orera, J., Messeguer, X., Blasco-Moreno, B., Villanueva-Cañas, J.L., Espinar, L., Díez, J., Carey, L.B., [Albà, M.M.](#) (2021). Uncovering de novo gene birth in yeast using deep transcriptomics. **Nature Communications**, vol. 12: 604.

Hong, S.Y., Sun, B., Straub, D., Blaakmeer, A., Mineri, L., Koch, J., Brinch-Pedersen, H., Holme, I.B., Burow, M., Lyngs Jørgensen, H.J., [Albà, M.M.](#), Wenkel, S. (2020) Heterologous microProtein expression identifies LITTLE

NINJA, a dominant regulator of jasmonic acid signaling. **Proceedings of the National Academy of Sciences USA**, vol. 117: 26197 - 26205.

Ruiz-Orera, J., Villanueva-Cañas, J.L., Albà, M.M. (2020) Evolution of new proteins from translated sORFs in long non-coding RNAs. **Experimental Cell Research**, vol. 391: 111940.

Reixachs-Solé, M., Ruiz-Orera, J., Albà, M.M., Eyra, E. (2020) Ribosome profiling at isoform level reveals evolutionary conserved impacts of differential splicing on the proteome. **Nature Communications**, vol. 11: 1768.

Blevins, W.R., Tavella, T., Moro, S.G., Blasco-Moreno, B., Closa-Mosquera, A., Diez, J., Carey, L.B., Albà, M.M. (2019) Extensive post-transcriptional buffering of gene expression in the response to severe oxidative stress in baker's yeast. **Scientific Reports**, vol. 9: 11005.

Ruiz-Orera, J., Albà M.M. (2019) Conserved regions in long non-coding RNAs contain abundant translation and protein-RNA interaction signatures. **Nucleic Acids Research Genomics and Bioinformatics**, vol. 1: e2.

Blevins, W.R., Carey, L.B., Albà, M.M. (2019) 'Transcriptomics data of 11 species of yeast identically grown in rich media and oxidative stress conditions'. **BMC Research Notes**, vol. 12: 250.

Ruiz-Orera, J., Albà, M.M. (2019) Translation of small ORFs: roles in regulation and evolutionary innovation. **Trends in Genetics**, vol. 35: 186-198.

Ruiz-Orera, J., Grau-Verdaguer, P., Villanueva-Cañas, J-L., Messeguer, X., Albà, M.M. (2018) Translation of neutrally evolving peptides provides a basis for *de novo* gene evolution. **Nature Ecology and Evolution**, vol. 2: 890 - 896.

Faherty, S.L.*, Villanueva-Cañas, J-L., Blanco, M.B., Albà, M.M.*, Yoder, A.D. (2018) Transcriptomics in the wild: Hibernation physiology in free-ranging dwarf lemurs. **Molecular Ecology**, vol 27: 709-722.*co-corresponding.

Domazet-Lošo, T., Carvunis, A.R., Albà, M.M., Šestak, M.S., Bakarić, R., Neme, R., Tautz, D. (2017) No evidence for phylostratigraphic bias impacting inferences on patterns of gene emergence and evolution. **Molecular Biology and Evolution**, vol. 34: 843–856.

Villanueva-Cañas, J-L., Ruiz-Orera, J., Agea, M.I., Gallo, M., Andreu, D., Albà, M.M. (2017) New genes and functional innovation in mammals. **Genome Biology and Evolution**, vol 9: 1888-1900.

Faherty, S.L., Villanueva-Cañas, J-L., Klopfer, P.H., Albà, M.M., Yoder, A.D. (2016) Gene expression profiling in the hibernating primate, *Cheirogaleus medius*. **Genome Biology and Evolution**, vol 8: 2413-2426.

Abascal, F., Corvelo, A., Cruz, F., Villanueva-Cañas, J-L., Vlasova, A., (40 more), Mailund, T., Albà, M.M., Gabaldón, T., Alioto, T., Godoy, J.A. (2016) Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian Lynx. **Genome Biology**, vol 17: 251.

Subirana, J.A., Albà, M.M., Messeguer, X. (2015) High evolutionary turnover of satellite families in *Caenorhabditis*. **BMC Evolutionary Biology**, vol 15: 218.

Ruiz-Orera, J., Hernández-Rodríguez, J., Chiva, C., Sabidó, E., Kondova, I., Bontrop, R., Marqués-Bonet, T., Albà, M.M. (2015). Origins of *de novo* genes in human and chimpanzee. **Plos Genetics**, vol 11: e1005721.

Baldo, L., Riera, J.L., Tooming-Klunderud, A., Albà, M.M., Salzburger, W. (2015) Gut microbiota dynamics during dietary shift in Eastern african cichlid fishes. **Plos ONE**, vol 10: e0127462.

Radó-Trilla, N., Arató, K., Pegueroles, C., Raya, A., de la Luna, S.*, Albà, M.M.* (2015) Key role of amino acid repeat expansions in the functional diversification of duplicated transcription factors. **Molecular Biology and Evolution**, vol 32: 2263-2272.*co-corresponding.

Santpere, G., Darre, F., Blanco, S., Alcamí, A., Villoslada, P., Albà, M.M., Navarro, A. (2014) Genome-wide analysis of wild-type Epstein-Barr virus genomes derived from healthy individuals of the 1,000 Genomes Project. **Genome Biology and Evolution**, vol 6: 846-860.

Gayà-Vidal, M., Albà, M.M. (2014) Uncovering adaptive evolution in the human lineage. **BMC Genomics**, vol 15: 599.

- Ruiz-Orera, J., Messeguer, X., Subirana, J.A., [Albà, M.M.](#) (2014) Long non-coding RNAs as a source of new peptides. **eLife**, vol 3: e03523.
- Villanueva-Cañas, J-L., Faherty, S.L., Yoder, A.D., [Alba, M.M.](#) (2014) Comparative Genomics of Mammalian Hibernators Using Gene Networks. **Integrative and Comparative Biology**, vol 54: 452-462.
- Pegueroles, C., Laurie, S., [Albà, M.M.](#) (2013) Accelerated evolution after gene duplication: a time-dependent process affecting just one copy. **Molecular Biology and Evolution** vol. 30: 1830-1842.
- Bornberg-Bauer, E., [Albà, M.M.](#) (2013) Dynamics and adaptive benefits of modular protein evolution. **Current Opinion in Structural Biology** vol. 23: 459-466.
- Toll-Riera, M., [Albà, M.M.](#) (2013) Emergence of novel domains in proteins. **BMC Evolutionary Biology** vol. 13: 47. [*highly accessed*].
- Villanueva-Cañas, J-L., Laurie, S., [Albà, M.M.](#) (2013) Improving genome-wide scans of positive selection by using protein isoforms of similar length. **Genome Biology and Evolution** vol. 5: 457-467.
- Trilling, M., Bellora, N., Rutkowski, A., de Graaf, M., Dickinson, P., Robertson, K., Prazeres da Costa, M., Ghazal, P., Friedel, C.C., [Albà, M.M.](#), Doelken, L. (2013). Deciphering the modulation of gene expression by type I and II interferons combining 4sU-tagging, translational arrest and in silico promoter analysis. **Nucleic Acids Research** vol. 41: 8107-8125.
- Mulero, et al. (including Bellora, N., [Albà, M.M.](#)) (2013) Chromatin-bound Ikb α is a modulator of PRC2-dependent repression in development and cancer. **Cancer Cell** vol. 24: 151-166.
- Laurie, S., Toll-Riera, M., Radó-Trilla, N., [Albà, M.M.](#) (2012) Sequence shortening in the rodent ancestor. **Genome Research**, vol. 22: 478-485.
- Radó-Trilla, N., [Albà, M.M.](#) (2012) Dissecting the role of low-complexity regions in the evolution of vertebrate proteins. **BMC Evolutionary Biology**, vol. 12: 155.
- Shikhagaie, M., Mercé-Maldonado, E., Isern, E., Muntasell, A., [Albà, M.M.](#), López-Botet, M., Hengel, H., Angulo, A. (2012) The HCMV-specific UL1 gene encodes a late phase glycoprotein incorporated in the virion envelope. **Journal of Virology**, vol. 86: 4091-101.
- Toll-Riera, M., Bostick, D., [Albà*](#), M.M., Plotkin*, J.B. (2012) Structure and age jointly influence rates of protein evolution. **PLoS Computational Biology**, vol. 8: e1002542. *co-corresponding
- Toll-Riera, M., Radó-Trilla, N., Martys, F., [Albà, M.M.](#) (2012) Role of Low-Complexity Sequences in the Formation of Novel Protein Coding Sequences. **Molecular Biology and Evolution**, vol. 29, 883-886.
- Engel, P., Perez-Carmona, N., [Albà, M.M.](#), Robertson, K., Ghazal, P., Angulo, A. (2011) Human cytomegalovirus-encoded UL7 molecule, a cellular homologue of the SLAM family receptor CD229, attenuates cytokine production. **Immunology and Cell Biology**, vol. 89: 753-66.
- Toll-Riera, M., Laurie, S., [Albà, M.M.](#) (2011) Lineage-specific Variation in Intensity of Natural Selection in Mammals. **Molecular Biology and Evolution**, vol. 28: 383-398.
- Mularoni, L., Ledda, A., Toll-Riera, M., [Albà, M.M.](#) (2010) Natural selection drives the accumulation of amino acid tandem repeats in human proteins. **Genome Research**, vol. 20: 745-754.
- Farré, D., [Albà, M.M.](#) (2010) Heterogeneous patterns of gene expression diversification in mammalian gene duplicates. **Molecular Biology and Evolution**, vol. 27:325-335. [*Evaluated by the Faculty of 1000*].
- Toll-Riera, M., Castelo, R., Bellora, N., [Albà, M.M.](#) (2009) Evolution of primate orphan genes. **Biochemical Society Transactions**, vol 37: 778-782.
- Rodilla, V., Villanueva, A., Obrador, A., Robert-Moreno, A., Fernandez-Majada, V., Bellora, N., [Albà, M.M.](#), Duñach, M., Capella, G., Bigas, A., Espinosa, L.I. (2009) Notch is downstream of Wnt signaling in colorectal cancer cells and

cooperates with beta-catenin to activate a specific gene program. **Proceedings of the National Academy of Sciences**, vol 106: 6315-6320.

Salichs, E., Ledda, A., Mularoni, L., Albà, M.M., De la Luna, S. (2009) Genome-wide analysis of histidine repeats reveals their role in the localization of human proteins to the nuclear speckles compartment. **Plos Genetics**, vol 5: e1000397.

Toll-Riera, M., Bosch, N., Bellora, N., Castelo, R., Armengol, Ll., Estivill, X., Albà, M.M. (2009) Origin of primate orphan genes: a comparative genomics approach. **Molecular Biology and Evolution**, vol 26: 603-612.

Bellora, N. Farré, D., Albà, M.M. (2007) Positional bias of general and tissue-specific regulatory motifs in mouse promoters. **BMC Genomics** vol 8: 459.

Farré, D., Bellora, N., Mularoni, L., Messeguer, X., Albà, M.M. (2007) Housekeeping genes tend to show reduced upstream sequence conservation. **Genome Biology**, vol. 8: R140.

Albà, M.M., Castresana, J. (2007) On homology searches by protein Blast and the characterization of the age of genes. **BMC Evolutionary Biology**, vol 7: 53.

Mularoni, L., Veitia, R.A., Albà, M.M. (2007) Highly constrained proteins contain an unexpectedly large number of amino acid tandem repeats. **Genomics**, vol 89: 316-325.

Bellora, N., Farré, D., Albà, M.M. (2007) PEAKS: Identification of regulatory motifs by their position in DNA sequences. **Bioinformatics**, vol 23: 243-244.

Furney, S.J., Albà, M.M., López-Bigas, N. (2006). Differences in the evolutionary history of disease genes affected by dominant or recessive mutations. **BMC Genomics**, vol. 7: 165.

Mularoni, L., Guigó, R., Albà, M.M. (2006). Mutation patterns of amino acid tandem repeats in the human proteome. **Genome Biology**, vol. 7: R33.

Blanco, E., Farré, D., Albà, M.M., Messeguer, X., Guigó, R. (2006). ABS: a database of annotated regulatory binding sites from orthologous promoters. **Nucleic Acids Research**, vol. 34: D63-67.

Albà, M.M., Castresana, J. (2005). Inverse Relationship between Evolutionary Rate and Age of Mammalian Genes. **Molecular Biology and Evolution**, vol. 22: 598 - 606.

Castresana, J., Guigó, R., Albà, M.M. (2004) Clustering of genes coding for DNA binding proteins in a region of atypical evolution of the human genome. **Journal of Molecular Evolution**, vol. 59: 72-79.

Gibbs et al. (including Albà, M.M.) (2004). Genome Sequence of the Brown Norway Rat yields Insights into Mammalian Evolution. **Nature**, vol. 428: 493 – 521.

Huang, H., Winter, E.E., Wang, H., Weinstock, K.G., Xing, H., Goodstadt, L., Stenson, P.D., Cooper, D.N., Smith, D., Albà, M.M., Ponting, C.P., Fechtel, K. (2004). Conservation of human disease genes in the rat genome. **Genome Biology**, vol. 5: R47.

Gendra, E., Moreno, A., Albà, M.M., Pagès, M. (2004). Interaction of the plant glycine-rich RNA binding protein MA16 with a novel nucleolar DEAD box RNA helicase protein from *Zea mays*. **The Plant Journal**, vol. 38: 875 – 886.

Albà, M.M., Guigó, R. (2004). Comparative analysis of amino acid repeats in rodents and humans. **Genome Research**, vol. 14: 549-554.

Farré, D., Roset, R., Huerta, M., Adsuara, J.E., Roselló, L., Albà, M.M., Messeguer, X. (2003). Identification of patterns in biological sequences at the ALGGEN server: PROMO and MALGEN. **Nucleic Acids Research**, vol. 31: 3651-3653.

Holzerlandt, R., Orengo, C.A., Kellam, P., Albà, M.M. (2002). Identification of novel herpesvirus homologues in the human genome. **Genome Research**, vol. 12:1739-1748.

Kellam, P., Albà, M.M. (2002). Virus Bioinformatics: Databases and recent applications. **Applied Bioinformatics**, vol. 1: 37-42.

Albà, M.M., Laskowski, R.A., Hancock, J.M. (2002). Detecting Cryptically Simple Protein Sequences using the SIMPLE Algorithm. **Bioinformatics**, Vol. 18: 672-688.

Messeguer, X., Escudero, R., Farré, D., Núñez, O., Martínez, J. and Albà, M.M. (2002). PROMO: detection of known transcription regulatory elements using species-tailored searches. **Bioinformatics**, vol. 18 333-334.

Albà, M.M., Das, R., Orengo, C., Kellam, P. (2001) Genome wide function conservation and phylogeny in the Herpesviridae. **Genome Research**, Vol. 11: 43-54.

Albà, M.M., Lee, D., Pearl, F.M.G., Shepherd, A.J., Martin, N., Orengo, C.A., Kellam, P. (2001) VIDA: A virus database system for the organization of virus genome open reading frames. **Nucleic Acids Research**, vol. 29: 133-136.

Jenner, R., Albà, M.M., Boshoff, C., Kellam, P. (2001) Kaposi's sarcoma-associated herpesvirus latent and lytic gene expression as revealed by DNA arrays. **Journal of Virology**, vol. 75: 891-902.

Lumbreras, V., Albà, M.M., Kleinow, T., Koncz, C., Pagès, M. (2001) Domain fusion between SNF1-related kinase subunits during plant evolution. **EMBO Reports**, vol. 2: 55-60.

Albà, M.M., Santibáñez-Koref, M.F., Hancock, J.M. (2001) The comparative genomics of polyglutamine repeats: extreme difference in the codon organization of repeat-encoding regions between mammals and Drosophila. **Journal of Molecular Evolution**, vol. 52: 249-259.

Albà, M.M. (2001) Replicative DNA polymerases. **Genome Biology**, Vol. 2(1): reviews 30021-30024.

Albà, M.M., Santibáñez-Koref, M.F., Hancock, J.M. (1999). Conservation of polyglutamine tract size between mouse and human depends on codon interruption. **Molecular Biology and Evolution**, vol 16: 1641-1644.

Albà, M.M., Santibáñez-Koref, M.F., Hancock, J.M. (1999). Amino acid reiterations in yeast are over-represented in particular classes of proteins and show evidence of a slippage-like mutational process. **Journal of Molecular Evolution**, vol 49: 789-797.

Albà, M.M., Pagès, M. (1998). Plant proteins containing the RNA recognition motif. **Trends in Plant Science**, vol 3:15-21.

Albà, M.M., Vinti, G., Messeguer, R., Pagès, M. (1998). Identification of RNAs associated *in vivo* with the maize MA16 RNA-binding protein by a PCR-based method. **Plant Physiology and Biochemistry**, vol 36: 913-918.

Niogret, M.F., Culiáñez-Macià, F.A., Goday, A., Albà, M.M., Pagès, M. (1996). Expression and cellular localization of rab28 mRNA and rab28 protein during maize embryogenesis. **The Plant Journal**, vol.9, 549-557.

Jensen, A.B., Busk, P.K., Figueras, M., Albà, M.M., Peracchia, G., Messeguer, R., Goday, A., Pagès, M. (1996). Drought signal transduction in plants. **Plant Growth Regulation**, vol 20, 105-110.

Albà, M.M., Culiáñez-Macià-F.A., Goday, A., Freire, M.A., Nadal, B., Pagès, M. (1994). The maize RNA-binding protein, MA16, is a nucleolar protein located in the dense fibrillar component. **The Plant Journal**, Vol.6, 825-834.

Goday, A., Jensen, A.B., Culiáñez-Macià, F.A., Albà, M.M., Figueras, M., Serratos, J., Torrent, M., Pagès, M. (1994). The maize abscisic acid-responsive protein Rab17 is located in the nucleus and interacts with nuclear localization signals. **The Plant Cell**, Vol.6, 351-360.

Commentaries/Reports:

Papadopoulos, C. & Albà, M.M. (2023). Newly evolved genes in the human lineage are functional. **Trends in Genetics**, Vol. 39: 235-236.

Albà, M.M. (2017). Zinc-finger domains in metazoans: evolution gone wild. **Genome Biology**, vol 18: 168.

Albà, M.M. (2000). Finding restriction sites – WebCutter. **Genome Biology**, Vol. 1(2): reports2048.

Albà, M.M. (2000). Making alignments prettier – Boxshade. **Genome Biology**, Vol. 1(2): reports2047.

Albà, M.M. (2000). Genome-wide analysis of vaccinia virus protein-protein interactions. **Genome Biology**, Vol. 1(2):

reports0059.

Albà, M.M. (2000). A comprehensive analysis of protein-protein interactions in *Saccharomyces cerevisiae*. **Genome Biology**, Vol. 1(2): reports0043.

Albà, M.M. (2000). Clustering of protein families - Protomap. **Genome Biology**, Vol. 1(1): reports236.

Albà, M.M. (1999). Links to molecular biology databases – The molecular biology database: an online compilation of relevant database resources. **Genome Biology**, Vol. 1(1): reportes235.

Albà, M.M. (1999). Analysis of protein sequences – The PredictProtein Server. **Genome Biology**, Vol. 1(1): reports225.

Book chapters:

Toll-Riera, M., Laurie, S., Radó-Trilla, N., Albà, M.M. (2011). Partial gene duplication and the formation of novel genes. **Gene Duplication / Book 1, Intech**. ISBN 978-953-307-387-3.

Morcillo-Suarez, C., Albà, M.M., Navarro, A. (2010) **Genoma y enfermedades complejas**. Tratado de Esclerosis Múltiple. Ed. Marge Medica Books.

Albà, M.M. (2009). Temporal aspects of gene evolution. **Evolución y Adaptación**. Sociedad Española de Biología Evolutiva.

Toll-Riera, M., Castresana, J., Albà, M.M. (2008). Accelerated Evolution of Genes of Recent Origin. **Evolutionary Biology: from concept to application**. Ed. P. Pontarotti. Springer.

Mularoni, L., Toll-Riera, M., Albà, M.M. (2008). Comparative Genetics of Trinucleotide Repeats in the Human and Ape Genomes. **Handbook of Human Evolution 2** (Ed. David N. Cooper & Hildegard Kehrer-Sawatzki). Ed. John Wiley & Sons Ltd., Chichester.

Albà, M.M., Tompa, P., Veitia, R.A. (2007). Amino-acid repeats and the structure and evolution of proteins. In *Gene and Protein Evolution*, **Genome Dynamics**. Ed. J-N Voff, Karger, Vol. 3: 119-130.

Freire, M.A., Albà, M.M., Jensen, A.B., Niogret, M.F., Goday, A., Pagès, M. (1994). Gene regulation by abscisic acid and water stress in maize. In "Biotechnology for Aridland Plants". Ed. G. Coruzzi and P. Puigdomenech. **NATO ASI Series**, Vol.H 81, 257-266.

Pagès, M., Vilardell, J., Jensen, A.B., Albà, M.M., Torrent, M., Goday, A. (1993). Molecular biological responses to drought in maize. In "Interacting Stresses on Plants in a Changing Climate". Ed. M.B. Jackson and C.R. Black. **NATO-ASI Series**, Vol.I 16, 583-591.

Conference papers:

Blevins, W.R., Albà, M.M., Carey, L (2018) Comparative transcriptomics and ribo-seq: Looking at de novo gene emergence in *Saccharomycotina*. Meeting of the Society for Molecular Biology and Evolution, **SMBE'18 Collection PeerJ preprints** 5:e3030v1.

Ruiz-Orera, J., Villanueva-Cañás, J-L., Blevins, W., Albà, M.M. (2018) *De novo* gene evolution: How do we transition from non-coding to coding? Meeting of the Society for Molecular Biology and Evolution, **SMBE'18 Collection PeerJ preprints** 5:e3031v2.

Bellora, N., Farré, D., Albà, M.M. (2008). Identification of regulatory motifs by positional bias in mammalian promoters. **Proceedings VIII Spanish Bioinformatics Symposium** (JdB'08)

Farré, D., Messeguer, X., Albà, M.M. (2002). PROMO: detection of known transcription regulatory elements common to multiple sequences. **Proceedings 3rd Annual Spanish Bioinformatics Conference** JBI'02.

Pagès, M., Albà, M.M., Culiáñez-Macià, F.A., Goday A. (1995). The maize RNA-binding protein, MA16, is a nucleolar protein located in the dense fibrillar component. **J. Cellular Biochemistry**, Suppl. 19A, 146.

Pagès, M., Albà, M.M., Arenas, C., Busk, P.K., Culiáñez-Macià, F.A., Figueras, M., Jensen, A.B., Jessop, A.C., Peracchia, G., Goday, A. (1994). Abscisic acid and water-stress responsive genes in maize. **Genet. Pol.** 35 B, pp 15-

24.

Textbooks:

López-Bigas, N., Albà, M.M., Eyras, E. (2006). Bioinformàtica. **Universitat Oberta de Catalunya** (UOC).