

ANA CONESA

Research Professor

Institute for Integrative Systems Biology (I2SysBio), CSIC – Universitat de València

ana.conesa@csic.es | conesalab.org | [ORCID 0000-0001-9597-311X](https://orcid.org/0000-0001-9597-311X) | [Google Scholar](https://scholar.google.com/citations?user=...)

Publications	182	Projects as PI	47	PhD students supervised	24
Citations (GS)	> 47,000	Lead-PI @ Multi-PI	17	Advisor/reviewer @ institutions	45
h-index (GS)	72	Research Contracts	6	Software tools developed	26
Talks/keynotes	188/29	Total raised	~19M\$	Start-up companies founded	2

SCIENTIFIC STATEMENT

I am Research Professor at the Spanish National Research Council (CSIC) I graduated as Agricultural Engineer at the Polytechnical University of Valencia in 1993 and obtained my PhD in Molecular Microbiology at the University of Leiden in the Netherlands with a research project at the Microbiology Department of the Dutch Institute for Food Research (TNO). I obtained a Ramon y Cajal award and joined the Valencia Agricultural Research Institute (Spain) in 2003 to develop bioinformatics tools for citrus genomics. I moved into CIPF in 2007 and became Senior Group Leader in 2010, creating the Genomics of Gene Expression Laboratory. From August 2014 to May 2021, I was Full professor at the Microbiology and Cell Science Department and Genetics Institute of the University of Florida. On May 2021, I joined the CSIC Institute for Integrative Systems Biology (I2SysBio) and became courtesy faculty of the University of Florida. In 2022 I became member of the Spanish Royal Academy of Engineer and of the Board of Directors of the International Society for Computational Biology (ISCB). I am ISCB Vice-president and President of the Spanish Society for Bioinformatics and Computational Biology. I am honorary member of the Spanish Society of Bioinformatics and Computational Biology, ISCB Fellow and lead-coordinator of the CSIC Network for Computational Biology and Bioinformatics, with over 350 scientists.

I am interested in understanding functional aspects of gene expression at the genome-wide level, across different organisms and in relation to pathological processes. My group has developed statistical methods and software tools that analyze the dynamics aspects transcriptomes, integrate these with other types of molecular data and annotate them functionally, with a special focus on Next Generation Sequencing (NGS) data. I am creator of popular bioinformatics software such Blast2GO, PaintOmics, maSigPro, NOISeq, Qualimap, SQANTI, tappAS, with tens of thousands of users world-wide, and pioneered the methodologies for transcriptome analysis using single-molecule sequencing technologies. These user-friendly tools bring complex bioinformatics algorithms to end biology and biomedical users to democratize large-scale genomics research. My research has been well-funded through national and international funding agencies including Horizon Europa, H2020, Marie Curie Actions, NIH, NASA, and USDA, as well as by private foundations such as Santander, JDRF and Helmsley. I have led multiple international research consortium projects, including STATegra (EU FP7, 11 partners, 8 countries, €6M), DEANN (Marie Curie Action, 16 partners, 14 countries, €0.9M), LongTREC (Marie Skłodowska Curie Action Doctoral Network, 12 partners, 10 countries, €2.7M), and a team of 6 PIs at UF to develop multi-omics models for Type 1 Diabetes progression. I have (co)-organized numerous bioinformatics and NGS conferences –including the major conference in the Computational Biology field ISMB- and delivered specialized bioinformatics courses in over 10 countries in 5 continents with over 500 attendants. I am co-founder and scientific advisor of Biobam Bioinformatics, a company operating since 2010 to create bioinformatics solutions for biologists. I serve a scientific advisor for multiple international research institutions and companies and in several CSIC governance committees.

EDUCATION

Ph.D. Molecular Microbiology, June 2001

University of Leiden / TNO

Leiden, The Netherlands

1996–2001

Thesis: Overproduction of Peroxidases by Filamentous Fungi

Agricultural Engineering Degree

Polytechnic University of Valencia

Valencia, Spain

1988–1993

Graduation Project: Development of a plant breeding program in common bean (*Phaseolus vulgaris*)

ACADEMIC POSITIONS

Research professor, I2SysBio

CSIC

Valencia, Spain

2021- present

Courtesy faculty, Microbiology and Cell Science

University of Florida

Gainesville, Florida, USA

2021- present

Professor Dept. Microbiology and Cell Science <i>University of Florida</i>	Gainesville, Florida, USA 2014-2021
Head of Genomics of Gene Expression Lab <i>Centro de Investigación Príncipe Felipe</i>	Valencia, Spain 2010-2018
Junior PI at Bioinformatics Department (permanent position) <i>Centro de Investigación Príncipe Felipe</i> Development of bioinformatics tools for functional genomics	Valencia, Spain 2008-2010
Ramon y Cajal Fellow at CIPF <i>Centro de Investigación Príncipe Felipe</i> Development of bioinformatics tools for functional genomics	Valencia, Spain 2007- 2008
Ramon y Cajal Fellow at Plant Genomics Center <i>Valencia Institute for Agricultural Research</i> Develop supporting bioinformatics research for the Citrus Genome Project	Valencia, Spain 2003- 2007
Project Leader Bioinformatics <i>TNO Nutrition and Food Research Institute</i> Setup the bioinformatics infrastructure for microarray gene expression analysis at the Department of Toxicology	Zeist, The Netherlands 2001-2003
PhD student at Molecular and Applied Microbiology Department <i>TNO Nutrition and Food Research Institute</i> Synthetic biology for the industrial production of peroxidases enzymes in fungal cellular factories Supervisor: Cees van de Hondel and Peter Punt	Zeist, The Netherlands 1996-2001
Research Fellow at Monoclonal Antibodies Laboratory <i>Institute for Plant Pathology (IPO)</i> Plantibodies to infer resistance to cyst nematodes in potato. Supervisor: Jack Stockermans	Wageningen, The Netherlands 1994-1995
Research Fellow at Molecular Flowering Department <i>Institute for Plant Breeding (CPRO)</i> Microsatellite markers in lilies Supervisor: Hans Sandbrink	Wageningen, The Netherlands 1993-1994
Introduction to Research grant from Valencian Government <i>Instituto Valenciano de Investigación Agraria</i> Molecular Markers in tomato. Supervisor: María José Asíns	Moncada, Spain 1992 July-August

HONOURS AND DISTINCTIONS

Jul 2023	Fellow of the International Society for Computational Biology
Dec 2022	Member of the “Científicas e Innovadoras” platform of the Spanish Ministry of Science and Innovation
2022-2026	Honorary Member of the Spanish Society for Bioinformatics and Computational Biology
Oct 2022	Member of the Spanish Royal Academy of Engineering

SCIENTIFIC APPOINTMENTS

Jan 2026 to date	President of the Spanish Society for Bioinformatics and Computational Biology
Jan 2025 to date	Vice-president of the International Society for Computational Biology (ISCB)
Jan 2022 to date	COSI representative at the Board of Directors of the International Society for Computational Biology
Jan 2022 to date	Member of the I2SysBio Scientific Committee
Oct 2022 to date	Chair of the I2SysBio Sustainability Committee
Feb 2023 to date	Member of ISCB Membership Taskforce
Feb 2023 to date	Member of the ISCB Green Science Committee
Mar 2023 to date	Member of the CSIC VIDA Programme Committee
May 2023 to date	Node of the Spanish National Bioinformatics Institute – ELIXIR-Spain
Sep 2023 to date	Coordinator CSIC Network in Bioinformatics and Computational Biology
Sep 2023 to date	Member of the CSIC Sustainability Committee
Oct 2023 to date	Director of the I2SysBio Theoretical and Computational Biology Programme

AWARDS AND FELLOWSHIPS

- El Mundo Award Best start up in Valencia 2013 to Biobam
- Mobility Grant Castillejo – Four-month sabbatical at UC-Berkeley (2012)
- Mobility Grant GA – Two month visit to Copenhagen University (2008)
- Ramón y Cajal Award for international talent attraction (2003-2008)
- Comett Fellowship for international mobility of graduate students (1993-1994)
- Undergraduate research grant, Polytechnical University of Valencia (1993)
- Research Fellowship at the Valencia Institute for Agricultural Research (1992)
- Fellowship at Interlegsa Breeding Company, Valencia (1992)
- Erasmus Fellowship for international mobility of undergraduate students (1991)

LANGUAGES

- Spanish (Mother tongue)
- English (Correct at Reading, Oral and Writing)
- Dutch (Correct at Reading, Oral and Writing)

SOFTWARE DEVELOPED

FUNCTIONAL ANNOTATION

- **Blast2GO** — Functional annotation & analysis of novel sequence data (Java desktop)
- **isoAnnot** — Functional annotation with isoform resolution (Python)
- **spongeScan** — Search for miRNA Multiple Recognition Elements in lncRNAs (Web)

QUALITY CONTROL IN NGS

- **Qualimap** — Quality analysis of mapped NGS data (Java desktop)
- **NOISeq** — Differential expression analysis of NGS data (R package)
- **MultiPower** — Power Analysis for multiomics data (R package)
- **SQANTI3** — Structural and Quality Analysis of Transcripts Isoforms (Python script)
- **SQANTI-Reads** — Structural and Quality Analysis of long reads (Python script)
- **SQANTI-SIM** — Simulation of long read transcript models (Python script)
- **SQANTI-TUSCO** — Benchmark for long-read transcriptomics data (Python script)
- **SQANTI-Epi** — Benchmark for long-read epigenomics data (Python script)

STATISTICAL ANALYSIS OF GENE EXPRESSION

- **maSigPro** — Analysis of time-series gene expression data (R package)
- **ASCA-genes** — Analysis of multifactorial gene expression data (R package)
- **SEA** — Analysis of serial gene expression data (Web site)
- **tappAS** — Functional profiling at the isoform resolution (Java desktop)
- **acorde** — Network analysis of isoform co-expression at single cells (R package)

MULTIOMICS DATA ANALYSIS

- **STATegraEMS** — Experiment Management System for multiomics (Java desktop)
- **Paintomics** — Integration of multiple omics on KEGG pathways (Web site)
- **RGmatch** — Linking genomics regions to gene models by NGS data (Python script)
- **MOSim** — Simulation of multiomics datasets (R package)
- **MORE** — Multiomics regulatory models (R package)
- **MultiBac** — Batch correction across omics (R package)
- **Padhoc** — Pathway Reconstructon on the fly (Python)
- **MirCure** — Quality control of microRNA annotations (Shiny app)
- **DeCovid** — Analysis of COVID19 disease map gene expression (Shiny app)
- **MAMBA** — Multi-omics Flux-Balance Analysis (Matlab)

PROJECTS AS PRINCIPAL INVESTIGATOR

CURRENT

47. **AGAIN24007** 22.Aug.2024-31.Dec.2026
Ayuda para la preparación de propuestas ERC
CSIC | Role: PI | Funding: 10,000 €
46. **CSIC-Juana Rienda** 01.Oct.2026-31.Dec.2030
EPI-ALZ: Integrating Epigenomics, Epitranscriptomics and Clinical Data for Stratification of Alzheimer's Disease Progression
CSIC (Programa Juana Rienda) | Role: PI | Funding: 420,000 €
45. **EVOLVE – 101307269** 01.Oct.2026-30.Sep.2029
EVOLVE: Translating Extracellular Vesicle Communication into AI Guided Breeding and Smart Biofertilization (WP7 leader)
European Commission, EIC Pathfinder | Role: Beneficiary / WP leader | Funding: 4,268,984 € (total) – 381,188 € (CSIC)
44. **2025_CMRC Commissioned Services** 01.Jan.2026-31.Dec.2026
TELLME: LLM-based narratives to explain and empower systems biology research
ELIXIR | Role: Lead-IP | Funding: 187,500 € (total) – 70,000 € (CSIC)
43. **2025_COCREA** 01.Jan.2026-31.Dec.2027
Omics data integration to unravel the role of the microbiome in reproductive health
CSIC | Role: IP | Funding: 139,750 € (total) – 59,000 € (CSIC)
42. **2025_COCREA** 01.Jan.2026-31.Dec.2027
Development of tools for epitranscriptomics analysis and association with disease
CSIC | Role: IP | Funding: 100,000 € (total) – 60,000 € (CSIC)
41. **2025_BIOGEOMA4** 01.Jan.2025-31.Dec.2025
Genomic Insights into Three Locally Adapted Diatoms from the Albufera Coastal Lagoon
Institut d'Estudis Catalans | Role: Co-IP | Funding: 80,000 € (total) – 10,000 € (Conesa lab share)
40. **MMT24-CONEXIÓN BCB-01** 01.Nov.2024-30.Oct.2028
Broad transformation of CSIC's digital capabilities through dedicated AI support from BCBHub
CSIC | Role: PI | Funding: 171,124 €
39. **ID: 01-167** 01.Oct.2024-30.Sep.2027
FAIRification of IsoSeq Evidence-driven annotation of the biodiversity
OSCARS/EOSC | Role: PI | Funding: 185,963 €
38. **PID2023-152976NB-I00** 01.Sep.2024-31.Aug.2027
Novel methodologies for multi-omics integrative analysis with cutting-edge sequencing technologies
MCIU | Role: PI | Funding: 275,000 €
37. **INFRA2024** 01.Jun.2024-31.May.2026
Impulsando la presencia del CSIC dentro de la ESFRI ELIXIR
CSIC | Role: PI-Coordinator | Funding: 100,000 €
36. **IMP/00019 – PMP24/00024** 01.Jan.2024-31.Dec.2026
IMPaCT-Data: Precision Medicine Data Science infrastructure – I2SysBio node
ISCIII | Role: PI of the CSIC node | Funding: 2,982,045 € (total) – 56,991 € (CSIC)
35. **HubBCB** 01.Sep.2023-31.Ago.2025
Conexión CSIC en Biología Computacional y Bioinformática
CSIC | Role: Coordinator | Funding: 200,000 €
34. **PROMETEO-CIPROM/2022/25** 01.Jul.2023-31.Dec.2026
Cells2Spine: Spatial Transcriptomics and Cell Communication Models applied to tissue regeneration and treatment in Spinal Cord Injury with Precision Nanomedicine
Generalitat Valenciana | Role: Coordinator | Funding: 597,364 € (total) – 115,404 € (CSIC)
33. **MSCA-DN-2021-101072892** 01.Oct.2022-3.Sep.2026
LongTREC: The Long Reads European Transcriptomics Consortium. The next generation transcriptome biology revealed by single molecule sequencing technologies
Horizon Europa | Role: Lead-PI | Funding: 2,701,476 € (total) – 251,971 € (CSIC)

PAST

32. **PID2020-119537RB-100** 01.Sep.2021-31.Aug.2024
Integración de datos multi-ómicos para la inferencia de modelos multi-capa de enfermedad
 Role: PI | Funding: 242,000 €
31. **1R21HG011280-01** 01.Sep.2020-31.Aug.2022
Development of methods for transcript quantification and differential expression analysis using long-read sequencing technologies
 NIH | Role: PI | Funding: 405,007 \$ (272,110 \$ transferred to CSIC)
30. **19-EXO19-0029** 01.Feb.2020-31.Jan.2024
Microbial Dark Matter
 NASA | Role: Co-PI (PI: Jamie Foster) | Funding: 663,314 \$ (total) – 136,000 \$ (UF)
29. **FSGC 08 TO No NNX15_033** 01.Aug.2019-31.Jul.2020
Facilitating knowledge exchange between microbiology and computer science students: a computationally intensive approach to discover new adaptation genes in extreme environment
 Florida Space Research Program | Role: PI | Funding: 24,907 \$
28. **2-SRA-2019-805-S-B** 01.Jul.2019-30.Jul.2021
Genotype by Environment interaction analysis to understand mechanisms of T1D pathogenesis
 JDRF-Pilot studies for mechanisms of T1D disease pathogenesis | Role: PI | Funding: 143,343 \$
27. **R01DK116954** 28.Feb.2018-27.Feb.2022
Critical role for alternative splicing in conferring risk for T1D
 NIH(R01) | Role: Co-PI (PI: Concannon) | Funding: 32,443 \$ (Conesa lab share)
26. **RFA-RM-17-001** 19. Sep.2017-19.Sep.2020
Galaxy platform for integrative metabolomics and transcriptomics analysis
 NIH(R03) | Role: PI | Funding: 152,500 \$
25. **2015-70016-23029** 01.Oct.2015-30.Sep.2022
A Novel Antimicrobial Approach To Combat Huanglongbing
 USDA | Role: Co-PI (PI: Lorca) | Funding: 138,487 \$ (Conesa lab share)
24. **UF Start-up funds** 01.Sep.2014-31.Dec.2019
Developing the Functional Iso-Transcriptomics framework
 Role: PI | Funding: 950,000 \$
23. **2018 SECIM** 01.Jul.2018-30.Jul.2019
Development of multiomics methods for the integrative study of the Yeast Metabolic Cycle
 U24DK097209 NIH Common Fund metabolomics program | Role: PI
22. **PT17/0009/0015**
Plataformas de apoyo a la investigación en ciencias y tecnologías de la salud de la convocatoria 2017 de la Acción Estratégica en Salud
 ISCIII | Role: PI Nodo Valencia | Funding: 31,900 €
21. **UFII Seed Funds 2017**
Understanding the functional role of alternative splicing
 University of Florida Informatics Institute | Role: PI | Funding: 49,580 \$
20. **PROMETEO/2016/093**
The Next Systems Biology: statistical methods for multiomics systems biology
 Generalitat Valenciana | Role: Lead PI | Funding: 190,774 €
19. **BIO2015-1658-R**
Novel methods for new challenges in the analysis of high-throughput sequencing data (NOVELSEQ)
 MINECO | Role: PI | Funding: 266,200 €
 The goal of this project is the development of new methods in the massive data analysis sequencing
18. **MSCA-ITN-2015. 2016-2019**
CHROME
 Horizon 2020 | Role: WP4 leader | Funding: 165,000 € (CIPF share)
 Computational methods for the integration of ChIP-seq, metabolomics and RNA-seq data to model chromatin metabolism
17. **Proyectos sinérgicos CIPF**
Identification and modelling of molecular and cellular events of the immune response associated to the appearance of minimal hepatic encephalopathy in cirrhotic patients
 Role: PI | Funding: 100,000 €

16. **Ayuda Complementaria Jerónimo Forteza**

Desarrollo de métodos estadísticos para la integración de múltiples datos ómicos y de secuenciación masiva

Generalitat Valenciana | Role: Lead PI | Funding: 9,600 €

Support finalization STATegra project

15. **TEDDY**

Integrative Analysis of TEDDY data to improve T1D diagnosis

Helmsley Charitable Trust | Role: Lead PI | Funding: 633,185 \$

Integration of multiomics, nutritional, demographic and clinical data from a cohort of 1.000 T1D patients to find Type 1 Diabetes triggers

14. **BIO2012-40244**

Development of Computational Approaches for the characterization and functional annotation of long-non-coding RNA (Annot-lncRNA)

MINECO | Role: PI | Funding: 90,000 €

The goal of this project is the development of computational approaches to unravel function of long non-coding RNAs

13. **GA-612583**

Developing a European American NGS Network (DEANN)

EU Marie Curie IRSES | Role: Lead PI | Funding: 934,500 € (total) – 268,000 € (CIPF)

Scientific network of European and Latin America researchers in the field of Next Generation Sequencing (DEANN) applied to the analysis of variation in human and natural endemic populations

Partners: TGAC(UK), UCL(UK), SLU(Sweden), Udine University(Italy); UPF(Spain), CIPF(Spain), IMEGEN(Mexico), CINVES-TAV(Mexico), Brasilia Univ. (Brazil), INTA (Argentina), CONICET (Argentina), INACH (Chile)

12. **GA-30600**

User-driven development of statistical methods for experimental planning, data gathering, and integrative analysis of next generation sequencing, proteomics and metabolomics data

FP7 HEALTH | Role: Lead PI | Funding: 6,000,000 € (total) – 577,919 € (CIPF)

Statistical methods for multiomics data integration

Partners: Imperial College(UK), IDIBELL(Spain), Karolinska Institute(Sweden), FORTH(Greece); CIPF(Spain), University Munich (Germany), Biomax(Germany), University Amsterdam (Holland), University Leiden (Holland), Qiagen Aarhus (Denmark), University California (USA)

11. **ACOMP/2012/058**

Generalitat Valenciana 2012 complementary actions Complementing Grant for Pathogenomics- Metabolomics and Interactomics of the relationship host-pathogen

RNA-seq analysis in pathogenic bacteria | Role: PI | Funding: 12,000 €

10. **FPA/2013**

Supporting technician for the Project “Development of transcriptional networks regulating virulence in filamentous fungi”

Jerónimo Forteza 2012 Programme | Role: PI | Funding: 92,000 €

RNA-seq analysis in fungi

9. **16ER**

Analysis of discordant twins to investigate correlation of gene expression changes and DNA methylation in Lupus

GentxGent 2012 | Role: PI and Scientific Coordinator | Funding: 20,500 €

RNA-seq y Methyl-seq analysis in a rare disease

Partners: CIPF (Spain) and Idibell (Spain)

8. **PIB2010AR-00266**

Genomics and Transcriptomics of detoxification pathways in Drosophila

Acción Internacional MICINN | Role: PI and Scientific Coordinator | Funding: 90,000 € (total) – 53,800 € (CIPF)

NGS-based genomic and transcriptomics analysis of natural fly strains fed under different nutritional conditions

Partners: CONICET (Argentina), UPF (Spain) and CIPF (Spain)

7. **BIO2009-10799**

Exploring novel genome-transcriptome relationships by Next Generation Sequencing approaches

MICINN Proyectos de Investigación Fundamental 2009 | Role: PI | Funding: 130,000 €

Desarrollo de plataformas informáticas para el estudio de la regulación genómica mediante técnicas de ultrasecuenciación

6. **BIO2008-04638-E**

Pathogenomics: Development of transcriptional networks regulating virulence in filamentous fungi

MICINN, Acciones Complementarias -ERA-NETs 2009 | Role: PI | Funding: 92,000 €

5. **BIO2008-05266-E/**

Pathomics: Metabolomics and Interactomics of the relationship host-pathogen

MICINN, Acciones Complementarias -ERA-NETs 2009 | Role: PI | Funding: 136,000 €

EARLIER FUNDING (PRE-2008, IVIA AND CIPF)

4. **Conselleria de Empresa, Universidad y Ciencia 2005** 01.Jan.2006-31.Dec.2007
CITRUS-SII: Sistemas integrados inteligentes en cítricos
Role: PI – IVIA | Funding: 19,975 €
3. **Conselleria de Cultura, Educación y Deporte 2004** 01.Jan.2004-31.Dec.2005
Desarrollo de sistemas de información para genómica de cítricos
Role: PI – IVIA | Funding: 13,170 €
2. **Conselleria de Industria, Comercio y Turismo 2004** 01.Jan.2004-31.Dec.2005
Modelado semántico de la información genética de cítricos
Role: PI – IVIA | Funding: 9,996 €

UNFUNDED PROJECTS

1. **LRGASP** 2019-2024
LRGASP: Long-read RNA-seq Genome Annotation Assessment Project
International consortium (unfunded) | Role: Consortium leadership

STUDENT FELLOWSHIPS

Competitive fellowships obtained by lab members with Ana Conesa as thesis supervisor or host PI.

12. **MSCA Postdoctoral Fellowship – GA 101269984** 2026-2028
TranscriptAccuracyAD
Sonia García-Ruiz | European Commission, MSCA
11. **PTA – Personal Técnico de Apoyo, PTA2025** 2026-
Silvia Talavera Marcos | Agencia Estatal de Investigación
10. **FPU25/03568** 2026-2030
Javier Hidalgo Moreno | Ministerio de Ciencia, Innovación y Universidades
9. **JAЕ Intro ICU** 2025
Sara Torres Rodríguez | CSIC | Co-supervised with Arnau Montagud
8. **JAЕ Intro ICU** 2025
Andrés Colomer | CSIC | Co-supervised with Carolina Monzó
7. **FPU 2025** 2025-
V́ctor Gaya | Ministerio de Ciencia, Innovación y Universidades
6. **MSCA Postdoctoral Fellowship – GA 101149931** 2024-2026
RBNAGE
Carolina Monzó | European Commission, MSCA
5. **JAЕ Intro** 2024
V́ctor Gaya | CSIC
4. **CIACIF/2023/124** 2023-
Carlos Blanco Ǵmez | Generalitat Valenciana
3. **ACIF/2019/081** 2019-
Pedro Salguero Garća | Generalitat Valenciana (VALi+d)
2. **ACIF/2018/290** 2018-
Francisco Joś Pardo Palacios | Generalitat Valenciana (VALi+d)
1. **FPU2013/02348** 2014-2018
Lorena de la Fuente | Ministerio de Educaci3n

RESEARCH CONTRACTS

6. **Swiss Cancer League** 01.Jan.2026
LUMINA - Long-read scRNA-seq for Unraveling the tumor Microenvironment and Immune Niche Architecture
Role: PI | Funding: 37,570 €
5. **Kwait University** 01.Jan.2025
Identification of Novel Drought-responsive Genes in the Date Palm (Phoenix dactylifera L.) Using a Combination of Illumina and Pacbio NGS-based RNA-seq Technologies
Role: PI | Funding: 48,000 €

4. **Slovenian Institute of Biology** 01.Oct.2017
Analysis and annotation of Solanum tuberosum Pacbio data
 Role: PI | Funding: 10,000 €
3. **IGENOMIX** 01.Oct.2014
Identificación de factores secretados y vinculados a alteraciones cromosómicas en embriones pre-implantacionales
 Role: PI | Funding: 40,000 €
2. **IMEGEN** 14.Mar.2014
Consulting RNA-seq data analysis
 Funding: 5,000 €
1. **ROSLIN Institute** 08.Jun.2009
Functional annotation of microarray data in livestock | Funding: 5,000 €

RESEARCH NETWORKS

Membership of research networks without direct funding to the lab.

4. **RED2024-RC** 2025-
Expansión del Instituto Nacional de Bioinformática (INB) para incrementar su impacto internacional
 Agencia Estatal de Investigación, Redes de Investigación | Role: Network member
3. **COST Action CHARME – CA15110** May 2016-Mar 2020
Harmonising standardisation strategies to increase efficiency and competitiveness of European life-science research
 European Cooperation in Science and Technology | Role: Network member
2. **RNALife – BFU2015-71978-REDT** 2016-2017
La vida del mRNA desde la transcripción a la degradación
 MINECO, Redes de Excelencia | PI: Susana Rodríguez Navarro | Role: Network member
1. **COST Action SeqAhead – BM1006** Mar 2011-Mar 2015
Next Generation Sequencing Data Analysis Network
 European Cooperation in Science and Technology | Role: Network member

TECHNOLOGY TRANSFER

- Co-founder and Scientific Advisor of Biobam Bioinformatics S.L. 2010. Biobam is a leading bioinformatics solution provider which accelerate research in disciplines such as agricultural genomics, microbiology and environmental NGS studies, amongst others. Biobam is committed to the development of user-friendly software solutions for biological research. Our mission is to transform complex data analysis procedures into an attractive and interactive task. Biobam is devoted to close the gap between experimental work, bioinformatics analysis and applied research. (<http://biobam.com>)
- Co-founder of Genometra S.L. 2011. Genometra is a service provider company for the bioinformatics analysis of high-throughput genomics data (<http://www/genometra.com>). The company ceased activity in 2018.

PUBLICATIONS

PREPRINTS AND MANUSCRIPTS UNDER REVIEW

- **MAMBA: a model-driven, constraint-based multiomic integration method**
 Manuel Ugidos, Carme Nuño-Cabanes, Sonia Tarazona, Alberto Ferrer, Lars Keld Nielsen, Susana Rodríguez-Navarro, Igor Marín de Mas, **Ana Conesa**
bioRxiv 2022.10.09.511458; doi: <https://doi.org/10.1101/2022.10.09.511458>.
- **SQANTI-browser: visualization and curation of SQANTI3-classified long-read transcriptomes within the UCSC Genome Browser**
 Alejandro Paniagua, Carlos Blanco, Andrés Colomer Fernández, Mark Diekhans, **Ana Conesa**, Carolina Monzó
bioRxiv 2026.05.25.727625; doi: <https://doi.org/10.64898/2026.05.25.727625>
- **A Multi-Omics Computational Framework for Inferring Phase-Specific Regulatory Networks in the Yeast Metabolic Cycle**
 Salvador Casani-Galdon, Shidong Xi, Jane Mellor, Sonia Tarazona, **Ana Conesa**
submitted

- Metabolic fingerprinting reveals a partitioned BRL3 role for abiotic stress response and carbon allocation in *Arabidopsis*

Andrés Rico, Saleh Alseekh, Norma Fábregas, **Ana Conesa**, Leyre Meliá, Fidel Lozano, Aditi Gupa, Ana Caño
submitted

- Benchmarking of image-based methods for spatial transcriptomics alignment

Víctor A. Gaya-Martín, Sonia Tarazona, **Ana Conesa**
Genomics, Proteomics and Bioinformatics, minor revision.

2026

182. Elucidating Metabolic Pathways of Microbial Dark Matter in Bahamian Thrombolites via Metagenome-Assembled Genomes

Rocío Hagüedus, Andrea Duscher, **Ana Conesa**, Jamie Foster
Astrobiology, accepted

181. Ten Simple Rules for Causal Analysis of Biomedical Omics Data

Gleb Svinin, Ramon Diaz-Urriarte, Rebecca Ting Jiin Loo, Nikhilesh Vasanth Kumar, Varsha Venkatesha Murthy, Dilara Uzuner Odongo, **Ana Conesa**, Gianluca Bontempi, Susana Vinga, Iliaria Granata, Daniel Domingo-Fernandez, Paola Lecca, Marieke L. Kuijjer, Jesse H. Krijthe, Ina Koch, Laurence Calzone, Simona Ester Rombo, Fatima Sanchez-Cabo, Enrico Glaab
PLoS Computational Biology, 2026 Aug 20. doi:10.1371/journal.pcbi.1014668

180. Deciphering Transcriptome Complexity via Long-read Sequencing

Chuwen Xu, Jia Li, Chenxi Yin, Keying Li, Shiwen Gao, Yue Yu, Cheng Chang, Ye Wang, Guoqing Tong, Liang Gong, Wen Hu, Guoliang Chai, Yilai Han, Qian Qin, Suoqin Jin, Xiufen Zou, Bo Li, **Ana Conesa**, Yunhao Wang, Dingjie Wang
iMeta, accepted

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8. Examining the role of glutamic Acid 183 in chloroperoxidase catalysis

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7. Calnexin overexpression increases manganese peroxidase production in *Aspergillus niger*

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6. Filamentous fungi as cell factories for heterologous protein production

Punt PJ, van Biezen N, **Conesa A**, Albers A, Mangnus J, van den Hondel C

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5. Fungal Peroxidases: Molecular Aspects and Applications

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4. The C-terminal propeptide of the *Caldariomyces fumago* chloroperoxidase: an intramolecular chaperone?

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3. The secretion pathway in filamentous fungi; a biotechnological view

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2. Expression of the *Caldariomyces fumago* chloroperoxidase in *Aspergillus niger* and characterization of the recombinant enzyme

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1. Studies on the Production of Fungal Peroxidases in *Aspergillus niger*
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LECTURES, SEMINARS AND INVITED TALKS

193. The SQANTIverse to evaluate and correct long-read transcriptomics data (Invited Speaker)
*A*STAR Genome Institute of Singapore, Seminar Series.* Singapore, September 18th, 2026
192. Transitioning from short to long read transcriptomics: accuracy, bias and analysis challenges (Keynote Speaker)
International Conference on Bioinformatics (InCoB/ISCB-APAC 2026). Penang, September 17th, 2026
191. From multi-omics integrative analysis to AI-assisted multilayered interpretations (Invited Speaker)
International Study Group for Systems Biology (ISGSB 2026). Ljubljana, September 8th, 2026
190. Write to publish: scientific paper writing (Invited Speaker)
NET4MAT Scientific Writing Webinar, CSIC. Online, April 24th, 2026
189. Grant writing (Invited Speaker)
CaLISTA Training School on Scientific Writing and Dissemination Skills (COST Action CA21109). Valencia, April 13th, 2026
188. From Blast2GO to the SQANTIverse: a female journey for bioinformatics excellence. Lights and shadows (Invited Speaker)
European Conference in Computational Biology (ECCB2026). Geneve, September 1st, 2026
187. The Good, the Bad and the Artifact: The SQANTIverse (Keynote Speaker)
Valencia Long-read transcriptomics (VALT2026). Valencia, July 1st, 2026
186. Insights into human transcriptomes by long-read RNA-sequencing (Invited Speaker)
European Society for Human Genetics (ESHG26) Conference. Gothenburg, June 15th, 2026
185. Long-read transcriptomics for beginners (Invited Speaker)
European Society for Human Genetics (ESHG26) Conference. Gothenburg, June 14th, 2026
184. Estado actual y tendencias de la Bioinformática (Keynote Speaker)
INNOTRANSFER: Del dato biológico al mercado, UPV. Valencia, Junio, 5th, 2026
183. Exploring new venues in single-molecule transcriptomics with the SQANTIverse (Invited Speaker)
Helmholtz Institute for RNA-based Infection Research (HIRI). Würzburg, April 28th, 2026
182. Advancing multi-omics data integration through tool development (Keynote Speaker)
Swiss Bioinformatics Workshop. Gothenburg, March 13th, 2026
181. Evaluation of strategies for evidence-driven genome annotation using lrRNA-seq (Invited Speaker)
Advances in Genomics Technologies Workshop (Sanger Institute). Hixton, October 27th, 2025
180. Isoform detection and genome annotation using long-reads transcriptome sequencing (Invited Speaker)
Uruguay Bioinformatics Workshop. Montevideo, October 15th, 2025
179. Round table: Future of RNA bioinformatics tools (Invited Speaker)
iRNA COSI at ISMB/ECCB 2025. Liverpool, June 24th, 2025
178. SQANTIverse: A comprehensive framework for analyzing long-read transcriptomics data (Invited Speaker)
Pacbio PRIMS2025. Boston, May 15th, 2025
177. A comprehensive framework for analyzing long-read transcriptomics data (Invited Speaker)
Luxembourg Centre of Systems Biomedicine, Seminars Series. On line, May 12th, 2025
176. The new biology revealed by single-molecule sequencing of the transcriptome (Keynote Speaker)
International Symposium in Human Genetics. Sorbonne University, Paris, May 6th 2025
175. SQANTIverse: A comprehensive framework for analyzing long-read transcriptomics data (Invited Speaker)
Pacbio PRIMS2025. Athenas, April 29th, 2025
174. Transitioning from short to long read transcriptomics: accuracy, bias and analysis challenges (Invited Speaker)
Instituto Italiano di Tecnologia. multiMilan, March 28th, 2025
173. Benchmarking of long-read transcriptomics methods (Keynote Speaker)
Modern benchmarking: advancing computational methods in molecular biology. Ascona, March 24th, 2025
172. SQANTIverse: A comprehensive framework for analyzing long-read transcriptomics data (Selected talk)
Festival of Genomics and Biodata London. ExCeL London, January 28th, 2025
171. Single-molecule sequencing of the transcriptome: the TODOs (Keynote Speaker)
Jornades de Bioinformàtica I Genòmica. University of Lleida, December 13th, 2024

170. SQANTIverse: A comprehensive framework for analyzing long-read transcriptomics data (Selected talk)
Biological Data Science. Cold Spring Harbor Laboratory, November 13th, 2024
169. Using lrRNA-seq in multi-sample experiments: design and bias considerations (Invited Speaker)
Long Reads Uppsala (LRUA24). Uppsala, October 22nd, 2024
168. Tools and discoveries from long read transcriptome sequencing (Keynote Speaker)
10th Utrecht Bioinformatics Center Symposium. Utecht University, October 7th
167. Discovering transcriptome complexity through single-molecule long-read sequencing (Invited Speaker)
Alicante Neurosciences Institute. Alicante, October 1st
166. Signal/noise ratio characterization and annotation of multi-omics experiments: pending tasks in Systems Biology (Invited Speaker)
Systems Biology ELIXIR Community Seminar. Online, September 5th, 2024
165. El ConesaLab o la Bioinformática para el análisis transcriptómico (Invited Speaker)
V Congreso de Bioinformática de Perú. Remote lecture, July 25th, 2024
164. Bias analysis for long-reads transcriptomics multi-sample datasets (Selected talk)
iRNA COSI at ISMB2024. Montreal, 12th-16th July 2024
163. Using long reads to understand complexity and specificity of the transcriptomes (Keynote Speaker)
Norwich Single-cell Symposium. Earlham Institute, Norwich, June 26th-27th June 2024
162. Single-molecule long read sequencing to unravel the complexity of the transcriptomes (Invited Speaker)
RIKEN Yokohama, May 20th 2024
161. Using long reads to understand complexity and specificity of the transcriptomes (Keynote Speaker)
Genome Workshop: Multi-omic discovery through long-read sequencing. Tokyo University, May 17th 2024
160. Long-read sequencing to study the transcriptome (Keynote Speaker)
High-content epigenome analysis in the next phase. Kyoto University, May 15th 2024
159. Novel insights in transcriptional complexity through single-molecule sequencing (Invited Speaker)
PacBioPRISM24. Lisbon, Portugal, April 24th, 2024
158. Evidence-driven annotation of the Florida manatee genome using long-reads (Invited Speaker)
Florida manatee research consortium. Online, March 20th, 2024
157. Quantifying isoform expression and transcriptome complexity by single-molecule sequencing (Selected talk)
ABGT 2024. Orlando, Florida, USA, February 6th, 2024
156. FAIRification of IsoSeq: evidence-driven annotation of biodiversity (Invited Speaker)
Invited seminar, EOSC. Online, 2024
155. Assessing transcriptome complexity by high-throughput single-molecule sequencing (Invited Speaker)
PacBio Day UCL London. London, UK, November 21st, 2023
154. Long-read sequencing for the analysis of the transcriptome (Invited Speaker)
Therapeutic targeting of mRNA splicing in cancer. Asilomar, California, USA, September 21st, 2023
153. Long-read sequencing for the analysis of the transcriptome (Keynote Speaker)
Annual Symposium of Polish Bioinformatics Society. Gliwice, Poland, September 13th, 2023
152. Using long reads technologies to reveal new insights into the functional complexity of the transcriptomes (Keynote Speaker)
Grapedia Annual Meeting. Valencia September 11th, 2023
151. Third-generation long-read transcriptome sequencing for unraveling transcriptome complexity (Keynote Speaker)
7th Denmark Bioinformatics Symposium. Aarhus (Denmark) September 7th, 2023
150. Las tecnologías de secuenciación de tercera generación nos revelan nuevos aspectos de la biología de los transcriptomas (Keynote Speaker)
Octavo Simposio Argentino de Jóvenes Investigadores en Bioinformática. Virtual August 3rd, 2023
149. Third-generation sequencing technologies to investigate the complexity of transcriptomes (Keynote Speaker)
SysReg COSI at ISMB/ECCB 2023. Lyon July 26th, 2023
148. Herramientas transcriptómicas para el modelado de sistemas biológicos complejos (Invited Speaker)
Congreso Biotec 2023 de la Sociedad Española de Biotecnología. Madrid July 17th, 2023
147. Análisis integrativo de datos multiómicos (Invited Speaker)
CSIC symposium in Computational Biology, IA and Data Science. Madrid July 3rd, 2023
146. Assessing long-read transcriptomics data for isoform identification and genome annotation (Invited Speaker)
European Reference Genomes Archive plenary. Virtual June 20th, 2023

145. Benchmarking of multiple long reads sequencing methods and platforms for transcriptome analysis (Invited Speaker)
Instituto Valenciano de Biomedicina. Valencia February 24th, 2023
144. Single molecule, long reads sequencing for the characterization of the transcriptome (Keynote Speaker)
Jornadas de Bioinformática Granada. Virtual February 23rd, 2023
143. Benchmarking of multiple long reads sequencing methods and platforms for transcriptome analysis (Invited Speaker)
Barcelona Supercomputing Center. Lisbon February 16th, 2023
142. Benchmarking of multiple long reads sequencing methods and platforms for transcriptome analysis (Invited Speaker)
PRBB Barcelona. Lisbon February 16th, 2023
141. Long-read sequencing to unravel the functional impact of alternative splicing (Invited Speaker)
Olissipo Winter School. Lisbon February 10th, 2023
140. Multiomics tools to model dynamic cellular systems in health and disease (Invited Speaker)
Olissipo Winter School. Lisbon February 9th, 2023
139. Lessons and perspectives learnt from the LRGASP project on long reads transcriptome sequencing (Invited Speaker)
European Bioinformatics Institute. Huxton, Cambridge January 27th, 2023
138. Benchmarking of multiple long reads sequencing methods and platforms for transcriptome analysis (Invited Speaker)
Festival of Genomics 2023. London, January 25th -26th, 2023
137. SQANTI3: A Set of Tools for Curation, Annotation and Quantification of Long Reads RNA Sequencing (lrrRNA-seq) Data (Selected talk)
XXX Plant and Animal Genome Conference. San Diego, January 13th -18th, 2023
136. PaintOmics, a Tool for the Integrative Analysis and Visualization of Multi-Omics Data (Selected talk)
XXX Plant and Animal Genome Conference. San Diego, January 13th -18th, 2023
135. Benchmarking of transcriptomics long reads technologies for transcript identification: the LRGASP project (Invited Speaker)
X Genomics and Bioinformatics Symposium. University of Valencia, December 15th -16th, 2022
134. Multi-omic integration to model dynamic biological systems (Invited Speaker)
International Food Data Science Workshop. Instituto de Tecnología de Alimentos (Valencia), November 30th – December 2nd, 2022
133. Diseño, análisis e interpretación de datos multiómicos en desarrollo y enfermedad (Opening lecture)
Seminarios de la Sociedad Española de Bioinformática y Biología Computacional. Online, November 21st, 2022
132. Benchmarking of transcriptomics long reads technologies for transcript identification: lessons from the LRGASP project (Invited Speaker)
Long Reads Uppsala Workshop. University of Uppsala, October 31st – November 2nd, 2022
131. The Conesa Lab: genomics tools for the people (Invited Speaker)
LASER TALKS, Universitat Politècnica de València. Center Cultural del Carmen, October 21st, 2022
130. From multi-omics data to multi-layered systems models: challenges and solutions (Invited Speaker)
Tri-Omics Summit, invited Speaker. Thistle Marble Arch Hotel, London, October 18th, 2022
129. The bioinformatics of multiomics data integration and modeling (Keynote Speaker)
7th European Student Council Symposium 2022/ECCB2022. Sitges, September 18th, 2022
128. Leveraging Long Reads Sequencing for Developing a Functional Iso-Transcriptomics Analysis Framework (Invited Speaker)
Computational Challenges in Very Large-Scale 'Omics'. University of California at Berkeley, United States, July 18th to 21th, 2022
127. The integration of multiomics data to infer multi-layered systems biology models (Keynote Speaker)
SysMod COSI at the Intelligent Systems for Computational Biology Conference. Madison, United States, July 10th to 14th 2022
126. Tools for transforming long reads into functional insights about isoform expression (Invited Speaker)
Long-reads sequencing workshop. The Jackson Laboratory for Genomic Medicine. Farmington, Connecticut May 19th 2022
125. Multiomics integration and third-generation sequencing boost biomedical research with new tools for data analysis (Invited Speaker)
Cabimer (Sevilla). May 13th, 2022
124. Annotation coverage across species and PTMs (Invited Speaker)
GENYO, Centro de Genómica e Investigación Oncológica. Granada, May 12th, 2022
123. Sample size calculation in multiomics experiments (Invited Speaker)
University of Melbourne, invited seminar. Online, May 12th, 2022
122. The Functional Iso-transcriptomics paradigm or long read sequencing applied to transcriptome research (Invited Speaker)
Genyo (Granada). Granada, March 23rd 2022

121. From multiomics data to multilayered systems biology models: do's and don'ts (Invited Speaker)
University of Granada, Department of Computer Science. Granada, March 22rd, 2022
120. Single molecule long reads sequencing as a new paradigm in transcriptomics research (Keynote Speaker)
Australian Mathematical Sciences Institute BioInfoSummer 2021. Virtual meeting, December 2nd 2021
119. Multi-omics integration and third-generation sequencing boost biomedical research with new tools for data analysis (Keynote Speaker)
Argentina Bioinformatics Conference. Virtual meeting, November 17th 2021
118. Statistical and bioinformatics methods for the integration of multi-omics data to understand disease mechanisms (Invited Speaker)
School of Medicine, Virginia University. Charlottesville, 27th October 2021
117. Interpretable integration of multiomics data to unravel disease mechanisms (Invited Speaker)
Cross disciplinary Study of Post-transcriptional and Post-translational modifications. NSF sponsored workshop. Virtual meeting, 18th October 2021
116. Multi-OMICs modelling of T1D links lipid impairment with T1D onset (Invited Speaker)
Ask the Expert. Sugar Science. Virtual meeting, 23rd September 2021
115. SQANTI3: A collaborative project for curation, annotation and quantification of long-read RNA sequencing (lrrRNA-seq) data (Invited Speaker)
ISMB/ECCB 2021. Online, July 1st, 2021
114. Challenges and solutions in for the integrative analysis of multi-omics data (Invited Speaker)
Belgrade Bioinformatics Conference 2021. Virtual meeting, 23rd June 2021
113. Considerations for quality control, quantification and differential expression analysis using lrrRNA-seq (Invited Speaker)
Earlham Institute Long Read RNA Symposium 2021. Virtual meeting, 16th June 2021
112. Methods and tools for the integration of multi-omics data to model biological processes (Selected talk)
Mechanisms of Oncogenesis program. UF Cancer Institute, 25th January 2021
111. Multi-omics and long reads technologies in genomics research: 2020 update (Invited Speaker)
Seminar at Plant Pathology Department, University of Florida. Gainesville, November 17th, 2020
110. Multi-omics and long reads technologies in genomics research: 2020 update (Invited Speaker)
Seminar at Animal Science Department, University of Florida. Gainesville, October 30th, 2020
109. The Functional Iso-Transcriptomics toolset to leverage long reads sequencing for unravelling isoform transcriptional networks from single cells (Keynote Speaker)
iRNA COSI at the European Conference in Computational Biology 2020, Tutorial. Virtual meeting, 13th July 2020
108. Full-Length RNA-Seq Analysis using PacBio long reads: from reads to functional interpretation (Selected talk)
European Conference in Computational Biology 2020, Tutorial. Virtual meeting, 12th July 2020
107. The functional iso-transcriptomics pipeline: from long reads to biological insights (Selected talk)
SMRT Informatics Leiden. May 2020
106. Leveraging long reads to unravel isoform-expression networks in single cells (Keynote Speaker)
SMRT Informatics Leiden. Online, May 2020
105. Bioinformatics tools for multi-omics integration and single molecule sequencing: application to human disease (Invited Speaker)
Topics in Cancer Seminar Series. Gainesville, December 6th, 2019
104. Tools for transforming multi-omics data into disease models (Selected talk)
Advances in Computational Biology. Barcelona, November 28th, 2019
103. From Long Reads to Transcript Function: Bioinformatics Tools for Iso-Transcriptomics Analysis (Keynote Speaker)
North America PacBio Users Group Meeting. Delaware University, September 25th, 2019
102. Tools for transforming multiomics data into disease models (Selected talk)
EMBO | EMBL Symposium: Multiomics to Mechanisms - Challenges in Data Integration. EMBL Heidelberg, September 13th, 2019
101. Multiomics approaches to model development and disease (Invited Speaker)
Institute for Integrative Systems Biology (I2SysBio). Valencia, July 16th, 2019
100. Multiomics and Third Generation Sequencing: at the forefront of genomics research (Invited Speaker)
Barcelona Supercomputing center (BSC). Barcelona, June 11th, 2019
99. Multiomics and Third Generation Sequencing: at the forefront of genomics research (Invited Speaker)
Centre for Research in Agro Genomics (GRAG). Barcelona, June 11th, 2019

98. From long reads to functional analysis of isoforms: bioinformatics tools to understand differential isoform expression in neural differentiation (Invited Speaker)
ENCODE Long reads meeting. Barcelona, June 9th- 10th, 2019
97. Multiomics and Third Generation Sequencing: at the forefront of genomics research (Invited Speaker)
Animal Science Program, University of Florida. Gainesville, April 22th, 2019
96. Multi-omics and third generation sequencing strategies for the future of genome research. The functional transcriptomics story (Keynote Speaker)
20 Years of Genomics. École normale supérieure, Paris, March 28th, 2019
95. From biomarkers to systems models: methods and software for multi-omics data integration (Keynote Speaker)
Challenges and perspectives in integrative bioinformatics. Paris, France, September 17th 2018
94. SQANTI: extensive characterization of long-read transcript sequences for quality control in full-length transcriptome identification and quantification (Selected talk)
European Conference in Computational Biology, ECCB2018. Athens, Greece, September 11th 2018
93. Bioinformatics methods for the integrative analysis of multi-omics and third generation sequencing data (Invited Speaker)
Spetses ChroMe summer school. Spetses Greece, August 26th 2018
92. Methods for multiomics data integration and third generation sequencing data analysis (Selected talk)
Bioinformatics Valencia (CIPF). Valencia, July 12th, 2018
91. Integrative analysis of multiomics TEDDY data reveals dysregulation at molecular events up to 12 months before seroconversion (Invited Speaker)
TEDDY project meeting. Washington DC, May 2nd 2018
90. Bioinformatics and Statistical Approaches for the Integration of Metabolomics and Transcriptomics Data (Invited Speaker)
2018 SECIM Metabolomics Symposium. Gainesville, Florida, April 26th 2018
89. Functional Profiling of Alternative Isoform expression on Mouse Neural Differentiation using Single Molecule Sequencing and tappAS (Selected talk)
Bermuda Principles. Impact on Splicing. 2nd Annual Conference. Bermuda, February 21st-25th, 2018
88. SQANTI and TAPPAS: Making sense of Iso-seq data (Invited Speaker)
SMRT Informatics Developers Conference @ PAG XVXXI. San Diego, January 17th, 2018
87. PaintOmics3: a web resource for the pathway analysis and visualization of multiomics data (Invited Speaker)
Jornadas de Bioinformática. Valencia, 2018
86. Multiomics data integration to unravel local gene regulatory networks (Invited Speaker)
International Workshop in Environmental Omics Integration and Modeling. CosmoCaixa, Barcelona, Spain, October 20th 2017
85. Tools and Methods for Multiomics Data Integration (Invited Speaker)
ChroMe project meeting. Oxford, July 12th, 2017
84. The STATegra road map for the design and analysis of multiomics perturbation experiments (Invited Speaker)
Leeds Advanced Statistical Research 2017/ Mimomics Workshop. University of Leeds, June 29th 2017
83. Unravelling novel transcriptome functional features (Selected talk)
Conference Lectures of the Bioinformatics Master of the University of Murcia. University of Murcia, May 19th, 2017
82. Functional Genomics and Transcriptomics: opportunities and challenges for analysis and modeling (Invited Speaker)
Biology Research Seminar, University of Florida. Gainesville, November 14th, 2016
81. Multiblock integration of T1D gene expression and metabolomics data to study T1D progression (Selected talk)
TEDDY fall meeting. Tysons Corner, Virginia, November 8th, 2016
80. Developing statistical approaches for the integration of multi-omics data (Invited Speaker)
Frontiers in Genomics Program. Universidad Autónoma de Mexico. Cuernavaca, 24th October 2016
79. Functional Genomics and Transcriptomics: opportunities and challenges for analysis and modeling (Invited Speaker)
Biocomplexity Group Seminar, University of Florida. Gainesville, October 4th, 2016
78. Functional transcriptomics in the post-NGS era: multiomics integration and new technologies (Plenary lecture)
Third International Conference of Computational Biomedicine, CBM 2016. Gainesville, Florida 25th-27th February 2016
77. Functional Analysis at Isoform Resolution (Selected talk)
Pacbio industrial workshop. XXIV Plant and Animal Genome Conference. San Diego, California 12th January 2016
76. Unravelling novel transcriptome functional features by NGS technologies (Opening lecture)
VI Argentinian Conference in Bioinformatics and Computational Biology. Bahia Blanca, Argentina, 14th-16th October 2015

75. Comparison of temporal gene expression profiles with other omics to understand gene expression regulation (Selected talk)
Workshop on Statistical Methods for Omics Data Integration and Analysis. Valencia, Spain. 14th-16th September 2015
74. Lessons and results of multi-omics data analysis (Keynote Speaker)
JOBIM 2015. Clermont-Ferrand, 6th- 9th July 2015
73. Integration of multi-omics data to study B-cell differentiation: experimental design and analysis issues (Keynote Speaker)
ABS4NGS Workshop. Paris, France, 22nd-23rd June 2015
72. STATegra: Statistical and Bioinformatics Resources for Analysis of Multi-Omics Projects (Selected talk)
5th NGS Conference (distinguished speaker). Boston, USA, 21st-22nd May 2015
71. Functional Alternative Isoform Expression Analysis Using Long Read Technologies (Selected talk)
Post-transcriptional Gene Regulation Workshop, Plant and Animal Genome Conference XXIII. San Diego, January 11th, 2015
70. Functional Alternative Isoform Expression Analysis Using Long Read Technologies (Selected talk)
Centro de Investigación Príncipe Felipe. Valencia, January 30th, 2015
69. The STATegra Initiative Develops Novel Methodologies for the Integrative Analysis of Multiple Types of NGS & Omics Data (Selected talk)
Bioinformatics Workshops, Plant and Animal Genome Conference XXIII. San Diego, January 13th, 2015
68. The STATegra NGS Experiment Management System (Selected talk)
Computer Demo Session, Plant and Animal Genome Conference XXIII. San Diego, 14th January 2015
67. Functional Annotation of a mouse neural differentiation process (Keynote Speaker)
Australian Bioinformatics Conference. Melbourne, Australia, 11th October 2014
66. The STATegra project: new tools for analysis and integration of multi-omics data (Keynote Speaker)
Conference of the Australasian Genomics Technologies Association. Melbourne, Australia, 13th October 2014
65. The STATegra project: new statistical tools for analysis and integration of diverse omics data (Invited Speaker)
EpiConcept Workshop 2014. Gran Canarias, Spain, 8th May 2013
64. NGS in Functional Genomics. NGS data integration (Invited Speaker)
SeqAhead Workshop: NGS after the Gold Rush. Norwich, UK, 6th May 2014
63. Bioinformatics for the Diverse Life Sciences (Invited Speaker)
Genetics Institute, University of Florida. Gainesville, Florida, USA, 17th February 2014
62. A Tour Though Data Integration Approaches at the GGE Lab (Selected talk)
Centro de Investigación Príncipe Felipe. Valencia, January 24th, 2014
61. The STATegra project: new statistical methods and tools for integrative omics data analysis (Invited Speaker)
ALLBIO Meeting. Uppsala, 7th-8th October 2013
60. Multidisciplinary multi-institutional PhDs (Invited Speaker)
ISCB/GOBLET Meeting. Berlin 19th July 2013
59. The STATegra project: new statistical methods and tools for integrative omics data analysis (Invited Speaker)
Workshop in Translational Genomics. Barcelona, 26th April 2013
58. Pathway-based linear models (Invited Speaker)
SeqAhead/STATegra High throughput and data integration workshop. Barcelona, 15th February 2013
57. Analysis of Fungal Transcriptomics with CLC Genomics Workbench and Blast2GO (Selected talk)
XXI Plant and Animal Genome Conference (Invited conference). San Diego, 15th January 2013
56. Transcriptome analysis with RNAseq: promises and biases (Invited Speaker)
Department of Genetics, Stanford University. Stanford, 28th September 2012
55. Pathway based methods to unravel functional relationships: application to pathway network inference and drug repurposing (Invited Speaker)
UCB Statistics and Genomics Seminars. Berkeley, 27th September 2012
54. NGS of a transdifferentiation system and other RNA-seq tricks (Invited Speaker)
Joining Forces Symposium. Zurich, 22nd June 2012
53. Functional Annotation of Sequence Data (Invited Speaker)
COST Action SeqAhead Course in Next Generation Sequencing. Uppsala, 31st May 2012
52. Next generation sequencing in transcriptomics: new views on the genome and much confusion (Invited Speaker)
Langebio Institute, CINVESTAV. Irapuato, Mexico, 8th May 2012
51. Transcriptional networks controlling virulence in filamentous fungal pathogen (Selected talk)
Joint Status Seminar of the ERA-Net PathoGenoMics. Tenerife, 23rd January 2012

50. Sequencing the Snake Venom Transcriptome for Its Applications in Biomedicine (Selected talk)
Plant and Animal Genome Conference XX. San Diego, California, 15th January 2012
49. Differential expression with RNA-seq: new potentials and new concerns (Invited Speaker)
Instituto Valenciano de Biomedicina. Valencia, 18th November 2011
48. NOISeq: a RNA-seq differential expression method robust for sequencing depth biases (Selected talk)
COST SeqAhead meeting. Brussels, 8th November 2011
47. Aplicaciones de las nuevas tecnologías de secuenciación masiva al estudio de la relación genoma-proteoma (Selected talk)
Conferencia de la Sociedad Española de Bioquímica y Biología Computacional. Barcelona, 7th September 2011
46. Differential expression in RNASeq: a matter of depth (Selected talk)
Conference of the International Society of Computational Biology/ European Conference in Computational Biology (ISCB/ECCB). Austria Center Vienna, 18th July 2011
45. Differential expression in RNASeq: a matter of depth (Selected talk)
Critical Assessment of Massive Data Analysis (CAMDA) 2011. Austria Center Vienna, 15th July 2011
44. Ontología Génica y Anotación Funcional (Invited Speaker)
AECID CYDET Curso Bioinformática y Genómica Vegetal. Cartagena de Indias, Colombia, 11th-13th July 2011
43. Differential expression in RNAseq Studies (Invited Speaker)
Practical Course on Bioinformatics and Network Biology. Centro de Investigación del Cáncer, Salamanca, Spain, 23rd June 2011
42. Blast2GO: A Gene Ontology annotation, visualization and analysis tool for functional genomics projects (Invited Speaker)
Practical Course on Bioinformatics and Network Biology. Centro de Investigación del Cáncer, Salamanca, Spain, 23rd June 2011
41. Introduction to NGS technology (Invited Speaker)
Data analysis workshop for massive sequencing data E.T.S. de Ingenierías Informática y de Telecomunicación. University of Granada, Spain, 13th June 2011
40. Differential expression with RNASeq: length and depth does matter (Selected talk)
Bioinformatics and High Throughput Sequencing 2011. Institute Pasteur Paris, France, 22nd March 2011
39. High performance sequencing and gene expression quantification (Selected talk)
RES Scientific Seminar of Supercomputing and Next Generation Sequencing. Parque Tecnológico de Andalucía, Málaga, Spain, 17th March 2011
38. Variable Selection for Multifactorial Genomic Data (Selected talk)
XXXII Congreso Nacional de Estadística e Investigación Operativa y VI Jornadas de Estadística Pública. Universidad Da Coruña, September 17th, 2010
37. Biología cuantitativa ¿cuántos son dos más dos? (Selected talk)
Departamento de Matemáticas. Universitat de València, Spain, May 2010
36. Pathway Analysis of Transcriptomics Data (Selected talk)
IX Jornadas Nacionales de Bioinformática. Calouste Gulbenkian Foundation, Lisbon, Portugal, 4th November 2009
35. Pathway Analysis of Transcriptomics Data (Selected talk)
Séptima reunión de la red valenciana de genómica y proteómica. Facultad de Farmacia de la Universitat de València, Spain, 12th November 2009
34. Pathway Network Analysis in Systems Biology (Selected talk)
XII Conferencia Española de Biometría. Universidad de Cádiz, Spain, 24th September 2009
33. The Joined GEPAS, Babelomics and Blast2GO Suites: Statistical and Functional Analysis of Genomics Data on the Web (Computer demo)
Plant and Animal Genome Conference, XVII. San Diego, USA, 14th January 2009
32. B2G-FAR: The Blast2GO Functional Annotation Repository (Computer demo)
Plant and Animal Genome Conference, XVII. San Diego, USA, 14th January 2009
31. PLS Analysis with Gene Ontology data: inferring the phenotype from the function of genes (Selected talk)
11th Conference on Chemometrics in Analytical Chemistry. Montpellier SupAgro, Montpellier, France, 3rd July 2008
30. Finding relationships between high throughout data sources through multiway projection methods (Invited Speaker)
MIPS, University of Munich. Munich, Germany, 4th March 2008
29. Systems Level Analysis of Time Course Omics Data (Invited Speaker)
Department of Statistics, University of Barcelona. Barcelona, Spain, November 2008
28. Systems Level Analysis of Time Course Omics Data (Selected talk)
(EMBNET) Conference 2008: 20th Anniversary Celebration. Martina Franca, Italy, 19th September 2008

27. Functional Genomics: Concepts, Databases and Methods (Invited Speaker)
First International Course in Environmental Genomics. DISAV, University of Piemonte Orientale, Italy, 15th December 2008
26. An approach to the characterization of the date palm genome (Selected talk)
II Congreso Internacional Oasis y Turismo Sostenible. La Tribuna del Agua de Expo Zaragoza, 9th August 2008
25. Finding relationships between high throughput data sources through multiway projection methods (Selected talk)
Jornadas Nacionales de Bioinformática. Centro de Investigaciones Príncipe Felipe, 13th February 2008
24. Partial Least Squares on Gene Functional Classes (Selected talk)
Critical Assessment of Gene Expression Data Analysis (CAMDA Conference). Centro de Investigación Príncipe Felipe, Valencia, Spain, 14th December 2007
23. High throughput functional annotation and analysis with the Blast2GO suite (Invited Speaker)
EMBRACE Gene Ontology Workshop. University of Bari, Italy 7th-9th November 2007
22. Multi-way methods for integrating data and knowledge in genomics research (Selected talk)
XI Española y Primer Encuentro Iberoamericano de Biometría. Universidad de Salamanca, Spain, 20st June 2007
21. N-way methods to functional genomics: can we integrate all data in a multidimensional box? (Selected talk)
Systems Biology Symposium. Universidad Complutense de Madrid, Spain, 8th June 2007
20. Bioinformática en genómica vegetal: anotación de funciones génicas y análisis de respuestas transcripcionales (Invited Speaker)
University of Malaga. Málaga, Spain, 4th May 2007
19. Anotación funcional de secuencias en especies no modelo (Invited Speaker)
Introduction to Bioinformatics. University of Alicante, Spain 19th December 2007
18. Blast2GO v2.0: A comprehensive functional annotation and analysis tool for the genomics of non-model species (Computer demo)
Plant and Animal Genome Conference, XV. San Diego, USA, 15th January 2007
17. A multi-way strategy for the integrative analysis of high dimensionality 'omics' data (Selected talk)
7th Spanish Symposium on Bioinformatics and Computational Biology. Zaragoza, November 22nd, 2006
16. Blast2GO: Conceptos de anotación funcional automática y su aplicación en una herramienta bioinformática (Invited Speaker)
BiT-Lab. Departamento de Arquitectura de Computadores, Universidad de Málaga, Málaga, Spain, 6th October 2006
15. Blast2GO: Conceptos de anotación funcional automática y su aplicación en una herramienta bioinformática (Invited Speaker)
Foro de Biotecnología de Plantas, Taller Bioinformática. Universidad de Murcia, Spain, 28th September 2006
14. maSigPro: A method to identify significantly differential expression profiles in time-course microarray experiments (Poster)
X Conferencia Española de Biometría. Oviedo, Spain, 27th May 2006
13. Vitamin: an Ontology-driven information System for Mutant Annotation (Selected talk)
4th European Conference on Computational Biology. Madrid, Spain, 28th September to 1st October 2005
12. Blast2GO: A universal Gene Ontology annotation, visualization and analysis framework for th egenomics research of non-model species (Selected talk)
4th European Conference on Computational Biology. Madrid, Spain, 28th September to 1st October 2005
11. Aplicación de la Genómica Funcional como Respuesta a Problemas Biológicos (Invited Speaker)
Instituto de Productos Lácteos de Asturias. Oviedo, Spain, May 25th, 2005
10. Analysis and interpretation of genome wide datasets: from sequence to function to biology (Invited Speaker)
School of Biosciences, University of Birmingham. Birmingham, UK, 2005
9. Finding significant differential gene expression profiles through maSigPro (Invited Speaker)
Departamento de Estadística, Universidad de Barcelona. Barcelona, Spain, 2005
8. Functional genomics in citrus or the bioinformatics of non-model species (Invited Speaker)
Department of Molecular Biology, University of Groninghem. Groningen, The Netherlands, 28th November 2005
7. Functional genomics in citrus or the bioinformatics of non-model species (Invited Speaker)
TNO Nutrition and Food Research. Zeist, The Netherlands, 3rd November 2005
6. Blast2GO (Selected talk)
GO Users Meeting organized by EMBL-EBI. Bergen, Norway, 14th September 2005
5. maSigPro: a method to identify significantly differential expression profiles in time-course microarray experiments (Poster)
5th Annual Spanish Bioinformatics Conference. UPC, Barcelona, 29th November – 2nd December 2004

4. **Blast2GO: a universal annotation and visualization tool for functional genomics research** (Poster)
5th Annual Spanish Bioinformatics Conference. UPC, Barcelona, 29th November – 2nd December 2004
3. **Blast2GO y maSigPro: herramientas bioinformáticas para Genómica Funcional en Investigación Agraria** (Selected talk)
Tercera reunión de la red valenciana de genómica y proteómica. IATA, Valencia, 28th October 2004
2. **Expression of *Caldariomyces fumago* chloroperoxidase in *Aspergillus niger*** (Selected talk)
VII International Fungal Biology Conference. Groningen, Netherlands, August, 1999
1. **Expression of the heme-peroxides in *Aspergillus*** (Selected talk)
Symposium NvvM section Mycology (oral presentation). Wageningen, October 29th, 1998

OUTREACH ACTIVITIES

15. **Iniciativas para medir y reducir la huella de carbono de la computación** (Invited talk)
Congreso de Sostenibilidad y Economía Circular Aplicada, PTI SosEcoCir (Plataforma Temática Interdisciplinar de Sostenibilidad y Economía Circular), CSIC. Madrid, May 6th 2026
14. **Scientific Writing**
NET4MAT Workshop. Valencia, April 24th 2026
13. **Grant Writing**
CaLISTA Training School Workshop. Valencia, April 13th 2026
12. **Technology and Humanism** (round table)
Alfonso X foundation. Murcia, February 19th 2026
11. **Women and Bioinformatics** (Invited talk)
University San Jorge. Zaragoza, February 13th 2026
10. **The BCBHub project to strengthen the CSIC bioinformatics community** (Invited talk)
IV Asamblea Conexión Nanomedicina CSIC. Madrid, November 14th 2025
9. **The unsustainable footprint of Artificial Intelligence** (Invited talk)
IDAEA Institute. Barcelona, November 13th 2025
8. **Cómo ser bioinformática y no morir en el intento** (Invited talk)
Invited talk, Montevideo. Online, October 15th 2025
7. **La Bioinformática en la era de la Inteligencia Artificial** (Invited talk)
School of Sciences, University of Alicante. Valencia, February 20th 2025
6. **Día internacional de la mujer y la niña en la ciencia – 11 de Febrero**
IES Cabanyal. Valencia, February 11th 2025
5. **The Long-reads Transcriptomics European Consortium MSCA-DN project (LongTREC): the making of** (Invited talk)
Workshop on EU funding opportunities, SEBiBC conference. Online, October 16th 2024
4. **Cómo ser IP. La Carrera Investigadora: de los inicios a la consolidación** (Invited talk)
Academia Joven de España. Madrid, 26th October 2022
3. **Medicina personalizada: el tratamiento está en tus genes** (Invited talk)
El País con tu futuro. Madrid, December 20th 2017
2. **Nuevos retos de la medicina personalizada** (Invited talk)
El País con tu futuro. Madrid, November 2015
1. **Nuevos retos de la medicina personalizada** (Invited talk)
MIT EmTech Valencia. Valencia, 5th November 2013

DOCTORAL THESES SUPERVISED

15. **Luidmyla Kondratova**
*From cis-regulatory elements to isoform quantification: a dual approach in *Phaseolus vulgaris* research*
University of Florida, April 2025.
14. **Francisco José Pardo Palacios**
Desarrollo de métodos bioinformáticos y experimentales para el estudio del impacto funcional de las isoformas alternativas
Universitat Politècnica de València, September 2024.

13. **Angeles Arzalluz-Lopez**
Understanding isoform expression and alternative splicing biology through single-cell RNAseq
Universitat Politècnica de València. March 26th, 2024.
12. **Rocío Amorín**
Elucidating the role of microbial dark matter in microbialite-forming ecosystems
University of Florida. September 18th, 2023.
11. **Manuel Guerrero Ugidos**
Desarrollo de métodos estadísticos para la Biología de Sistemas multiómica
Universitat Politècnica de València. 2023
10. **María Teresa Rubio Martínez-Abarca**
Métodos de integración de datos multiómicos para el estudio de enfermedades
Universitat Politècnica de València, June 30th 2022.
9. **Salvador Casaní Gabaldón**
Bioinformatics methods to link metabolic and epigenetic regulation
Universitat València, defense on February 8th 2021.
8. **Tatyana Zamkovaya**
Network analysis of Microbial Dark Matter
University of Florida, 2020
7. **Pedro Furió Tarí**
Development of bioinformatic tools for massive sequencing analysis
Universitat Politècnica de València, 2020
6. **Lorena de la Fuente**
Development of a Bioinformatics Approach for the Functional Analysis of Alternative Splicing
Universitat Politècnica de València, 2019.
5. **Rafael Hernández de Diego**
Development of Bioinformatics Resources for the Integrative Analysis of Next Generation Omics Data
Universitat Politècnica de València, 2016.
4. **Sonia Tarazona Campos**
Statistical methods for transcriptomics: from microarray to RNA-seq
Universitat Politècnica de València, 2014
3. **Stefan Goetz**
Functional characterization of genome-wide sequence data: development of methods and tools for high-throughput analysis
Universitat Politècnica de València, 2010.
2. **Sonia Prado López**
Efectos del oxígeno en la expresión genética y diferenciación de líneas de células madre embrionarias humanas (hESC)
Universitat de València, 2009.
1. **Maria José Nueda Roldán**
Statistical methods for Time Course Microarray data
Universitat Politècnica de València, 2009.

IN PROGRESS

- Alejandro Paniagua, Universitat de València
- Priyansh Srivastava, Universitat de València
- Tianyuan Liu, Universitat de València
- Fabian Jetzinger, Universitat de València
- Enrique Vidal, Universitat Politècnica de València
- Carlos Blanco Gómez, Universitat de València
- Julen Santiago, Universitat de València
- Víctor Gaya, Universitat de València
- Pablo Atienza, Universitat de València

PhD THESIS DEFENCE COMMITTEES

34. **Ángela del Pozo Maté** July 17th, 2026
Facultad de Medicina, Universidad Autónoma de Madrid
A benchmark study of outlier-detection tools for RNA-Seq data in rare disease diagnostics
Role: Secretary of the committee
33. **David Niklas Wissel** July 7th, 2026
Department of Computer Science, ETH Zürich
Characterizing the limits of multi-omics survival models and long-read transcriptomics for precision medicine
32. **Justin Waletich** November 5th, 2024
University of Florida
Characterizing stem cell organization in the colonial marine hydroid hydractinia symbiolongicarpus
31. **Veredas Coleto Alcúdia** November 2024
Universitat Autònoma de Barcelona (CRAG)
Computational approaches for the identification of biomarkers involved in relevant agricultural traits
30. **Josie Gleeson** April 2024
The University of Melbourne, Australia
Investigating the human brain transcriptome and epitranscriptome: insights from long-read sequencing and transcriptional risk profiling
Role: Thesis examiner
29. **Anna Delgado Tejedor** March 2024
Universitat Pompeu Fabra
Decoding the epitranscriptomic complexity through computational methods based on long-read sequencing
28. **Laurel Evie Woodridge** January 2024
University College London
Investigating multi-omics signatures to understand cardiovascular risk and atherosclerosis in systemic lupus erythematosus
Role: External examiner
27. **Sonia García Ruiz** September 7th, 2023
UCL Great Ormond Street Institute of Child Health
Assessing splicing accuracy and its determinants across human tissues using RNA sequencing
26. **Joanna Ficek-Pascual** Augustus 17th, 2023
LMU Munich
Computational methods for dissecting cancer heterogeneity using multi-modal data: from bulk to spatial resolution
25. **Nerea Castillo Marco** June 2023
Universitat de València
Molecular investigation on the etiology of preeclampsia and new strategies for its early diagnosis
24. **Sharon Thompson** 2023
Microbiology and Cell Science Department, University of Florida
Investigation of the impact of diet on the probiotic organism lactobacillus johnsonii n6.2
23. **Adrian Barry Sousa** 2023
Microbiology and Cell Science Department, University of Florida
Microbial communities of the upper Floridan aquifer, U.S.A.: composition, structure, and contributions to biogeochemical cycling
22. **Adelena Nanni** 2022
Genetics and Genomics Doctoral Programme, University of Florida
Insights into the regulation of expression and quantification of Transcripts using modern analytical approaches
21. **Alexandra L. Wiscovitch Bonilla** 2022
Genetics and Genomics Doctoral Programme, University of Florida
Single-cell sexual dimorphisms in non-sexual organs
20. **Katheleen Miller** 2022
Microbiology and Cell Science Department, University of Florida
Exploring adaptation to pressure extremes relevant to earth and mars via growth, transcriptomic, and epigenetic modulation within the genus carnobacterium
19. **Christina Davis** 2022
Microbiology and Cell Science Department, University of Florida
Ecology of subglacial lake microbial communities in west antarctica
18. **Richard Kuo** July 28th, 2022
College of Medicine and Veterinary Medicine. The University of Edinburgh
Identifying Long Non-Coding RNA in the Chicken Transcriptome

17. **Luis Ferrández Peral** June 8th, 2022
Departament de ciències experimentals i de la salut. Universitat Pompeu Fabra
Evolution of the transcriptomic regulation in the primate lineage
16. **Alvaro Montesinos** February 17th, 2022
Departamento de Bioquímica y Biología Molecular y Celular, Universidad de Zaragoza
*Dynamics of almond (*Prunus amygdalus* (L.) Batsch, syn. *P. dulcis* (Mill.)) tree architecture and scion/rootstock interaction*
15. **Jordi Martorell** Abril 27th, 2021
Centro Pzifer, Universidad de Granada
Computational and statistical methods for integrated analysis of biomedical data
14. **Julia Betancourt** 2021
Genetics and Genomics Doctoral Programme, University of Florida
Single-cell analysis reveals targets of an endocrine disruptor in the developing genitalia
13. **Isabel Betegón Putze** November 10th, 2020
Animal Biology, Plant Biology and Ecology Department. Universitat Autònoma de Barcelona
Spatiotemporal analysis of brassinosteroid signaling in the vascular stem cells
12. **Kelsey s. Aadland** 2020
Genetics and Genomics Doctoral Programme, University of Florida
Conservation of early miRNA biogenesis in animal and plant lineages
11. **Krishna Bhattarai** 2020
Horticultural Sciences Department, University of Florida
*Genetic mapping and next-generation sequencing to identify quantitative trait loci and candidate genes for powdery mildew resistance in gerbera (*Gerbera hybrida*)*
10. **Joany Bablilonia** 2019
Microbiology and Cell Science Department, University of Florida
Comparative metagenomics and metabolomics for characterizing stromatolite ecological community function
9. **Morgan Smith** 2019
Genetics and Genomics Doctoral Programme, University of Florida
The Characterization of Sirpγ and its role in Type I Diabetes
8. **Stefanos Fafalios**
Computer Science Department, Creta University
Towards a universal molecular classifier December, 2019
7. **Jordi Durban i Sánchez** 2015
Facultat de Biològiques, Universidad de Valencia
Aplicacions de Next Generation Sequencing en organismes no model : caracterització dels transcriptomes de verins de serps
6. **Stanley Kimbung** 2014
University of the Western Cape
5. **Tamara Garrido Gómez** May 29th, 2012
Facultad de Medicina, Universidad de Valencia
Estudio proteómico del endometrio humano
4. **Patricia Díaz Gimeno** 2011
Departamento de Pediatría, Obstetricia y Ginecología, Universidad de Valencia
Desarrollo de una herramienta molecular diagnóstica de la Receptividad endometrial
3. **Rubén Noglas Cadenas** 2010
Facultad de Informática, Universidad Complutense de Madrid
2. **Laura Pascual Bañuls** 2010
Departamento de Biotecnología, Universidad de Valencia
1. **Aureliano Bombarely Gómez** 2007
Departamento de Biología y Bioquímica, Universidad de Málaga

MASTER AND GRADUATE THESES SUPERVISED

35. **Raul López** 2026
Master en Bioinformática. Universitat de Valencia
Desarrollo de un pipeline bioinformático para el análisis funcional de isoformas de splicing

34.	Wouter Maarsen Master in Bioinformatics, University of Nijmegen, The Netherlands <i>Development of an lrrNA-seq benchmarking platform</i>	2025
33.	Julia Lienard Bioinformatics Masters, Lund University, Sweden <i>Exploring Transcript divergency in a type I diabetes in vitro model using long read RNA sequencing</i>	2025
32.	Víctor Gaya Master en Bioinformática. Universitat de Valencia <i>Development of image alignment methods for Spatial Transcriptomics data of Spinal Cord</i>	2024
31.	Kimia Salek Master in biotechnology for food science. Università degli Studi di Padova <i>Benchmarking splice-aware long-read aligners with a focus on micro-exon detection</i>	2024
30.	Arianna Febbo Master en Bioinformática. Università degli studi di Milano <i>Development of a multiomics single-cell simulator</i>	2023
29.	Enrique Sapena Ventura Master en Bioinformática. Universitat de Valencia <i>LRGASP: OpenEBench implementation</i>	2023
28.	Alejandro Escobar Simón Master en Biomedicina y Biotecnología, Universitat de Valencia <i>Estudio de la inestabilidad transcripcional asociada a envejecimiento, desarrollo y/o enfermedad mediante tecnologías de secuenciación de tercera generación</i>	2023
27.	Alessandra Martínez Master en Bioinformática, Universitat de Valencia <i>Development of isoAnnot: a new pipeline for Transcriptome functional annotation at isoform Resolution</i>	2023
26.	Idoia Alvarez Master en Bioinformática, Universitat de Valencia <i>Anotación de sitios de unión de miRNA y señales de localización celular en isoformas</i>	2023
25.	Cristina Araiz Grado de Biotecnología, Universitat Politècnica de Valencia <i>Análisis multiómico con MAMBA</i>	2023
24.	Eva Navarre Grado de Biotecnología, Universitat Politècnica de Valencia <i>Análisis multiómico de datos circadianos</i>	2022
23.	Isidro Sobrino Grado de Biotecnología, Universitat Politècnica de Valencia <i>Optimización, validación y aplicación a un caso real de una herramienta bioinformática para el análisis transcriptómico de organismos no modelo utilizando lecturas largas</i>	2022
22.	Enrique Sales Grado de Biotecnología, Universitat Politècnica de Valencia <i>Análisis multiómico de datos circadianos</i>	2022
21.	Alejandro Paniagua Máster de Bioinformática, Universidad de Valencia <i>Evidence-driven annotation of the Trichechus manatus latirostris genome using long-reads</i>	2022
20.	Jorge Mestre Máster de Bioinformática, Universidad de Valencia <i>SQANTISIM: a simulator of controlled novelty and degradation of transcripts sequenced by long-reads</i>	2022
19.	Pedro Salguero Máster de Bioinformática, Universidad de Valencia <i>tappAS: marco computacional para el análisis del impacto funcional del splicing alternativo</i>	2019
18.	David Richard Toole M.S. Microbiology and Cell Science, University of Florida <i>Picrust2 and Tax4fun2: a comparison of bacterial functional predictions tools in Southwest Florida soils</i>	2018
17.	Héctor Carmona Salido Máster de Bioinformática, Universidad de Valencia <i>Multi-omics integration to elucidate the effects of hyperamonemia in minimal hepatic encephalopathy</i>	2018

16. **Víctor Sánchez Gaya** 2017
Licenciatura biotecnología, Universidad Politécnica de Valencia
Estudio del efecto de la exposición a pesticidas en el neurodesarrollo mediante la integración de datos ómicos
15. **Francisco Huertas López** 2017
Master de Bioinformática, Universidad de Murcia
DNA Methylation and Metagenomic sequencing data integration in a colorectal cancer study
14. **Jordi Martorell** 2015
Licenciatura biotecnología, Universidad Politécnica de Valencia
Análisis de expresión alternativa de isoformas en el tiempo mediante datos de RNA-seq
13. **Rodrigo García Valiente** 2015
Máster de Bioinformática, Universidad de Valencia
Desarrollo de recursos computacionales para la anotación y caracterización funcional del ARN largo no codificante en especies no modelo
12. **Rafael Hernández de Diego** 2012
Licenciatura biotecnología, Universidad Politécnica de Valencia
Caracterización funcional de lncRNAs a partir de datos de NGS
11. **David Jovani Sales** 2012
Licenciatura biotecnología, Universidad Politécnica de Valencia
Estudio de la organización funcional de los genes humanos y la regulación de la expresión de sus funciones en distintos tejidos mediante técnicas de secuenciación de nueva generación
10. **Aaron Weimann** 2012
Master Program in Bioinformatics, Saarland University (Germany)
Functional Profiling and Quantitative Comparison of Microbial Communities
9. **Federico José García López** 2009
Licenciatura biotecnología, Universidad Politécnica de Valencia
Desarrollo de un método bioinformático de integración y visualización de datos de t. transcriptómica y metabolómica
8. **Jorge Ruiz Otera** 2010
Licenciatura biotecnología, Universidad Politécnica de Valencia
Análisis funcional del splicing alternativo mediante técnicas de ultrasecuenciación
7. **Óscar David Sánchez Jiménez** 2007
Departamento de Física Aplicada, Universidad de Valencia
Técnicas del modelado conceptual aplicadas a la información biológica
6. **María José Nueda Roldán** 2005
Tesina. Polytechnical University Valencia, Spain
Departamento de Estadística e Investigación Operativa Aplicadas y Calidad Métodos estadísticos aplicados a la transcriptómica
5. **María Teresa Peralta** 2004
Escuela de Ingeniería de Telecomunicaciones
Graduation Project (TFG) Polytechnical University Valencia, Spain Normalización de datos de microarrays
4. **Stefan Goetz** 2004
Departamento de Física Aplicada
Graduation Project (TFG) Polytechnical University Valencia, Spain Blast2GO: An universal annotation tool for the functional annotation of sequence data
3. **Paul Roepman** 2002
Graduate MSc student thesis. University of Wageningen, The Netherlands
cDNA microarray analysis. Effects of quercetin on colon cancer cells
2. **J.J.H.P Bartels** 2000
Fontys Hogeschool Eindhoven, The Netherlands
The production of lignin peroxidase in Aspergillus niger
1. **Gerri Weelink** 1999
Hogeschool Drenthe, Emmen, The Netherlands
The trans activity of the chloroperoxidase pro-peptide in Aspergillus niger

TEACHING

ORGANISATION OF AND LECTURING AT SPECIALISED BIOINFORMATICS COURSES

- Microarray Data Analysis, CIPF, Valencia, March 2008
- Microarray Data Analysis, CIPF, Valencia, March 2009
- Course in Automated Functional Annotation and Data Mining, Valencia, September 2009
- Course in Automated Functional Annotation and Data Mining, Florida, October 2009
- I Jornada de Tecnologías para la Salud, Valencia, November, 2009 (Only lecturer)
- Course in Automated Functional Annotation and Data Mining, Cape Town, December 2009
- Course in Automatic Functional Annotation and Data Mining, Oeiras, May 2010
- Microarray Data Analysis using GEPAS and BABELOMICS, Oeiras, May 2010
- Massive Data Analysis, CIPF, Valencia, June 2010
- Course in Automated Functional Annotation and Data Mining, Valencia, October 2010
- Course in Automated Functional Annotation and Data Mining, Florida, November 2010
- Course in Automated Functional Annotation and Data Mining, Cape Town, December 2010
- Massive Data Analysis, CIPF, Valencia, March 2011
- Course in Automated Functional Annotation and Data Mining, Davis, July 2011
- Course in Automated Functional Annotation and Data Mining, Valencia, October 2011
- Transcriptómica y modelización de proteínas empleando Supercomputación, Castilla y León, November, 2011
- Course in Transcriptome Assembly, Automated Functional Annotation and Data Mining, Oeiras, February 2012
- Course in Automated Functional Annotation and Data Mining, Irapuato. Mexico, May 2012
- Course in Automated Functional Annotation and Data Mining, Davis, July 2012
- Course in Automated Functional Annotation and Data Mining, Valencia, October 2012
- Course in Blast2GO and Babelomics, Portici, Italy, November 2012
- Course in Automated Functional Annotation and Data Mining, Brisbane, Australia, January 2013
- IX International Course of Massive Data Analysis, Valencia, March 2013
- Course in Automated Functional Annotation and RNA-seq, Oeiras, March 2013
- Course in Automated Functional Annotation and Data Mining, Valencia, October 2013
- Course in Automated Functional Annotation and Data Mining, Sao Paulo, November 2013
- Course in RNA-seq and Functional Annotation, Buenos Aires (Argentina), November 2013
- Course in Automated Functional Annotation and Data Mining, La Paz (México), January 2014
- NGS Course in transcriptomics, Cancun (México), April 2016
- Multiomics and Integrative Analysis of Gene Expression, Valencia, January 2017.
- Workshop in Multiomics Data Integration and Technology Transfer, Mexico City, November 2017.
- Bioinformatics III (Multiomics Technologies) at ChroMe ETN Network, Stockholm, December 2017.
- Multiomics and Integrative Analysis of Gene Expression, Valencia, March, 2018.
- Full-Length RNA-Seq Analysis using PacBio long reads: from reads to functional interpretation, Virtual ISMB2020 Conference, July 2020
- Full-Length RNA-Seq Analysis using PacBio long reads: from reads to functional interpretation, Virtual ECCB2020 New Trends in Bioinformatics, September 2020
- PacBio Iso-Seq Workshop Online UCDavis, September 30th – October 2nd, 2020
- tappAS for functional analysis of lrrRNA-seq data, Madison, USA, July 2022
- LongTREC Summer School, Earlham Institute, July 14th – 17th, 2025
- Montevideo School in Bioinformatics, Pasteur Institute, October 13th – 15th, 2025
- VALT Summer School, Valencia, June 25th – 27th, 2026
- BCBHub Summer School in Advanced Bioinformatics, Oviedo, July 20th – 24th, 2026

REGULAR TEACHING

- R for Functional Genomics, University of Florida, 3 Credits, 2015-17
- Human Genetics, University of Florida, 3 Credits, 2017
- Invited lecturer at the Polytechnical University of Valencia, 2004-2007
- Invited lecturer at the Máster de Bioinformática, Universidad Complutense Madrid, 2007-2008
- Invited lecturer at the Máster de Bioinformática, Universidad Valencia, 2013
- Invited lecturer at the Máster de Bioinformática, Universidad Murcia, 2013, 2025
- Invited lecturer at the Máster de Bioinformática, Polytechnical University of Valencia, 2018
- Member of 32 UF graduate student committees

- Supervisor 10 undergrad student internships, Polytechnic University of Valencia, 2004-2017
- Supervisor 3 undergrad student internships, University of Valencia, 2006-2017
- Supervisor undergraduate student theses, Polytechnic University of Valencia, 2004

ORGANISATION OF CONFERENCES

- Critical Assessment of Microarray Data Analysis Conference 2007 (CAMDA)
- Jornadas Nacionales de Bioinformática, CIPF, January 2008
- SeqAhead Workshop on High Performance Computing for Next Generation Sequencing Analysis (HPC4NGS), 2012
- The Next NGS Challenge Conference, CIPF, May 2013 (Chair)
- HiTSeq conference within ISMB, Boston (July 2014) and Dublin (July 2015), Orlando (July 2016), Prague (July 2017), Basel (July 2019), Virtual formats (July 2020 and July 2021), Madison (2022), Lyon (2023), Montreal (2024)
- SMODIA2015 Workshop, CIPF, September 2015 (Chair)
- UF Genetics Institute Symposium 2019-2017
- Organization Bioinformatics@Valencia, July 2018 (Chair)
- UF Genetics Institute Symposium, November 2019 (Chair)
- CSHL Genomics Informatics, November 2019 (Discussion leader)
- European Conference in Computational Biology 2020 (GENES track chair) and 2022 (Chair Proceedings)
- Primer Congreso de la Sociedad Española de Biología Computacional y Bioinformática, Valencia, 2024.
- Asamblea de la Conexión de Biología Computacional y Bioinformática del CSIC (Valencia, 2025, Madrid 2025, Madrid 2025)
- Valencia Long-reads transcriptomics (Valencia, June 29th to July 1st 2026)

ADVISORY ACTIVITY AND INSTITUTIONAL SERVICE

- Scientific Advisory Board member of the Instituto Biosanitario de Granada, Spain
- Member of the Scientific Advisory Board of the Interdisciplinary Center for Biotechnological Research, University of Florida
- Scientific Advisory Board member of the Informatics Institute, University of Florida
- Scientific Advisory Board member of the Bioinformatics Core ICBR, University of Florida
- Scientific Advisory Board member of the Scientific Computing Program, University of Florida
- Scientific Advisory Board member of the French Bioinformatics Institute (IFB).
- Committee member Juan de la Cierva Postdoctoral awards, Spanish Ministry of Economy and Competitiveness, 2016
- Panel Member at the “Relationship between genome and epigenome” Workshop organized European Commission’s Directorate General for Research and Innovation (DG RTD) and Cooperation in Science and Technology (COST), Brussels, 14th-15th February 2013.
- Panel Member at the “Big data in health research: an EU action plan” Workshop organized European Commission’s Directorate General for Research and Innovation (DG RTD), Luxemburg 30th October 2015.
- Evaluation Committee member BioExcel H2020 project 2016-2017
- Member Biotechnology Evaluation Committee Plan Nacional (Spain), 2017
- Member NSF Advances in Biological Informatics (ABI) Career Panel, 2017
- Senior Programme Committee Member as HiTSeq COSI Chair, ISMB Conference 2018
- Member of Barcelona Supercomputing Center Access Committee, 2017-2019
- Member of Scientific Committee of I2SysBio, from 2022
- Member of HPC Advisory Committee of I2SysBio, from 2022
- Chair of Sustainability Committee of I2SysBio, from 2022
- Evaluator for EU ESFRI Landmarks projects, 2023
- Scientific Advisory Board member of IMAGING VLC, 2023
- Expert Evaluator of the EU ESFRI Landmark Elixir, 2023
- Scientific Advisory Board Member of the Plant Biotechnology and Genomics Center (Centro de Biotecnología y Genómica de Plantas, CBGP, UPM-INIA/CSIC), 2023
- Expert Evaluator of the Department of Molecular Life Sciences, University of Zurich, 2023.
- Chair of GreenISCB, from 2023
- Technical Evaluation Committee member for the Biology-Molecular and Cellular Biology of the Spanish Science Agency national research projects, 2025.

- Member of the ERC Synergy 2024 Life Sciences panel.
- Scientific Advisory Board Member of the Center of Research in Agro-Genomics (CRAG), 2025

SOCIETY MEMBERSHIP

- International Society of Computational Biology (ISCB)
- Green Science Working Group ISCB
- Chair HitSeq
- Chair of the ELIXIR RNA-data Focus Group
- Member of the ELIXIR Systems Biology Community
- Sociedad Iberoamericana de Bioinformática (SoiBio)
- Sociedad Española de Biotecnología (Sebio)
- GOBLET, global organization for Bioinformatics training
- American Association for Advance in Science
- Sociedad Española de Biología Computacional y Bioinformática.

REVIEWING AND EDITORIAL ACTIVITIES

REVIEWER OF JOURNALS

Nature, Nature Methods, Nature Neurosciences, Nature Metabolism, Nature Protocols, Nature Biotechnology, Nature Neurosciences, Nature Evolution, Nature Reviews Molecular Cell Biology, Scientific Reports, Scientific data, Nature Communications, Genome Research, Genome Biology, Bioinformatics, Bioinformatics Advances, Briefings in Bioinformatics, Communications Biology, RNA, BMC Bioinformatics, BMC Systems Biology, eLife, BMC Neuroscience, BMC Genomics, BMC Research Notes, BMC Neuroscience, GENES, PLoS ONE, PLoS Computational Biology, Nucleic Acid Research, Genomics, Journal of Genomics, Journal of Chemometrics, Bioinformatics Advances, Plant Biology, Bioinformatics and Biology insights, JZUS-B (Biomedicine & Biotechnology), Genome Medicine, International Journal of Plant Genomics, BBA – Biochimica et Biophysica Acta, Cancer Genetics, Human Heredity, iScience, NAR Cancer, NAR Genomics and Bioinformatics, RNA Biology.

REVIEWER FOR FUNDING AGENCIES

ANEP (Spain), The European Research Council (ERC), ERC Synergy grants, The Executive Agency for Higher Education, Research, Development and Innovation Funding (Romania), European Commission, European COST Action, Natural Environment Research Council (UK), Institute of Computer Science Foundation for Research & Technology-Hellas (FORTH) (Greece), UK Fight for Sight, Argentina Science, Technology and Productive Innovation Agency, National Science Foundation (USA), National Institutes of Health (NIH), Alzheimer Research UK, NWO The Netherlands, European Science Foundation, French National Research Agency (France), Novo-Nordisk Foundation Center for Biosustainability (Denmark), King Abdullah University of Science and Technology (South Arabia), Karolinska Institute (SE), Agencia Estatal de Investigación (AEI, Spain), Research Foundation Flanders (FWO, Belgium), Slovenian Research Agency (ARIS), Genome Canada, Ontario Institute for Cancer Research (OICR, Canada), CRDF Global.

REVIEWER AT CONFERENCES

CAMDA, Jornadas de Bioinformática, Bioinformatics Italy 2012, Bioinformatics 2014, ISMB conferences, Genome Informatics, RECOMB 2026.

EDITORIAL COMMITMENTS

- Associated Editor of Scientific Data (Nature publishing)
- Associated Editor of Genes (MDPI-Open Access)
- Editor of Scientific Data Multiomics Collection (Nature publishing)
- Editor of BMC System Biology Special Issue in Data Integration (BioMed Central)
- Editor of BMC Bioinformatics Special Issue in Multiomics analysis (BioMed Central)
- Guest Editor of Genome Research Special Issue in Long reads Methods (2024)