



# Jaime A Castro-Mondragon

BIOINFORMATICIAN (SCIENTIST LEVEL II)

Nykode Therapeutics AS

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## Personalia

### Date of birth

13/02/90

### Citizenship

MEXICAN

### Children

2

### Paternity leave

SPRING 2021, AUTUMN 2024

## Education

### Aix-Marseille Universite

Marseille, France

PHD IN BIOINFORMATICS

2014 - 2017

- Graduated with honors. Thesis supervised by PhD Jacques van Helden. 6 publication derived from the thesis work.

### Institute de biology de l'Ecole Normale Supérieure

Paris, France

MASTER IN SYSTEMS BIOLOGY

2013 - 2014

- Thesis supervised by PhD Jacques van Helden.

### Universidad Nacional Autónoma de México

Cuernavaca, Mexico

BACHELOR IN GENOMIC SCIENCES

2009 - 2013

- Graduated with honors. Thesis supervised by PhD Julio Collado-Vides and PhD Alejandra Medina-Rivera

## Research/Working Experience

### Nykode Therapeutics AS

Oslo, Norway

BIOINFORMATICIAN (SCIENTIST II)

2022 - Present

- Design and analysis of RNA-seq data. Establishment of bioinformatic workflows (prediction of MHC-binding peptides, protease cleavage sites, RNA secondary structure). Train ML models to highlight protein features explaining experimental observations.

### University of Oslo

Oslo, Norway

POST-DOCTORAL RESEARCHER

2017 - 2022

- My main project focused on study the likely association between mutations at cis-regulatory regions and dysregulation the miRNA networks. Besides this project, I co-lead two releases of the JASPAR database working on the clustering of motifs, data curation, and establishing a motif discovery pipeline. Supervisor: Anthony Matelier.

## Awards and Honors

TRAVEL FELLOWSHIP TO PRESENT A TALK AT ISMB/ECCB 2019

2019

PHD SCHOLARSHIP FROM ECOLE DOCTORALE SCIENCES DE LA VIE ET DE LA SANCTE

2014 - 2017

CONACYT (CONSEJO NACIONAL DE CIENCIA Y TECNOLOGIA) SCHOLARSHIP FOR MASTER STUDIES

2013 - 2014

## Teaching Experience

- Teaching assistant. Master level

**Bachelor in genomic sciences program**

Cuernavaca, Mexico

2013

- Teaching assistant. Bachelor level

**Bachelor in genomic sciences program**

Cuernavaca, Mexico

2013

- Teaching assistant. Bachelor level

## Publications

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See the complete list of publications (including preprints) and citations in my google scholar profile: [pcevKk0AAAA](#)

ORCID profile: 0000-0003-4069-357X

\* = equal contributions (first-author)

^ = equal contributions (second-author)

# = co-corresponding authors

### PEER-REVIEWED

1. Taboada-Castro H, Hernandez-Alvarez AJ, **Castro-Mondragon JA**, and Encarnacion-Guervara S. *RhizoBindingSites v2.0 Is a Bioinformatic Database of DNA Motifs Potentially Involved in Transcriptional Regulation Deduced From Their Genomic Sites*. Bioinformatics and Biology Insights. (2024)
2. Rauluseviciute I, Launay T, Barzaghi G, Nikumbh S, Lenhard B, Krebs AR, **Castro-Mondragon JA**, and Mathelier A. *Identification of transcription factor co-binding patterns with non-negative matrix factorization*. Nucleic Acids Research (2024)
3. Rauluseviciute I\*, Riudavets-Puig R\*, Blanc-Mathieu R^, **Castro-Mondragon JA**^, Ferenc K^, Kumar V^, Berhanu Lemma R^, Lucas J^, Cheneby J, Baranasic D, Khan A, Fornes O, Gundersen S, Johansen M, Hovig E, Lenhard B#, Sandelin A#, Wasserman WW#, Parcy F#, and Mathelier A#. *JASPAR 2024: 20th anniversary of the open-access database of transcription factor binding profiles*. Nucleic Acids Research (2024)
4. **Castro-Mondragon JA**, Ragle Aure M, Lingjærde OC, Langerød A, Martens JWM, Børresen-Dale AL, Kristensen VN, and Mathelier A. *Cis-regulatory mutations associate with transcriptional and post-transcriptional deregulation of gene regulatory programs in cancers*. Nucleic Acids Research (2022)
5. Saha S\*, Spinelli L\*, **Castro-Mondragon JA**, Kervadec A, Lynott M, Kremmer L, Roder L, Sallouha J, Torres M, Brun C, Vogler G, Bodmer R, Colas AR#, Ocorr K#, and Perrin L#. *Genetic architecture of natural variations of cardiac performance in flies*. eLife (2022)
6. Santana-Garcia W\*, **Castro-Mondragon JA**\*, Padilla-Galvez M, Nguyen NTT, Elizondo-Salas A, Ksouri N, Gerbes F, Thieffry D, Vincens P, Contreras-Moreira B#, van Helden J#, Thomas-Chollier M#, Medina-Rivera A#. *RSAT 2022: regulatory sequence analysis tools\**. Nucleic Acids Research (2022)
7. **Castro-Mondragon JA**\*, Riudavets-Puig R\*, Rauluseviciute I\*, Berhanu Lemma R, Turchi L, Blanc-Mathieu R, Lucas J, Boddie P, Khan A, Manosalva Perez N, Fornes O, Leung TY, Aguirre A, Hammal F, Schmelter D, Baranasic D, Ballester B, Sandelin A#, Lenhard B#, Vandepoele K, Wasserman WW#, Parcy F#, and Mathelier A#. *JASPAR 2022: the 9th release of the open-access database of transcription factor binding profiles*. Nucleic Acids Research (2021)
8. Santiago-Algarra D, Souaid C, Singh H, Dao TML, Hussain S, Medina-Rivera A, Ramirez-Navarro L, **Castro-Mondragon JA**, Sadouni N, Charbonnier G, Spicuglia S. *Epromoters function as a hub to recruit key transcription factors required for the inflammatory response*. Nature Communications (2021)
9. Riudavets-Puig R, Boddie P, Khan A, **Castro-Mondragon JA**, and Mathelier A. *UniBind: maps of high-confidence direct TF-DNA interactions across nine species*. BMC Genomics (2021)
10. Ragle Aure M, Fleischer T, Bjørklund S, Ankill J, **Castro-Mondragon JA**, OSBREAC (Oslo Breast Cancer Research Consortium), Børresen-Dale AL, Tost J, Sahlberg KK, Mathelier A, Tekpli X#, Kristensen VN#. *Crosstalk*

between microRNA expression and DNA methylation drives the hormone-dependent phenotype of breast cancer. *Genome Medicine* (2021)

11. Ksouri N, **Castro-Mondragon JA**, Montardit-Tarda F, van Helden J, Contreras-Moreira B#, and Gogorcena Y#. *Tuning promoter boundaries improves regulatory motif discovery in non-model plants: the peach example*. *Plant Physiology* (2021)
12. Taboada-Castro H, **Castro-Mondragon JA**, Aguilar-Vera A, Hernandez-Alvarez AJ, van Helden J, and Encarnacion-Guervara S. *RhizoBindingSites, a Database of DNA-Binding Motifs in Nitrogen-Fixing Bacteria Inferred Using a Footprint Discovery Approach*. *Frontiers in Microbiology* (2020)
13. Fornes O\*, **Castro-Mondragon JA\***, Khan A\*, van der Lee Robin, Zhang X, Richmond PA, Modi BP, Correard S, Gheorghe M, Baranasic D, Santana-Garcia Walter, Tan G, Cheneby J, Ballester B, Parcy F, Sandelin A#, Lenhard B#, Wasserman WW#, and Mathelier A#. *JASPAR 2020: update of the open-access database of transcription factor binding profiles*. *Nucleic Acids Research* (2019)
14. Nguyen NTT\*, Contreras-Moreira B\*, **Castro-Mondragon JA**, Santana-Garcia W, Ossio R, Robles-Espinoza CD, Bahin M, Collombet S, Vincens P, Thieffry D, van Helden J#, Medina-Rivera A#, Thomas-Chollier M#. *RSAT 2018: regulatory sequence analysis tools 20th anniversary*. *Nucleic Acids Research* (2018)
15. Taboada H\*, Meneses N\*, Dunn MF\*, Vargas-Lagunas C, Buchs N, **Castro-Mondragon JA**, Heller M, and Encarnacion S. *Proteins in the periplasmic space and outer membrane vesicles of Rhizobium etli CE3 grown in minimal medium are largely distinct and change with growth phase*. *Microbiology* (2018)
16. Khan A\*, Fornes O\*, Stigliani A\*, Gheorghe M, **Castro-Mondragon JA**, van der Lee R, Bessy A, Chèneby J, Kulkarini S, Tan G, Baranasic D, Arenillas D, Sandelin A#, Vandepoele K, Lenhard B#, Ballester B, Wasserman W#, Parcy F, Mathelier A#. *JASPAR 2018: update of the open-access database of transcription factor binding profiles and its web framework*. *Nucleic Acids Research* (2017)
17. Dao LM\*, Galindo-Albarran AO\*, **Castro-Mondragon JA^**, Andireu-Soler C^, Medina-Rivera A^, Souadi C, Charbonnier G, Griffon A, Vanhille L, Stephen S, Alomairi J, Soler C, Stephen T, Martin D, Torres M, Fernandez N, Soler E, van Helden J, Puthier D, Spicuglia S. *Genome-wide characterization of mammalian promoters with distal enhancer functions*. *Nature Genetics* (2017)
18. **Castro-Mondragon JA**, Jaeger S, Thieffry D, Thomas-Chollier M#, and van Helden J#. *RSAT matrix-clustering: dynamic exploration and redundancy reduction of transcription factor binding motif collections*. *Nucleic Acids Research* (2017)
19. **Castro-Mondragon JA\***, Rioualen C\*, Contreras-Moreira B, van Helden J. *RSAT::Plants: Motif Discovery in ChIP-Seq Peaks of Plant Genomes*. *Plant Synthetic Promoters - Springer Protocol* (2016)
20. Contreras-Moreira B#, **Castro-Mondragon JA**, Rioualen C, Cantalapiedra CP, van Helden J. *RSAT::Plants: Motif Discovery Within Clusters of Upstream Sequences in Plant Genomes*. *Plant Synthetic Promoters - Springer Protocol* (2016)
21. Gama-Castro S\*, Salgado H\*, Santos-Zavaleta A, Ledezma-Tejeida D, Muñiz-Rascado L, García-Sotelo JS, Alquicira-Hernández K, Martínez-Flores I, Pannier L, **Castro-Mondragon JA**, Medina-Rivera A, Solano-Lira H, Bonavides-Martínez C, Pérez-Rueda E, Alquicira-Hernández S, Porrón-Sotelo L, López-Fuentes A, Hernández-Koutouchéva A, Del Moral-Chávez V, Rinaldi F, Collado-Vides J. *RegulonDB version 9.0: high-level integration of gene regulation, coexpression, motif clustering and beyond*. *Nucleic Acids Research* (2015)
22. Medina-Rivera A\*, Defrance M\*, Sand O\*, Herrmann C, **Castro-Mondragon JA**, Delerce J, Jaeger S, Blanchet C, Vincens P, Caron C, Staines DM, Contreras-Moreira B, Artufel M, Charbonnier-Khamvongsa L, Hernandez C, Thieffry D, Thomas-Chollier M#, van Helden J#. *\* RSAT 2015 : Regulatory Sequence Analysis Tools\**. *Nucleic Acids Research* (2015)
23. Rogel MA, Bustos P, Santamaría RI, González V, Romero D, Miguel AC, Lozano L, **Castro-Mondragon JA**, Martínez-Romero J, Ormeño-Orrillo E, Martínez-Romero E. *Genomic basis of symbiovar mimosae in Rhizobium etli*. *BMC Genomics* (2014)

## PREPRINTS

No preprints at this moment.

## Reviewed manuscripts

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Web of Science (prev. Publons) profile: 1499198

Reviewed manuscripts in the following journals: Bioinformatics, Genetics, Molecular Plant, Nucleic Acids Research, Genome biology, Genome Biology and Evolution, Frontiers in Genetics, eLife.

## Presentations

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### TALKS

#### ISMB/ECCB 2019

Basel, Switzerland

COMBINING TRANSCRIPTIONAL AND POST-TRANSCRIPTIONAL REGULATION TO PREDICT MUTATIONS ALTERING THE GENE REGULATORY PROGRAM IN CANCER CELLS

2019 - Present

#### 1st Student Symposium on Computational Genomics

Mainz, Germany

RSAT MATRIX-CLUSTERING: DYNAMIC EXPLORATION AND REDUNDANCY REDUCTION OF TRANSCRIPTION FACTOR BINDING MOTIF COLLECTIONS.

2016 - Present

### POSTERS

1. *Combining transcriptional and post-transcriptional regulation to predict mutations altering the gene regulatory program in cancer cells.* ISM/ECCB, 2019. (doi: <https://f1000research.com/posters/8-1286>)
2. *Characterization of mutations that dysregulate driver microRNAs in cancer.* 4th anual NORBIS conference, 2018.
3. *Clustering and redundancy reduction of transcription factor binding motifs.* 1st Student Symposium on Computational Genomics, 2016.
4. *Clustering and redundancy reduction of transcription factor binding motifs.* 15th ECCB (doi: 10.7490/f1000research.111391.1) 2016.
5. *Comparing and clustering multiple collections of DNA motifs using RSAT* 12th BC2 (doi: 10.7490/f1000research.1111391.1) 2015.
6. *Comparing, clustering and aligning Transcription Factor Binding Motifs with RSAT.* 13th ECCB. (**Castro J**, Thomas-Chollier M, Thieffry D and van Helden J Comparing, clustering and aligning transcription factor binding motifs with RSAT. F1000Posters 2014,5:1845 (poster)), 2014.
7. *Novel computational predictions of regulons based on the observed autoregulation of the network.* 5th IECA Conference 2011. Gene Regulatory Networks in the Enterobacteriaceae, 2011.

## Languages

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#### SPANISH

- Native speaker

#### ENGLISH

- Fluent

#### FRENCH

- Fluent

#### NORWEGIAN

- Intermediate (Level A2)

## Computational skills

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### R

PROFICIENT. USE OF GGLOT, TIDYVERSE, RMARKDOWN, RCPP, S4 OBJECTS, PLOTLY.

### Perl

PROFICIENT

## Git

PROFICIENT

## CI/CD (github actions)

BEGINNER

## Snakemake

PROFICIENT. DEVELOPMENT OF PIPELINES FOR ANALYSIS OF HIGH-THROUGHPUT DATA

## Python

INTERMEDIATE. USE OF PANDAS, POLARS, SEABORN, PLOTLY, NUMPY, SCIKIT-LEARN, OBJECT-ORIENTED CLASSES.

## Docker

INTERMEDIATE

## Make

INTERMEDIATE

## Bash

INTERMEDIATE

## D3

INTERMEDIATE

## aws S3

BEGINNER

## Other

EXPERIENCE WITH BIOLOGICAL DATABASES LIKE TCGA, ICGC, ROADMAP EPIGENOMICS, ENCODE, HUMAN PROTEIN ATLAS

# References

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## Professor Jacques van Helden

*Aix-Marseille Universite, Marseille,  
France*

PHD SUPERVISOR, COLLABORATOR

- Jacques.van-Helden@france-bioinformatique.fr (<https://orcid.org/0000-0002-8799-8584>)

## PhD Alejandra Medina-Rivera

*Laboratorio Internacional de  
Investigacion sobre el Genoma  
Humano, Queretaro, Mexico*

BACHELOR THESIS SUPERVISOR, COLLABORATOR

- amedina@liigh.unam.mx (<https://liigh.unam.mx/amedina/>)

## PhD Anthony Mathelier

*Norway Centre of Molecular  
Medicine, Oslo, Norway*

POSTDOC SUPERVISOR, COLLABORATOR

- anthony.mathelier@ncmm.uio.no (<https://mathelierlab.com/>)

## PhD Andreas Midbøe Hoff

*Nykode Therapeutics AS, Oslo,  
Norway*

HEAD OF IN SILICO AND ARTIFICIAL INTELLIGENCE DEPARTMENT

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