Research/Working Experience

```
## # A tibble: 2 x 5
##   what                         when           with              where why
##   <chr>                        <chr>          <chr>             <chr> <lis>
## 1 Bioinformatician (Scientist II) 2022 - Present Nykode Therapeutic~ Oslo~ <chr>
## 2 Post-doctoral researcher     2017 - 2022    University of Oslo  Oslo~ <chr>
```

Education

```
## # A tibble: 3 x 5
##   what                        when         with                      where why
##   <chr>                       <chr>        <chr>                     <chr> <lis>
## 1 PhD in bioinformatics       2014 - 2017 Aix-Marseille Universite  Mars~ <chr>
## 2 Master in systems biology   2013 - 2014 Institute de biology de ~ Pari~ <chr>
## 3 Bachelor in genomic sciences 2009 - 2013 Universidad Nacional Aut~ Cuer~ <chr>
```

Computational skills

```
## # A tibble: 14 x 5
##    what                                          when  with  where why
##    <chr>                                         <chr> <chr> <chr> <lis>
##  1 Proficient. Use of ggplot, tidyverse, Rmarkdown, Rcp~ <NA>  R     <NA>  <chr>
##  2 Proficient. Use of regular expressions, CGI and obje~ <NA>  Perl  <NA>  <chr>
##  3 Proficient. Creating development branches, merging p~ <NA>  Git   <NA>  <chr>
##  4 Beginner. Test functionality of my own code.         <NA>  CI/C~ <NA>  <chr>
##  5 Proficient. Development of pipelines for analysis of~ <NA>  Snak~ <NA>  <chr>
##  6 Proficient. Use of pandas, polars, seaborn, plotly, ~ <NA>  Pyth~ <NA>  <chr>
##  7 Intermediate. Installation of software requiring mul~ <NA>  Dock~ <NA>  <chr>
##  8 Intermediate.                                        <NA>  GNU ~ <NA>  <chr>
##  9 Intermediate                                         <NA>  Bash  <NA>  <chr>
## 10 Intermediate. Development of interactive hierarchica~ <NA>  D3    <NA>  <chr>
## 11 Beginner. Basic manipulation of files in a bucket.   <NA>  aws ~ <NA>  <chr>
## 12 Beginner. Development of pipelines for analysis of h~ <NA>  next~ <NA>  <chr>
## 13 Intermediate. Development of interactive websites.   <NA>  HTML~ <NA>  <chr>
## 14 Experience with biological databases like TCGA, ICGC~ <NA>  Other <NA>  <chr>
```

Languages

Spanish	English	French	Norwegian
Native	Fluent	Fluent	Intermediate (A2)

Publications

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, Kulkarni 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-Koutoucheva 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

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.

Personalia

```
## # A tibble: 2 x 5
##   what     when  with          where why
##   <chr>    <chr> <chr>         <chr> <list>
## 1 13/02/90 <NA>  Date of birth <NA>  <chr [0]>
## 2 Mexican  <NA>  Citizenship   <NA>  <chr [0]>
```

References

```
## # A tibble: 4 x 5
##   what                                            when  with  where why
##   <chr>                                           <chr> <chr> <chr> <lis>
## 1 PhD Supervisor, Collaborator                    <NA>  Prof~ Aix-~ <chr>
## 2 Bachelor Thesis Supervisor, Collaborator        <NA>  PhD ~ Labo~ <chr>
## 3 Postdoc Supervisor, Collaborator                <NA>  PhD ~ Norw~ <chr>
## 4 Head of In Silico and Artificial Intelligence Departm~ <NA>  PhD ~ Nyko~ <chr>
```