

Mariela Cortés López, Ph.D.

Postdoctoral Associate at WCM | NYGC

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Employment

Weill Cornell Medicine / New York Genome Center 2022 - current

Postdoctoral Associate - [Dan Landau's Lab](#)

Developing single-cell approaches to study the influence of mutations and transcriptome regulation in the evolution of cellular phenotypes during disease.

University of Nevada, Reno 2016 - 2017

Research Assistant - [Pedro Miura's Lab](#)

Scientific technician position, collaborating in RNA related bioinformatics projects.

University of Nevada, Reno 2015 - 2016

Undergraduate Researcher - [Pedro Miura's Lab](#)

Internship and bachelor thesis project. Developing a computational pipeline to analyze RNA-Seq data in order to identify circRNA transcripts. Collaboration in several projects inside the group but also with other groups from UNR (Dr. Alexander van der Linden group) and external (Dr. Brian Johnson from UC Davis and Dr. Joe Chakkalakal from Rochester University).

MIT Earth and Atmospheric Sciences Summer 2014

Summer Undergraduate Researcher - Roger Summon's Lab (as part of MISTI-Mexico)

Participation in MISTI-Mexico Workshop (June 26th, 2014). Training in basic analysis of MS data.

Centro de Ciencias Genómicas, Cuernavaca, Mexico 2013 - 2015

Undergraduate Researcher - Otto Geiger's Lab

Project: "Bacteria with a phospholipid methyltransferase activity can synthesize their own choline and glycine betaine" Training in molecular biology and lipidomics techniques.

Education

Institute of Molecular Biology, Mainz, Germany 2017 - 2022

Ph.D., Biology - [Julian König's Lab](#)

Dissecting alternative splicing networks using high throughput mutagenesis approaches. Development of saturation mutagenesis experiments and data analysis frameworks for disease-relevant splicing events: *RON* exon 11, *CD19* exon 2 and *Alu* exonisation in *BRCA2*. Thesis: “[Decoding splicing regulatory networks in cancer-relevant genes](#)”

Universidad Nacional Autónoma de México, Cuernavaca, Mexico

2012 - 2016

BSc., Genomics Licenciatura en Ciencias Genómicas Thesis: “CircRNA accumulation in the aging mouse brain”

Publications

JOURNAL ARTICLES

Luo H⁺, **Cortés-López M⁺**, Tam CL, Xiao M, Wakiro I, Chu KL, Pierson A, Chan M, Chang K, Yang X, Fecko D, Han G, Ahn EE, Morris QD, Landau DA, Kharas MG. [SON is an essential m(6)A target for hematopoietic stem cell fate](<https://www.ncbi.nlm.nih.gov/pubmed/37582363/>). *Cell Stem Cell*. 2023 Dec 7;30(12):1658-1673.e10. doi: 10.1016/j.stem.2023.11.006. PubMed PMID: 38065069.

Cortés-López M⁺, Chamely P⁺, Hawkins AG⁺, Stanley RF⁺, Swett AD, Ganesan S, Mouhieddine TH, Dai X, Kluegel L, Chen C, Batta K, Furer N, Vedula RS, Beaulaurier J, Drong AW, Hickey S, Dusaj N, Mullokandov G, Stasiw AM, Su J, Chaligné R, Juul S, Harrington E, Knowles DA, Potenski CJ, Wiseman DH, Tanay A, Shlush L, Lindsley RC, Ghobrial IM, Taylor J, Abdel-Wahab O, Gaiti F, Landau DA. [Single-cell multi-omics defines the cell-type-specific impact of splicing aberrations in human hematopoietic clonal outgrowths](#). *Cell Stem Cell*. 2023 Sep 7;30(9):1262-1281.e8. doi: 10.1016/j.stem.2023.07.012. Epub 2023 Aug 14. PubMed PMID: 37582363; NIHMSID:NIHMS1921094.

Ziegler N, **Cortés-López M**, Alt F, Sprang M, Ustjanzew A, Lehmann N, El Malki K, Wingerter A, Russo A, Beck O, Attig S, Roth L, König J, Paret C, Faber J. [Analysis of RBP expression and binding sites identifies PTBP1 as a regulator of CD19 expression in B-ALL](#). *Oncoimmunology*. 2023;12(1):2184143. doi: 10.1080/2162402X.2023.2184143. eCollection 2023. PubMed PMID: 36875548; PubMed Central PMCID: PMC9980455.

Cortés-López M⁺, Schulz L⁺, Enculescu M⁺, Paret C, Spiekermann B, Quesnel-Vallières M, Torres-Diz M, Unic S, Busch A, Orekhova A, Kuban M, Mesitov M, Mulorz MM, Shraim R, Kielisch F, Faber J, Barash Y, Thomas-Tikhonenko A, Zarnack K, Legewie S, König J. [High-throughput mutagenesis identifies mutations and RNA-binding proteins controlling CD19 splicing and CART-19 therapy resistance](#). *Nat Commun*. 2022 Sep 22;13(1):5570. doi: 10.1038/s41467-022-31818-y. PubMed PMID: 36138008; PubMed Central PMCID: PMC9500061.

Schulz L, Torres-Diz M⁺, **Cortés-López M⁺**, Hayer KE⁺, Asnani M⁺, Tasian SK, Barash Y, Sotillo E, Zarnack K, König J, Thomas-Tikhonenko A. [Direct long-read RNA sequencing identifies a subset of questionable exons likely arising from reverse transcription artifacts](#). *Genome Biol*. 2021 Jun 28;22(1):190. doi: 10.1186/s13059-021-02411-1. PubMed PMID: 34183059; PubMed Central PMCID: PMC8240250.

Braun S⁺ , Enculescu M⁺ , Setty ST⁺ , **Cortés-López M**, de Almeida BP, Sutandy FXR, Schulz L, Busch A, Seiler M, Ebersberger S, Barbosa-Morais NL, Legewie S, König J, Zarnack K. [Decoding a cancer-relevant splicing decision in the RON proto-oncogene using high-throughput mutagenesis.](#) *Nat Commun.* 2018 Aug 17;9(1):3315. doi: 10.1038/s41467-018-05748-7. PubMed PMID: 30120239; PubMed Central PMCID: PMC6098099.

Cortés-López M⁺, Gruner MR⁺ , Cooper DA, Gruner HN, Voda AI, van der Linden AM, Miura P. [Global accumulation of circRNAs during aging in *Caenorhabditis elegans*.](#) *BMC Genomics.* 2018 Jan 3;19(1):8. doi: 10.1186/s12864-017-4386-y. PubMed PMID: 29298683; PubMed Central PMCID: PMC5753478.

Liu W, Klose A, Forman S, Paris ND, Wei-LaPierre L, **Cortés-López M**, Tan A, Flaherty M, Miura P, Dirksen RT, Chakkalakal JV. [Loss of adult skeletal muscle stem cells drives age-related neuromuscular junction degeneration.](#) *Elife.* 2017 Jun 6;6. doi: 10.7554/eLife.26464. PubMed PMID: 28583253; PubMed Central PMCID: PMC5462534.

Gruner H⁺ , **Cortés-López M**⁺, Cooper DA, Bauer M, Miura P. [CircRNA accumulation in the aging mouse brain.](#) *Sci Rep.* 2016 Dec 13;6:38907. doi: 10.1038/srep38907. PubMed PMID: 27958329; PubMed Central PMCID: PMC5153657.

⁺ indicates co-first author.

REVIEWS

Cortés-López M, Miura P. [Emerging Functions of Circular RNAs.](#) *Yale J Biol Med.* 2016 Dec;89(4):527-537. eCollection 2016 Dec. Review. PubMed PMID: 28018143; PubMed Central PMCID: PMC5168830.

BOOK CHAPTERS

Cooper DA, **Cortés-López M**, Miura P. [Genome-Wide circRNA Profiling from RNA-seq Data.](#) *Methods Mol Biol.* 2018;1724:27-41. doi: 10.1007/978-1-4939-7562-4_3. PubMed PMID: 29322438; PubMed Central PMCID: PMC6261425.

Conference participation (Selected)

Nanopore Community Meeting

Houston, Texas

November 2023

Talk: “GoT-Splice: unraveling cell-type-specific impact of splicing factor mutations”

CEGS Annual Meeting

New York, NY

October 2023

Talk: “Defining the cell-type specific impact of splicing aberrations with GoT-Splice”

Penn RNA Group

University of Pennsylvania (Virtual) October 2021
Talk: “Building blocks of immune escape: exons, introns, exitrons, and falsitrons”, together with Prof. Andrei Thomas-Tikhonenko

EI Long Read RNA Symposium

Earlham Institute (Virtual) July 2021
Talk: “Questionable junctions: Using direct RNA-seq to identify RT artifacts”

RNA 2021 RNA Society Meeting

Virtual May 2021
Talk: “Massive parallel reporter assay decodes *CD19* alternative splicing in CART-19 therapy resistance”

RNA 2019 RNA Society Meeting

Krakow, Poland June 2019
Poster presentation: “The patterns of *Alu* exonisation in human cancers”

RMU-RNA Salon

Frankfurt, Germany April 2019
Short Talk: “The patterns of *Alu* exonisation in human cancers”

Otto Warburg International Summer School and Research Symposium on RNA regulation and non-coding RNA function

CAS-MPG Partner Institute for Computational Biology Shanghai, China August 2017
Poster presentation: “Analysis of the cis-regulatory landscape controlling *RON* splicing”. Best poster award.

Keystone Symposium in Non Coding RNA and Enhancers

Santa Fe, NM, USA February 2016
Poster presentation: “CircRNA accumulation in the aging mouse brain” with colleague Hannah Gruner.