



Daniel Rafael Saldaña Torres

Bioinformatician

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PROFESSIONAL SUMMARY

Bioinformatician with 6+ years of experience in transcriptomic data analysis, NGS, and molecular structure data processing. Proficient in Python, R, and Bash scripting with strong skills in data science techniques including machine learning. Proven success in sRNA annotation and protein modeling across multiple organisms. Published researcher seeking to apply computational expertise in a remote-first environment.

SKILLS

Category	Skills & technologies
Programing & Scripting	R (Advanced), python (proficient) and bash (proficient)
Bioinformatic tools	Transcriptomics/NGS: Bowtie, Samtools, IGV, JBrowse, Shortstack Structural Bioinformatics: PyMOL, UCSF Chimera, AlphaFold, ViennaRNA, Rosetta
Databases & Resources	NCBI, EMBL-EBI, KEGG, RCSB PDB
Version Control	Git, GitHub, Conda
Data Science & Machine Learning	Scikit-learn and Caret packages

PROFESSIONAL EXPERIENCE

IPICYT, San Luis Potosí, México

2021 – current

PhD student

- Applied k-means clustering to identify organism-specific sRNA expression patterns across interaction timepoints, revealing dynamic regulatory patterns during mutualistic establishment.
- Conducted Gene Ontology enrichment analysis for differentially accumulated sRNA clusters, identifying biological processes modulated during plant-fungus interactions.
- Characterized dynamic conformational changes in AGO-sRNA-target complexes by modeling different protein states using multiple templates, identifying key non-conserved contacts in intermediate conformations.

IPICYT, San Luis Potosí, México

2019 – 2021

Master student

- Implemented an organism-specific RNAseq mapping and *loci* annotation pipeline, achieving 90% genome mapping rate and identified 354 *loci* in *Arabidopsis* and 227 in *Trichoderma*.
- Developed a scoring algorithm incorporating thermodynamics and plant sRNA targeting parameters to predict non-canonical sRNA-target interactions for previously uncharacterized tsRNAs ≥ 24 nt.

UANL, Monterrey, México

2014-2019

Bachelor student

- Identified 80 miRNAs across *Ae. aegypti* life stages (eggs, females, males) from RNAseq data, using miRDeep2 to annotate microRNAs critical for mosquito development and viral transmission.
- Performed conservation analysis that revealed 55 miRNAs shared across insect orders, with 62.4% present in Diptera and 34 unique to holometabolous insects, establishing evolutionary relationships.

- Authored and contributed to 3 peer-reviewed publications as the lead or consulted bioinformatician.

EDUCATION

- **PhD. degree in Molecular Biology (*in progress*)** | Instituto Potosino de Investigación Científica y Tecnológica A.C. (IPICYT), *San Luis Potosí, San Luis Potosí, México* | 2021 – current
- **Sc. M. degree in Molecular Biology** | Instituto Potosino de Investigación Científica y Tecnológica A.C. (IPICYT), *San Luis Potosí, San Luis Potosí, México* | 2019 – 2021
- **Bachelor's degree in Genomic Biotechnology** | *Universidad Autónoma de Nuevo León (UANL), Monterrey, Nuevo León, México* | 2014 – 2019

CERTIFICATIONS

Associate Data Scientist | *DataCamp* – July 2025

PUBLICATIONS

- Jiménez-Martínez, M. L., Ramírez-Ahuja, M. d. L., **Saldaña-Torres, D. R.**, et al. (2024). "De Novo miRNAs from *Anisopteromalus calandrae* (Hymenoptera: Pteromalidae) Conserved in the Order Hymenoptera". *Insects*. doi:[10.3390/insects15121007](https://doi.org/10.3390/insects15121007)
- Rodríguez-Sánchez, I.P., **Saldaña-Torres, D.R.**, et al. (2021). "*miRNAs of Aedes aegypti* (Linnaeus 1762) conserved in six orders of the class Insecta". *Scientific Reports*. doi: [10.1038/s41598-021-90095-9](https://doi.org/10.1038/s41598-021-90095-9).
- **Daniel Rafael Saldaña-Torres**, et al. (2018). "Genomic Mining, Evolution Analysis, and Structural Characterization of the Sepik Virus". *Southwestern Entomologist*. doi: [10.3958/059.043.0128](https://doi.org/10.3958/059.043.0128).