

Miguel Tellez

Rockville, MD · mtellez1846@gmail.com · [linkedin.com/in/miguel-tellez-62010a78](https://www.linkedin.com/in/miguel-tellez-62010a78) · miguel.nascentpoly.com · Willing to relocate · Authorized to work in the US for any employer

SUMMARY

Molecular biologist with 10+ years of research experience, including nearly six years in industry cell line development, gene editing and nucleic-acid assay development. At AstraZeneca, led three stem cell line development campaigns using multiplex CRISPR-Cas9 homology-directed targeted integration, built qPCR genotyping and dPCR transgene-stability assays that supported manufacturing scale-up, and wrote a Primer3/BLAST desktop application that automates assay design with CHO-genome off-target screening. Brings Python automation and data-pipeline skills from founding a software company in 2026.

EXPERIENCE

Nascent Poly LLC · Rockville, MD *Founder* · Mar 2026 – Oct 2026

- Founded a software company; designed and shipped a deterministic natural-language classification engine with a REST API, command-line tools and client libraries, and a production web platform (Django, JavaScript) for a client business.
- Built and operated a 4-node NVIDIA GPU cluster for model training and inference; wrote CI quality gates, automated test suites and data pipelines in Python.
- Applies Python automation, statistics and reproducible-workflow practice to assay development and data review.

AstraZeneca · Gaithersburg, MD *Scientist, Cell Line Development* · May 2022 – Mar 2026 *QC Analyst / Research Associate (contract)* · Jun 2021 – May 2022

- Led three stem cell line development campaigns using targeted transgene insertion; developed a multiplex homology-directed repair method for CRISPR-Cas9 targeted integration.
- Built Primer Design & Off-Target Analysis, a desktop application (Python, Primer3, NCBI BLAST+) that automates qPCR/dPCR assay design with genome-wide off-target screening against the CHO genome (CriGri-PICRH-1.0), alignment checks against alternative sequences, multiplex-reaction support and amplicon risk categorization; packaged as a one-click Windows executable with a command-line batch mode so colleagues without Python could run it.
- Joined the cell line development team when the cardiac program paused and built qPCR genotyping assays for its engineered cell lines.
- In CHO cell line development (Biopharmaceutical Development), ran dPCR analysis of transgene stability across manufacturing scale-up; established workflows for efficient assay development and wet-lab execution.
- As a contractor, performed qPCR analysis of pluripotency and differentiation markers supporting the human ventricular progenitor cardiac regeneration program (Poch et al., *Nature Cell Biology*, 2022).
- Methods: TaqMan qPCR, ddPCR and dPCR assay design; vector design and construction; CHO transfection, cloning and scale-up; embryonic stem cell culture and small-molecule cardiac differentiation; flow cytometry; Hamilton liquid-handler scripting.

Cian Diagnostics · Frederick, MD *Scientist, R&D* · Nov 2020 – Jun 2021 *Microbiologist / Biochemist* · May 2020 – Nov 2020

- Introduced Illumina next-generation sequencing to the laboratory and developed SARS-CoV-2 sequencing assays; authored standard operating procedures.
- Performed SARS-CoV-2 RT-qPCR patient-sample testing under laboratory SOPs with instrument

calibration, quality control and complete documentation.

Johns Hopkins University School of Medicine · Baltimore, MD *Research Associate, Kralli Laboratory* · Jul 2017 – Mar 2020

- Characterized Mcrip2, a novel gene in mitochondrial thermogenesis: designed and executed AAV overexpression and lentiviral knockdown studies in cancer cell lines and primary inguinal adipocytes.
- Optimized immunofluorescence conditions to localize Mcrip2 in U2OS cells; built and validated plasmids and reagents for the project.
- Closed two departmental seminars and led a journal club.

California State University, Fullerton *Undergraduate Researcher, Linder Laboratory* · Jul 2014 – May 2017

- Purified and characterized a novel small copper carrier in blood plasma and urine (FPLC, size-exclusion chromatography, centrifugal filtration, Cu-67 radiotracer); led a team of four.
- First author on an Experimental Biology 2016 abstract; co-author on three further abstracts and papers; five conference presentations; Howell-CSUPERB Research Scholar Award.

EDUCATION

M.S., Cellular and Molecular Biology · Johns Hopkins University School of Medicine · 2019 **B.S., Biochemistry** · California State University, Fullerton · 2017

PUBLICATIONS

- Gioilli BD, Kidane TZ, Fieten H, **Tellez M**, Dalphin M, Nguyen A, Nguyen K, Linder MC. Secretion and uptake of copper via a small copper carrier in blood fluid. *Metallomics*. 2022;14(3):mfac006.
- **Tellez M**, Alsky T, Dalphin M, Flynn S, Munoz A, Ibarra D, Truong H, Linder MC, Lutsenko S, Weldy S. Purification and characterization of a small copper carrier found in mammalian blood plasma and in the urine of mice and dogs with copper overload. *FASEB J*. 2016;30(S1):1026.2.
- Nguyen K, Roque T, Carrillo H, Giolli B, Kidane T, **Tellez M**, Linder M. A small copper carrier in blood plasma: purification, characterization, and metabolism. *FASEB J*. 2021;35(S1).
- Flynn S, Dalphin M, **Tellez M**, Fieten H, Weldy S, Muchenditsi A, Lutsenko S, Linder M. Relation of copper toxicosis in dogs and Wilson disease to the appearance of a small copper carrier (SCC) in blood plasma and urine. *FASEB J*. 2015;29(S1):921.2.

SKILLS

- **Nucleic acids:** TaqMan qPCR, ddPCR and dPCR assay design; qRT-PCR; primer design; DNA/RNA extraction and quantification; Illumina NGS.
- **Gene editing and vectors:** CRISPR-Cas9 HDR targeted integration (multiplex); shRNA; AAV and lentiviral vectors; plasmid design and construction; BSL-2 viral work.
- **Cells:** mammalian cell culture; embryonic stem cell maintenance and cardiac differentiation; CHO transfection, cloning and scale-up; knockout line development; flow cytometry; aseptic technique.
- **Protein and analytical:** western blot; immunofluorescence; anion-exchange, size-exclusion and metal-affinity purification; atomic absorption spectroscopy; radioisotope handling.
- **Automation and software:** Hamilton Basic; Python (automation, data pipelines, statistics); GraphPad Prism, SnapGene, FlowJo, ImageJ, BioEdit, BLAST, UCSC Genome Browser.