# ANTONIO MAFFIA, PHD

Oakland, 94612, CA · 510-610-8741 · antonio.maffia01@gmail.com · LinkedIn · Website

#### **Senior Scientist**

Creative and results-driven Senior Scientist with 5+ years of experience in molecular biology, functional genomics, and cell-based high-throughput screening. Proven success in project management, experimental design, data analysis, and resolving process scalability challenges. Effective in cross-functional teams with a track record of driving R&D innovation.

#### **Key Achievements:**

- Accelerated protein engineering throughput 1,000 × by implementing pooled lentiviral CRISPR screening strategies.
- Boosted cell-based drug screening capacity 100x through a scalable gene-editing pipeline and automated phenotypic assays.
- Orchestrated cross-functional collaborations, streamlining project management and data-driven decision-making across R&D teams and pharma partners.

Technical Core Skills: Molecular Biology · High-Throughput Screening · Mammalian Cells Engineering · Functional Genomics · Cell-Based Assay Development

Operational Core Skills: Project Management · Cross-functional Collaboration · Communication · Adaptability

### PROFESSIONAL EXPERIENCE

#### Mammoth Biosciences · Brisbane, CA

May 2023 - Nov 2024

#### **Senior Scientist I**

- Designed and implemented high-throughput pooled lentiviral CRISPR screens, accelerating cell-based protein engineering workflows 1,000×.
- Developed and optimized combinatorial lentiviral library pipelines, achieving above 80% accuracy in library representation for engineered mammalian systems.
- Scaled mRNA nucleofection workflows 4×, increasing reproducibility and efficiency of epigenetic effector
- Led project coordination across 6 cross-functional teams, improving strategic alignment and reducing decision timelines by 30%.

#### University of California, Berkeley · Berkeley, CA **Research Scientist**

Mar 2020 - May 2023

- Engineered novel hESC-derived cancer models for synthetic lethality screening in partnership with GlaxoSmithKline (GSK); enabled pooled CRISPR screens of ~25,000 targets.
- Co-developed a scalable nucleofection and immunofluorescence platform to generate and screen 100–200× more knockout cell lines for phenotypic profiling.
- Developed a new embryonic stem cell model that achieved a 10,000× increase in immortalization efficiency, supporting regenerative medicine applications.
- Co-first author on a Nature Communications publication demonstrating a high-throughput, cell-based platform for telomere-related therapeutic discovery.

# Institute of Molecular Genetics · Pavia, Italy

Oct 2018 - Feb 2020

- **Research Scientist**
- Engineered 2 CRISPR/HDR cell lines disrupting key DNA-repair protein modifications, creating platforms for therapeutic target discovery.
- Mentored 2 graduate students and 5+ colleagues, driving experimental design, data analysis, and manuscript development for multiple publications.
- Led chemical screening campaigns of DNA-structure binders, uncovering modulators of DNA repair and cell-cycle control for targeted cancer therapies.
- Published findings in top peer-reviewed journals, advancing understanding of genomic stability mechanisms in vivo.

#### **TECHNICAL SKILLS**

#### Molecular & Cellular Biology

**Cell Line Engineering:** Transgenic, Knockout, Knock-in & Stable Clonal Cell Lines · Reporter Cell Lines · High-throughput Knockout Cell Lines Generation

Molecular Biology: Recombinant DNA Cloning (Golden Gate, Gibson Assembly, Restriction Cloning) · Combinatorial Lentiviral Libraries · Gene Knockout Libraries · Site-directed Mutagenesis · Expression Vector Design for Mammalian & Bacterial Systems · DNA & siRNA Transfection · High-throughput Transfection · DNA/mRNA Nucleofection Optimization · Human Genomic DNA & RNA Extraction · RNA-seq · Digital PCR (ddPCR) · PCR · RT-PCR Cell Culture: Human Embryonic Pluripotent Stem Cells · Cancer & Patient-Derived Immortalized Lines · Clonal Cell Lines · High-throughput Knockout Line Generation · Stem

**Flow Cytometry:** Cell Sorting  $\cdot$  Cell Cycle Analysis  $\cdot$  Viability Assays  $\cdot$  Surface Marker Staining & Detection

**Assays & Imaging:** · High-throughput Immunofluorescence · Immunofluorescence & Protein Colocalization · BioID · Split-Tag · BiFC · Chromosome FISH · Live Cell Imaging · FRAP · *In-vitro* Enzymatic Assays

#### Gene Editing, Screening & Sequencing

**CRISPR Screens & Editing:** CRISPR/Cas9 · CRISPRi · CRISPRa · Genome-wide & Targeted Pooled Screens · Arrayed Screens · Lentiviral & RNP Delivery · NGS Analysis · Dropout Screens · Editing Efficiency

Sequencing Technologies: NGS Library Prep · Illumina · Nanopore

Cells Differentiation. Lentiviral Production, Titration, Transduction

**High-throughput Screening Platforms:** Platform Design & Automation · Cell-Based Assay Development · Phenotypic Analysis Workflows · Automated Gene Editing Pipelines

#### **Biochemistry & Technology Platforms**

**Biochemistry:** Recombinant Protein Expression  $(E.\ coli) \cdot \text{Tag Human Enzyme Purification} \cdot \text{Ni-NTA} \cdot \text{HiTRAP Buffer Exchange} \cdot \text{Antibody Purification} \cdot \text{SDS-PAGE} \cdot \text{Western Blot} \cdot \text{Immunoprecipitation} \cdot \text{Pull-down} \cdot \text{Co-immunoprecipitation}$  **Automation Tools:** Tecan  $\cdot$  Hamilton  $\cdot$  Integra Viaflo  $\cdot$  Tecan Fluent  $\cdot$  Qpix Colony Picking

**Liquid Handling & DNA Analysis:** KingFisher · ZAG DNA Analyzer · Agilent TapeStation **Microscopy:** Perkin Elmer Opera Phenix · ZEISS LSM 900 · Leica TCS SP8 **Sequencing & Flow Cytometry Platforms:** Illumina NextSeq, MiSeq · BD Facs Aria Fusion ·

BD LSR Fortessa · BD FACS Symphony · Biorad S3

#### **Data Analysis, Visualization & Soft Skills**

 $\textbf{Data Tools:} \ \mathsf{JMP} \cdot \mathsf{CRISPResso} \cdot \mathsf{Fiji/ImageJ} \cdot \mathsf{GraphPad} \cdot \mathsf{FlowJo} \cdot \mathsf{FCS} \ \mathsf{Express} \cdot \mathsf{Galaxy} \ \mathsf{Project} \ \mathsf{Platform} \cdot \mathsf{Microsoft} \ \mathsf{Office} \ \mathsf{Suite} \cdot \mathsf{Adobe} \ \mathsf{Illustrator} \ \& \ \mathsf{Photoshop} \ \mathsf{Platform} \cdot \mathsf{Microsoft} \ \mathsf{Colored Suite} \cdot \mathsf{Adobe} \ \mathsf{Illustrator} \ \mathsf{Colored Suite} \ \mathsf{Colore$ 

**Programming & Stats:** Python · R

**Soft Skills:** Leadership · Strategic Thinking · Problem Solving · Risk Management · Troubleshooting · Communication & Presentation · Collaboration & Teamwork · Adaptability & Resilience · Project Management · Attention to Detail · Decision-Making · Innovation & Curiosity

#### **EDUCATION & CREDENTIALS**

University of Pavia · Pavia, IT PhD Fellow

Oct 2015 - Sep 2018

- Developed a patient-derived Xeroderma Pigmentosum cell line, enabling the first in vivo DNA polymerase activity assays via targeted protein engineering.
- **Elucidated novel DNA damage response mechanisms** by profiling human cell sensitivity to G-quadruplex binders, uncovering new targets for repair pathway intervention.

Technische Universität · Darmstadt, DE

Mar 2015 - Jun 2015

- **Visiting Student Researcher**
- Built high-throughput live-cell imaging pipelines, quantifying temporal recruitment kinetics of DNA damage proteins in cancer models.
- Optimized fluorescent-tagged protein constructs, enhancing imaging precision and signal fidelity for dynamic DNA repair studies.

University of Pavia · Pavia, IT

Oct 2013 - Jul 2015

**Master Student** 

• Mapped tumor suppressor-mediated DNA repair recruitment, using immunofluorescence and biochemical assays to define key protein interactions in human cells.

University of Milano-Bicocca  $\cdot$  Milan, IT

Oct 2010 - Jul 2013

**Bachelor Student** 

• Streamlined bacterial enzyme purification workflows, increasing yield and catalytic activity to support downstream biochemical and structural analyses.

#### **SELECTED PUBLICATIONS**

(a more comprehensive list is available upon request)

- Turkalo K. T.\* Maffia, A\*., Regalado, G. S., Blanchette, M., Spierings, C. J., Lansdorp, P. M., Hockemeyer, D. (2023). A non-genetic switch triggers alternative telomere lengthening and cellular immortalization in ATRX deficient cells. *Nature Communications*, 14(1). \*Authors have equally contributed to the work.
- Maffia, A., Ranise, C., & Sabbioneda, S. (2020). From R-Loops to G-Quadruplexes: Emerging New Threats for the Replication Fork. *International Journal of Molecular Sciences.* 21 (4).
- Cipolla, L., Bertoletti, F., **Maffia, A.**, Liang, C. C., Lehmann, A. R., Cohn, M. A., Sabbioneda, S. (**2019**). UBR5 interacts with the replication fork and protects DNA replication from DNA polymerase n toxicity. *Nucleic acids research*, *47* (*21*).
- Cipolla, L., **Maffia, A.**, Bertoletti, F., & Sabbioneda, S. (**2016**). The regulation of DNA damage tolerance by ubiquitin and ubiquitin-like modifiers. *Frontiers in genetics*, *7 (105)*.

## **OUTREACH & ENGAGEMENT**

- Scientific Presentations: Delivered talks and poster presentations at international and national conferences, including the EMBO Workshop (2022), University of Leiden (2018), and 6th EU-US DNA Damage Conference (2017).
- **Peer-Review Activities:** Invited reviewer for journals such as *Frontiers in Oncology* and *Frontiers in Genetics* (2022).
- **Community Leadership:** Co-directed scientific outreach activities, organized PhD/postdoc events, and contributed to the UC Berkeley SARS-CoV-2 PCR test initiative (2020–2022).