Federico Rossi

Senior Bioinformatician (Bioinformatic analysis | Data Management |
Clinical Validation) – PhD Medical and Molecular Genetics

Lausanne – Switzerland

WORK EXPERIENCE

SOPHiA GENETICS   Lausanne, Switzerland
Senior Bioinformatician   March 2023 - Present
- Validation of robot-based workflow for next generation sequencing product
- Lead Stability Study on CE-IVD next generation sequencing product
- Data Management in Post-Market Follow-Up Study on CE-IVD next generation sequencing product
- Supervision of Change Control Procedure on software for data analysis

Bioinformatician   February 2021–February 2023
- Development of software for the quality-check of next generation sequencing product
- Clinical Validation of CE-IVD next generation sequencing product

European Institute of Oncology – Cancer Epigenetics Lab   Milano, Italy
Postdoctoral Research in Bioinformatics   July 2019-January 2021
- Pipeline development for next generation sequencing data analysis
- ChIP-seq, RNA-seq, HiC data analysis
- Software development for secondary data analysis

King's College London – Epigenetics and Bioinformatics Lab   London, UK
PhD Student   January 2016-March 2020
- Optimisation of protocols for the extraction and sequencing of DNA from low-DNA-content tissues
- Whole-Genome Sequencing and Whole-Genome-Bisulfite Sequencing library preparation
- Analysis of Whole-Genome Sequencing and Whole-Genome-Bisulfite Sequencing data

EDUCATION

King's College London – Epigenetics and Bioinformatics Lab   London, UK
PhD, Medical and Molecular Genetics.   January 2016-March 2020
Thesis: Optimisation of protocols for extraction and high-throughput sequencing of
DNA from low-DNA-content tissues

Pisa University & Scuola Superiore Sant'Anna   Pisa, Italy
MS: Plant and Microbial Biotechnology (Graduated with "cum laude")   October 2013-October 2015

Pisa University & Scuola Superiore Sant'Anna   Pisa, Italy
BS: Plant and Microbial Biotechnology (Graduated with "cum laude")   October 2010-October 2013

SKILLS

- **Programming:** R (8 years), Python (1 year), Bash (8 years)
- **Bioinformatic Pipeline Development:** Git (Github/Gitlab) (4 years), Docker (2 years), Snakemake (4 years)
- **Bioinformatic data analysis:** data analysis of WGS (3 years), targeted panels-enriched sequencing (2 years), WGBS (3 years), ChIP-seq (2 years), RNA-seq (2 years), HiC (2 years) data
- **Documentation of processes and software**: Change Control Procedure (2 years), Data Management (2 years), Risk Analysis (2 years), Stability Study (2 years), Clinical Validation (2 years)
- **Languages**: English (fluent), Spanish (elementary proficiency), Italian (native)

PUBLICATIONS

- E. Conway, **F. Rossi**, D. Fernandez-Perez, E. Ponzo, K.J. Ferrari, M. Zanotti, D. Manganaro, S. Rodighiero, S. Tamburri, D. Pasini. *BAP1 enhances Polycomb repression by counteracting widespread H2AK119ub1 deposition and chromatin condensation.* Molecular Cell, 81, 17, 2021.
- **F. Rossi**, A. Crnjar, R.J. Oakey, R. Feliciano, A.R. Mateos, C. Molteni, R. Schulz. *DNA extraction and high-throughput sequencing of oak heartwood : assesing the feasibility of genome-wide epigenetic profiling.* PloSOne 16, 11, 2021.
- N. Zaghet, K. Madsen, **F. Rossi**, D. Fernandez-Perez, P.G. Amendola, S. Demharter, U. Pfisterer, K. Khodosevich, D. Pasini, A. E. Salcini. *Coordinated maintenance of H3K36/K27 methylation by histone demethylases preserves germ cell identity and immortality.* Cell Reports, 37, 8, 2021.