# Ira Horecka

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## WORK EXPERIENCE

**University of Toronto**                                                        **Sept. 2021 – Present**
*PhD Student, Molecular Genetics*                                                        *Toronto, ON*
- Developed RISK, a scalable tool for annotating and visualizing large biological networks.
- Quantified crosstalk between biological pathways using genetic interaction data from *S. cerevisiae.*
- Identified moonlighting proteins and predicted drug targets using genetic and chemical-genetic datasets.
- Validated predictions with statistical benchmarking and comparative analyses against established methods.
- Built full-stack web tools using Python and React to visualize crosstalk networks and genetic interactions.
- Built interactive tools for enrichment analysis and visualization across networks, matrices, and linear gene data.
- Collaborated with experimentalists and engineers to refine usability and validate predictions.

**Personalis, Inc.**                                                        **Jul. 2020 – Aug. 2021**
*Laboratory Process Automation Engineer*                                                        *Menlo Park, CA*
- Served as a core Hamilton VENUS developer; wrote error-safe API wrappers for four external devices.
- Integrated Python with Hamilton methods to enhance code readability and capacity.
- Built full-stack utility web apps to assist automation system operators.

**Five Prime Therapeutics**                                                        **Dec. 2017 – Sept. 2019**
*Research Associate II*                                                        *South San Francisco, CA*
- Led molecular biology workflows and collaborated with systems engineering.
- Developed automation protocols; trained users on Tecan, Beckman FX, and Qpix platforms.
- Used Python and R for automation scripting, statistical analysis, and visualization.

**Bayer**                                                        **Nov. 2016 – Dec. 2017**
*Associate Scientist*                                                        *Berkeley, CA*
- Improved protein recovery 7.5x by optimizing a chromatography step.
- Co-developed a scalable downstream process from bench to pilot scale.

## EDUCATION

**University of California, Santa Cruz**                                                        **June 2016**
*BS, Biochemistry and Molecular Biology*                                                        *Santa Cruz, CA*

## SKILLS

- Programming: Python, R, Git; Tools: NetworkX, Cytoscape; Stats: overrepresentation testing, data visualization
- Wet Lab: liquid handler protocols, molecular cloning, protein purification

## PROJECTS

- Projects include RISK (network annotation), API wrappers, and scientific tools available on GitHub and [irahorecka.com](irahorecka.com).

## SELECTED PUBLICATIONS

- Clarke, Jesse, et al. "A conserved signaling network monitors delivery of sphingolipids to the plasma membrane in budding yeast" *Molecular Biology of the Cell,* vol. 28, no. 20, 2017, pp. 2580 - 2599.
- van Leeuwen, Jolanda, et al. "Exploring Genetic Suppression Interactions on a Global Scale" *Science,* vol. 354, no. 6312, 2016, pp. aag0839.