

# Ira Horecka

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## WORK EXPERIENCE

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### 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

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### University of California, Santa Cruz

June 2016

*BS, Biochemistry and Molecular Biology*

*Santa Cruz, CA*

## SKILLS

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- Programming: Python, R, Git; Web: HTML/CSS, JavaScript, React; GUI: PyQt
- Software: Flask, NetworkX, Cytoscape, Sigma.js; CLI and API development
- Analysis: statistical testing, enrichment analysis, network algorithms, data visualization
- Lab Techniques: Golden Gate cloning, Expi293 transfection, Sanger sequencing, ELISA, chromatography
- Packaging: >10 PyPI libraries; modular scientific tools; wet lab automation scripting (TECAN, Biomek, Qpix)

## SELECTED PUBLICATIONS

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- 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.