



Filip Horvat

PHD STUDENT, BIOINFORMATICIAN

Institute of Molecular Genetics, Prague, Czech Republic

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Research Interests

Bioinformatics; computational biology; transcriptomics; developmental biology; small RNAs; retrotransposons

Employment

Institute of Molecular Genetics, Laboratory of Epigenetic Regulations

PHD STUDENT - BIOINFORMATICS

Prague

2017 - current

- Bioinformatic analysis of RNA dynamics in mammalian oocytes and early embryos
- Maternal mRNA degradation
- Roles and distribution of small RNAs and long non-coding RNAs
- Profiling and analysis of retrotransposon expression and silencing

Institute of Molecular Genetics, Laboratory of Epigenetic Regulations

SPECIALIST OF SCIENCE AND RESEARCH - BIOINFORMATICS

Prague

2016 - 2017

- Control of gene expression during mammalian oocyte-to-embryo transition

University of Zagreb, Faculty of Science, Bioinformatics Group

INTERN - BIOINFORMATICS

Zagreb

2015 - 2016

- Management, interpretation, visualization and statistical analysis of high-throughput sequencing data

Max F Perutz Laboratories, DNA Damage Response and Transcription Regulation

INTERN - WET LAB

Vienna

Apr 2015 - Sep 2015

- Activity of PARG protein in relation to loss of post-translational modifications in human cells

Education

Charles University, Faculty of Science

PHD IN DEVELOPMENTAL AND CELL BIOLOGY

Prague

2017 - current

University of Zagreb, Faculty of Science

MASTER IN MOLECULAR BIOLOGY

Zagreb

2013 - 2016

University of Zagreb, Faculty of Science

BACHELOR IN MOLECULAR BIOLOGY

Zagreb

2009 - 2013

Skills

Programming languages

R (ADVANCED), BASH (INTERMEDIATE), PYTHON (BEGINNER)

R framework

SHINY, RMARKDOWN, BIOCONDUCTOR, TIDYVERSE, GGPLOT2, PLOTLY

Other computational tools

UNIX/LINUX, COMMAND LINE INTERFACE, NEXTFLOW, GIT

Languages

ENGLISH (FLUENT), GERMAN (BASIC), CROATIAN (NATIVE)

Peer-reviewed Publications

- Kataruka, S., Kinterova, V., **Horvat, F.**, Kulmann, M. I. R., Kanka, J., & Svoboda, P. (2022). Physiologically relevant miRNAs in mammalian oocytes are rare and highly abundant. *EMBO Reports*, 23(2), e53514.
- Petrzilek, J., Pasulka, J., Malik, R., **Horvat, F.**, Kataruka, S., Fulka, H., & Svoboda, P. (2022). De novo emergence, existence, and demise of a protein-coding gene in murids. *BMC Biology*, 20(1), 1–14.
- Zapletal, D., Taborska, E., Pasulka, J., Malik, R., Kubicek, K., Zanova, M., Much, C., Sebesta, M., Buccheri, V., **Horvat, F.**, et al. (2022). Structural and functional basis of mammalian microRNA biogenesis by dicer. *Molecular Cell*, 82(21), 4064–4079.
- Loubalova, Z., Fulka, H., **Horvat, F.**, Pasulka, J., Malik, R., Hirose, M., Ogura, A., & Svoboda, P. (2021). Formation of spermatogonia and fertile oocytes in golden hamsters requires piRNAs. *Nature Cell Biology*, 23(9), 992–1001.
- Ganesh, S., **Horvat, F.**, Drutovic, D., Efenberkova, M., Pinkas, D., Jindrova, A., Pasulka, J., Iyyappan, R., Malik, R., Susor, A., et al. (2020). The most abundant maternal lncRNA Sirena1 acts post-transcriptionally and impacts mitochondrial distribution. *Nucleic Acids Research*, 48(6), 3211–3227.
- Kataruka, S., Modrak, M., Kinterova, V., Malik, R., Zeitler, D. M., **Horvat, F.**, Kanka, J., Meister, G., & Svoboda, P. (2020). MicroRNA dilution during oocyte growth disables the microRNA pathway in mammalian oocytes. *Nucleic Acids Research*, 48(14), 8050–8062.
- Demeter, T., Vaskovicova, M., Malik, R., **Horvat, F.**, Pasulka, J., Svobodova, E., Flemr, M., & Svoboda, P. (2019). Main constraints for RNAi induced by expressed long dsRNA in mouse cells. *Life Science Alliance*, 2(1).
- Taborska, E., Pasulka, J., Malik, R., **Horvat, F.**, Jenickova, I., Jelić Matošević, Z., & Svoboda, P. (2019). Restricted and non-essential redundancy of RNAi and piRNA pathways in mouse oocytes. *PLoS Genetics*, 15(12), e1008261.
- Horvat, F.**, Fulka, H., Jankele, R., Malik, R., Jun, M., Solcova, K., Sedlacek, R., Vlahovicek, K., Schultz, R. M., & Svoboda, P. (2018). Role of Cnot6l in maternal mRNA turnover. *Life Science Alliance*, 1(4).
- Franke, V., Ganesh, S., Karlic, R., Malik, R., Pasulka, J., **Horvat, F.**, Kuzman, M., Fulka, H., Cernohorska, M., Urbanova, J., et al. (2017). Long terminal repeats power evolution of genes and gene expression programs in mammalian oocytes and zygotes. *Genome Research*, 27(8), 1384–1394.

Book Chapters

- Horvat, F.**, & Svoboda, P. (2019). Microarray-based transcriptomics of early mammalian development. In *Advances in disease models*. OPTIO CZ.