


# Ieva Rauluševičiūtė

Doctoral Research fellow

 [ieva.rauluseviciute@ncmm.uio.no](mailto:ieva.rauluseviciute@ncmm.uio.no)

 +47 967 07 578

 @IevaRau

## Experience

<b>April 2020 -</b>	<b>Doctoral Research Fellow, Computational Biology &amp; Gene Regulation Group at the Centre for Molecular Medicine Norway (NCMM), Nordic EMBL Partner for Molecular Medicine, University of Oslo, Oslo, Norway</b> Computational analysis of transcription factor binding and gene regulation
<i>February 2019 - May 2019</i>	Staff engineer at the Department of Clinical and Molecular Medicine, NTNU, Trondheim, Norway
<i>July 2018 - February 2019</i>	Intern at the Department of Clinical and Molecular Medicine, NTNU, Trondheim, Norway
<i>June 2017 - June 2018</i>	MSc student at the Department of Clinical and Molecular Medicine, NTNU, Trondheim, Norway MSc thesis <i>"Computational analysis of DNA methylation and gene expression patterns in prostate cancer"</i> Supervisors dr. Morten Beck Rye and prof. Finn Drabløs
<i>February 2015 - June 2016</i>	BSc student at Human Genome Research Centre, Faculty of Natural Science, Vilnius University, Lithuania BSc thesis <i>"Novel DNA methylation biomarkers in prostate cancer"</i> Supervisors dr. Kristina Daniūnaitė and prof. Sonata Jarmalaitė
<i>June 2015 - September 2015</i>	Vilnius iGEM 2015 team project <i>"Coliclock"</i> for iGEM 2015, Boston, USA Institute of Biotechnology, Vilnius University, Lithuania Supervisor prof. Virginijus Šikšnys

## Selected publications

<i>2021</i>	Castro-Mondragon JA*, Riudavets-Puig R*, <b>Rauluseviciute I*</b> , Berhanu Lemma R, Turchi L, Blanc-Mathieu R, et al. JASPAR 2022: the 9th release of the open-access database of transcription factor binding profiles. Nucleic Acids Res. 2021 Nov 30;gkab1113. doi:10.1093/nar/gkab1113
<i>2020</i>	<b>Rauluseviciute I</b> , Drabløs F, Rye MB. DNA hypermethylation associated with upregulated gene expression in prostate cancer demonstrates the diversity of epigenetic regulation. BMC Med Genomics. 2020 Jan 8;13(1):6. doi:10.1186/s12920-020-0657-6
<i>2019</i>	<b>Rauluseviciute I</b> , Drabløs F, Rye MB. DNA methylation data by sequencing: experimental approaches and recommendations for tools and pipelines for data analysis. Clin Epigenetics. 2019 Dec 12;11(1):193. doi:10.1186/s13148-019-0795-x

## Education

---

<b>August 2016 - June 2018</b>	<b>MSc in Molecular Medicine, Norwegian University of Science and Technology (NTNU), Trondheim, <i>Norway</i></b>
<i>September 2012 - June 2016</i>	Bachelor's degree in Genetics, Vilnius University, <i>Lithuania</i>
<i>September 2000- July 2012</i>	Graduated Kaišiadorys A. Brazauskas gymnasium, <i>Lithuania</i>

## Conference posters and talks

---

<i>2021</i>	ISMB/ECCB 2021, <i>virtual</i> . Research talk and poster presentation. CSHL Biology of Genomes, <i>virtual</i> . Poster presentation.
<i>2016</i>	COINS 2016, <i>Vilnius, Lithuania</i> . Poster presentation.
<i>2015</i>	2015 iGEM competition, <i>Boston, USA</i> . Project and poster presentations.

---

**Languages:** Lithuanian is mother tongue; fluent in English, elementary proficiency in German; beginner in Norwegian and Italian.

**Computational skills:** R, Bash and Python. Pipeline building with Snakemake.

**Communication and organisational skills:** extensive experience with public speaking (science related, environment protection related topics); organisational skills through local and international volunteering and iGEM experience.