Curriculum Vitae

Education

2011 - 2016	PhD degree in bioinformatics at the Department of Genetics, University Medical Centre Groningen, the Netherlands
2009 – 2011	Master’s degree in Computational and Applied Linguistics at Saint-Petersburg State University (with honours)
2005 – 2009	Bachelor degree in Computational and Applied Linguistics at Saint-Petersburg State University
2003 – 2005	Lyceum N 239, specializing in mathematics and physics

Scientific activity and work

2024 - present	**Institute of Genetic and Biomedical Research (IRGB), National Research Council (CNR), Cagliari, Italy** Postdoc in the Women4Health project: interaction between sex hormones, circulating proteome, gut and vaginal microbiota.
2020 - 2024	**Department of Genetics, University Medical Center Groningen, the Netherlands** Postdoc (personal NWO VENI grant): sex differences in cardiovascular disease and risk factors; analysis of associations between gut microbiome and human genome.
2016 - 2019	**Department of Genetics, University Medical Center Groningen, the Netherlands** Postdoc: Proteomics, protein level QTL mapping, Mendelian Randomization.
2020-2021	**Laboratory of Genomic Diversity, Center for Computer Technologies, ITMO University, Russia** Postdoc: Vertebrate genome assembly and annotation.

2016 – 2019	**Dobzhansky Center for Genome Bioinformatics, Saint-Petersburg State University, Russia** Postdoc: Human population genetics, WGS data analysis, GWAS.
2011 – 2015	**Department of Genetics, University Medical Center Groningen, the Netherlands** PhD student: eQTL mapping, allele-specific expression analysis, RNA-seq data analysis.
Summer of 2011	**Reverso - Softissimo, Paris** Internship: automatic transcription software development.
2009 – 2011	**St. Petersburg State University, Department of Computational Linguistics** Master’s project: “Development of an ontology-based short text classification system”.
2010 – 2011	**St. Petersburg Institute in Bioinformatics** Student: SABA course in bioinformatics.
2010 - 2011	**ABBYY** Lexicographer: Developing an automatic Russian <-> French translation tool.
Summer of 2010	**Department of Genetics, University Medical Center Groningen, the Netherlands** Internship: Development of a search engine with query expansion from medical ontologies.
2006 – 2009	**St. Petersburg State University, Department of Phonetics and Speech Technologies** Second bachelor specialization in Phonetics and Speech Technologies. Development of a phonetic database for speech synthesis.
2006 – 2009	**St. Petersburg State University, Department of Computational Linguistics** Bachelor project: “Linguistic aspect of informational retrieval: query expansion with the help of a thesaurus”.

Presentations, posters

September 2025, Heidelberg	**EMBL Symposium: The human microbiome** Poster: "Gut bacterial genes involved in female sex hormone metabolism"
September 2023, Heidelberg	**EMBL Symposium: The human microbiome** Poster: "Host Genetic Regulation of Human Gut Microbial Structural Variation"
May 2019, Moscow	**Centenary of Human Population Genetics** Oral presentation: "The Genome Russia Project: a reference database of whole genome sequences across Russia"
August 2018, Virginia	**Recent Advances in Conservation Genetics** Participation in the international summer school
July 2018, St. Petersburg	**Bioinformatics: from Algorithms to Applications 2018** Poster: "Tracing ancient human history of Russia through genomics"
June 2018, Milan	**European Society of Human Genetics** Oral presentation: "Plasma protein levels - a link between host microbiome, genetics, metabolites and disease-related phenotypes"
July 2017, Prague	**ISMB/ECCB (European Conference on Computational Biology)** Poster: "Systems human genome and metagenome analysis on circulating proteins in a population cohort"
May 2017, Copenhagen	**European Society of Human Genetics** Poster: "Annotation of genetic variation within Genome Russia project"
August 2015, Cambridge	**Leena Peltonen School of Human Genomics** Oral presentation: "Genetic variants affect expression of nearly all genes, but only in a specific context".
June 2015, Glasgow	**European Society of Human Genetics** Oral presentation: "Genetic variants affect expression of nearly all

	genes, but only in a specific context".
September 2014, Groningen	**Data Integration Course For Biologists** Lectures for students: "Calling genotypes from public RNA-sequencing data enables identification of genetic variants that affect gene expression levels".
July 2014, St.Petersburg	**Bioinformatics summer school** Oral presentation: "Calling genotypes from public RNA-sequencing data enables identification of genetic variants that affect gene expression levels".
July 2014, Leiden	**BioSB/NBIC, Advanced NGS Course: RNA-seq data analysis** Lectures for students: “Variant calling in RNA-seq data and eQTL mapping”.
November 2013, Leiden	**NBIC, Advanced NGS Course: RNA-seq data analysis** Lectures for students: “Variant calling in RNA-seq data”.
June 2013, Paris	**European Society of Human Genetics** Oral presentation: “Novel genetic variants associated with alternative polyadenylation and expression of noncoding transcripts”.
April 2013, Leiden	**European Medical Genetics Conference** Oral presentation: “Novel genetic variants associated with alternative polyadenylation and expression of coding and noncoding transcripts”.
September 2012, St.Petersburg	**SysPatho Workshop** Poster: "The power of meta-analysis of RNA-seq datasets for the eQTL detection".
June 2012, Nurnberg	**European Society of Human Genetics** Poster: “The power of meta-analysis of RNA-seq datasets for eQTL identification”.

Publications

First or last author:

1. Wu J, <...>, Zhernakova DV. The interplay of sleep characteristics with health factors and gut microbiome. *Nat Commun. 2026 Feb 13;17(1):2731. doi: 10.1038/s41467-026-68791-9.*
2. Wu J, <...>, Zhernakova DV. Epigenome-wide association study on the plasma metabolome suggests self-regulation of the glycine and serine pathway through DNA methylation. *Clin Epigenetics. 2024 Aug 13;16(1):104. doi: 10.1186/s13148-024-01718-7*.

3. Zhernakova DV el al. Host Genetic Regulation of Human Gut Microbial Structural Variation. *Nature 2024, Jan;625(7996):813-821. doi: 10.1038/s41586-023-06893-w.*

4. Zhernakova DV el al. Age-dependent sex differences in cardiometabolic risk factors. *Nat Cardiovasc Res 1, 844–854 (2022). doi: 10.1038/s44161-022-00131-8.*

5. Doestzada M, Zhernakova DV el al. Systematic analysis of relationships between plasma branched-chain amino acid concentrations and cardiometabolic parameters: an association and Mendelian randomization study. *BMC Med. 2022 Dec 15;20(1):485. doi: 10.1186/s12916-022-02688-4.*

6. Zhernakova DV et al. Genome-wide sequence analyses of ethnic populations across Russia. *Genomics. 2019 Mar 19. doi: 10.1016/j.ygeno.2019.03.007.*

7. Zhernakova DV, Le TH, Kurilshikov A et al. Individual variations in cardiovascular-disease-related protein levels are driven by genetics and gut microbiome. *Nat Genet. 2018 Sep 24.*

8. Zhernakova DV et al. Analytical "bake-off" of whole genome sequencing quality for the Genome Russia project using a small cohort for autoimmune hepatitis. *PLoS One. 2018 Jul 11;13(7)*

9. Zhernakova DV et al. Identification of context-dependent expression quantitative trait loci in whole blood. *Nat Genet. 2017 Jan;49(1):139-145*

10. Zhernakova DV, Deelen P et al. Calling genotypes from public RNA-sequencing data enables identification of genetic variants that affect gene-expression levels. *Genome Med. 2015 Mar 27;7(1):30.*

11. Zhernakova DV et al. DeepSAGE reveals genetic variants associated with alternative polyadenylation and expression of coding and non-coding transcripts. *PLOS Genet. 2013 Jun;9(6).*

12. Zhernakova DV et al. Linguistic aspects of informational retrieval: query expansion with the help of a thesaurus. Actual problems of theoretical and practical linguistics: collection of scientific articles / *ed.: E. P. Sosnina. – Ulyanovsk: UlGTU, 2009.*

Other:

1. Vinerbi E et al. *Lactobacillus iners* dominates the vaginal microbiota of healthy Italian women of reproductive age. *mSystems. 2025 Dec 17;10(12):e0098325. doi: 10.1128/msystems.00983-25.*

2. Spreckels JE et al. Host and environmental determinants of human milk oligosaccharides and microbiota in the Lifelines NEXT cohort. *Cell Rep. 2025 Aug 26;44(8):116124. doi: 10.1016/j.celrep.2025.116124.*

3. Andreu-Sánchez S et al. Global genetic diversity of human gut microbiome species is related to geographic location and host health. *Cell. 2025 Jul 24;188(15):3942-3959.e9. doi: 10.1016/j.cell.2025.04.014.*

4. Li Y et al. Genome-wide Studies Reveal Genetic Risk Factors for Hepatic Fat Content. *Genomics Proteomics Bioinformatics. 2024 Jul 3;22(2):qzae031. doi: 10.1093/gpbjnl/qzae031.*

5. Ryakhovsky SS et al. The mixed liver and kidney transcriptome dataset of *Darevskia valentini rock lizard*. *BMC Res Notes. 2022 Nov 8;15(1):345. doi: 10.1186/s13104-022-06228-4.*

6. Chen L et al. Influence of the microbiome, diet and genetics on inter-individual variation in the human plasma metabolome. *Nat Med. 2022 Nov;28(11):2333-2343. doi: 10.1038/s41591-022-02014-8.*

7. Ochkalova S et al. First Genome of Rock Lizard *Darevskia valentini* Involved in Formation of Several Parthenogenetic Species. *Genes (Basel). 2022 Sep 1;13(9):1569. doi: 10.3390/genes13091569.*

8. Andreu-Sánchez S et al. Genetic, parental and lifestyle factors influence telomere length. *Commun Biol. 2022 Jun 9;5(1):565. doi: 10.1038/s42003-022-03521-7.*

9. Bourgonje AR et al. The Effect of Phenotype and Genotype on the Plasma Proteome in Patients with Inflammatory Bowel Disease. *J Crohns Colitis. 2022 Mar 14;16(3):414-429. doi: 10.1093/ecco-jcc/jjab157.*

10. Ryakhovsky SS et al. De novo transcriptome assembly and annotation of parthenogenetic lizard *Darevskia unisexualis* and its parental ancestors *Darevskia valentini* and *Darevskia raddei nairensis*. *Data Brief. 2021 Dec 6;39:107685. doi: 10.1016/j.dib.2021.107685.*

11. Shevchenko AK et al. Genome-wide association study reveals genetic variants associated with HIV-1C infection in a Botswana study population. *Proc Natl Acad Sci U S A. 2021 Nov 23;118(47):e2107830118. doi: 10.1073/pnas.2107830118.*

12. Tamazian G et al. Draft de novo Genome Assembly of the Elusive Jaguarundi, *Puma yagouaroundi*. *J Hered. 2021 Nov 1;112(6):540-548. doi: 10.1093/jhered/esab036.*

13. Kurilshikov A et al. Large-scale association analyses identify host factors influencing human gut microbiome composition. *Nat Genet. 2021 Feb;53(2):156-165. doi: 10.1038/s41588-020-00763-1.*

14. Chen L et al. Genetic and Microbial Associations to Plasma and Fecal Bile Acids in Obesity Relate to Plasma Lipids and Liver Fat Content. *Cell Rep. 2020 Oct 6;33(1):108212. doi: 10.1016/j.celrep.2020.108212.*

15. Folkersen L et al. Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. *Nat Metab. 2020 Oct;2(10):1135-1148. doi: 10.1038/s42255-020-00287-2.*

16. Fan M et al. New Gene Variants Associated with the Risk of Chronic HBV Infection. *Virol Sin. 2020 Aug;35(4):378-387. doi: 10.1007/s12250-020-00200-x.*

17. Kliver S et al. Assembly of the *Boechera retrofracta* Genome and Evolutionary Analysis of Apomixis-Associated Genes. *Genes (Basel). 2018 Apr; 9(4): 185.*

18. Wang S et al. Identified OAS3 gene variants associated with coexistence of HBsAg and anti-HBs in chronic HBV infection*. J Viral Hepat. 2018 Mar 27.*

19. Yousefi S et al. A SNP panel for identification of DNA and RNA specimens. *BMC Genomics. 2018 Jan 25;19(1):90.*

20. Bonder MJ et al. Disease variants alter transcription factor levels and methylation of their binding sites *Nat Genet. 2017 Jan;49(1):131-138*

21. Bonder MJ et al. The effect of host genetics on the gut microbiome. *Nat Genet. 2016 Nov;48(11):1407-1412*

22. Barban N et al. Genome-wide analysis identifies 12 loci influencing human reproductive behavior. *Nat Genet. 2016 Oct 31.*

23. Slieker RC et al. Age-related accrual of methylomic variability is linked to fundamental ageing mechanisms. *Genome Biol. 2016 Sep 22;17(1):191.*

24. Dekkers KF et al. Blood lipids influence DNA methylation in circulating cells. *Genome Biol. 2016 Jun 27;17(1):138.*

25. Ricaño-Ponce I, Zhernakova et al. Refined mapping of autoimmune disease associated genetic variants with gene expression suggests an important role for non-coding RNAs. *J Autoimmun. 2016 Apr;68:62-74*

26. Gutierrez-Achury J et al. Functional implications of disease-specific variants in loci jointly associated with coeliac disease and rheumatoid arthritis. *Hum Mol Genet. 2016 Jan 1;25(1):180-90*

27. Kogelman LJ, Zhernakova DV et al. An integrative systems genetics approach reveals potential causal genes and pathways related to obesity. *Genome Med. 2015 Oct 20;7:105*

28. Shah et al. Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. *Am J Hum Genet. 2015 Jul 2;97(1):75-85*

29. Kumar V et al. Systematic annotation of celiac disease loci refines pathological pathways and suggests a genetic explanation for increased interferon-gamma levels. *Hum Mol Genet. 2015 Jan 15;24(2):397-409.*

30. Hrdlickova B et al. Expression profiles of long non-coding RNAs located in autoimmune disease-associated regions reveal immune cell-type specificity. *Genome Med. 2014 Oct 28;6(10):88.*

31. Kogelman LJ et al. Identification of co-expression gene networks, regulatory genes and pathways for obesity based on adipose tissue RNA Sequencing in a porcine model. *BMC Med Genomics. 2014 Sep 30;7:57.*

32. Westra HJ et al. Systematic identification of trans eQTLs as putative drivers of known disease associations. *Nat Genet. 2013 Oct;45(10).*

33. Kumar V et al. Human disease-associated genetic variation impacts large intergenic non-coding RNA expression. *PLOS Genet. 2013;9(1).*

Scientific interests

Gut microbiome, transcriptomics and proteomics, sex differences in omics phenotypes, population genetics.

Languages

Russian: native speaker,

English: fluent,

French: upper-intermediate.