

# Alla Mikheenko

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## Education

### Ph.D. in Computational Biology & Bioinformatics

Center for Algorithmic Biotechnology at St. Petersburg State University

Saint Petersburg, Russia

Jun 2015 - Jan 2021

- Thesis: "Development of computational methods for analysis and visualization of eukaryotic genome assemblies"
- PhD supervisor: Prof. Pavel Pevzner (University of California at San Diego)

### Doctor of Medicine

Ulyanovsk State University

Ulyanovsk, Russia

Sep 2008 - Jun 2014

- Graduated with Distinction

## Work Experience

### Postdoctoral Research Fellow

University College of London

London, UK

Sep 2022 - present

### Postdoctoral Research Fellow

Saint Petersburg State University

Saint Petersburg, Russia

Jan 2021 - Aug 2022

## Software

All software is open source.

- QUAST** Versatile (meta)genome assembly evaluation. 200,000+ downloads
- IsoQuant** Transcript discovery and quantification with long RNA reads
- VerityMap** Accurate mapping of long reads to extra-long tandem repeats
- AGB** Interactive visualization of assembly graphs

## Bioinformatics Expertise

- Genomics data analysis** Next-generation and long-read genome sequencing data, metagenomics, ChIP-seq.
- Transcriptomics data analysis** Single-cell, spatial, bulk RNA-Seq data.
- Proteomics data analysis** Mass spectrometry-based quantitative proteomics data.

## Other Skills

- Programming** Proficiency in Python (Pandas, NumPy, PyTorch, Scikit-learn. etc.) and R; HTML, JavaScript; algorithm design.
- Machine learning** Supervised/unsupervised learning, ensemble methods, regularization and optimization, deep learning (CNNs, RNNs, GANs).
- Miscellaneous** Linux, Shell (Bash/Zsh),  $\text{\LaTeX}$ , Git, cluster workload managers (SGE, Slurm).

## Publications

**h-index:** 18 (Google Scholar) **citations:** 3,700 (Google Scholar)

### SELECTED JOURNAL ARTICLES

1. Prjibelski AD\*, **Mikheenko A\***, Joglekar A, et al. Accurate isoform discovery with IsoQuant using long reads. **Nature Biotechnology**. 2023;41: 915–918 (co-first authorship).
2. Bzikadze AV\*, **Mikheenko A\***, Pevzner PA. Fast and accurate mapping of long reads to complete genome assemblies with VerityMap. **Genome Research**. 2022;32: 2107-2118 (co-first authorship).
3. **Mikheenko A**, Saveliev V, Hirsch P, Gurevich A. WebQUAST: online evaluation of genome assemblies. **Nucleic Acids Research**. 2023;51(W1): W601–W606.
4. **Mikheenko A**, Prjibelski AD, Joglekar A, Tilgner HU. Sequencing of individual barcoded cDNAs on Pacific Biosciences and Oxford Nanopore reveals platform-specific error patterns. **Genome Research**. 2022;32: 726-737.

5. Rhie A, Nurk S, Cechova M, ..., **Mikheenko A**, et al. The complete sequence of a human Y chromosome. **Nature**. 2023; 1-11.
6. Hardwick SA, Hu W, Joglekar A, ..., **Mikheenko A**, et al. Single-nuclei isoform RNA sequencing unlocks bar-coded exon connectivity in frozen brain tissue. **Nature Biotechnology**. 2022; 40: 1082–1092.
7. Nurk S, Koren S, Rhie A, Rautiainen M, Bzikadze AV, **Mikheenko A**, et al. The complete sequence of a human genome. **Science**. 2022;376 (6588): 44-53.
8. Altemose N, Logsdon GA, Bzikadze AV, ..., **Mikheenko A**, et al. Complete genomic and epigenetic maps of human centromeres. **Science**. 2022;376 (6588).
9. Rhie A, Mc Cartney A, Shafin K, ..., **Mikheenko A**, et al. Chasing perfection: validation and polishing strategies for telomere-to-telomere genome assemblies. **Nature Methods**. 2022; 19: 687–695.
10. Logsdon GA, Vollger MR, Hsieh P, ..., **Mikheenko A**, et al. The structure, function and evolution of a complete human chromosome 8. **Nature**. 2021;593: 101–107.
11. **Mikheenko A**, Bzikadze AV, Gurevich A, Miga KH, Pevzner PA. TandemTools: mapping long reads and assessing/improving assembly quality in extra-long tandem repeats. **Bioinformatics**. 2020;36: i75–i83 (presented at ISMB 2020).
12. **Mikheenko A**, Prjibelski A, Saveliev V, Antipov D, Gurevich A. Versatile genome assembly evaluation with QAST-LG. **Bioinformatics**. 2018;34: i142–i150 (presented at ISMB 2018).
13. **Mikheenko A**, Kolmogorov M. Assembly Graph Browser: interactive visualization of assembly graphs. **Bioinformatics**. 2018;35: 3476-3478.
14. Mohimani H, Gurevich A, Shlemov A, **Mikheenko A**, Korobeynikov A, Cao L, et al. Dereplication of microbial metabolites through database search of mass spectra. **Nature Communications**. 2018;9: 1–12.
15. Gurevich A, **Mikheenko A**, Shlemov A, et al. Increased diversity of peptidic natural products revealed by modification-tolerant database search of mass spectra. **Nature Microbiology**. 2018;3: 319–327.
16. Mohimani H, Gurevich A, **Mikheenko A**, et al. Dereplication of peptidic natural products through database search of mass spectra. **Nature Chemical Biology**. 2017;13: 30–37.

## PREPRINTS

1. Miloto C, Carcole M, Giblin A, ..., **Mikheenko A**, et al. PolyGR and polyPR knock-in mice reveal a conserved neuroprotective extracellular matrix signature in C9orf72 ALS/FTD neurons. Accepted to Nature Neuroscience.
2. Pardo-Palacios FJ, Wang D, Reese F, ..., **Mikheenko A**, et al. Systematic assessment of long-read RNA-seq methods for transcript identification and quantification. Submitted to Nature Methods.

## PAPERS IN PREPARATION

1. **Mikheenko A**, Ndayambaje S, et al. Differential effects of the TDP-43 knockdown on cellular functions of neuronal and glial cells.
2. Ryan V, **Mikheenko A**, et al. Concordant effects of TDP-43 and FUS loss in soma and neurites of cultured neuronal cells.
3. **Mikheenko A**, Armas J, Arozena AA, et al. Gains and losses of TDP-43 function in mice with ALS-associated mutations of TARDBP.
4. Brown AL, Zanollo M, **Mikheenko A**, et al. TDP-43 cryptic exons in neurons: insights from invitro experiments and in vivo detection.
5. Bryce-Smith S, Brown AL, Mehta P, ..., **Mikheenko A**, et al. TDP-43 loss induces cryptic 3' end processing in neurons and ALS.

## Grants & Awards

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2021 **Essential Open Source Software for Science program**, Chan Zuckerberg Initiative  
 2019 **Young Scientists Award**, Saint Petersburg State University

*key personnel  
winner*

## Teaching

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- 2022 **Lecturer**, NGS Data Analysis, Sirius University of Science and Technology, Russia (Bioinformatics Master's students)
- 2021-2022 **Undergraduate Research Mentor**, Mentoring research projects of Computer Science undergraduate students, St. Petersburg State University, Russia
- 2019 **Lecturer**, Introduction to Bioinformatics, St. Petersburg State University, Russia (Biology and Bioinformatics Master's students)

## Professional development

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- An Introduction to Evidence-Based Undergraduate STEM Teaching (Cornell University)** Online course
- Advancing Learning Through Evidence-Based STEM Teaching (Cornell University)** Online course
- Teaching & Learning in the Diverse Classroom (Columbia University)** Online course
- Inclusive Teaching (Cornell University)** Online course
- Machine learning (Stanford University)** Online course
- Neural networks and computer vision (Samsung Research)** Online course
- Pharmacology Modeling School (Skolkovo Institute in partnership with AstraZeneca)** Educational workshop

## Major Collaborations

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- 2015-2018 **AstraZeneca**, Development of computational pipeline for identifying and prioritization mutations in the genomic data of cancer patients.
- 2019-2023 **T2T consortium**, Development of highly sensitive and precise algorithm for detecting assembly errors in highly repetitive regions.
- 2015-2022 **Pavel Pevzner (University of California at San Diego)**, Development of computational tools for genomics data
- 2020-present **Hagen Tilgner (Weill Cornell Medicine)**, Development of computational tools for transcriptomics data
- 2015-2019 **Hosein Mohimani (Carnegie Mellon University)**, Development of computational tools for proteomics data
- 2023-present **Michael Ward (NIH)**, Analysis of transcriptomics and proteomics data of mouse models and cell lines.

## Academic References

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- **Pietro Fratta** (postdoctoral advisor)  
Professor of Cellular and Molecular Neuroscience  
Department of Neuromuscular Diseases, University College of London  
pfratta@ucl.ac.uk
- **Pavel Pevzner** (PhD advisor)  
Distinguished Professor of Computer Science  
Department of Computer Science, University of California at San Diego  
ppevzner@ucsd.edu
- **Hagen Tilgner**  
Associate Professor of Neuroscience  
Brain and Mind Research Institute, Weill Cornell Medicine  
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