

Dr. Olga O. Bochkareva (Dranenko)

Date of Birth: Sept. 10, 1988
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List of all publications: <https://orcid.org/0000-0003-1006-6639>
Languages: English (fluent), German (A1), Russian (native)



Research interests:

- Architecture and evolution of bacterial chromosomes: genome rearrangements, horizontal gene transfer, homologous recombination, multi-chromosome bacterial species.
- Evolution of protein sequences and operons structure.
- Evolution of bacterial communities: pan-genomics, metagenomics, taxonomy.
- Pathogenicity, resistance, microbe-host interactions.

Work experience:

2023 – present principal investigator/senior postdoc, CUBE, Department of Microbiology and Ecosystem Science, University of Vienna, Vienna, Austria.

2019 – 2023 postdoctoral researcher, Institute of Science and Technology, Vienna, Austria. Prof. Fyodor Kondrashov group.

2017- 2019 junior research scientist, Department of Life Sciences, Skolkovo Institute of Science and Technology, Moscow, Russia. Prof. Mikhail Gelfand group.

2012- 2019 junior research scientist, Kharkevich Institute for Information Transmission Problems RAS, Moscow, Russia. Prof. Mikhail Gelfand group.

Education:

2012–2019 Ph.D., Kharkevich Institute for Information Transmission Problems RAS. PhD thesis: *“Reconstruction of evolutionary history of genome rearrangements in bacteria”*, Supervisor: Prof. Mikhail S. Gelfand.

2010–2012 Master of Science (applied mathematics and physics), Department of Molecular and Biological Physics, Moscow Institute of Physics and Technology. Master thesis *“Bacterial microevolution and genome rearrangements”*, Supervisor: Prof. Mikhail S. Gelfand.

2005–2010 Bachelor of Science (applied mathematics and physics), Department of Molecular and Biological Physics, Moscow Institute of Physics and Technology.

Funding and Awards:

2023 ESPRIT Programme (“Early Stage Programme: Research, Innovation and Training”), funding from **Austrian Science Fund**, total amount – **294.015€**.

2019 ISTplus postdoctoral fellowship. Funding from the European Union’s Horizon 2020 research and innovation programme under the **Marie Skłodowska-Curie grant** agreement No 754411

Publications:

8 peer-reviewed publications, 3 first and 3 last authorships, 89 citations (GoogleScholar on 1/03/2023)

(* - equal contribution)

1. Maximilian Baumgartner, Rebecca Zirnbauer, Sabine Schlager, Daniel Mertens, Nikolaus Gasche, Barbara Sladek, Craig Herbold, **Olga Bochkareva**, Vera Emelianenko, Harald Vogelsang, Michaela Lang, Anton Klotz, Birgit Moik, Athanasios Makristathis, David Berry, Stefanie Dabsch, Vineeta Khare & Christoph Gasche Atypical enteropathogenic *E. coli* are associated with disease activity in ulcerative colitis **Gut Microbes**, 2022, Nov 22; 14(1):2143218 <https://doi.org/10.1080/19490976.2022.2143218>
2. Natalia O Dranenko, Maria Tutukina, Mikhail S. Gelfand, Fyodor Kondrashov & **Olga O Bochkareva** Chromosome-encoded IpaH ubiquitin ligases indicate non-human pathogenic *Escherichia* **SciRep** 2022 Apr 27, 12:6868 doi: 10.1038/s41598-022-10827-3
3. Alexey Zabelkin, Yulia Yakovleva, **Olga Bochkareva*** & Nikita Alexeev* **(last co-authorship)**. PaReBrick: PARallel REarrangements and BReaks identification toolkit. **Bioinformatics** 2021 Oct 03; 38(2):357-363 <https://doi.org/10.1093/bioinformatics/btab691>
4. Zaira Seferbekova, Alexey Zabelkin, Yulia Yakovleva, Robert Afasizhev, Nikita Alexeev, Mikhail S Gelfand & **Olga O Bochkareva (last authorship)** High rates of genome rearrangements and pathogenicity of *Shigella* spp. **Frontiers Microbiology** 2021 Apr 12; 12:831. doi:10.3389/fmicb.2021.628622
5. Olga Sigalova, Andrei V Chaplin, **Olga O Bochkareva**, Pavel V Shelyakin, Vsevolod A Filaretov, Evgeny E Akkuratov, Valentina Burskaya & Mikhail S Gelfand *Chlamydia* pan-genomic analysis reveals balance between host adaptation and selective pressure to genome reduction. **BMC Genomics**. 2019 Sep 12;20(1):710. doi: 10.1186/s12864-019-6059-5.
6. Pavel V Shelyakin*, **Olga O Bochkareva***, Anna A Karan & Mikhail S Gelfand **(first co-authorship)** Micro-evolution of three *Streptococcus* species: selection, antigenic variation, and horizontal gene inflow. **BMC Evol. Biol.** 2019. Mar 27;19(1):83. doi: 10.1186/s12862-019-1403-6.
7. **Olga O Bochkareva**, Elena V Moroz, Iakov I Davydov & Mikhail S Gelfand Genome rearrangements and selection in multi-chromosome bacteria *Burkholderia* spp. **BMC Genomics**. 2018 Dec 27;19(1):965. doi: 10.1186/s12864-018-5245-1.
8. **Olga O Bochkareva**, Natalia O Dranenko, Elena S Ocheredko, German M Kanevsky, Yaroslav N Lozinsky, Vera A Khalaycheva, Irena I Artamonova & Mikhail S Gelfand Genome rearrangements and phylogeny reconstruction in *Yersinia pestis*. **PeerJ**. 2018 Mar 27;6:e4545. doi: 10.7717/peerj.4545.

Preprints and submitted papers:

- Natalia O Dranenko, Aleksandra D Rodina, Yaroslav V Demenchuk, Mikhail S. Gelfand & **Olga O Bochkareva** Evolutionary trajectories of secondary replicons in multipartite genomes **bioRxiv** 2023 Apr 09: 536151; doi:10.1101/2023.04.09.536151

Working papers:

- Alper Yurtseven, Sofia Buyanova, Amay A. Agrawal, **Olga O. Bochkareva** & Olga V. Kalinina Machine learning and phylogenetic analysis improves predicting antibiotic resistance in *M. tuberculosis*
- Alexey Zabelkin & **Olga O. Bochkareva** *BADLON: linear collinear Blocks Analysis: Distribution, Location, and compositiON*

Invited Talks

1. Detection of genome rearrangements responsible for bacterial phenotype switching. **2022 Helmholtz Institute for Pharmaceutical Research Saarland (HIPS)** Saarland, Germany
2. How bacteria switch to dark side. **2022 SMTB'22 University of Tartu**, Tartu, Estonia
3. Microbes: taxonomy, genome structure and molecular evolution **2022** workshop organized by **Institute of Bioinformatics (online)**
4. Role of genome rearrangements in formation of bacterial phenotypes, **2021 EMBL, Heidelberg** Germany
5. Comparative genomics of prokaryotes (cookbook), **2020** Summer School of **Bioinformatics Institute, online**
6. Structure and evolution of bacterial chromosomes **2019 Bioinformatics Institute** Open Lectures series, St. Petersburg, Russia
7. Comparative genomics of prokaryotes (cookbook), **2019** workshop organized by **Bioinformatics Institute**, St. Petersburg, Russia

Conference Talks:

1. Detection of genome rearrangements responsible for bacterial phenotype switching. **SASBi'22** Stellenbosch, South Africa
2. Evolutionary benefits of bacterial genomes with chromids **MCCMB'21** Moscow, Russia
3. Genome rearrangements in bacteria. **BiATA'19** St. Petersburg, Russia
4. Evolution of bacterial chromosomes. **Chromosome'18** Novosibirsk, Russia

Supervised students:

2021 Natalia Dranenko, IITP RAS, Russia

The Classification of *ipaH* Genes in *Shigella* and Enteroinvasive *Escherichia*, **MCCMB'21** poster presentation published in **SciRep** doi: 10.1038/s41598-022-10827-3

2021 Ariadna Semenova, Moscow State University, Russia

Insertion sequences in *B. mallei*: adaptation to intracellular lifestyle, **MCCMB'21** poster presentation

2020 Yulia Yakovleva, Alexey Zabelkin Bioinformatics Institute, Russia

PaReBrick: PArallel REarrangements and BReakpoints identification toolkit

published in **Bioinformatics** doi:10.1101/2021.05.18.444676

2020 Kristina Perevoshchikova, Moscow State University, Russia

Evolutionary benefits of bacterial genomes with chromids, **MCCMB'21** oral presentation

2019 Zaira Seferbekova, Moscow State University, Russia

Impact of mobile elements into pathogenicity of *Shigella*

published in **Frontiers Microbiology** 10.1186/s12862-019-1403-6

2019 Moldir Zhiyenbayeva, graduate student at HSE, Moscow, Russia. Co-advising master project

"Comparative Genomics of *Bacillus* spp.". PI: Mikhail Gelfand.

2018 Natalia Dranenko, graduate student at MIPT, Moscow, Russia. Co-advising bachelor project

"Reconstruction of OxyR ancestor sequence in bacteria". PI: Mikhail Gelfand.

Collaborations:

2021-present Dr. Roderich Kromhild, IST Austria, Klosterneuburg, Austria. Project: Fitness effects of short random peptides.

2020-2022 Dr. Nikina Alexeev, ITMO University, Saint Petersburg, Russia. Project: Development of the bioinformatic toolkit for whole-genome analysis.

2020-present Dr. Michaela Lang, Medical University of Vienna, Vienna, Austria. Project: Genetic factors under biofilms formation in pathogenic *E.coli*.

2016-2018 Prof. Marc Robinson-Rechavi, Evolutionary Bioinformatics Lab, Department of Ecology and Evolution, Université de Lausanne, Lausanne, Switzerland. Project: Positive selection and horizontal gene transfer in prokaryotes.

2010-2014 Prof. Pavel Pevzner, University of California at San Diego, California, USA. Project: Application of the MGRA (Multiple Genome Rearrangements and Ancestors) algorithm to microbial data.

Management experience:

Summer School of Theoretical and Molecular Biology (<https://molbioschool.org/en/>)

- **2020 – 2022 Vice-director** - recruiting project leaders, lecturers and course instructors; design of lectures and courses; management of courses execution and labs; and moderation of scientific discussions.
- **2020 – 2022 Head of Laboratory** – 4 project leaders and 4-6 students.
- **2016 – 2019 Project Leader** - design and supervision a research-based teaching project.

Teaching experience:

Lecturer/course instructor:

Designed and delivered courses

- **Fall 2020 “Comparative genomics of prokaryotes”**, course for master students (Bioinformatics Institute, St Petersburg, Russia), in Russian. Final evaluation by students: 9.3 out of 10 (the highest evaluation across all courses during the term)

Teacher assistant:

Designed and delivered selected lectures and labs, prepared and supervised course projects and home assignments

- **Spring 2019 “Bioinformatics”**, course for master and PhD students (Skoltech, Moscow, Russia), in English
- **Autumn 2018 “Comparative Genomics”**, course for master and PhD students (joint program Skoltech/HSE, Moscow, Russia), in English

Reviewer:

in Microbial Genomics, BMC Genomics, GENE, Journal of Bioinformatics and Computational Biology, PeerJ, Frontiers Microbiology

Professional skills:

Bioinformatics (comparative and evolutionary genomics): genome assembly and annotation, phylogeny reconstruction, rearrangements reconstruction, sequences alignment, ancestral sequences reconstruction, HGT identification, selection identification, statistics.

Programming: (Bio-)Python, R

Academic writing (+LaTeX), **data visualization**