

## Dr. Olga O. Bochkareva (Dranenko)

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**Web page (current lab):** <https://ist.ac.at/en/research/kondrashov-group/>.  
**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:

**June 2019 - present** 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

**2012- 2019** junior research scientist, Kharkevich Institute for Information Transmission Problems RAS, Moscow, Russia

### 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. Bachelor thesis *“The convergence of the over-relaxation method depending on the iteration parameter choice for the 2-D Poisson equation”*, Supervisor: *Prof. Sergey Surzhikov*, Ishlinsky Institute for Problems in Mechanics RAS.

### Funding and Awards:

**2022-2025** ESPRIT Programme (“Early Stage Programme: Research, Innovation and Training”), funding from **Austrian Science Fund**, total amount – **294.015€**.

**2019-2021** 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, 77 citations** (GoogleScholar on 20/11/2022)

(\* - 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:**

## 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. See also a list of specialized tools I use in my [CookBook](#).

**Programming:** (Bio-)Python, R

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