

Dr. Olga O. Bochkareva

Date of Birth: Sept. 10, 1988
Citizenship: Russia
Address: 3400 Institute of Science and Technology Austria
Am Campus 1, Klosterneuburg, Austria
E-mail: olga.bochkareva@ist.ac.at
Mobile phone: +43 664 88326272
Web page (personal): <https://www.bochkareva.me/>
Web page (current lab): <https://ist.ac.at/en/research/kondrashov-group/>.
List of all publications: <https://orcid.org/0000-0003-1006-6639>
Languages: Russian (native), English (fluent), German (A1)
Married, two children

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, Kharkevich Institute for Information Transmission Problems RAS, Moscow, Russia

2017- 2019 junior research scientist, Department of Life Sciences, Skolkovo Institute of Science and Technology, 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:

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:

6 peer-reviewed publications, 3 first and 2 last authorships, 49 citations (GoogleScholar on 15/10/2021)

(* - equal contribution)

1. Alexey Zabelkin, Yulia Yakovleva, **Olga Bochkareva***, Nikita Alexeev*. PaReBrick: PArallel REarrangements and BReaks identification toolkit. **Bioinformatics** 2021 Oct 03 <https://doi.org/10.1093/bioinformatics/btab691>
2. Zaira Seferbekova, Alexey Zabelkin, Yulia Yakovleva, Robert Afasizhev, Nikita Alexeev, Mikhail S Gelfand, **Olga O Bochkareva** High rates of genome rearrangements and pathogenicity of *Shigella* spp. **Frontiers Microbiology** 2021 Apr 12; 12:831. doi:10.3389/fmicb.2021.628622
3. 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.
4. Pavel V Shelyakin*, **Olga O Bochkareva***, Anna A Karan, Mikhail S Gelfand 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.
5. **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.
6. **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:

1. Natalia O Dranenko, Maria Tutukina, Mikhail S. Gelfand, Fyodor Kondrashov, **Olga O Bochkareva** Chromosome-encoded IpaH ubiquitin ligases indicate non-human pathogenic *Escherichia* **BioRxiv** October 19, 2021 doi: 10.1101/2021.10.19.464960

Supervised projects:

2021 Natalia Dranenko, IITP RAS, Russia

The Classification of *ipaH* Genes in *Shigella* and Enteroinvasive *Escherichia*, **MCCMB'21** poster presentation

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 Molder 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:

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

2020-present Prof. Christoph Gasche, 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.

Teaching experience:

Summer School of Theoretical and Molecular Biology

2020 – 2021 Head of STEM department - design of lectures and courses, recruiting lecturers and course instructors, management of courses execution, and moderation of scientific discussions.

2020 – 2021 Head of Laboratory – 4 project leaders and 4-6 students.

2016 – 2019 Project Leader - design and supervision a research-based teaching project.

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)

Invited lectures and other teaching contributions:

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

2020 Structure and evolution of bacterial chromosomes Bioinformatics Institute Open Lectures ([youtube](#))

2020 Comparative genomics of prokaryotes, cookbook, Summer School of Bioinformatics Institute ([youtube](#))

Reviewer:

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

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**