

## Dr. Olga O. Bochkareva

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### The impact and importance of the main research outputs:

I'm working on the intersection of comparative genomics, algorithmic biology, and evolutionary biology to build a deep understanding of bacterial genome organization and the molecular mechanisms providing complex dynamic genotype-phenotype connections. How many genotypes are present simultaneously in a pure bacterial colony? What is responsible for the rates of genotype switching in a one cell line? What are the limitations of the classic model 'one bacterial colony - one genome' which is still a basis of genome assemblers? Under the confines of a single laboratory we develop computational methods and set-up experimental assays of engineered cultures to study complex genetic mechanisms leading to bacterial adaptation to dynamic environments characterized by multiple pressures: fluctuating nutrient availability, phages, host immune system etc. I have developed a set of the methods for analysis of structural variants (PaReBRick, BADLON) which provide a basis for holistic prediction of phase variable systems and the genotype-to-phenotype connection they moderate. Mainly working on fundamental knowledge about bacterial genome complexity, I create efficient pipelines which might be used as a basis for clinical and industrial applications.

### Work experience:

**2023 – present** ESPRIT Principal Investigator, CUBE, Centre for Microbiology and Environmental Systems Science, University of Vienna, Austria.

**2019 – 2023** postdoctoral researcher, Institute of Science and Technology (ISTA), Austria. Prof. Fyodor Kondrashov group.

**2017 – 2019** junior research scientist, Department of Life Sciences, Skolkovo Institute of Science and Technology, Moscow, Russia.

**(Career break) 2014 – 2017** maternity leave (twins)

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

### Funding and Awards:

**(under review)** "Genetic heterogeneity of Bacteroides PULs", total amount **664.218€**

**Austrian Science Fund**, Principal Investigator Project, one postdoc and one PhD positions are included

**2023** "Large-scale genomic features and bacterial phenotypes", total amount – **294,015€**

**Austrian Science Fund** ESPRIT Programme ("Early Stage Programme: Research, Innovation and Training")

**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

## Education:

**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.

**2012** Master of Science (applied mathematics and physics), Department of Molecular and Biological Physics, Moscow Institute of Physics and Technology.

**2010** Bachelor of Science (applied mathematics and physics), Moscow Institute of Physics and Technology.

## Publications:

**10 peer-reviewed publications, 3 first and 3 last authorships** (\* - equal contribution)

1. K Jain, R Hauschild, **OO Bochkareva**, R Roemhild, G Tkacik, CC Guet Pulsatile basal gene expression as a fitness determinant in bacteria **Proc. Natl. Acad. Sci. U.S.A.** 2025 Apr 07, 122(15) e2413709122 doi:10.1073/pnas.2413709122
2. A Yurtseven, S Buyanova, AA Agrawal, **OO Bochkareva** & OV Kalinina. Machine learning and phylogenetic analysis improves predicting antibiotic resistance in *M. tuberculosis* 2023 **BMC Microbiol** 23, 404 doi:10.1186/s12866-023-03147-7
3. M Baumgartner, R Zirnbauer, S Schlager, D Mertens, N Gasche, B Sladek, C Herbold, **OO Bochkareva**, V Emelianenko, H Vogelsang, M Lang, A Klotz, B Moik, A Makristathis, D Berry, S Dabsch, V Khare & C Gasche. Atypical enteropathogenic *E. coli* are associated with disease activity in ulcerative colitis **Gut Microbes**, 2022, Nov 22; 14(1):2143218 doi: 10.1080/19490976.2022.2143218
4. NO Dranenko, M Tutukina, MS Gelfand, F Kondrashov & **OO Bochkareva** Chromosome-encoded IpaH ubiquitin ligases indicate non-human pathogenic *Escherichia* **SciRep** 2022 Apr 27, 12:6868 doi:10.1038/s41598-022-10827-3
5. A Zabelkin, Y Yakovleva, **O Bochkareva\*** & N Alexeev\*. PaReBrick: PArallel REarrangements and BReaks identification toolkit. **Bioinformatics** 2021 Oct 03; 38(2):357-363 doi:0.1093/bioinformatics/btab691
6. Z Seferbekova, A Zabelkin, Y Yakovleva, R Afasizhev, N Alexeev, MS Gelfand & **OO Bochkareva**. High rates of genome rearrangements and pathogenicity of *Shigella* spp. **Frontiers Microbiology** 2021 Apr 12; 12:831. doi:10.3389/fmicb.2021.628622
7. O Sigalova, AV Chaplin, **OO Bochkareva**, PV Shelyakin, VA Filaretov, EE Akkuratov, V Burskaya & MS 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.
8. PV Shelyakin\*, **OO Bochkareva\***, AA Karan & MS 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.
9. **OO Bochkareva**, EV Moroz, II Davydov & MS 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.
10. **OO Bochkareva**, NO Dranenko, ES Ocheredko, GM Kanevsky, YN Lozinsky, VA Khalaycheva, II Artamonova & MS Gelfand. Genome rearrangements and phylogeny reconstruction in *Yersinia pestis*. **PeerJ**. 2018 Mar 27;6:e4545. doi:10.7717/peerj.4545.

### Preprints and submitted papers:

- LH Isakova, E Streltsova, **OO Bochkareva**, PK Vlasov, FA Kondrashov Descent from a common ancestor restricts evolutionary exploration of protein sequence space Submitted in PNAS Material available here: <https://github.com/oist/sequence-space-dimension>
- C Zioutis, M Lang, F Pereira, **O Bochkareva**, E Kolodyazhnaya, J Osvatic, KD McCoy, S Künzel, H Fokt, JF Baines, D Berry Rapid genetic diversification of *Bacteroides thetaiotaomicron* in mono-associated mice revealed through deep population-level sequencing. bioRxiv 2025.06.24.661302 doi: 10.1101/2025.06.24.661302
- M Lang, C Zioutis, A Heberlein, N Ivanovova, J Schwarz, S Köstlbacher, **O Bochkareva**, KJ Flanagan, FC Pereira, D Berry Nutrient landscape shapes the genetic diversification of the human gut commensal *Bacteroides thetaiotaomicron* bioRxiv 2025.06.24.661248 doi:10.1101/2025.06.24.661248
- NO Dranenko, AD Rodina, YV Demenchuk, MS Gelfand & **OO Bochkareva**. Evolutionary trajectories of secondary replicons in multipartite genomes bioRxiv 2023 Apr 09: 536151; doi:10.1101/2023.04.09.536151
- EV Vostokova, NO Dranenko, MS Gelfand, **OO Bochkareva**. Genome rearrangements and host adaptation in *Wolbachia* bioRxiv 2023 Oct doi:10.1101/2023.10.25.563763

### Papers in preparation:

- An evolutionary-conserved mechanism of phase variation in dominant members of the mammalian gut microbiota. N Gruber, B Hekele, S Khadem, N Dranenko, E Kolodyazhnaya, R Romhild, M Hennessey, F Kondrashov, D Berry, C Guet, **O Bochkareva**
- Stress-induced adaptive mutation modulated by luxS. M Hennessey-Wesen, **O Bochkareva**, J Merrin, CC Guet, B Hof

## Other contributions to the research community

### Invited Talks

2024 Trinity College Dublin, Ireland; 2024 Okinawa Institute of Science and Technology, Japan; 2022 Helmholtz Institute for Pharmaceutical Research Saarland (HIPS) Saarland, Germany; 2022 SMTB'22 University of Tartu, Tartu, Estonia; 2021 EMBL, Heidelberg Germany

### Supervised students:

>15 term papers, 2 BS theses, 4 MS theses, 2 co-supervised PhD theses

### New courses development and implementation to educational programs:

- **Semester course**, “Comparative genomics of prokaryotes” for master and PhD students.

Taught for Bioinformatics Institute (St Petersburg, Russia) in Fall 2020, final evaluation by students: 9.3 out of 10 (the highest evaluation across all courses during the term).

- **Bioinformatics workshops** for a broad audience.

### Services for the scientific community and volunteering

- **Summer School of Theoretical and Molecular Biology**

design of the research project, hiring lab staff, lecturers and course instructors; design of lectures and courses; management of courses execution and labs; student supervision.

- **Bioinformatics Institute** (non-governmental non-profit Bioinformatics research and educational institution)

giving open lectures and workshops for broad audience interested in bioinformatics

- **Member of Scholars-Without-Borders programme**

supporting students and academics from Ukraine, Belarus or Russia affected by the war

- **Member of Women In Biology Initiative**

supporting the careers of female scientists at all levels

**Languages:** English (fluent), German (A2), Russian (native)

**Contact details of referees:**

**Prof. Mikhail Gelfand:**

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**Prof. Fyodor Kondrashov:**

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**Prof. Calin Guet:**

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**Prof. David Berry:**

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