

ALEXANDER PREDEUS

NGS BIOINFORMATICS, GENOMICS, SYSTEMS BIOLOGY, IMMUNOLOGY

CONTACT

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EDUCATION

DOCTORATE DEGREE

Organic Chemistry
Michigan State University
2003 – 2009

MASTER'S DEGREE

Chemistry
Moscow State University
1998 – 2003

SKILLS

TECHNICAL

Unix administration
High-performance clusters
Cloud environment (AWS, GC)
Pipeline development
Software/algorithm design
[Git/GitHub](#)
Client support (Jira)

SUMMARY

I am a professional bioinformatician with a broad experience in processing and analysis of NGS data. I have developed tens of high-throughput pipelines, as well as advanced web-based solutions and novel standalone tools. I have supervised M.S. and Ph.D. students, and managed teams of bioinformaticians and computer scientists, working in both academic and service-oriented settings. My main scientific interests lie in applying computational and systems biology approaches to genomic and transcriptomic data. I greatly enjoy generating biological hypotheses from big data and collaborating with experimental scientists to validate them.

EXPERIENCE

PRINCIPAL BIOINFORMATICIAN, CELLULAR GENETICS INFORMATICS

Wellcome Sanger Institute, Hinxton, UK | Dec 2020 – Present

- Designed and prototyped an internal portal of uniformly reprocessed single cell RNA-seq data
- Developed, ran, and improved numerous bioinformatic software tools and pipelines supported by CellGenIT
- Reprocessed several thousand public and internal scRNA-seq, Visium, multiome, CITE-seq, and bulk RNA-seq datasets
- Introduced management improvements into CellGenIT support workflow
- Helped establish curation pipeline for submission of Sanger-generated data to CZI CELLXGENE data portal
- Established working collaborations with most research groups in the Cellular Genetics programme
- Line managed five bioinformaticians

POSTDOCTORAL RESEARCH ASSOCIATE, JAY HINTON LABORATORY

University of Liverpool, Liverpool, UK | Jan 2018 – Nov 2020

- Processed, quality-controlled, assembled, and analysed data generated by 10k Salmonella genomes project
- Developed a novel pipeline to process multi-strain bacterial RNA-Seq
- Developed a custom pipeline for analysis of TraDIS experiments
- Performed bacterial GWAS to find genomic determinants of invasive non-typhoidal salmonellosis
- Participated in numerous collaborations related to genome assembly, analysis, and bacterial RNA-seq processing

SKILLS

PROGRAMMING

R – advanced

Python – intermediate

Bash – advanced

Perl – advanced

C, C++, FORTRAN – basic

PROFESSIONAL

Line management

Project design and management

Scientific writing

Grant writing

REFERENCES

PROF. SARAH TEICHMANN

Wellcome Sanger Institute, UK

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PROF. MUZLIFAH HANIFFA

Wellcome Sanger Institute, UK

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PROF. JAY HINTON

University of Liverpool, UK

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DR. VLADIMIR KISELEV

Alethiomics, UK

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LANGUAGES

RUSSIAN | Native

UKRAINIAN | Native

ENGLISH | Fluent

EXPERIENCE

DIRECTOR OF RESEARCH

Bioinformatics Institute, Saint Petersburg, Russia | Jul 2015 – Dec 2017

- Established an independent research program in NGS bioinformatics, involving graduate students and young scientists from various Universities and hospitals of Saint Petersburg
- Analysed and published the first compendium of exome-wide allele frequencies in Russian population
- Created several bioinformatic tools used for exome and sequencing panel data analysis in medical genomics
- Developed novel statistical approaches to analyse and functionally characterise pleiotropy in the UK Biobank GWAS dataset
- Established a broad international collaboration network for biologists and medical professionals using NGS methods, including Washington University in St. Louis, Yale University, and University of Copenhagen

POSTDOCTORAL RESEARCH ASSOCIATE, MAX ARTYOMOV LABORATORY

Washington University in St. Louis, School of Medicine | Jul 2012 – Jul 2015

- Performed computational processing of NGS experiments: quality control, alignment, and analysis of several hundred RNA-Seq and ChIP-Seq samples
- Used Markov genome segmentation analysis to identify active enhancer and promoter regions of VDJ loci
- Analysed the epigenetic code influencing active repertoire in murine T-cells
- Developed a comprehensive gene co-expression database based on the published expression experiments, and implemented as GeneQuery web tool
- Discovered a new non-coding RNA involved in regulation of macrophage polarization
- Analysed expression and metabolic changes in adipose tissue of human CALERIE project participants upon calorie restriction
- Participated in numerous collaborative projects with experimental biologists, interpreting human and murine expression data

TEACHING

- Was lead bioinformatic instructor in Wellcome Connecting Science course “Single Cell Technologies and Analysis”, 2021-2022
- Contributed several chapters to singlecellcourse.org
- Created a massive open online course (MOOC) named “Introduction to Next-Generation Sequencing” based on Stepik online education platform
- Co-developed the workshop concept, and taught RNA-Seq and ChIP-Seq analysis courses at Systems Biology Workshop in Sydney, Australia (Garvan Institute of Medical Research) in 2016
- Co-developed the workshop concept, and taught RNA-Seq and ChIP-Seq analysis courses at five Systems Biology Workshops in Saint Petersburg, Russia, 2014 - 2018

PUBLICATIONS

As of September 2023, I have published 50 papers and 12 preprints, with 6 as a first or co-first author, and 8 as a communicating author. Full list of my publications is available in my [Google Scholar profile](#). Selected publications are listed below.

- Easter, Quinn T., Bruno F. Matuck, German B. Stark, Catherine L. Worth, Alexander V. Predeus, Brayon Fremin, Khoa T. Huynh, et al. "Polybacterial intracellular coinfection of epithelial stem cells in periodontitis." **bioRxiv** (August 24, 2023). <https://doi.org/10.1101/2023.08.23.554343>
- Predeus, Alexander V., Anna Arutyunyan, Laura Jardine, Chenqu Suo, Emma Dann, Regina Hoo, Martin Prete, Muzlifah Haniffa, Thomas J. Mitchell, Roser Vento-Tormo, Matthew D. Young. "X-inactivation states of single cell transcriptomes reveal cellular phylogenies in human females." **bioRxiv** (November 13, 2022). <https://doi.org/10.1101/2022.11.10.515645>
- Hoo R., Elias R. Ruiz-Morales, Iva Kelava, Carmen Sancho-Serra, Cecilia I. Mazzeo, Sara Chelaghma, Elizabeth Tuck, Alexander V. Predeus, David Fernandez-Antoran, Ross F. Waller, Marcus Lee, Roser Vento-Tormo. "Early infection response of the first trimester human placenta at single-cell scale." **bioRxiv** (January 02, 2023). <https://doi.org/10.1101/2023.01.02.522155>
- Spadaro, O., Y. Youm, I. Shchukina, S. Ryu, S. Sidorov, A. Ravussin, K. Nguyen, et al. "Caloric Restriction in Humans Reveals Immunometabolic Regulators of Health Span." **Science** 375, no. 6581 (February 11, 2022): 671–77. <https://doi.org/10.1126/science.abg7292>
- Barbitoff, Yury A., Ruslan Abasov, Varvara E. Tvorogova, Andrey S. Glotov, and Alexander V. Predeus. "Systematic Benchmark of State-of-the-Art Variant Calling Pipelines Identifies Major Factors Affecting Accuracy of Coding Sequence Variant Discovery." **BMC Genomics** 23, no. 1 (December 2022): 155. <https://doi.org/10.1186/s12864-022-08365-3>
- Perez-Sepulveda, Blanca M., Darren Heavens, Caisey V. Pulford, Alexander V. Predeus, Ross Low, Hermione Webster, Gregory F. Dykes, et al. "An Accessible, Efficient and Global Approach for the Large-Scale Sequencing of Bacterial Genomes." **Genome Biology** 22, no. 1 (December 2021): 349. <https://doi.org/10.1186/s13059-021-02536-3>
- Powers, TuShun R., Amanda L. Haeberle, Alexander V. Predeus, Disa L. Hammarlöf, Jennifer A. Cundiff, Zeus Saldaña-Ahuactzi, Karsten Hokamp, Jay C. D. Hinton, and Leigh A. Knodler. "Intracellular Niche-Specific Profiling Reveals Transcriptional Adaptations Required for the Cytosolic Lifestyle of Salmonella Enterica." **PLOS Pathogens** 17, no. 8 (August 30, 2021): e1009280. <https://doi.org/10.1371/journal.ppat.1009280>
- Pulford, Caisey V., Blanca M. Perez-Sepulveda, Rocío Canals, Jessica A. Bevington, Rebecca J. Bengtsson, Nicolas Wenner, Ella V. Rodwell, et al. "Stepwise Evolution of Salmonella Typhimurium ST313 Causing Bloodstream Infection in Africa." **Nature Microbiology** 6, no. 3 (March 2021): 327–38. <https://doi.org/10.1038/s41564-020-00836-1>
- Barbitoff, Yury A., Dmitrii E. Polev, Andrey S. Glotov, Elena A. Serebryakova, Irina V. Shcherbakova, Artem M. Kiselev, Anna A. Kostareva, Oleg S. Glotov, and Alexander V. Predeus. "Systematic Dissection of Biases in Whole-Exome and Whole-Genome Sequencing Reveals Major Determinants of Coding Sequence Coverage." **Scientific Reports** 10, no. 1 (December 2020): 2057. <https://doi.org/10.1038/s41598-020-59026-y>
- Shikov, Anton E., Rostislav K. Skitchenko, Alexander V. Predeus, and Yury A. Barbitoff. "Phenome-Wide Functional Dissection of Pleiotropic Effects Highlights Key Molecular Pathways for Human Complex Traits." **Scientific Reports** 10, no. 1 (December 2020): 1037. <https://doi.org/10.1038/s41598-020-58040-4>
- Beliavskaia, Alexandra Y., Alexander V. Predeus, Sofya K. Garushyants, Maria D. Logacheva, Jun Gong, Songbao Zou, Mikhail S. Gelfand, and Maria S. Rautian. "New Intranuclear Symbiotic Bacteria from Macronucleus of Paramecium Putrinum - 'Candidatus Gortzia Yakutica.'" **Diversity** 12, no. 5 (May 15, 2020): 198. <https://doi.org/10.3390/d12050198>
- Canals, Rocío, Disa L. Hammarlöf, Carsten Kröger, Siân V. Owen, Wai Yee Fong, Lizeth Lacharme-Lora, Xiaojun Zhu, et al. "Adding Function to the Genome of African Salmonella Typhimurium ST313 Strain D23580." **PLOS Biology** 17, no. 1 (January 15, 2019): e3000059. <https://doi.org/10.1371/journal.pbio.3000059>
- Barbitoff, Yury A., Igor V. Bezdvornykh, Dmitrii E. Polev, Elena A. Serebryakova, Andrey S. Glotov, Oleg S. Glotov, and Alexander V. Predeus. "Catching Hidden Variation: Systematic Correction of Reference Minor Allele Annotation in Clinical Variant Calling." **Genetics in Medicine** 20, no. 3 (March 2018): 360–64. <https://doi.org/10.1038/gim.2017.168>
- Predeus, Alexander V., Suhasni Gopalakrishnan, Yue Huang, Jun Tang, Ann J. Feeney, Eugene M. Oltz, and Maxim N. Artyomov. "Targeted Chromatin Profiling Reveals Novel Enhancers in Ig H and Ig L Chain Loci." **The Journal of Immunology** 192, no. 3 (February 1, 2014): 1064–70. <https://doi.org/10.4049/jimmunol.1302800>
- Gopalakrishnan, Suhasni, Kinjal Majumder, Alexander Predeus, Yue Huang, Olivia I. Koues, Jiyoti Verma-Gaur, Salvatore Loguercio, et al. "Unifying Model for Molecular Determinants of the Preselection V β Repertoire." **Proceedings of the**