

Alexander Brechalov, Ph.D.

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SUMMARY

Data analyst specializing in machine learning and bioinformatics. Experienced in developing user-friendly data analysis tools and conducting experimental research projects. My background combines technical proficiency in data science with a strong understanding of bioinformatics, enabling me to deliver insightful, data-driven solutions.

SKILLS & TECHNOLOGIES

• Python

- Data analysis & visualization: **Pandas, NumPy, SciPy, Seaborn, Matplotlib**
- Version control: **GitHub**
- Machine Learning: **SciKit-Learn, Keras, PyTorch, HuggingFace**
- Web scraping / development: **Flask, Redis, BeautifulSoup**

• Other languages: **Perl, R**

• OS & command line: **bash, Linux**

• Data analysis APIs: **MS Office, LibreOffice, Vector NTI, SnapGene**

PROJECTS

PIFiA: Machine Learning Tool for Comprehensive Analysis of Microscopic Data

2020 – 2022

Role: Machine Learning Engineer

- *Designed and developed essential components for data analysis within the PIFiA tool*
- *Engineered data-driving algorithms to facilitate microscopic image clustering*
- *Extracted valuable biological insights from the analysis of results*

Access PIFiA at: <https://thecellvision.org/pifia/>

JOURNAL ADVISOR: Transformer-Based Web Tool Facilitating Academic Publishing

2021 – 2022

Role: Machine Learning Project Lead

- *Led the end-to-end development of the project, from conception to successful launch*
- *Gathered and organized dataset comprising 6 million manuscripts from over 4,000 scientific journals*
- *Deployed neural network on remote servers, enabling over 20-fold acceleration of calculations*
- *Developed and implemented a user-friendly web tool to streamline academic publishing*

Explore Journal Advisor at: <https://journal-advisor.com/>

ALEX: generalist protein annotation

2022 – 2024

Role: Machine Learning Engineer, Project Manager

- *Created and developed the project concept*
- *Managed a group of 4 scientists, developed training pipeline of generalist visual transformer*
- *Created and organized the most comprehensive set of microscopic images, encompassing over 70% of human proteome and comprising ~4,000,000 single-cell images from 12+ databases*

Codebook: Characterization of Novel Transcription Factors

2018 – 2023

Role: Researcher and Data Analyst

- *Conducted experiments and optimized protocols*
- *Organized a diverse dataset and developed an efficient indexing system for different types of genomic data*
- *Conducted in-depth analysis of genomic data, comparing and contrasting various datatypes*

WORK EXPERIENCE

Postdoctoral Fellow Donnelly Centre for Cellular and Biomolecular Research, University of Toronto, Canada	2018 – 2023
Junior Researcher Engelhardt Institute of Molecular Biology, Russian Academy of Sciences, Moscow, Russia	2017 – 2018
Junior Researcher (part time) Institute of Gene Biology, Russian Academy of Sciences, Moscow, Russia	2012 – 2017

EDUCATION

Doctor of Philosophy, Molecular Biology Engelhardt Institute of Molecular Biology, Russian Academia of Sciences, Moscow, Russia Sofia Georgieva's lab.	2009 – 2017
Continuing education courses, Bioinformatics Kharkevich Institute for Information Transmission Problems, Moscow, Russia	2013 – 2014
Exchange student, Chemical Engineering Luleå Technical University, Luleå, Sweden	2008 – 2009
M.Sc. in Industrial Biotechnology Northern Arctic Federal University (Arkhangelsk State Technical University), Arkhangelsk, Russia	2003 – 2009

PUBLICATIONS

1. Razdaibiedina A, **Brechalov A.**, MIREAD: Simple Method for Learning High-quality Representations from Scientific Documents. The 61st Annual Meeting of the Association for Computational Linguistics (ACL'23).
2. Razdaibiedina A, **Brechalov A.** et al. PIFIa: a self-supervised approach for protein functional annotation from single-cell imaging data. Submitted to Molecular and System Biology.
3. Soshnikova NV, Azieva AM, Klimenko N, Khamidullina AI, Feoktistov AV, Sheynov AA, **Brechalov AV**, Tatarskiy VV, Georgieva SG. A novel chromatin-remodeling complex variant, dcPBAF, is involved in maintaining transcription in differentiated neurons. Front. Cell Dev. Biol., 14 Nov 2023
4. Razdaibiedina A, and **Brechalov A.** Learning multi-scale functional representations of proteins from single-cell microscopy data. ICLR2022 Machine Learning for Drug Discovery.
5. Popova VV *, **Brechalov AV** *, Georgieva SG, Kopytova DV. Nonreplicative functions of the origin recognition complex. Nucleus. 2018;9(1):460-473. *Authors contribute equal to this work.
6. Tatarskiy VV Jr, Simonov YP, Shcherbinin DS, **Brechalov AV**, Georgieva SG, Soshnikova NV. Stability of the PHF10 subunit of PBAF signature module is regulated by phosphorylation: role of β -TrCP. Sci Rep. 2017 Jul 17;7(1):5645.
7. **Brechalov AV**, et al. PHF10 isoforms are phosphorylated in the PBAF mammalian chromatin remodeling complex. Mol Biol (Mosk). 2016 Mar-Apr;50(2):320-6.
8. Soshnikova NV, Simonov YP, **Brechalov AV**, Portseva TN, Pankratova EV, Georgieva SG. The level of the PHF10 protein, a PBAF chromatin-remodeling complex subunit, correlates with the Mts1/S100A4 expression in human cancer cell lines. Dokl Biochem Biophys. 2016 Mar;467(1):162-4.
9. Portseva TN, **Brechalov AV**, et al. Transcription factor Oct-1 stimulates the release of Mts1/S100A4 protein by the cancer cells. Dokl Biochem Biophys. 2016 Mar;467(1):121-3.
10. Kopytova DV, Popova VV, Kurshakova MM, Shidlovskii YV, Nabirochkina EN, **Brechalov AV**, Georgiev GP, Georgieva SG. ORC interacts with THSC/TREX-2 and its subunits promote Nxf1 association with mRNP and mRNA export in Drosophila. Nucleic Acids Res. 2016 Jun 2;44(10):4920-33.
11. **Brechalov AV**, et al. Mammalian cells contain two functionally distinct PBAF complexes incorporating different isoforms of PHF10 signature subunit. Cell Cycle. 2014;13(12):1970-9.
12. **Brechalov AV**, et al. Functioning of macromolecular complexes at successive stages of gene expression as self-coordinated molecular machines. Biofizika. 2011 Sep-Oct;56(5):831-9.