

# Roman Novikov

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## About

Data and Bioinformatics Engineer with over 4 years of experience in developing scalable data pipelines for genomic data analysis. Expertise in liquid biopsy research, biomarker discovery, and high-throughput sequencing workflows. Proficient in modern bioinformatics tools and frameworks, including CWL, Docker, and AWS, with a proven ability to optimize workflows for the development of cancer biomarkers. Strong interdisciplinary collaboration skills with a focus on translating computational science into impactful clinical outcomes.

## Skills

Languages	Python, Bash, JavaScript
Technologies	FastAPI, Docker, Kubernetes, Jenkins, AWS, PostgreSQL, ClickHouse, MongoDB, Tortoise ORM, Apache Kafka, Apache Airflow
Bioinformatics Tools	Picard, BWA, SAMtools, Bedtools, CWL, Nextflow

## Experience

<b>Hero.io</b> <i>Data Engineer</i>	<i>October 2024 - Present</i> <i>Dubai, UAE</i>
<ul style="list-style-type: none"><li>Designed and optimized robust ETL pipelines using Apache Airflow, FastAPI and Tortoise ORM for transforming and validating data across multiple sources.</li><li>Collaborated on automating data scraping and cleansing techniques to ensure high-quality inputs for ML models.</li></ul>	
<b>BostonGene</b> <i>Software Engineer</i>	<i>October 2022 - October 2024</i> <i>Waltham, MA</i>
<ul style="list-style-type: none"><li>Automated the validation of raw NGS data from liquid biopsy samples using Python and AWS, improving processing efficiency by 40% and reducing error rates by 30%.</li><li>Developed and maintained standardized bioinformatics pipelines with CWL, and Docker, leading to a 30% faster integration of new features.</li><li>Streamlined workflows in LIMS systems, enhancing interdepartmental collaboration and data accuracy.</li></ul>	
<i>Data Analyst</i>	<i>July 2021 - October 2022</i> <i>Waltham, MA</i>
<ul style="list-style-type: none"><li>Developed an analytical system using FastAPI significantly speeding up sample verification processes by 60%.</li><li>Automated data validation processes for large datasets, increasing processing efficiency by 40% and reducing error rates by 30%.</li></ul>	

## Education

<b>Moscow Institute of Physics and Technology</b> <i>Master's degree in Applied Mathematics and Physics</i> <i>Major in Computational Bioinformatics</i> <i>Professional qualification in Data Science</i> <b>Grade:</b> 3.90 GPA (Top 2%) <b>Graduate project:</b> Comprehensive analysis of quality control data for liquid biopsy samples based on cell-free DNA using NGS. <b>Awards:</b> Scholarship of Vladimir Potanin Foundation	<i>September 2022 - June 2024</i> <i>Moscow, Russia</i>
<b>Lomonosov Moscow State University</b> <i>Bachelor's degree in Biology, Major in Bioengineering</i> <b>Grade:</b> 3.83 GPA (Top 5%) <b>Graduate project:</b> Design of a nucleic acid biosensor based on two dCas9 proteins.	<i>Septembre 2017 - June 2021</i> <i>Moscow, Russia</i>

## Projects

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### iGEM Projects (2019 and 2020)

March 2019 - November 2020

Moscow, Russia

Led computational modeling efforts in two award-winning CRISPR/Cas biosensor projects for the international iGEM competition. Developed biosensors for hepatitis C and Lyme disease detection, achieving high sensitivity and specificity. Successfully presented results in Boston.

## Publications

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Shaytan, A. K., **Novikov, R. V.**, Vinnikov, R. S., et al. (2022). From DNA-Protein Interactions to the Genetic Circuit Design Using CRISPR-dCas Systems. *Frontiers in Molecular Biosciences*, 9, 1070526. [Link](#).

**Novikov, R. V.**, Gribkova, A. K., Kacher, J. G., et al. (2021). Design of Nucleic Acid Biosensors Based on CRISPR/Cas Systems and Reporter Split Proteins. *Moscow University Biological Sciences Bulletin*, 76(2), 52–58. [Link](#).

**Novikov, R. V.**, Bondarenko, E. A., Malyuchenko, N. V., Feofanov, A. V., Studitsky, V. M., Shaytan, A. K. (2020). Determining the Binding Constant of LANA Protein Fragment with Nucleosome. *Moscow University Biological Sciences Bulletin*, 75(4), 252–256. [Link](#).