CV and publications of Dr. Alexey Larionov

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Summary

Initially qualified as a medical doctor in Russia (Bachelor in Medicine as recognized by UK NARIC) I specialized in medical oncology and then did my PhD about peripheral estrogen production in breast cancer patients in Petrov Institute of Oncology in St. Petersburg (PhD degree is also recognized by UK NARIC).

I moved to the UK in 2000 to continue translational research in medical oncology in the Breast Research Unit in Edinburgh University, where I studied molecular markers and mechanisms of response to hormonal treatments in breast cancer. My tasks ranged from handling and annotating the clinical samples using clinical documentation, to setting up experimental and data analysis procedures (from RNA extraction to gene expression analysis). During this employment I contributed to several well-cited studies (e.g. https://doi.org/10.1200/JCO.2008.16.8849), wrote my first paper in data analysis (https://doi.org/10.1186/1471-2105-6-62) and presented in multiple international scientific meetings.

Using novel molecular methods (quantitative PCR, then microarrays, then sequencing) I got interested in bioinformatics and obtained MSc in Applied Bioinformatics (2012, Cranfield University, UK). Then I worked as a post-doctoral bioinformatician in Medical Department of Cambridge University (UK) developing pipelines for sequencing data analysis and studying mechanisms of heritable predisposition to cancers and rare diseases. Here I analyzed various datasets, ranging from familial pedigree sequencing data, through internally sequenced cohorts of hundreds of patients, to populational analysis of thousands of samples from the Genomic England project. During this employment I also contributed to several well-cited studies (e.g. https://doi.org/10.1016/S2468-1253(18)30079-7 or https://doi.org/10.1093/hmg/ddac089), and continued collaboration with my Edinburgh colleagues writing on hormonal and targeted treatments in breast cancer (e.g. https://doi.org/10.3389/fonc.2018.00089 or http://www.springer.com/us/book/9783319179711). Also, I got involved and interested in teaching.

In 2021 I moved to Cranfield University (UK) as a Lecturer in Bioinformatics, where I am currently focusing on teaching in MSc Applied Bioinformatics course, and applying modern sequencing techniques to study soil microbiome (e.g. https://doi.org/10.1016/j.soilbio.2025.109712).

Throughout my research and academic career I contributed to tens of research papers that attracted more than 5,000 citations (overall h-index 27 ,as calculated by Google Scholar on 21Jan2026 : https://scholar.google.com/citations?hl=en&user=hGLjJ-kAAAAJ). I have presented my research in multiple international scientific meetings. I am a Fellow of the High Education Academy, UK (after completing PgCert in Academic Practices in Edinburgh University in 2013). I participated as a co-Investigator in several UK Research Councils grants, I reviewed and edited multiple manuscripts, currently I am an editorial board member of British Journal of Cancer Reports (https://www.nature.com/bjcreports).

Please see details of my employment, education and the list of selected publications below.

Employment

2021-Present: Lecturer in Bioinformatics, Cranfield University, UK
Faculty of Engineering and Applied Sciences

https://www.cranfield.ac.uk/people/dr-alexey-larionov-32582716

My main tasks in this position include research and teaching.

- **Research Activities**
    - Translate recent molecular genetic advances from biomedical research to the environmental and agrifood context. Current research projects where I am a Co-Investigator:
        - Restoring ecosystems after anthropogenic impacts (NERC NE/V006444/1)
        - Developing regenerative technologies in tea breeding and production (BBSRC BB/Y003241/1)
    - Manage postdoctoral researchers and supervise PhD projects. Currently supervised PhD projects:
        - Application of long-read sequencing to detection of mycotoxin-producing fungi
        - Application of Self Organizing Maps (SOMs) for dimensionality reduction and classification in SC (single-cell) transcriptomics data analysis
    - Contribute to publications and grant applications: see my publications list, research and PhD projects.
- **Teaching activities**
    - Delivery of lectures and seminars, marking assignments, supervising and marking thesis projects for the Cranfield MSc Applied Bioinformatics course. Modules taught in the last academic year:
        - Introduction to Bioinformatics using Python
        - Introduction to Epigenetics and Metagenomics analysis
        - Advanced NGS analysis and genome assembly
    - Marking thesis and oral presentations (remotely) for the data analysis and bioinformatics related projects for Environmental Engineering course of the joint Cranfield-Jiangsu MSc programs.
- **Other Activities**
    - I co-supervise Medical Genetics MSc projects at Cambridge University
    - I co-organize Cancer Genomics and Transcriptomics course for EBI (European Bioinformatics Institute, Hinxton), and I deliver transcriptomics data analysis sessions for this course.
    - Other standard *ad-hoc* academic tasks, such as reviewing and editing (e.g. I am a member of BJC-Reports editorial board)

Previous employment

***2013-2021:* Research Associate (Bioinformatics), Cambridge University, UK**
Department of Medical Genetics, School of Clinical Medicine

My main task during the employment in the Medical Genetics Department at Cambridge University was to provide bioinformatics support to diverse research projects in heritable predisposition to cancer.

- I analyzed data for a wide range of different projects: from small rare-disease family datasets to large cohorts derived from the 100-Thousand Genomes (Genomics England) proget.

- I designed and implemented pipelines in different computational environments including HPC clusters and cloud computing (AWS)
- I implemented various types of bioinformatics analysis including secondary bioinformatics (from FASTQ to VCF), variant annotation and prioritization, rare variant association analyses, selection of variants based on functional and biological criteria, etc.
- My teaching tasks included supervising research projects and marking theses for the postgraduate course in Genomic Medicine, taught by the Department of Medical Genetics.
- Along with the tasks carried out for my employment in Cambridge, I published about hormonal and targeted treatments in breast cancer (carrying over from my previous research in Edinburgh) and continued teaching in the Endocrine Physiology and Pharmacology course in Edinburgh University.
- My other academic activities included writing (I have contributed to a number of well-cited papers in reputable journals, see publications 2013-2021), reviewing, editing, and I completed multiple courses in a broad range of bioinformatics methods during this employment.

2008-2013: **Research Fellow, Edinburgh University, UK**

Edinburgh Cancer Research Centre

My main task was to study transcriptional profiles of breast cancer biopsies to understand and predict response and resistance to aromatase inhibitors (a hormonal treatment) in breast cancer.
The specific tasks and responsibilities included:

- Selection of optimal sets of informative genes (based on differential gene expression between responders and non-responders)
- Design and validation of classification algorithms for response prediction (comparing regression models, SVM and decision tree- based algorithms)
- Low level microarray data analysis (mainly R-libraries for Illumina and Affymetrix RNA microarrays)
- Supervision and support for PhD, MSc and MD students within the research group
- Preparation of publications, grant applications and presenting results at international conferences

Along with bioinformatics and wet-lab tasks during that employment I completed MSc in Applied Bioinformatics (Cranefield University, 2012) and PgCert in Academic Practices (Edinburgh University, 2013), reviewed papers for multiple journals and reviewed grants.

2002 – 2007: **Research Fellow, NHS Lothian, UK**

Breast Research Unit, Edinburgh Western General Hospital

Tasks and responsibilities: Study mechanisms and markers of endocrine resistance in breast cancer, validate micro-array gene expression results with RT-qPCR:

- Development of real-time quantitative PCR methodology for gene expression measurements in clinical samples of breast cancer
- Organizing clinical samples storage and clinical annotations
- Extraction of RNA from tumour biopsies, design and validation of PCR primers, qPCR data analysis

During that employment I performed qPCR analysis in hundreds of samples for multiple genes pre-selected from previous micro-array results. Also, I developed and published a standard curve based method for qPCR data analysis, which has already been cited more than 1000 times (Larionov et al, BMC bioinformatics, 2005).

***2001 – 2002:* Clinical Research Associate, PSI Pharma Support Inc., St. Petersburg, Russia**
Monitoring patients' well-being and regulatory compliance in breast cancer clinical trials.

***2000:* Postdoctoral Research Fellow, Edinburgh University, UK**
The fellowship was awarded by the Royal Society.
I studied local estrogen production in breast cancer tissue and in other peripheral tissues (this resulted into two well-cited 1-st author papers).

***1992 – 1999:* Postgraduate student** (specialization in clinical oncology) then **PhD student** (oncology) then **Researcher** in Petrov Institute of Oncology, St. Petersburg, Russia

Education

2011-2013	**Postgraduate Certificate in Academic Practices** Edinburgh University, UK
2010-2012	**MSc in Applied Bioinformatics** (bursary awarded by BBSRC) Cranfield University, UK
2001-2002	**Postgraduate Certificate in computer sciences** State Polytechnical University, St. Petersburg, Russia
1994-1997	**PhD in medicine** – recognized by UK NARIC Petrov Institute of Oncology, St. Petersburg, Russia
1992-1994	**Postgraduate specialization in medical oncology** Petrov Institute of Oncology, St. Petersburg, Russia
1984-1992	**Bachelor degree in medicine** (diploma with distinction) – recognized by UK NARIC Pavlov State Medical University, St. Petersburg, Russia

Selected publications

Articles

These are only papers published within the last 5 years (since 2021) or cited at least 100 times. The citations count was taken from Google Scholar on 23 Jan 2026: https://scholar.google.co.uk/citations?hl=en&user=hGLjJ-kAAAAJ

Recent articles (published within the last 5 years: 2021-present)

Sizmur T & **Larionov** A (**2025**) The soil microbial methylome: a tool to explore the role of epigenetic memory in driving soil abiotic legacy effects. *Soil Biology and Biochemistry* https://doi.org/10.1016/j.soilbio.2025.109712

Larionov A *et al* (**2023**) The contribution of germline pathogenic variants in breast cancer genes to contralateral breast cancer risk in BRCA1/BRCA2/PALB2-negative women. *Cancers* https://doi.org/10.3390/cancers15020415 ***Cited 1 time***

Yngvadottir B, … **Larionov** A *et al* (**2022**) Frequency of pathogenic germline variants in cancer susceptibility genes in 1336 renal cell carcinoma cases. *Human Molecular Genetics* https://doi.org/10.1093/hmg/ddac089 ***Cited 36 times***

Fewings E, … **Larionov** A *et al* (**2021**) Investigating the clinical, pathological and molecular profile of oncocytic adrenocortical neoplasms: a case series and literature review. *Endocrine Oncology*. https://doi.org/10.1530/EO-21-0011 ***Cited 2 times***

Earlier articles (published before 2021, cited at least 100 times)

Larionov AA (**2018**) Current therapies for human epidermal growth factor receptor 2-positive metastatic breast cancer patients. *Front Oncol.* 8:89, https://doi.org/10.3389/fonc.2018.00089 ***Cited 109 times***

Fewings E, **Larionov** A *et al* (**2018**) Germline pathogenic variants in PALB2 and other cancer-predisposing genes in families with hereditary diffuse gastric cancer without CDH1 mutation: a whole-exome sequencing study. *Lancet Gastroenterol Hepatol.* https://doi.org/10.1016/S2468-1253(18)30079-7 ***Cited 125 times***

Turnbull AK, ... **Larionov** AA, *et al* (**2015**) Accurate prediction and validation of response to endocrine therapy in breast cancer. *J Clin Oncol*. https://doi.org/10.1200/JCO.2014.57.8963 ***Cited 138 times***

Sokolenko AP, ... **Larionov** AA, *et al* (**2012**) High prevalence and breast cancer predisposing role of the BLM c.1642 C>T (Q548X) mutation in Russia. *Int J Cancer* https://doi.org/10.1002/ijc.26342 ***Cited 111 times***

Miller WR & **Larionov** AA (**2012**) Understanding the mechanisms of aromatase inhibitor resistance. *Breast Cancer Res.* https://doi.org/10.1186/bcr2931 ***Cited 142 times***

Hrstka R, … **Larionov** A *et al* (**2010**) The pro-metastatic protein anterior gradient-2 predicts poor prognosis in tamoxifen-treated breast cancers. *Oncogene*. https://doi.org/10.1038/onc.2010.228 ***Cited 132 times***

Miller WR & **Larionov** AA (**2010**) Changes in expression of oestrogen regulated and proliferation genes with neoadjuvant treatment highlight heterogeneity of clinical resistance to the aromatase inhibitor, letrozole. *Breast Cancer Res.* https://doi.org/10.1186/bcr2611 ***Cited 100 times***

Creighton CJ, … **Larionov** AA *et al* (**2009**) Residual breast cancers after conventional therapy display mesenchymal as well as tumor-initiating features. *PNAS* https://doi.org/10.1073/pnas.0905718106 ***Cited 1,728 times***

Miller WR, **Larionov** A *et al* (**2009**) Gene expression profiles differentiating between breast cancers clinically responsive or resistant to letrozole. *J Clin Oncol.* https://doi.org/10.1200/JCO.2008.16.8849 ***Cited 121 times***

Miller WR, **Larionov** A *et al* (**2007**) Changes in breast cancer transcriptional profiles after treatment with the aromatase inhibitor, letrozole. *Pharmacogenet Genomics*. https://doi.org/10.1097/FPC.0b013e32820b853a ***Cited 121 times***

Mackay A, … **Larionov A** *et al* (**2007**) Molecular response to aromatase inhibitor treatment in primary breast cancer. *Breast Cancer Res*. https://doi.org/10.1186/bcr1732 ***Cited 136 times***

Tomlinson V, … **Larionov** A *et al* (**2005**) Translation elongation factor eEF1A2 is a potential oncoprotein that is overexpressed in two-thirds of breast tumours. *BMC Cancer*. https://doi.org/10.1186/1471-2407-5-113 ***Cited 205 times***

Larionov A *et al* (**2005**) A standard curve based method for relative real time PCR data processing. *BMC Bioinformatics* https://doi.org/10.1186/1471-2105-6-62 ***Cited 1,166 times***

Book chapters

Larionov A (**2016**) Novel translational research of neo-adjuvant endocrine therapy. Chapter in *Personalized Treatment of Breast Cancer*. Editors: Masakazu Toi, Eric Winer, John Benson, Suzanne Klimberg. Springer, ISBN: 978-4-431-55551-3

Larionov A & Miller WR (**2015**) Prediction of Response to Aromatase Inhibitors in Breast Cancer. Chapter in *Resistance to Aromatase Inhibitors in Breast Cancer*. Editor: Alexey A Larionov, Series: *Resistance to Targeted Anti-Cancer Therapeutics*. Springer, ISBN: 978-3-319-17971-1

Sims A, **Larionov** A, *et al*. (**2013**) Use of microarray analysis to investigate EMT gene signatures. Chapter in *Adhesion Protein Protocols*. Editor Amanda S. Coutts, Springer ISBN 978-1-62703-538-5

Book edited

A. Larionov (editor) **(2015)** Resistance to aromatase inhibitors in breast cancer. Springer, ISBN: 978-3-319-17971-1 http://www.springer.com/us/book/9783319179711

Conference talks

Larionov A *et al* **(2020)** The contribution of germline pathogenic variants beyond BRCA1/2/PALB2 to contralateral breast cancer in women with a younger onset breast cancer. *Oral presentation* in the Joint Meeting of UK / Dutch Clinical Genetics Societies & Cancer Genetics Groups, 10 – 11 February, 2020, **Hinxton, UK**

Larionov A **(2014)** Recent findings from translational research of neoadjuvant endocrine therapy. *Invited lecture*. Kyoto Breast Cancer Consensus Conference, 20-22 February 2014, **Kyoto, Japan**

Larionov A **(2013)** An invited faculty member for biomarker discovery *panel discussion*. Controversies in Breast Cancer conference, 9-10 February 2013, **Kolkata, India**

Larionov A (**2010**) Molecular heterogeneity of endocrine resistance in breast cancer: profiling of clinical specimens. *Oral presentation* in BIT Life Sciences' 3rd World Cancer Congress-Breast Cancer Conference: 25-27April 2010, **Shanghai, China**

Larionov A *et al* (**2007**) Reproducibility and interpretation of quantitative gene expression measurements in breast cancer biopsies. *Oral presentation* in the 10th Nottingham International Breast Cancer Conference, 18 – 20 September, 2007, **Nottingham, UK**

Larionov A *et al* (**2004**) Data processing in real time PCR. *Oral presentation* in the 1st International qPCR Symposium & Application Workshop Transcriptomics, Clinical Diagnostics & Gene Quantification, 3rd - 6th March, 2004, **Freising-Weihenstephan, Germany**