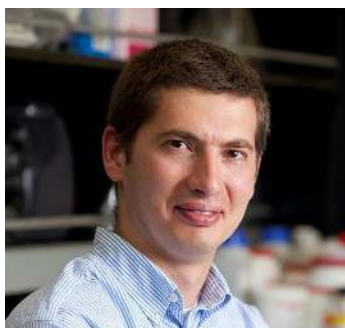




[Mark Daly](#) (PhD) / Broad Institute, Massachusetts General Hospital

Mark Daly is an institute member of the Broad Institute and co-director of the Program in Medical and Population Genetics. His research primarily focuses on the development and application of statistical methods for the discovery and interpretation of genetic variation responsible for complex human disease. As founding chief of the Analytic and Translational Genetics Unit at Massachusetts General Hospital, he also has an expanded focus on the interpretation of genome sequence and the use of genome information in clinical settings. Daly's group has developed numerous methods and widely used software tools, including GENEHUNTER and HAPLOVIEW, genetic analysis tools used in thousands of laboratories worldwide, and GRAIL and DAPPLE, web-based utilities for the interpretation of genome-wide association results. The team has also contributed to additional widely distributed tools developed in the Broad community such as PLINK and GATK. Daly's earlier work at the Whitehead Institute and Whitehead/MIT Center for Genome Research was instrumental in developing an understanding of patterns of variation in the human and mouse genomes, and in the use of these patterns in disease gene mapping. More recently, Daly's group also participates in numerous studies using exome sequencing to articulate the genetic origins of rare, inherited diseases, early-onset and pediatric cancers, and severe adverse drug responses.



Maxim Artyomov (PhD) / Washington University in St. Louis

Maxim Artyomov is an Assistant Professor at Immunology & Pathology Department of Washington University in St. Louis. Dr. Artyomov's lab applies next generation sequencing and novel computational techniques to address fundamental questions in immunology. His recent work is devoted to development of high-throughput RNA-seq approaches and applications of this technology to uncover relation between genes implicated in autoimmunity through genome-wide association studies. Dr. Artyomov obtained his PhD from MIT in 2009 working at Arup Chakraborty's lab where he studied stochastic behavior in the signal transduction networks at early stages of T-cell activation. For his postdoctoral studies Dr. Artyomov joined Broad Institute of MIT and Harvard, working with Aviv Regev to explore (both experimentally and computationally) the transcriptional networks that govern activation of dendritic cells in response to immune stimuli. Dr. Artyomov also serves as Co-Chair of Scientific Advisory Board (along with Doug Lauffenburger) for Cambridge based Immuneering Inc.



Alexander Predeus (PhD) / Bioinformatics Institute, SPB

Alexander has graduated from Moscow State University (Department of Chemistry) in 2003. In the fall of 2003 he joined the graduate school of Michigan State University to continue his studies in chemistry with Prof. William D. Wulff. His research focused on organometallic and supramolecular chemistry. He graduated with a Ph.D. in chemistry in 2009. Following this, Alexander has shifted his interests towards biological chemistry. During the two-year postdoctoral appointment with Prof. Michael Feig, Alexander have

studied molecular dynamics methodology, and used it to get insights into mechanisms of action of RNA Polymerase II, MSH2-MSH6 DNA repair enzyme, and molecular crowding. After this Alexander have joined the lab of Prof. Maxim Artyomov to pursue his interest in fast-growing field of next-generation sequencing (NGS). He worked on integrative analysis of genetic and epigenetic information obtained by next-generation sequencing (RNA-Seq, CHIP-Seq of transcription factors and histone modifications, Dnase I hypersensitivity) applied to immune cells. Another project involved analysis of co-expression patterns in publicly available datasets and creation of databases that would allow the discovery of biological similarities between unrelated samples based on gene co-expression. His other scientific interests include developing best practices in analysis of transcriptomic, genome-interaction, and Hi-C data, and its biological interpretation. In the Summer of 2015 Alexander has joined Bioinformatics Institute as a research director.



Nikita Artomov / Harvard University, Massachusetts General Hospital, Broad Institute

Nikita is a graduate student at Harvard University. He is working in the lab of Mark Daly at Analytic and Translational Genetics Unit (Massachusetts General Hospital) and Broad Institute. He is working on development of computational pipelines for full genome/exome sequencing data processing starting from raw data to the analysis ready dataset and following data analysis (GATK, Picard, etc.). Mostly working with germline cancer sequencing data of the patients with early onset and rare cancer type. He is interested in the development

of tools for functional analysis incorporating protein-protein interaction maps for extracting affected protein pathways from sequencing studies.