

# SODBO SHARAPOV, PhD

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Statistical geneticist, computational biologist with nine years of experience in the field of human genetics. Inspired by genetics as a tool to study complex traits and multifactorial diseases. Author of 23 peer-reviewed publications (381 citations, h=9) in *Nature Communications*, *Science Advances*, *Communications Biology*, *Human Molecular Genetics*, *JCI Insights* and others.

## CURRENT POSITIONS

### **Institute of Cytology and Genetics**

Researcher

Siberian Branch of Russian Academy of Sciences

Laboratory of Recombination and Segregation analysis

630090 Novosibirsk  
Prospekt Lavrentyeva 10  
Russia

### **Novosibirsk State University**

Researcher

Laboratory of Theoretical and Applied Functional Genomics

630090, Novosibirsk,  
2 Pirogova Str.  
Russia

### **Novosibirsk State University**

Lector, assistant

Chair of Cytology and Genetics, Department of Natural Sciences

630090, Novosibirsk,  
2 Pirogova Str.  
Russia

### **Moscow Institute of Physics and Technologies**

Lector, assistant

141701, Dolgoprudny,  
Moscow, Russia

## EDUCATION

### **Novosibirsk State University**

Ph.D. fellowship in statistical genetics

Advisor: Dr. Yurii Aulchenko

Title: Genetic control of human blood plasma protein N-glycosylation

Novosibirsk, Russia  
2014 – 2018

### **Novosibirsk State University**

Master of Science, magna cum laude,

Bioinformatics/biology

Advisor: Dr. Yurii Aulchenko

Title: Gene interactions in the control of human serum metabolome

Novosibirsk, Russia  
2009 - 2014

### **University of Liege**

Nextflow training course

Liege, Belgium  
2020

### **Erasmus MC**

Erasmus Summer Program in Genetic Epidemiology

Rotterdam, The Netherlands  
2013

## RESEARCH EXPERIENCE / EMPLOYMENT HISTORY

### **Institute of Cytology and Genetics**

Junior Researcher

Research assistant

Novosibirsk, Russia

05.2015 to present

09.2012 – 04.2015

- Group leader (team of four members)
- Executing genome-wide association analyses (GWAS), including analysis of large-scale human cohorts (UK Biobank), SNP-array and WES/WGS data
- Coordinating and executing multi-center genome-wide association meta-analysis of human total plasma glycome with researchers from various backgrounds (biochemistry, epidemiology, clinicians, medical doctors etc.)
- Performing quality control of genotype data from different sources: SNP-arrays, WES/WGS data
- Performing quality control of GWAS summary statistics
- Conducting post-GWAS analysis using GWAS summary statistics: fine mapping, colocalization, eQTL analysis, LD score regression, genetic correlation analysis, meta-analysis, Mendelian randomization, variant prioritization
- Developing, testing and application of GWAS-MAP - database of GWAS summary statistics and API for conducting joint *in silico* post-GWAS analysis (Mendelian randomization, colocalization analysis, meta-analysis)
- Development of novel methods and software for the genetic association analysis
  - Developing and testing of OmicABEL: high performance linear mixed model (C++)
    - <https://github.com/GenABEL-Project/OmicABEL>
  - Development of R package for family-based regional association analysis (FFB-SKAT)
    - <http://mga.bionet.nsc.ru/soft/FFBSKAT/>

### **Helmholtz Zentrum München**

Visiting scientist

Munich, Germany

2013 - 2016

- Developing network-based conditional genetic association analysis of human metabolome
- Analysis of gene x gene and gene x environment interactions in the control of human serum metabolome
- Supporting large-scale gene-interaction analysis on SuperMUC supercomputer

### **PolyOmics, PolyKnomics**

Computational biologist (contract work)

's-Hertogenbosch, The Netherlands

2013 - present, part-time

- Executing the GWAS and post-GWAS analysis and preparing reports for the “PainOmics” European Union FP7 project
- Defining genetic control of human healthspan using GWAS of UKBiobank data
- Software packaging (Debian packages)
- Developing automated and portable pipe-line for quality control of human glycome data
  - R, bash, singularity, Docker
- Creating R packages for pedigree analysis
  - <https://rdr.io/cran/RVPedigree/>

**Knomics Ltd**

Moscow, Russia

## Internship

July, 2017

- Agile/Scrum training paradigm of teamwork and project management
- Support statistical genetics projects

**TEACHING EXPERIENCE****Biostatistics**

Novosibirsk State University

- Lector, leading practical sessions

2022 - present

**Models and methods of quantitative genetics**

Novosibirsk State University

- Lector, leading practical sessions

2012 - 2021

**Coursera course “From Diseases to Genes and Back”**

Novosibirsk State University,

- Co-creator
- [www.coursera.org/learn/disease-genes/](http://www.coursera.org/learn/disease-genes/)

2017

**Research Summer School on Statistical Omics 2014, 2015**

Split, Croatia

- Co-leading the student projects
- Title: Genome-wide association and genomic prediction for human blood lipids using multivariate analysis and machine learning methods (<http://school2015.statisticalomics.org/projects>)
- Title: Discovering the difference in genetic control of plasma and IgG glycosylation (<http://school2014.statisticalomics.org/projects>)

2014, 2015

**LEADERSHIP EXPERIENCE****Laboratory of Recombination and Segregation analysis**

Institute of Cytology and

Genetics

- Leading a glyco-genomics research line in the group with up to four employs
- Leading (as a main analyst and first author) consortia of 10 scientific groups. Two first-author publications.

2017 – present

**Laboratory of theoretical and Applied Functional Genomics**

Novosibirsk State

- Finding industry clients and negotiating with them
- Holding ownership of the intellectual property
- Developing budget
- Setting reproduceable workflows in the lab

University

2018 - present

**Winner of the life sciences hackathon “LifeCode”**

Novosibirsk State

- Building a team, organizing the team work
- Solved a problem of the biotech company, that sales direct-to-customer genetic tests of *BRCA1* and *BRCA2* genes for early diagnosis of breast cancer

University

2017

**Supervision of Alexander Zlobin (B.Sc.)**

- Title: Population specific analysis of Yakut exomes

Novosibirsk State  
University  
2014-2015

**Leader of student fellow**

- Managing relationships between students and  
Department of Natural Sciences

Novosibirsk State  
University  
2012-2014

## GRANTS AND FELLOWSHIPS

1. DAAD & Russian Ministry of Education and Science #3735, 2015-2016  
“Development and application of novel approaches for finding genetic interactions in the framework of genome-wide association studies”  
Approx. budget - 10000 Euros
2. BS and MS Scholarship program at Novosibirsk State University, 2009-2014  
Russian Ministry of Education and Science  
Approx. budget - 20000 Euros
3. Ph.D. fellowship at the Novosibirsk State University, 2014-2018  
Russian Ministry of Education and Science  
Approx. budget - 12000 Euros

## MAIN AWARDS

1. “Best poster in basic research” and conference fellowship, ESHG 2021 conference, Vienna, Austria 2021
2. “Best young scientist” award from the Government of Novosibirsk, 2021
3. “Early research career Scholarship for young scientists”, ICQG6, Brisbane, Australia, 2020
4. “Diploma magna cum laude”, Novosibirsk State University 2014
5. “Best thesis defense” award at Department of Natural Sciences, Novosibirsk State University, 2014
6. Second place award at the International Student Scientific Conference, Novosibirsk, 2014

## INVITED TALKS

1. “Genetic of human protein N-glycome”, Michel Georges group, University of Liege, Liege, Belgium, 2020
2. “Genetics of multifactorial diseases”, paid invited talk at “yRisk” private company, Moscow, Russia, 2019
3. “Letters everywhere”, Scientific popularization event – “Science Slam” at the People’s Friendship University of Russia, Moscow, Russia, 2017
4. “Genes and destiny”, Popular science event – “Science Slam” at the Novosibirsk State University, Novosibirsk, Russia, 2016

5. "Genes and destiny", Popular science event – "Open Space Picnic" at the Novosibirsk State University, Novosibirsk, Russia, 2016
6. "Dissecting phenomenon of variance heterogeneity in gene-gene interaction scan on human serum metabolome ", Fabian Theis group, Institute of Computational Biology, Munich, Germany, 2015

## PEER-REVIEWED PUBLICATIONS

1. Arianna Landini, Irena Trbojević-Akmačić, Pau Navarro, Yakov A. Tsepilov, **Sodbo Z. Sharapov**, Frano Vučković, Ozren Polašek Caroline Hayward, Tea Petrović, Marija Vilaj, Yurii S. Aulchenko, Gordan Lauc, James F. Wilson, Lucija Klarić (2022). Genetic regulation of post-translational modification of two distinct proteins. *Nature Communications* 13, 1586 (2022). <https://doi.org/10.1038/s41467-022-29189-5> (IF=14.9)
2. Vyacheslav Petrov, **Sodbo Sharapov**, Lev Shagam, Arina Nostaeva, Marija Pezer, Dalin Li, Maja Hanić, Dermot McGovern, Edouard Louis, Souad Rahmouni, Gordan Lauc, Michel Georges, Yurii Aulchenko. Association between human gut microbiome and N-glycan composition of total plasma proteome. (2022). *Frontiers Microbiology*, 13:811922. <https://doi.org/10.3389/fmicb.2022.811922> (IF= 4.0)
3. Ivanov, A.A., Ukladov, E.A., Kremis, S.A., **Sharapov S.Z.**, et al. Investigation of cytotoxic and antioxidative activity of 1,2,3-triazolyl-modified furocoumarins and 2,3-dihydrofurocoumarins. *Protoplasma* (2022). <https://doi.org/10.1007/s00709-022-01739-0>, (IF=3.4)
4. Zaytseva O.O., **Sharapov S.Z.**, Perola M., Esko T., Landini A., Hayward C., Wilson J.F., Lauc G., Aulchenko Y.S., Klarić L., Tsepilov Y.A. (2021). Investigation of the causal relationships between human IgG N-glycosylation and 12 common diseases associated with changes in the IgG N-glycome. *Human Molecular Genetics*. <https://doi.org/10.1093/hmg/ddab335> (IF=6.2)
5. Krištić, J., **Sharapov, S. Z.**, & Aulchenko, Y. S. (2021). Quantitative Genetics of Human Protein N-Glycosylation. In *The Role of Glycosylation in Health and Disease. Advances in Experimental Medicine and Biology* (pp. 151–171). Springer. [https://doi.org/10.1007/978-3-030-70115-4\\_7](https://doi.org/10.1007/978-3-030-70115-4_7) (IF=2.6)
6. Rahman, M. S., Winsvold, B. S., Chavez Chavez, S. O., Børte, S., Tsepilov, Y. A., **Sharapov, S. Z.**, Aulchenko, Y. S., Hagen, K., Fors, E. A., Hveem, K., Zwart, J. A., van Meurs, J. B., Freidin, M. B., & Williams, F. M. *Annals of the Rheumatic Diseases*, 80(9), 1227–1235. <https://doi.org/10.1136/annrheumdis-2020-219624> (IF=19.1)
7. Ning, Z., Tsepilov, Y. A., **Sharapov, S. Z.**, Wang, Z., Grishenko, A. K., Feng, X., Shirali, M., Joshi, P. K., Wilson, J. F., Pawitan, Y., Haley, C. S., Aulchenko, Y. S., & Shen, X. (2021). Nontrivial Replication of Loci Detected by Multi-Trait Methods. *Frontiers in Genetics*, 12. <https://doi.org/10.3389/fgene.2021.627989>, (IF=3.8)
8. Liu, D., Zhu, J., Zhao, T., et al. (2021) Associations Between Genetically Predicted Plasma N-Glycans and Prostate Cancer Risk: Analysis of Over 140,000 European Descendants.

<https://doi.org/10.2147/PGPM.S319308> (IF=3.9)

9. Shadrina, A. S., Zlobin, A. S., Zaytseva, O. O., Klarić, L., **Sharapov, S. Z.**, D Pakhomov, E., Perola, M., Esko, T., Hayward, C., Wilson, J. F., Lauc, G., Aulchenko, Y. S., & Tsepilov, Y. A. (2021). Multivariate genome-wide analysis of immunoglobulin G N-glycosylation identifies new loci pleiotropic with immune function. *Human Molecular Genetics*, 30(13), 1259–1270. <https://doi.org/10.1093/hmg/ddab072> (IF=6.2)
10. **Sharapov, S. Z.**, Shadrina, A. S., Tsepilov, Y. A., Elgaeva, E. E., Tiys, E. S., Feoktistova, S. G., Zaytseva, O. O., Vuckovic, F., Cuadrat, R., Jäger, S., Wittenbecher, C., Karssen, L. C., Timofeeva, M., Tillin, T., Trbojević-Akmačić, I., Štambuk, T., Rudman, N., Krištić, J., Šimunović, J., Momčilović, A., Vilaj, M., Jurić, J., Slana, A., Gudelj, I., Klarić, T., Puljak, L., Skelin, A., Kadić, A. J., Van Zundert, J., Chaturvedi, N., Campbell, H., Dunlop, M., Farrington, S. M., Doherty, M., Dagostino, C., Gieger, C., Allegri, M., Williams, F., Schulze, M. B., Lauc, G., & Aulchenko, Y. S. (2021). Replication of 15 loci involved in human plasma protein N-glycosylation in 4802 samples from four cohorts. *Glycobiology*, 31(2), 82–88. <https://doi.org/10.1093/glycob/cwaa053> (IF=4.1)
11. Shashkova, T. I., Gorev, D. D., Pakhomov, E. D., Shadrina, A. S., **Sharapov, S. Z.**, Tsepilov, Y. A., Karssen, L. C., & Aulchenko, Y. S. (2020). The GWAS-MAP platform for aggregation of results of genome-wide association studies and the GWAS-MAP|homo database of 70 billion genetic associations of human traits. *Vavilov Journal of Genetics and Breeding*, 24(8), 876–884. <https://doi.org/> (IF=0.6)
12. Klarić, L., Tsepilov, Y. A., Stanton, C. M., Mangino, M., Sikka, T. T., Esko, T., Pakhomov, E., Salo, P., Deelen, J., McGurnaghan, S. J., Keser, T., Vučković, F., Ugrina, I., Krištić, J., Gudelj, I., Štambuk, J., Plomp, R., Pučić-Baković, M., Pavić, T., Vilaj, M., Trbojević-Akmačić, I., Drake, C., Dobrinić, P., Mlinarec, J., Jelušić, B., Richmond, A., Timofeeva, M., Grishchenko, A. K., Dmitrieva, J., Bermingham, M. L., **Sharapov, S. Z.**, Farrington, S. M., Theodoratou, E., Uh, H.-W., Beekman, M., Slagboom, E. P., Louis, E., Georges, M., Wuhler, M., Colhoun, H. M., Dunlop, M. G., Perola, M., Fischer, K., Polasek, O., Campbell, H., Rudan, I., Wilson, J. F., Zoldoš, V., Vitart, V., Spector, T., Aulchenko, Y. S., Lauc, G., & Hayward, C. (2020). Glycosylation of immunoglobulin G is regulated by a large network of genes pleiotropic with inflammatory diseases. *Science Advances*, 6(8), eaax0301. <https://doi.org/10.1126/sciadv.aax0301>. (IF=14.1)
13. Sunuwar, L., Frkatović, A., **Sharapov, S.**, Wang, Q., Neu, H. M., Wu, X., Haritunians, T., Wan, F., Michel, S., Wu, S., Donowitz, M., McGovern, D., Lauc, G., Sears, C., & Melia, J. (2020). Pleiotropic ZIP8 A391T implicates abnormal manganese homeostasis in complex human disease. *JCI Insight*, 5(20), e140978, <https://doi.org/10.1172/jci.insight.140978>. (IF=8.3)
14. **Shadrina, A. S.**, Shashkova, T. I., Torgasheva, A. A., Sharapov, S. Z., Klarić, L., Pakhomov, E. D., Alexeev, D. G., Wilson, J. F., Tsepilov, Y. A., Joshi, P. K., & Aulchenko, Y. S. (2020). Prioritization of causal genes for coronary artery disease based on cumulative evidence from experimental and in silico studies. *Scientific Reports*, 10(1), 10486. <https://doi.org/10.1038/s41598-020-67001-w>. (IF=4.4)

15. Tsepilov, Y. A., Freidin, M. B., Shadrina, A. S., **Sharapov, S. Z.**, Elgaeva, E. E., Zundert, J. van, Karssen, L. C., Suri, P., Williams, F. M. K., & Aulchenko, Y. S. (2020). Analysis of genetically independent phenotypes identifies shared genetic factors associated with chronic musculoskeletal pain conditions. *Communications Biology*, 3(1), 329. <https://doi.org/10.1038/s42003-020-1051-9>. (IF=6.3)
16. **Sharapov, S. Z.**, Tsepilov, Y. A., Klaric, L., Mangino, M., Thareja, G., Shadrina, A. S., Simurina, M., Dagostino, C., Dmitrieva, J., Vilaj, M., Vuckovic, F., Pavic, T., Stambuk, J., Trbojevic-Akmacic, I., Kristic, J., Simunovic, J., Momcilovic, A., Campbell, H., Doherty, M., Dunlop, M. G., Farrington, S. M., Pucic-Bakovic, M., Gieger, C., Allegri, M., Louis, E., Georges, M., Suhre, K., Spector, T., Williams, F. M. K. K., Lauc, G., & Aulchenko, Y. S. (2019). Defining the genetic control of human blood plasma N-glycome using genome-wide association study. *Human Molecular Genetics*, 28(12), 2062–2077. <https://doi.org/10.1093/hmg/ddz054>. (IF=6.2)
17. Shadrina, A. S., **Sharapov, S. Z.**, Shashkova, T. I., & Tsepilov, Y. A. (2019). Varicose veins of lower extremities: Insights from the first large-scale genetic study. *PLOS Genetics*, 15(4), e1008110. <https://doi.org/10.1371/journal.pgen.1008110>. (IF=5.9)
18. Zenin, A., Tsepilov, Y., Sharapov, S., Getmantsev, E., Menshikov, L. I., Fedichev, P. O., & Aulchenko, Y. (2019). Identification of 12 genetic loci associated with human healthspan. *Communications Biology*, 2(1), 41. <https://doi.org/10.1038/s42003-019-0290-0>. (IF=6.3)
19. Tsepilov, Y. A., **Sharapov, S. Z.**, Zaytseva, O. O., Krumsek, J., Prehn, C., Adamski, J., Kastenmüller, G., Wang-Sattler, R., Strauch, K., Gieger, C., & Aulchenko, Y. S. (2018). A network-based conditional genetic association analysis of the human metabolome. *GigaScience*, 7(12), giy137. <https://doi.org/10.1093/gigascience/giy137>. (IF=6.5).
20. Frolova, T. S., **Sharapov, S. Z.**, Sinitsyna, O. I., Tolstikova, T. G., Grigoriev, I. A., Morozov, S. V., & Yushkova, Y. V. (2018). New Ionic Conjugates Based on  $\alpha$ -Tocopheryl Succinate as Potential Cytotoxic Agents. *Russian Journal of Bioorganic Chemistry*, 44(3), 330–336. (IF=0.8)
21. Xia Shen, Lucija Klarić, **Sodbo Sharapov**, Massimo Mangino, Zheng Ning, Di Wu, Irena Trbojević-Akmačić, Maja Pučić-Baković, Igor Rudan, Ozren Polašek, Caroline Hayward, Timothy D Spector, James F Wilson, Gordan Lauc, Yurii S Aulchenko. Multivariate discovery and replication of five novel loci associated with Immunoglobulin G N-glycosylation // Nat. Commun. Nature Publishing Group, 2017. Vol. 8, № 1. P. 447. (IF=14.9)
22. AS Zlobin, **S Zh Sharapov**, VP Gur'ev, MR Bevova, Ya A Tsepilov, TM Sivtseva, UA Boyarskikh, EA Sokolova, Yu S Akul'chenko, ML Filipenko, VL Osakovskii. Population Specific Analysis of Yakuts Exomes // Доклады Академии наук. 2017. Vol. 474, № 4. P. 505–509 (IF=0.99).
23. Diego Fabregat-Traver, **Sodbo Zh Sharapov**, Caroline Hayward, Igor Rudan, Harry Campbell, Yurii Aulchenko, Paolo Bientinesi. High-performance mixed models based genome-wide association analysis with omicABEL software // F1000Research. Faculty of 1000 Ltd, 2014. Vol. 3. (IF=2.3)



## PENDING PUBLICATIONS AND PREPRINTS

1. Lagou, V., Jiang, L., Ulrich, A., Zudina, L., González, K. S. G., Balkhiyarova, Z., Faggian, A., Chen, S., Todorov, P., **Sharapov, S.**, David, A., Marullo, L., Mägi, R., Rujan, R.-M., Ahlqvist, E., Thorleifsson, G., Gao, H., Evangelou, E., Benyamin, B., Scott, R., Isaacs, A., Zhao, J. H., Willems, S. M., Johnson, T., Gieger, C., Grallert, H., Meisinger, C., Müller-Nurasyid, M., Strawbridge, R. J., Goel, A., Rybin, D., Albrecht, E., Jackson, A. U., Stringham, H. M., Corrêa, I. R., Eric, F.-E., Steinthorsdottir, V., Uitterlinden, A. G., Munroe, P. B., Brown, M. J., Julian, S., Holmen, O., Thorand, B., Hveem, K., Wilsgaard, T., Mohlke, K. L., Kratzer, W., Mark, H., Koenig, W., Boehm, B. O., Tan, T. M., Tomas, A., Salem, V., Barroso, I., Tuomilehto, J., Boehnke, M., Florez, J. C., Hamsten, A., Watkins, H., Njølstad, I., Wichmann, H.-E., Caulfield, M. J., Khaw, K.-T., van Duijn, C., Hofman, A., Wareham, N. J., Langenberg, C., Whitfield, J. B., Martin, N. G., Montgomery, G., Scapoli, C., Tzoulaki, I., Elliott, P., Thorsteinsdottir, U., Stefansson, K., Brittain, E. L., McCarthy, M. I., Froguel, P., Sexton, P. M., Wooten, D., Groop, L., Dupuis, J., Meigs, J. B., Deganutti, G., Demirkan, A., Pers, T. H., Reynolds, C. A., Aulchenko, Y. S., Kaakinen, M. A., Jones, B., Prokopenko, I., on behalf of the Meta-Analysis of Glucose, & (MAGIC), I. T. C. (2021). Random glucose GWAS in 493,036 individuals provides insights into diabetes pathophysiology, complications and treatment stratification. *MedRxiv*. doi:10.1101/2021.04.17.21255471
2. Associations between genetically predicted plasma N-glycans and pancreatic cancer risk.

## SELECTED ORAL AND POSTER PRESENTATIONS

1. Sharapov S., et al. Meta-analysis of genome-wide association studies for N-glycosylation in 10,000 individuals. // ESHG 2021, Vienna, Austria
2. Sharapov S., et al. Mapping genes involved in control of N-glycosylation of blood glycoproteins through a large genome-wide association study. // MCCMB'21. 10th Moscow Conference on Computational Molecular Biology, Moscow, Russia, 2021
3. Sharapov S., "Results of genome-wide association study of plasma proteome N-glycosylation in 10,000 samples". BGRS/SB-2020: 12th International Multiconference "Bioinformatics of Genome Regulation and Structure/Systems Biology". Novosibirsk, Russia, 2020
4. Sharapov S., "Genome-wide association study identifies tissue-specific regulation of human protein N-glycosylation". International Conference on Quantitative Genetics (ICQG6), Brisbane, Australia, November 2020
5. Sharapov S., et al. Genetic control of human blood plasma N-glycome. // «VI Congress of the Russian biochemists", Sochi, Russia, October 2019
6. Sharapov S., et al. Genome-wide association study finds new loci affecting N-glycosylation of human blood plasma proteins. // MCCMB'19. 9th Moscow Conference on Computational Molecular Biology, Moscow, Russia, 2019
7. Sharapov S., et al. Genetic loci, associated with glycosylation of human total plasma proteins: a 2019 update. // ISABS Conference on Forensic and Anthropologic Genetics, Split, Croatia, 2019



8. Sharapov S., et al. Defining the genetic control of human blood plasma glycome using genome-wide association study. // BGRS\SB-2018. Bioinformatics of Genome Regulation and Structure\Systems Biology, Novosibirsk, Russia, 2018
9. Sharapov S., et al. Understanding the genetic control of human blood plasma glycome using genome-wide association study. // 2<sup>nd</sup> GlycoCom, Dubrovnik, Croatia, 2018
10. Sharapov S., et al. Dissecting variance heterogeneity in human serum metabolome. BGRS\SB-2016. Bioinformatics of Genome Regulation and Structure\Systems Biology, Novosibirsk, Russia, 2016
11. Sharapov S., et al. Genetic interactions in control of human metabolome: a genome-wide variance heterogeneity analysis. Bertinoro Computational Biology, Bertinoro, Italy, 2014.
12. Sharapov S., et al. Genome-wide environmental sensitivity analysis of human metabolomics data // BGRS\SB-2014. Bioinformatics of Genome Regulation and Structure\Systems Biology, Novosibirsk, Russia, 2014
13. Sharapov S., et al. Searching for statistical genetic interactions in the control of human blood metabolome. // International Student Scientific Conference, Novosibirsk, Russia, 2014
14. Sharapov S., et al. Genome-wide environmental sensitivity analysis of human metabolomics data. // EMGM 2014, European Mathematical Genetics Meeting, Cologne, Germany, 2014.
15. Sharapov S., et al. Identification of gene-gene interactions in genome-wide association analysis. // AC.CES. The Aachen Conference on Computational Engineering Science, Aachen, Germany, 2013