SODBO SHARAPOV

sharapovsodbo@gmail.com

Statistical geneticist, computational biologist with eight years of experience in the field of human genetics. Ph.D. candidate (defense in April 27, 2022). Inspired by genetics as a tool to study complex traits and multifactorial diseases.

Author of 20 peer-reviewed publications (360 citations, h=9) in *Nature Communications*, *Science Advances*, *Communications Biology*, *Human Molecular Genetics*, *JCI* Insights and others.

CURRENT POSITIONS

Institute of Cytology and Genetics	630090 Novosibirsk
Researcher	Prospekt Lavrentyeva 10
Siberian Branch of Russian Academy of Sciences	Russia
Laboratory of Recombination and Segregation analysis	
Novosibirsk State University	630090, Novosibirsk,
Researcher	2 Pirogova Str.
Laboratory of Theoretical and Applied Functional Genomics	Russia
Novosibirsk State University	630090, Novosibirsk,
Lector, assistant	2 Pirogova Str.
Chair of Cytology and Genetics, Department of Natural Sciences	Russia
Moscow Institute of Physics and Technologies	141701, Dolgoprudny,
Lector, assistant	Moscow, Russia

EDUCATION

Novosibirsk State University	Novosibirsk, Russia
Ph.D. fellowship	2014 – 2018
Advisor: Dr. Yurii Aulchenko	
Title: Genetic control of human blood plasma protein N-glycosylation	
Novosibirsk State University	Novosibirsk, Russia
MS, magna cum laude, Bioinformatics/biology	2009 - 2014
Advisor: Dr. Yurii Aulchenko	
Title: Gene interactions in the control of human serum metabolome	
University of Liege	Liege, Belgium
Nextflow training course	2020
Erasmus MC	Rotterdam, The Netherlands
Erasmus Summer Program in Genetic Epidemiology	2013

RESEARCH EXPERIENCE / EMPLOYMENT HISTORY

Institute of Cytology and Genetics   Novosibirsk, Russia
Junior Researcher   05.2015 to present
Research assistant   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
- 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/

Novosibirsk State University   Novosibirsk, Russia
Researcher   2015 – present

- 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)

Helmholtz Zentrum München   Munich, Germany
Visiting scientist   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

PolyOmica, PolyKnomics   's-Hertogenbosch, The Netherlands
Computational biologist (contract work)   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://rdrr.io/cran/RVPedigree/

Knomics Ltd   − 2017

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

TEACHING EXPERIENCE

Biostatistics − Lector, leading practical sessions	Novosibirsk State University 2022 - present
Models and methods of quantitative genetics − Leading practical sessions − Lector, leading practical sessions	Novosibirsk State University 2012 - 2017 2018 - 2021
Coursera course "From Diseases to Genes and Back" − Co-creator − www.coursera.org/learn/disease-genes/	Novosibirsk State University, Novosibirsk, Russia 2017
Research Summer School on Statistical Omics 2015 − Co-leading the student project − Title: Genome-wide association and genomic prediction for human blood lipids using multivariate analysis and machine learning methods (http://school2015.statisticalomics.org/projects)	Split, Croatia 2015
Research Summer School on Statistical Omics 2014 − Co-leading the student project. − Title: Discovering the difference in genetic control of plasma and IgG glycosylation (http://school2014.statisticalomics.org/projects)	Split, Croatia 2014

LEADERSHIP EXPERIENCE

Laboratory of Recombination and Segregation analysis − 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.	Institute of Cytology and Genetics Novosibirsk, Russia 2017 – present

Laboratory of theoretical and Applied Functional Genomics
- – Finding clients and negotiating with them
- – Holding ownership of the intellectual property
- – Developing budget
- – Setting reproduceable workflows in the lab

Novosibirsk State University,
Novosibirsk, Russia
2018 - present

Winner of the life sciences hackathon "LifeCode"
- – 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

Novosibirsk State University,
Novosibirsk, Russia
2017

Supervision of Alexander Zlobin (B.Sc.)
- – Title: Population specific analysis of Yakut exomes

Novosibirsk State University,
Novosibirsk, Russia
2014-2015

Leader of student fellow
- – Managing relationships between students and Department of Natural Sciences

Novosibirsk State University,
Novosibirsk, Russia
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

INVITED TALKS

1. "Genetic of human protein N-glycome", 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 ", Institute of Computational Biology, Munich, Germany, 2015

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

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 (accepted for publication).
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* (accepted for publication).
3. 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)**
4. 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 **(IF=2.6)**
5. 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=16.1**)

6. 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)**

7. 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. *Pharmgenomics. Pers. Med.,* Volume 14, 1211–1220. https://doi.org/10.2147/PGPM.S319308 **(IF=3.88)**

8. 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=5.1)**

9. **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**)

10. 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=0.5**)

11. 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., Wuhrer, 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=13.1**)

12. 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=6.0**)

13. **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=4.0**)

14. 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=4.2**)

15. **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=5.1**)

16. 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=5.5**)

17. 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**)

18. 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=6.87**).

19. 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 α-Tocopheryl Succinate as Potential Cytotoxic Agents. Russian Journal of Bioorganic Chemistry, 44(3), 330–336. (**IF= 0.838**)

20. 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 GN-glycosylation // Nat. Commun. Nature Publishing Group, 2017. Vol. 8, № 1. P. 447. (**IF=12.12**)

21. 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**).

22. 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=1.13**)

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., Wootten, 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. Landini, A., Trbojević-Akmačić, I., Navarro, P., Tsepilov, Y. A., **Sharapov, S. Z.**, Vučković, F., Polašek, O., Hayward, C., Petrovic, T., Vilaj, M., Aulchenko, Y. S., Lauc, G., Wilson, J. F., & Klarić, L. (2021). Same role but different actors: genetic regulation of post-translational modification of two distinct proteins. BioRxiv. doi:10.1101/2021.05.04.442584

3. 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. // 2nd 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