

Сведения о ведущей организации

Полное наименование организации	Федеральное государственное бюджетное учреждение науки Институт общей генетики им. Н.И. Вавилова Российской академии наук
Сокращенное наименование организации	ФГБУН ИОГЕН РАН
Место нахождения	Москва, ул. Губкина, д. 3
Почтовый адрес	119991, ГСП-1 Москва, ул. Губкина, д. 3
Телефон	+7 (499) 135-62-13
Адрес электронной почты	iogen@vigg.ru
Адрес официального сайта	http://vigg.ru/
Список основных публикаций работников организации по теме диссертации за последние 5 лет (не более 15)	<ol style="list-style-type: none">1. Simovski B, Kanduri C, Gundersen S, Titov D, Domanska D, Bock C. Coloc-stats: a unified web interface to perform colocalization analysis of genomic features. <i>Nucl Acids Res.</i> 2018; 46: W186–W193.2. Khamis AM, Motwalli O, Oliva R, Jankovic BR, Medvedeva YA, Ashoor H, et al. A novel method for improved accuracy of transcription factor binding site prediction. <i>Nucl Acids Res.</i> 2018; 46: e72.3. Zhivotovsky LA, Teterina AA, Mukhina NV, Stroganov AN, Rubtsova GA, Afanasiev KI. Effects of genetic drift in a small population of Atlantic cod (<i>Gadus morhua kildinensis</i> Derjugin) landlocked in a meromictic lake: genetic variation and conservation measures. <i>Conservation Genetics.</i> 2017; 17: 229-238.4. Savitskaya E, Lopatina A, Medvedeva S, Kapustin M, Shmakov S, Tikhonov A, et al. Dynamics of <i>Escherichia coli</i> type I-E CRISPR spacers over 42 000 years. <i>Mol Ecol.</i> 2017; 26: 2019-20265. Stavrovskaya ED, Niranjana T, Fertig EJ, Wheelan SJ, Favorov AV, Mironov AA. StereoGene: rapid estimation of genome-wide correlation of continuous or interval feature data. <i>Bioinformatics.</i> 2017; 33: 3158-3165.6. Lisenkova AA, Grigorenko AP, Tyazhelova TV, Andreeva TV, Gusev FE, Manakhov AD, et al. Complete mitochondrial genome and evolutionary analysis of <i>Turritopsis dohrnii</i>, the “immortal” jellyfish with a reversible life-cycle. <i>Molecular Phylogenetics and Evolution.</i> 2017; 107: 232-238.7. Hon CC, Ramilowski JA, Harshbarger J, Bertin N, Rackham OJL, Gough J. An atlas of human long non-coding RNAs with accurate

5' ends. *Nature*. 2017; 543: 199-204.

8. Panchin AY, Makeev VJ, Medvedeva YA. Preservation of methylated CpG dinucleotides in human CpG islands. *Biology Direct*. 2016;11: 11.
 9. Hill SM, Heiser LM, Cokelaer T, Unger M, Nesser NK, Carlin DE, et al. Inferring causal molecular networks: empirical assessment through a community-based effort. *Nature methods*. 2016;13: 310–318.
 10. Vorontsov IE, Khimulya G, Lukianova EN, Nikolaeva DD, Eliseeva IA, Kulakovskiy IV, et al. Negative selection maintains transcription factor binding motifs in human cancer. *BMC Genomics*. 2016;17: 395.
 11. Kulakovskiy IV, Vorontsov IE, Yevshin IS, Soboleva AV, Kasianov AS, Ashoor H, et al. HOCOMOCO: expansion and enhancement of the collection of transcription factor binding sites models. *Nucl Acids Res*. 2016;44: D116–D125.
 12. Pronina IV, Loginov VI, Burdenny AM, Fridman MV, Kazubskaya TP, Dmitriev AA, et al. Expression and DNA methylation alterations of seven cancer-associated 3p genes and their predicted regulator miRNAs (miR-129-2, miR-9-1) in breast and ovarian cancers. *Gene*. 2016;576: 483–491.
 13. Krasnov GS, Dmitriev AA, Kudryavtseva AV, Shargunov AV, Karpov DS, Uroshlev LA, et al. PPLine: An Automated Pipeline for SNP, SAP, and Splice Variant Detection in the Context of Proteogenomics. *J Proteome Res*. 2015;14: 3729–3737.
 14. Kurmangaliyev YZ, Favorov AV, Osman NM, Lehmann K-V, Campo D, Salomon MP, et al. Natural variation of gene models in *Drosophila melanogaster*. *BMC Genomics*. 2015;16: 198.
 15. Kozlov K, Gursky VV, Kulakovskiy IV, Dymova A, Samsonova M. Analysis of functional importance of binding sites in the *Drosophila* gap gene network model. *BMC Genomics*. 2015;16: S7.
-