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
адрес	119991, ГСП-1 Москва, ул. Губкина, д. 3
Телефон	+7 (499) 135-62-13
почты	iogen@vigg.ru
та	http://vigg.ru/
работников организации по теме диссертации за последние 5 лет (не более 15)	1. Filippova EA, Loginov VI, Burdennyi AM, Braga EA, Pronina IV, Kazubskaya TP, Kushlinskii DN, Utkin DO, Fridman MV, Khodyrev DS, Kushlinskii NE. Hypermethylated Genes of MicroRNA in Ovarian Carcinoma: Metastasis Prediction Marker Systems. Bull Exp Biol Med. 2019 [Epub ahead of print] 2. Kelley DZ, Flam EL, Guo T, Danilova LV, Zamuner FT, Bohrson C, Considine M, Windsor EJ, Bishop JA, Zhang C, Koch WM, Sidransky D, Westra WH, Chung CH, Califano JA, Wheelan S, Favorov AV, Florea L, Fertig EJ, Gaykalova DA. Functional characterization of alternatively spliced GSN in head and neck squamous cell carcinoma. Transl Res. 2018; 202:109-119. 3. Stavrovskaya ED, Niranjan T, Fertig EJ, Wheelan SJ, Favorov AV, Mironov AA. StereoGene: rapid estimation of genome-wide correlation of continuous or interval feature data. Bioinformatics. 2017; 33: 3158-3165. 4. 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. 5. Andreeva TV, Tyazhelova TV, Rykalina VN, Gusev FE, Goltsov AY, Zolotareva OI, Aliseichik MP, Borodina TA, Grigorenko AP, Reshetov DA, Ginter EK, Amelina SS, Zinchenko RA, Rogaev EI. Whole exome sequencing links dental tumor to an autosomal-dominant mutation in ANO5 gene associated with gnathodiaphyseal dysplasia and muscle dystrophies. Sci Rep. 2016; 6:26440. 6. Panchin AY, Makeev VJ, Medvedeva YA. Preservation of methylated CpG dinucleotides in human CpG islands. Biology Direct. 2016;11: 11. 7. Protasova MS, Grigorenko AP, Tyazhelova TV, Andreeva TV, Reshetov DA, Gusev FE, Laptenko AE, Kuznetsova IL, Goltsov AY, Klyushnikov SA, Illarioshkin SN, Rogaev EI. Whole-genome

	sequencing identifies a novel ABCB7 gene mutation for X-linked congenital cerebellar ataxia in a large family of Mongolian ancestry. Eur J Hum Genet. 2016: 24(4):550-5. 8. Salnikova LE, Kolobkov DS. Germline and somatic genetic predictors of pathological response in neoadjuvant settings of rectal and esophageal cancers: systematic review and meta-analysis. Pharmacogenomics J. 2016; 16:249-65. 9. Pronina IV, Loginov VI, Burdennyy 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. 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. Balanovsky O, Zhabagin M, Agdzhoyan A, Chukhryaeva M, Zaporozhchenko V, Utevska O, Highnam G, Sabitov Z, Greenspan E, Dibirova K, Skhalyakho R, Kuznetsova M, Koshel S, Yusupov Y, Nymadawa P, Zhumadilov Z, Pocheshkhova E, Haber M, A Zalloua P, Yepiskoposyan L, Dybo A, Tyler-Smith C, Balanovska E. Deep phylogenetic analysis of haplogroup G1 provides estimates of SNP and STR mutation rates on the human Y-chromosome and reveals migrations of Iranic speakers. PLoS One. 2015; 10:e0122968.