

**СПИСОК ПУБЛИКАЦИЙ д.б.н. ЩЕРБАКОВА Д.Ю.**  
**ПО ТЕМЕ ОППОНИРУЕМОЙ ДИССЕРТАЦИИ**

1. Sherbakov D.Yu., Bukin Yu.S., Kravtsova L.S., Romanova E.V., Mincheva E.V., Peretolchina T.E., Poroshina A.E., Sirotinina E.A., Voylo M.A. Mechanisms of fast transformations of Baikal biota: multidisciplinary approach // Limnology and Freshwater Biology. – 2018. – № 1. – P. 32-35. DOI: 10.31951/2658-3518-2018-A-1-32
2. Bukin Y.S., Petunina J.V., Sherbakov D.Yu. The Mechanisms for Genetic Diversity of Baikal Endemic Amphipod *Gmelinoides fasciatus*: Relationships between the Population Processes and Paleoclimatic History of the Lake // Russian Journal of Genetics. – 2018. – Vol.54 (9). P.1059–1068.
3. Adelshin R.V., Sidorova E.A., Bondaryuk A.N., Trukhina A.G., Sherbakov D.Yu., White III R.A., Andaev E.I., Balakhonov S.V. “886-84-like” tick-borne encephalitis virus strains: Intraspecific status elucidated by comparative genomics // Ticks and Tick-borne Diseases. – 2019. – Vol.10(5). – P.1168-1172. DOI:10.1016/j.ttbdis.2019.06.006
4. Pobedintseva M.A., Makunin A.I., Kichigin I.G., Kulemzina A.I., Serdyukova N.A., Romanenko S.A., Vorobieva N.V., Interesova E.A., Korentovich M.A., Zaytsev V.F., Mischenko A.V., Zadelenov V.A., Yurchenko A.A., Sherbakov D.Yu., Graphodatsky A.S., Trifonov V.A. Population genetic structure and phylogeography of sterlet (*Acipenser ruthenus*, *Acipenseridae*) in the Ob and Yenisei river basins // Mitochondrial DNA Part A. – 2019. – Vol.30(1). – P.156-164. DOI:10.1080/24701394.2018.1467409
5. Romanova E.V., Sherbakov D.Yu. Different rates of molecular evolution of mitochondrial genes in Baikalian and non-Baikalian amphipods // Limnology and Freshwater Biology. – 2019. – №6. – P.339-344. DOI:10.31951/2658-3518-2019-A-6-339
6. Romanova E.V., Bukin Y.S., Mikhailov K.V., Logacheva M.D., Aleoshin V.V., Sherbakov D.Yu. Hidden cases of tRNA gene duplication and remolding in mitochondrial genomes of amphipods // Molecular Phylogenetics and Evolution. – 2020. – Vol.144, Art №106710. – P.1-21. DOI:10.1016/j.ympev.2019.106710
7. Romanova E.V., Bukin Yu.S., Sherbakov D.Yu. Bioinformatic tools for tRNA gene analyses in mitochondrial DNA sequence data // Data in brief. – 2020. – №29, Art№ 105284. – P.1-7. DOI:10.1016/j.dib.2020.105284
8. Kovalenkova M.V., Bukin Yu.S., Sitnikova T.Ya., Sherbakov D.Yu. The phylogeny based on the intron of ATP synthase  $\alpha$ -subunit gene reveals a substrate role in the origin of the gastropod species flock from Lake Baikal // Limnology and Freshwater Biology. – 2020. – №2. – P.405-411. DOI:10.31951/2658-3518-2020-A-2-405

9. Romanova E.V., Bukin Y.S., Mikhailov K.V., Logacheva M.D., Aleoshin V.V., Sherbakov D.Yu. Detection of the extra tRNA genes in mitochondrial genomes of amphipods using lineage-specific models // Limnology and Freshwater Biology. – 2020. – №4. – P.812-813. DOI: 10.31951/2658-3518-2020-A-4-812
10. Poroshina A.A., Sherbakov D.Y., Peretolchina T.E., Diagnosis of the mechanisms of different types of discordances between phylogenies inferred from nuclear and mitochondrial markers // Vavilov Journal of Genetics and Breeding. – 2020. – Vol. 24(4). – P.420–426. DOI: 10.18699/VJ20.634
11. Sirotinina E.A., Romanova E.V., Sherbakov D.Yu. Dynamics of gene order rearrangements in mitochondrial genomes of Baikalian amphipods // Limnology and Freshwater Biology. – 2020. – №4. – P.818-819. DOI:10.31951/2658-3518-2020-A-4-818
12. Romanova E. V., Bukin Y. S., Mikhailov K. V., Logacheva M. D., Aleoshin V. V., & Sherbakov D. Y. The mitochondrial genome of a freshwater pelagic amphipod *macrohectopus branickii* is among the longest in metazoan // Genes. – 2021. – Vol. 12(12). 2030. DOI:10.3390/genes12122030
13. Bukin Y.S., Kravtsova L.S., Peretolchina T.E., Fedotov A.P., Tupikin A.E., Kabilov M.R., Sherbakov D.Y., Mincheva E.V. DNA metabarcoding of benthic algae and associated eukaryotes from Lake Baikal in the face of rapid environmental changes // Vavilovskii Zhurnal Genet Seleksii. – 2022. – Vol. 26(1). – P. 86-95. DOI: 10.18699/VJGB-22-12.
14. Kirichenko A.D., Poroshina A.A., Sherbakov D.Y., Sadovsky M.G., Krutovsky K.V. Comparative analysis of alignment-free genome clustering and whole genome alignment-based phylogenomic relationship of coronaviruses // PLoS One. – 2022. – Vol. 17(3). – P. e0264640. DOI: 10.1371/journal.pone.0264640.