

Публикации официального оппонента к.б.н. Константина Николаевича Козлова по теме оппонируемой диссертации

1. К.Н. Козлов, Л.Ю. Новикова, И.В. Сеферова, М.Г. Самсонова, МАТЕМАТИЧЕСКАЯ МОДЕЛЬ ВЛИЯНИЯ КЛИМАТИЧЕСКИХ ФАКТОРОВ НА РАЗВИТИЕ СОИ, БИОФИЗИКА, 2018, том 63, вып. 1, с. 175–176
2. Gursky, V.V., Kozlov, K.N., Kulakovskiy, I.V., Zubair, A., Marjoram, P., Lawrie, D.S., Nuzhdin, S.V., Samsonova, M.G, Translating natural genetic variation to gene expression in a computational model of the Drosophila gap gene regulatory network, PLoS ONE, Volume 12, Issue 9, September 2017, Article number e0184657
3. Konstantin Kozlov, Vera Kosheverova, Rimma Kamentseva, Marianna Kharchenko, Alena Sokolkova, Elena Kornilova and Maria Samsonova, Quantitative analysis of the heterogeneous population of endocytic vesicles, 2017, Journal of Bioinformatics and Computational Biology, Vol. 15, No. 2 (2017) 1750008
4. A.A. Chertkova, J. S. Schiffman, S. V. Nuzhdin, K. N. Kozlov, M.G. Samsonova, V. V. Gursky, In silico evolution of the Drosophila gap gene regulatory sequence under elevated mutational pressure, BMC Evolutionary biology, 2017, Volume 17, Pages 1-12, DOI 10.1186/s12862-016-0866y
5. Kozlov Konstantin, Samsonov Alexander M., Samsonova Maria. A software for parameter optimization with Differential Evolution Entirely Parallel method // PeerJ Computer Science. — 2016. — August. — Vol. 2. — P. e74. <https://doi.org/10.7717/peerj-cs.74>.
6. Konstantin Kozlov, Vitaly Gursky, Ivan Kulakovskiy, Arina Dymova and Maria Samsonova, Analysis of functional importance of binding sites in the Drosophila gap gene network model. BMC Genomics 2015, 16(Suppl 13):S7, doi:10.1186/1471-2164-16-S13-S7 Published: 2015.
7. К.Н. Козлов, А.М.Самсонов, М.Г. Самсонова, «Метод полностью параллельной разностной эволюции для адаптации моделей в системной биологии», БИОФИЗИКА, 2015, том 60, вып. 6, с. 1219–1220
8. K. Kozlov, D. Chebotarev, M. Hassan, M. Triska, P. Triska, P. Flegontov, and T. Tatarinova, Differential evolution approach to detect recent admixture, BMC Genomics 16 (2015), p. S9, Available at <http://www.biomedcentral.com/1471-2164/16/S8/S9>.
9. Ivanisenko NV, Mishchenko EL, Akberdin IR, Demenkov PS, Likhoshvai VA, Kozlov KN, Todorov DI, Gursky VV, Samsonova MG, Samsonov AM, Clausznitzer D, Kaderali L, Kolchanov NA, Ivanisenko VA. A new stochastic model for subgenomic hepatitis C virus replication considers drug resistant mutants. PLoS One. 2014 Mar 18;9(3):e91502.
10. Konstantin Kozlov, Vitaly Gursky, Ivan Kulakovskiy and Maria Samsonova Sequence-Based Model of Gap Gene Regulatory Network BMC Genomics 2014, 15(Suppl 12):S6 BMC Genomics 2014, 15(Suppl 12):S6
11. Anastasia Terskikh, K.Kozlov Quantitative characterization of receptor-mediated endocytosis by segmentation of confocal images . In “Bertichte aus der Medizinischen Informatik und Bioinformatik.” German Russian Network of Computational Systems Biology, Report 2014, 55-57
12. Myasnikova E., Kozlov, K.N. Statistical method for estimation of the predictive power of a gene circuit model. J Bioinform Comput Biol. 2014 Apr;12(2):1441002. doi: 10.1142/S0219720014410029