

Портфолио преподавателя
Медведева Юлия Анатольевна



Ученая степень	кандидат биологических наук
Ученое звание	-
Должность	рук. группы регуляторной транскриптомики и эпигеномики
Эл. почта	ju.medvedeva@gmail.com
Образование и повышение квалификации	Высшее, МГТУ им. Н.Э. Баумана, МГУ им. М.В. Ломоносова
Область научных интересов	Эпигенетика, транскриптомика, анализ омиксных данных, биоинформатика, машинное обучение.
Премии и награды (при наличии)	Стипендия Министерства Экономики и Конкурентноспособности Испании, 2014г; Премия SABIC (Саудовская Аравия) для кандидатов наук, 2012 г; Премия SABIC (Саудовская Аравия) для кандидатов наук, 2011 г.
Избранные публикации	<ol style="list-style-type: none"> Antonov IV, Mazurov E, Borodovsky M, Medvedeva YA. Prediction of lncRNAs and their interactions with nucleic acids: benchmarking bioinformatics tools. Brief Bioinform. (2018) Apr 24. doi: 10.1093/bib/bby032. Antonov I, Marakhonov A, Zamkova M, Medvedeva YA. ASSA: Fast identification of statistically significant interactions between long RNAs. J Bioinform Comput Biol. (2018) Jan 29:1840001 Artemov AV, Mogue NS, Rastorguev SM, Zhenilo S, Mazur AM, Tsygankova SV, Boulygina ES, Kaplun D, Nedoluzhko AV, Medvedeva YA, Prokhortchouk EB. Genome-Wide DNA Methylation Profiling Reveals Epigenetic Adaptation of Stickleback to Marine and Freshwater Conditions. Mol Biol Evol. (2017) Sep 1;34(9):2203-2213. de Rie D, Abugessaisa I, Alam T, Arner E, Arner P, Ashoor H, Åström G, Babina M, Bertin N, Burroughs AM, Carlisle AJ, Daub CO, Detmar M, Deviatiiarov R, Fort A, Gebhard C, Goldowitz D, Guhl S, Ha TJ, Harshbarger J, Hasegawa A, Hashimoto K, Herlyn M, Heutink P, Hitchens KJ, Hon CC, Huang E, Ishizu Y, Kai C, Kasukawa T, Klinken P, Lassmann T, Lecellier CH, Lee W, Lizio M, Makeev V, Mathelier A, Medvedeva YA, Mejhert N, Mungall CJ, Noma S, Ohshima M, Okada-Hatakeyama M, Persson H, Rizzu P,

- Roudnický F, Sætrom P, Sato H, Severin J, Shin JW, Swoboda RK, Tarui H, Toyoda H, Vitting-Seerup K, Winteringham L, Yamaguchi Y, Yasuzawa K, Yoneda M, Yumoto N, Zabierowski S, Zhang PG, Wells CA, Summers KM, Kawaji H, Sandelin A, Rehli M; FANTOM Consortium, Hayashizaki Y, Carninci P, Forrest ARR, de Hoon MJL. An integrated expression atlas of miRNAs and their promoters in human and mouse. *Nat Biotechnol.* (2017) Sep;35(9):872-878. doi: 10.1038/nbt.3947.
5. Hon CC, Ramilowski JA, Harshbarger J, Bertin N, Rackham OJ, Gough J, Denisenko E, Schmeier S, Poulsen TM, Severin J, Lizio M, Kawaji H, Kasukawa T, Itoh M, Burroughs AM, Noma S, Djebali S, Alam T, **Medvedeva YA**, Testa AC, Lipovich L, Yip CW, Abugessaisa I, Mendez M, Hasegawa A, Tang D, Lassmann T, Heutink P, Babina M, Wells CA, Kojima S, Nakamura Y, Suzuki H, Daub CO, de Hoon MJ, Arner E, Hayashizaki Y, Carninci P, Forrest AR. An atlas of human long non-coding RNAs with accurate 5' ends. *Nature.* (2017) Mar 9;543(7644):199-204.
6. Kulakovskiy IV, Vorontsov IE, Yevshin IS, Soboleva AV, Kasianov AS, Ashoor H, Ba-Alawi W, Bajic VB, **Medvedeva YA**, Kolpakov FA, Makeev VJ. (2015) HOCOMOCO: expansion and enhancement of the collection of transcription factor binding sites models. *Nucleic Acids Res.* 2015 Nov 19. pii: gkv1249.
7. **Medvedeva YA**, Lennartsson A, Ehsani R, Kulakovskiy IV, Vorontsov IE, Panahandeh P, Khimulya G, Kasukawa T; FANTOM Consortium, Drabløs F. (2015) EpiFactors: a comprehensive database of human epigenetic factors and complexes. *Database (Oxford).* 2015 Jul 7;2015:bav067. doi: 10.1093/database/bav067.
8. A.Khamis, A.Hamilton, **Y.Medvedeva**, T.Alam, I.Alam, M.Essack, B.Umylny, B.Jankovic, N.Naeger, M.Suzuki, M.Harbers, G.Robinson, and V.Bajic (2015) Insights into the Transcriptional Architecture of Behavioral Plasticity in the Honey Bee *Apis mellifera*. *Scientific Reports*, Jun 15;5:11136
9. Alam T*, **Medvedeva YA***, Jia H, Brown JB, Lipovich L, Bajic VB (2014). Promoter analysis reveals globally differential regulation of human long non-coding RNA and protein-coding genes. *PLoS One.* Oct 2;9(10):e109443. (*shared first authors).
10. A.R.R. Forrest, H. Kawaji, M. Rehli, J.K. Baillie, M.J.L. de Hoon, V. Haberle, T. Lassmann, I.V. Kulakovskiy, M. Lizio, M. Itoh, R. Andersson, C.J. Mungall, T.F. Meehan, S. Schmeier, N. Bertin, M. Jørgensen, E. Dimont, E. Arner, C. Schmidl, U. Schaefer, **Y. A. Medvedeva**, C. Plessy, M. Vitezic, J. Severin, C.A. Semple, Y. Ishizu, M. Francescato, et al. (2014) A promoter level mammalian expression atlas. *Nature.* 507(7493):462-70.
11. **Y.A. Medvedeva**, A. Khamis, I.V. Kulakovskiy, W. Ba-Alawi, Md.S.I. Bhuyan, H. Kawaji, T. Lassmann, M. Harbers, A.R.R. Forrest and V.B. Bajic (2014). Effects of cytosine methylation on transcription factor binding sites. *BMC genomics.* 26;15(1):119.
12. Pardo LM, P.Rizzu, M.Francescato, M.Vitezic, G.G.Leday, J.Sanchez, A.Khamis, H.Takahashi, W.D. van de Berg, **Y.A.Medvedeva**, M.A. van de Wiel, C.O. Daub, P.Carninci, P.Heutink (2013) Regional differences in gene expression and promoter usage in aged human brains. *Neurobiology of Aging* pii: S0197-4580(13)00023-7.
13. Kulakovskiy IV, **Medvedeva YA**, Schaefer U, Kasianov AS, Vorontsov IE, Bajic VB, Makeev VJ. (2013) HOCOMOCO: a comprehensive collection of human transcription factor binding sites models. *Nucleic Acids Res.* Jan;41(Database issue):D195-202.

	<p>14. Favorov A, Mularoni L, Cope LM, Medvedeva Y, Mironov AA, Makeev VJ, Wheelan SJ. (2012) Exploring massive, genome scale datasets with the GenometriCorr package. <i>PLoS Comput Biol.</i> May;8(5):e1002529.</p> <p>15. Kulakovskiy IV, Belostotsky AA, Kasianov AS, Esipova NG, Medvedeva YA, Eliseeva IA, Makeev VJ. (2011) A deeper look into transcription regulatory code by preferred pair distance templates for transcription factor binding sites. <i>Bioinformatics</i>, Oct 1;27(19):2621-4.</p> <p>16. Medvedeva YA, Fridman MV, Oparina NJ, Malko DB, Ermakova EO, Kulakovskiy IV, Heinzl A, Makeev VJ. (2010) Intergenic, gene terminal, and intragenic CpG islands in the human genome. <i>BMC Genomics</i>. Jan 19;11:48.</p>
Преподаваемые дисциплины	Дополнительные главы биоинформатики; интеллектуальный анализ данных в биоинформатике; научное руководство программы аспирантуры профиля 03.01.09 Математическая биология, биоинформатика
Общий стаж работы, лет	15
Стаж работы по специальности, лет	15