CURRICULUM VITAE

Kulakovskiy Ivan Vladimirovich

[In Russian] Кулаковский Иван Владимирович

Official address

Engelhardt Institute of Molecular Biology Russian Academy of Sciences

EIMB RAS, Vavilova 32, Moscow 119991, Russia

Vavilov Institute of General Genetics Russian Academy of Sciences

VIGG RAS, Gubkina 3, Moscow 119991, Russia

E-mail

ivan-dot-kulakovskiy-at-gmail-dot-com

Google Scholar profile

http://scholar.google.com/citations?user=0f5hVB4AAAAJ&hl=en

Degrees

Ph.D.: November 2009 in Bioinformatics (Kharkevich Institute for information transmission problems Russian Academy of Sciences)

Construction of optimal models for transcription factor binding sites

using information from different experimental sources
(Supervisor Prof. Dr. V.G. Tumanyan, EIMB RAS)

M.Sc.: July 2006 in Computer Science (Moscow State University of Forest)

Organizing computational pipelines for complex genomic analysis
(Supervisor Assist. Prof. E.K. Baranova); graduation with honors

Bachelor: June 2005 in Computer Science (Moscow State University of Forest)

Interactive electronic spreadsheets (Supervisor Prof. A.V. Korolkov);
graduation with honors

Scientific interests

computational biology, bioinformatics, systems biology, regulatory genomics,

next-generation sequencing, protein-DNA recognition, motif discovery & motif finding

Peer reviewer

Genome Biology, Bioinformatics, PloS ONE, BMC Genomics, BMC Bioinformatics, Algorithms for Molecular Biology, Journal of Bioinformatics and Computational Biology, Nucleic Acids Research,

Молекулярная биология [in Russian]

Positions held

2016-

Lead researcher, Engelhardt Institute of Molecular Biology, Russian Academy of Sciences (Moscow), Laboratory of Computational Methods for Systems Biology

2014-

Senior research fellow, Vavilov Institute of General Genetics Russian Academy of Sciences (Moscow), Department of Computational Systems Biology

2013-2016

Senior research fellow, Engelhardt Institute of Molecular Biology, Russian Academy of Sciences (Moscow), Laboratory of Computational Methods for Systems Biology

2012-2013

Research fellow, Vavilov Institute of General Genetics Russian Academy of Sciences (Moscow), Department of Computational Systems Biology

2010-2013

Research fellow, Engelhardt Institute of Molecular Biology Russian Academy of Sciences (Moscow), Laboratory of Bioinformatics and Systems Biology

2010-2011

Research fellow, Research Institute for Genetics and Selection of Industrial Microorganisms (Moscow), Laboratory of Bioinformatics

2009-2010

Junior research fellow, Research Institute for Genetics and Selection of Industrial Microorganisms (Moscow), Laboratory of Bioinformatics

2006-2009

Graduate student, programmer, Engelhardt Institute of Molecular Biology Russian Academy of Sciences (Moscow), Laboratory of Bioinformatics and Systems biology

2005-2006

Technician, Engineer, Central Scientific Research Institute for Machine Building (Korolev), Mission Control Center, Telemetry Department

Publications in peer-reviewed journals

1. (2017) L.A. Uroshlev, I.V. Kulakovskiy, N.G. Esipova, V.G. Tumanyan, S.V. Rahmanov, V.J. Makeev; Role of structural water for prediction of cation binding sites in apoproteins. *J Biomol Struct Dyn*, doi: 10.1080/07391102.2016.1273136.

2. (2017) N. Andreeva, E. Kulakovskaya, A. Zvonarev, A. Penin, I. Eliseeva, A. Teterina, A. Lando, I.V. Kulakovskiy, T. Kulakovskaya; Transcriptome profile of yeast reveals the essential role of PMA2 and uncharacterized gene YBR056W-A (MNC1) in adaptation to toxic manganese concentration. *Metallomics*, doi: 10.1039/c6mt00210b

3. (2017) A.M. Schwartz, D.E. Demin, I.E. Vorontsov, A.S. Kasyanov, L.V. Putlyaeva, K.A. Tatosyan, I.V. Kulakovskiy, D.V. Kuprash; Multiple single nucleotide polymorphisms in the first intron of the IL2RA gene affect transcription factor binding and enhancer activity. *Gene*, 602:50-56, doi: 10.1016/j.gene.2016.11.032

4. (2016) I.V. Kulakovskiy, I.E. Vorontsov, I.S. Yevshin, A.V. Soboleva, A.S. Kasianov, H. Ashoor, W. Ba-Alawi, V.B. Bajic, Y.A. Medvedeva, F.A. Kolpakov, V.J. Makeev; HOCOMOCO: expansion and enhancement of the collection of transcription factor binding sites models. *Nucleic Acids Res.,* 44(D1):D116-25, doi: 10.1093/nar/gkv1249

5. (2016) I.E. Vorontsov, G.Khimulya, E.N. Lukianova, D.D. Nikolaeva, I.A. Eliseeva, I.V. Kulakovskiy, V.J. Makeev; Negative selection maintains transcription factor binding motifs in human cancer. *BMC Genomics*, 17(Suppl 2):395, doi: 10.1186/s12864-016-2728-9

6. (2016) N. Zolotarev, A. Fedotova, O. Kyrchanova, A. Bonchuk, A.A. Penin, A.S. Lando, I.A. Eliseeva, I.V. Kulakovskiy, O. Maksimenko, P. Georgiev; Architectural proteins Pita, Zw5,and ZIPIC contain homodimerization domain and support specific long-range interactions in Drosophila. *Nucleic Acids Res.*, doi: 10.1093/nar/gkw371

7. (2016) A.M. Schwartz, L.V. Putlyaeva, M.Covich, A.V. Klepikova, K.A. Akulich, I.E. Vorontsov, K.V. Korneev, S.E. Dmitriev, O.L. Polanovsky, S.P. Sidorenko, I.V. Kulakovskiy, D.V. Kuprash; Early B-cell factor 1 (EBF1) is critical for transcriptional control of SLAMF1 gene in human B cells. *BBA – Gene Regulatory Mechanisms*, doi: 10.1016/j.bbagrm.2016.07.004

8. (2015) K. Kozlov, V.V. Gursky, I.V. Kulakovskiy, A. Dymova, M. Samsonova; Analysis of functional importance of binding sites in the Drosophila gap gene network model. *BMC Genomics,* 16 Suppl 13:S7. doi: 10.1186/1471-2164-16-S13-S7

9. (2015) D. Papatsenko, H. Darr, I.V. Kulakovskiy, A. Waghray, V.J. Makeev, B.D. MacArthur, I.R. Lemischka; Single-Cell Analyses of ESCs Reveal Alternative Pluripotent Cell States and Molecular Mechanisms that Control Self-Renewal. *Stem Cell Reports*, 5(2):207-20. doi: 10.1016/j.stemcr.2015.07.004

10. (2015) Y.A. Medvedeva, A. Lennartsson, R. Ehsani, I.V. Kulakovskiy, I.E. Vorontsov, P. Panahandeh, G. Khimulya, T. Kasukawa, The FANTOM Consortium and F. Drabløs; EpiFactors: a comprehensive database of human epigenetic factors and complexes. *Database*, bav067, doi:10.1093/database/bav067

11. (2014) K. Kozlov, V. Gursky, I. Kulakovskiy, M. Samsonova; Sequence-based model of gap gene regulatory network. *BMC Genomics*, 15(Suppl 12):S6, doi:10.1186/1471-2164-15-S12-S6

12. (2014) 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 *et al.*; A promoter-level mammalian expression atlas. *Nature*, 507: 462–470, doi: 10.1038/nature13182

13. (2014) D.N. Lyabin, A.N. Doronin, I.A. Eliseeva, G.P. Guens, I.V. Kulakovskiy, L.P. Ovchinnikov; Alternative Forms of Y-Box Binding Protein 1 and YB-1 mRNA. *PLoS One,* 9(8):e104513, doi: 10.1371/journal.pone.0104513

14. (2014) Y.A. Medvedeva, A.M. Khamis, I.V. Kulakovskiy, W. Ba-Alawi, M.S.I. Bhuyan, H. Kawaji, T. Lassmann, M. Harbers, A.R.R. Forrest, V.B. Bajic, The FANTOM

consortium; Effects of cytosine methylation on transcription factor binding sites. *BMC Genomics*, 15(1): 119, doi: 10.1186/1471-2164-15-119

15. (2014) V.G. Levitsky, <u>I.V. Kulakovskiy</u>, N.I. Ershov, D.Y. Oschepkov, V.J. Makeev, T.C. Hodgman, T.I. Merkulova; Application of experimentally verified transcription factor binding sites models for computational analysis of ChIP-Seq data. *BMC Genomics*, 15(1): 80, doi: 10.1186/1471-2164-15-80.

16. (2013) I.A. Eliseeva, I.E. Vorontsov, K.E. Babeyev, S.M. Buyanova, M.A. Sysoeva, F.A. Kondrashov, <u>I.V. Kulakovskiy</u>; In silico motif analysis suggests an interplay of transcriptional and translational control in mTOR response. *Translation*, 1(2), doi: 10.4161/trla.27469

17. (2013) I.E. Vorontsov, <u>I.V. Kulakovskiy</u>, V.J. Makeev; Jaccard index based similarity measure to compare transcription factor binding site models. *Algorithms for Molecular Biology*, 8(23), doi: 10.1186/1748-7188-8-23

18. (2013) <u>I. Kulakovskiy</u>, V. Levitsky, D. Oshchepkov, L. Bryzgalov, I. Vorontsov, V. Makeev; From binding motifs in ChIP-Seq data to improved models of transcription factor binding sites. *Journal of Bioinformatics and Computational Biology (J Bioinform Comput Biol)*, 11(1): 1340004, doi: 10.1142/S0219720013400040

19. (2013) <u>I.V. Kulakovskiy</u>, Y.A. Medvedeva, U. Schaefer, A.S. Kasianov, I.E. Vorontsov, V.B. Bajic, V.J. Makeev; HOCOMOCO: a comprehensive collection of human transcription factor binding sites models. *Nucleic Acids Research*, 41(D1): D195-D202, doi: 10.1093/nar/gks1089

20. (2012) N.I. Moiseeva, T.P. Stromskaya, E.Yu. Rybalkina, A.V. Vaiman, M.A. Malyshkina, E.R. Kim, I.A. Eliseeva, <u>I.V. Kulakovskiy</u>, L.P. Ovchinnikov, and A.A. Stavrovskaya; Effects of extracellular YB-1 protein on cultured cells of human breast cancer. *Biochemistry (Moscow) Supplement Series A: Membrane and Cell Biology*, 7(1): 21-28, doi: 10.1134/S1990747812050133

21. (2012) M. Ridinger-Saison, V. Boeva, P. Rimmele, <u>I. Kulakovskiy</u>, I. Gallais, B. Levavasseur, C. Paccard, P. Legoix-Ne, F. Morle, A. Nicolas, P. Hupe, E. Barillot, F. Moreau-Gachelin, C. Guillouf; Spi-1/PU.1 activates transcription through clustered DNA occupancy in erythroleukemia. *Nucleic Acids Research*, 40(18): 8927-8941, doi: 10.1093/nar/gks659

22. (2011) <u>I.V. Kulakovskiy</u>, A.A. Belostotsky, A.S. Kasianov, N.G. Esipova, Y.A. Medvedeva, I.A. Eliseeva, V.J. Makeev; A deeper look into transcription regulatory code by preferred pair distance templates for transcription factor binding sites. *Bioinformatics*, 27(19): 2621-4, doi: 10.1093/bioinformatics/btr453

23. (2011) <u>I.V. Kulakovskiy</u>, A.S. Kasianov, A.A. Belostotsky, I.A. Eliseeva, V.J. Makeev; Preferred distances between transcription factor binding sites. *Biophysics*, 56(1): 114-6, doi:10.1134/S0006350911010155

24. (2010) <u>I.V. Kulakovskiy</u>, V.A. Boeva, A.V. Favorov, V.J. Makeev; Deep and wide digging for binding motifs in ChIP-Seq data. *Bioinformatics*, 26(20): 2622-3, doi: 10.1093/bioinformatics/btq488

25. (2010) Y.A. Medvedeva, M.V. Fridman, N.J. Oparina, D.B. Malko, E.O. Ermakova, <u>I.V. Kulakovskiy</u>, A. Heinzel, V.J. Makeev; Intergenic, gene terminal, and intragenic

CpG islands in the human genome. *BMC Genomics*, 11:48, doi: 10.1186/1471-2164-11-48

26. (2010) Y.A. Medvedeva, I.V. Kulakovskiy, N.J. Oparina, A.V. Favorov, V.J. Makeev; GC-skew near PolII start sites and its association with Sp1 binding site variants. *Biophysics*, 55(6): 976-85

27. (2010) S. Rahmanov, I. Kulakovskiy, L. Uroshlev, V. Makeev; Empirical potentials for ion binding in proteins. *Journal of Bioinformatics and Computational Biology*, 8(3): 427-35

28. (2009) I.V. Kulakovskiy, A.V. Favorov, V.J. Makeev; Motif discovery and motif finding from genome-mapped DNAse footprint data. *Bioinformatics*, 25(18): 2318-25

29. (2009) I.V. Kulakovskiy, V.J. Makeev; Discovery of DNA motifs recognized by transcription factors through Integration of different experimental sources. *Biophysics*, 54(6): 667-74

Book chapters

1. (2016) N. Andreeva, L. Lichko, L. Trilisenko, I.V. Kulakovskiy, and T. Kulakovskaya; Yeast Polyphosphatases PPX1 and PPN1: Properties, Functions, and Localization. Chapter in *Inorganic Polyphosphates in Eukaryotic Cells*, edited by Kulakovskaya, Tatiana, Pavlov, Evgeny, Dedkova, Elena N., Springer International Publishing, 15-33. ISBN 978-3-319-41073-9, doi: 10.1007/978-3-319-41073-9

2. (2014) I.V. Kulakovskiy, V.J. Makeev; Motif Discovery and Motif Finding in ChIP-Seq Data. Invited chapter in *Genome Analysis: Current Procedures and Applications*, edited by Maria Poptsova, Caister Academic Press, 83-100. ISBN 978-1-908230-29-4

3. (2013) I.V. Kulakovskiy, V.J. Makeev; DNA Sequence Motif: A Jack of All Trades for ChIP-Seq Data. Invited chapter in *Advances in Protein Chemistry and Structural Biology*, Vol. 91, edited by Rossen Donev, Burlington: Academic Press, 135-171. ISBN 978-0-12-411637-5, Elsevier Inc

Publications in peer-reviewed journals [In Russian]

1. (2012) Н.И. Моисеева, Т.П. Стромская, Е.Ю. Рыбалкина, А.В. Вайман, М.А. Малышкина, Е.Р. Ким, И.А. Елисеева, И.В. Кулаковский, Л. П. Овчинников, А.А. Ставровская; Влияние внеклеточного белка YB-1 на культивируемые клетки опухолей молочной железы. *Биологические мембраны*, 29(5): 340-348

2. (2011) И.В. Кулаковский, А.С. Касьянов, А.А. Белостоцкий, И.А. Елисеева, В.Ю. Макеев; Предпочтительные расстояния между участками ДНК, связывающими белковые факторы, регулирующие инициацию транскрипции. *Биофизика*, 56(1): 136-9

3. (2010) Ю.А. Медведева, И.В. Кулаковский, Н.Ю. Опарина, А.В. Фаворов, В.Ю. Макеев; Ассиметрия GC-состава в окрестностях стартов транскрипции (с участием ДНК-зависимой РНК-полимеразы II) и ее связь с расположением участков адсорбции белка Sp1 на ДНК. *Биофизика*, 55(6): 976-85

4. (2009) И.В. Кулаковский, В.Ю. Макеев; Интеграция данных, полученных различными экспериментальными методами, для определения мотивов в последовательностях ДНК, распознаваемых факторами, регулирующими транскрипцию. *Биофизика*, 54(6): 965-74

Invited talks

1. (2016) April 6, Seminar @Mathematical Biology and Bioinformatics Laboratory, Peter the Great Saint-Petersburg Polytechnic University; Comprehensive collection of transcription factor binding motifs in human and mouse: current state, software tools, practical applications in regulatory genomics.

   Коллекция моделей мотивов сайтов связывания для факторов транскрипции мыши и человека: обзор данных, программных инструментов и практических приложений для задач регуляторной геномики.

2. (2015) June 2-6, IV International Conference "Modern Problems of Genetics, Radiobiology, Radioecology, and Evolution" dedicated to the 115th anniversary of the birth of N.W.Timofeeff-Ressovsky and his international scientific school, St.Petersburg, Russia; **[plenary talk]** I.V. Kulakovskiy; Is there a nucleotide-level genetic code for gene expression control?

3. (2014) [In Russian] May 23, Seminar @Biophysics Department, Faculty of Physics, Lomonosov Moscow State University, Moscow, Russia; Interplay of transcriptional and translational control in mTOR response as seen by motif analysis in silico.

   Взаимосвязанная регуляция транскрипции и трансляции в mTOR-ответе с точки зрения анализа последовательностей.

4. (2014) March 24, Seminar @Institut de Medicina Predictiva I Personalitzada del Càncer, Barcelona, Spain; Sequence analysis suggests an interplay of transcriptional and translational control in mTOR response.

5. (2012) November 22-24, The Third International Scientific and Practical Conference "Postgenomic methods of analysis in biology, and laboratory and clinical medicine", POSTGENOME'2012, Kazan, Russia; How transcription start site can affect translational regulation? A case study on mRNA targets of mTOR cascade.

6. (2012) June 25–29, The Eighth International Conference on Bioinformatics of Genome Regulation and Structure/Systems Biology, BGRS\SB'12, Novosibirsk, Russia; **[keynote talk]** Comprehensive collection of human transcription factor binding site models.

7. (2010) November 8-10, LIX Bioinformatics Colloquium, Paris, France; Deep and wide digging for binding motifs in ChIP-Seq data.

8. (2010) June 15-17, Bioinformatics after Next Generation Sequencing, Zvenigorod, Russia; ChIPMunk: digging for transcription factor binding motifs in ChIP-Seq data.

9. (2010) April 21-22, Seminar @Institute of Computer Science, Faculty of Natural Sciences III, Martin Luther University Halle-Wittenberg, Germany; Motif discovery using positional preferences and data integration.

Conference abstracts

1. (2016) November 6-9, RECOMB/ISCB Conference on Regulatory & Systems Genomics with DREAM Challenges & Cytoscape Workshop, Phoenix, Arizona, USA; A.S. Lando, I.E. Vorontsov, V. Boeva, G.V. Sapunov, I.A. Eliseeva, V.J. Makeev, I.V. Kulakovskiy; Preselection of training cell types improves prediction of transcription factor binding

sites.

2. (2016) September 3-7, 15th European Conference on Computational Biology, ECCB 2016, The Hague, Netherlands

   2.1. I.A. Eliseeva, I.E. Vorontsov, <u>I.V. Kulakovskiy</u>; Can transcription determine mRNA translation in mammals? Digging evidence with sequence analysis.

   2.2. <u>I.V. Kulakovskiy</u>, I.E. Vorontsov, I. Yevshin, H. Ashoor, W. Ba-Alawi, A.S. Kasianov, Y. Medvedeva, V. Bajic, F. Kolpakov, V. Makeev; HOCOMOCO: data integration for building collection of reliable transcription factor binding sites models.

3. (2016) August 29-September 2, 10th anniversary International Multiconference "Bioinformatics of Genome Regulation and Structure\Systems Biology" (BGRS\SB-2016), Novosibirsk, Russia

   3.1. **[talk]** I.E. Vorontsov, Y.A. Medvedeva, V.J. Makeev, <u>I.Kulakovskiy</u>; HOCOMOCO COmprehensive MOdel COllection as a practical gateway to regulatory motif-ome of human and mouse transcription factors. p. 335

   3.2. K. Kozlov, A.V. Svichkarev, V.V. Gursky, <u>I.V. Kulakovskiy</u>, S.Y. Surkova, and M.G. Samsonova; Two models of the drosophila gap gene network with variation of maternal input. p. 149

4. (2016) June 14-16, SocBiN Bioinformatics 2016, Moscow, Russia

   4.1. **[talk]** I.V. Kulakovskiy; HOCOMOCO collection of transcription factor binding sites models: Expansion, enhancement and practical applications. p. 24

   4.2. I.E. Vorontsov, I.V. Kulakovskiy, G. Khimulya, E.N. Lukianova, I.A. Eliseeva, D. Nikolaeva, V.J. Makeev; Selection of somatic mutations within transcription factor binding motifs in human cancers. p. 41

   4.3. I.A. Eliseeva, I.E. Vorontsov, I.V. Kulakovskiy; Can transcription determine future of mRNAs? A case study on mTOR translational control in mammals. p. 20

5. (2015) July 16-19, Moscow Conference on Computational Molecular Biology (MCCMB'15); **[talk]** I.E. Vorontsov, <u>I.V. Kulakovskiy</u>, G.N. Khimulya, D.D. Nikolaeva, V.J. Makeev; Selection pressure on breast cancer somatic mutations revealed by bioinformatics sequence analysis.

6. (2015) July 10-14, 23rd Annual International Conference on Intelligent Systems for Molecular Biology / 14th European Conference on Computational Biology, ISMB/ECCB 2015, Dublin, Ireland; **[talk @VarI Special Interest Group]** I.E. Vorontsov, <u>I.V. Kulakovskiy</u>, G. Khimulya, D. Nikolaeva, V.J. Makeev; Sequence analysis of regulatory variants reveals selection pressure on somatic mutations in breast cancer.

7. (2015) January 12-15, 6th International Conference on Bioinformatics Models, Methods and Algorithms, BIOINFORMATICS 2015, Lisbon, Portugal; I.E. Vorontsov, <u>I.V. Kulakovskiy</u>, G. Khimulya, D.D. Nikolaeva, V.J. Makeev; PERFECTOS-APE: Predicting Regulatory Functional Effect of SNPs by Approximate P-value Estimation. p.102-108, DOI: 10.5220/0005189301020108

8. (2014) June 23-28, The ninth international conference on bioinformatics of genome regulation and structure\systems biology, BGRS\SB-2014, Novosibirsk, Russia

8.1. K.N. Kozlov, V.V. Gursky, <u>I.V. Kulakovskiy</u>, V.V. Muzhichenko, M.G. Samsonova; Sequence-based model of gap gene regulatory network. p. 87

8.2. D.Y. Oshchepkov, V.G. Levitsky, <u>I.V. Kulakovskiy</u>, N.I. Ershov, V.J. Makeev, T.I. Merkulova; Experimentally verified transcription factor binding sites models applied for computational analysis of ChIP-Seq data. p. 119

9. (2014) March 27-28, Integrative and Computational Biology, V IMPPC Annual Conference and 4DCellFate Workshop, Barcelona, Spain

9.1. I.A. Eliseeva, I.E. Vorontsov, K.E. Babeyev, S.M. Buyanova, M.A. Sysoeva, F.A. Kondrashov, <u>I.V. Kulakovskiy</u>; mTOR mRNA targets and transcription-translation rendezvous: a peep through sequence analysis keyhole.

9.2. I.E. Vorontsov, <u>I.V. Kulakovskiy</u>, V.J. Makeev; Large non-redundant collection of binding motifs for human transcription factors.

9.3. Y.A. Medvedeva, A. Khamis, <u>I.V. Kulakovskiy</u>, W. Ba-Alawi, M.S.I. Bhuyan, H. Kawaji, T. Lassmann, A.R.R. Forrest, M.Herbers, The FANTOM consortium, V.B. Bajic; Effects of cytosine methylation on transcription factor binding sites.

9.4. <u>I. Kulakovskiy</u>, I. Vorontsov, G. Khimulya, V. Makeev; Comparison and classification of transcription factor binding sites models with application to functional annotation of regulatory sequence variants.

10. (2013) July 21-23, 21st Annual International Conference on Intelligent Systems for Molecular Biology, 12th European Conference on Computational Biology, ISMB/ECCB 2013, Berlin, Germany

10.1. **[talk** @Regulatory Genomics Special Interest Group**]** <u>I. Kulakovskiy</u>; diChIPMunk: utilizing ChIP-Seq data to construct advanced dinucleotide models of transcription factor binding sites.

10.2. I. Vorontsov, <u>I. Kulakovskiy</u>, V. Makeev; Jaccard Index to Compare Position Weight Matrices of Transcription Factor Binding Sites.

10.3. <u>I.V. Kulakovskiy</u>, V.G. Levitsky, D.G. Oshchepkov, I.E. Vorontsov, V.J. Makeev; diChIPMunk: deriving dinucleotide TFBS models from ChIP-Seq data.

11. (2013) July 25-28, Moscow Conference on Computational Molecular Biology, MCCMB'13, Moscow, Russia; **[talk]** <u>I.V. Kulakovskiy</u>, V.G. Levitsky, D.G. Oshchepkov, I.E. Vorontsov, V.J. Makeev; From ChIP-Seq data to improved transcription factor binding sites models.

12. (2013) July 6-11, 38th FEBS Congress, Saint Petersburg, Russia; M. Fridman, <u>I. Kulakovskiy</u>, D. Lvovs, N. Oparina, V. Makeev; Distribution of tandem repeats in human genome. *FEBS Journal*, Volume 20 Supplement 1, p. 20

13. (2013) February 11-14, 4th International Conference on Bioinformatics Models, Methods and Algorithms, BIOINFORMATICS 2013, Barcelona, Spain; **[talk]** <u>I.V. Kulakovskiy</u>, V.G. Levitsky, D.G. Oshchepkov, I.E. Vorontsov, V.J. Makeev; Learning advanced TFBS models from ChIP-Seq data. p.146-150, DOI: 10.5220/0004238201460150

14. (2012) November 22-24, The Third International Scientific and Practical Conference "Postgenomic methods of analysis in biology, and laboratory and clinical medicine", POSTGENOME'2012, Kazan, Russia; I.E. Vorontsov, <u>I.V. Kulakovskiy</u>, V.J. Makeev;

Comparing DNA motifs specifically recognized by transcription factors.

15. (2012) October 29 - November 2, FANTOM5 Timecourses meeting, Workshop: Motifs and composite elements for time-courses, RIKEN Yokohama Institute, Tsurumi, Japan

    15.1. <u>I.V. Kulakovskiy</u>, Y.A. Medvedeva, I.E. Vorontsov, V.J.Makeev; Preferred pair distance templates for detection of TFBS composite elements in FANTOM5 Timecourse data.

    15.2. **[talk]** I.A. Eliseeva, K.E. Babeev, S.M. Buyanova, M.A. Sysoeva, F.A. Kondrashov, <u>I.V. Kulakovskiy</u>; Sequence analysis of TSSs for mRNAs translationally regulated by mTOR cascade.

16. (2012) September 9-12, 11th European Conference on Computational Biology, ECCB'12, Basel, Switzerland; <u>I.V. Kulakovskiy</u>, Y.A. Medvedeva, A.S. Kasianov, I.E. Vorontsov, U. Schaefer, V.B. Bajic, V.J. Makeev; Comprehensive collection of human transcription factor binding sites models (HOCOMOCO).

17. (2012) September 11-14, SysPatho Workshop "System biology and medicine", St.Petersburg, Tsarskoe selo; V.G. Levitsky, D.Y. Oshchepkov, G.V. Vasiliev, N.I. Ershov, T.I. Merkulova, <u>I.V. Kulakovskiy</u>, V.J. Makeev; In silico verification of TFBS in ChIP-Seq data. p. 43

18. (2012) June 25–29, The Eighth International Conference on Bioinformatics of Genome Regulation and Structure/Systems Biology, BGRS\SB'12, Novosibirsk, Russia

    18.1. V.G. Levitsky, D.Y. Oshchepkov, G.V. Vasiliev, N.I. Ershov, T.I. Merkulova, <u>I.V. Kulakovskiy</u>, V.J. Makeev; In silico verification of ChIP-Seq data. p. 181

    18.2. N.Y. Oparina, M. Fridman, <u>I.V. Kulakovskiy</u>, V.J. Makeev; Place makes a sequence: the influence of high and low copy repeats on the origin and fate of microsatellites in vertebrate genomes. p. 224

19. (2011) July 21-24, The International Moscow Conference on Computational Molecular Biology, MCCMB'11, Moscow, Russia

    19.1. M. Fridman, N. Oparina, <u>I. Kulakovskiy</u>, V. Makeev; The role of recombination in the multiplication of Alu-associated microsatellites, p.113

    19.2. <u>I.V. Kulakovskiy</u>, A.A. Belostotsky, A.S. Kasianov, Y.A. Medvedeva, I.A. Eliseeva, V.J. Makeev; Preferred Pair Distance Templates for Analysis of Transcription Regulation Code, p.182-4

    19.3. V.J. Makeev, <u>I.V. Kulakovskiy</u>, I.S. Yevshin, T.F. Valeev; BioUML: the ChIPMunk Plugin for Motif Discovery in ChIP-Seq Data, p.212-3

    19.4. L. Uroshlev, S. Rakhmanov, <u>I. Kulakovskiy</u>, V. Makeev; GPGPU-assisted prediction of ion binding sites in proteins; p.375

20. (2011) July 15-19, 19th Annual International Conference on Intelligent Systems for Molecular Biology & 10th European Conference on Computational Biology, BioREG SIG (Bioinformatics for Regulatory Genomics), Vienna, Austria
[talk] <u>I.V. Kulakovskiy</u>, A.A. Belostotsky, A.S. Kasianov, I.A. Eliseeva, V.J. Makeev; Preferred Pair Distance Templates reveal functional transcription factor binding sites.

21. (2011) June 14-18, Albany 2011: The 17th conversation, Albany, NY, USA

    21.1. <u>I.V. Kulakovskiy</u>, Y.A. Medvedeva, V.J. Makeev; Cis-Regulatory Modules: Identification *in silico* and Understanding of Gene Regulatory Networks. *Jounal of Biomolecular Structure & Dynamics*, Volume 28, Issue #6, p.1126-7

    21.2. **[talk]** <u>I.V. Kulakovskiy</u>, A.A. Belostotsky, V.J. Makeev; Preferred Pair Distance Templates for Identification of Functional Binding Sites for Interacting Transcription Factors. *Jounal of Biomolecular Structure & Dynamics*, Volume 28, Issue #6, p.1127-8

22. (2010) September 26-29, 9th European Conference on Computational Biology, ECCB'10, Ghent, Belgium; <u>I.V. Kulakovskiy</u>, V.A. Boeva, A.V. Favorov, V.J. Makeev; Fast and accurate digging for binding motifs in ChIP-Seq data using ChIPMunk software.

23. (2010) June 20-27, The 7th International Conference on Bioinformatics of Genome Regulation and Structure\Systems Biology, BGRS\SB'10, Novosibirsk, Russia

    23.1. A.A. Belostotsky, <u>I.V. Kulakovskiy</u>, V.J. Makeev; Identification of eukaryotic transcription regulatory regions using protein-protein interaction data. p.41

    23.2. M.V. Fridman, <u>I.V. Kulakovskiy</u>, N.J. Oparina, V.J. Makeev; Frequent repeats in mammal genomes and active retroposones. p.74

    23.3. <u>I.V. Kulakovskiy</u>, V.A. Boeva, A.V. Favorov, V.J. Makeev; ChIPMunk: discovery of transcription factor binding motifs in ChIP-Seq data. p.152

    23.4. S.V. Rahmanov, <u>I.V. Kulakovskiy</u>, L.A. Uroshlev, V.J. Makeev; Local geometry of protein surface is highly optimized for hydration. p.240

    23.5. L.A. Uroshlev, <u>I.V. Kulakovskiy</u>, S.V. Rahmanov, V.M. Makeev; GPGPU-computing for prediction of small ligand binding sites in proteins. p.296

24. (2010) April 14-17, The 4th ESF Conference on Functional Genomics & Disease, Dresden, Germany

    24.1. A.A. Belostotsky, <u>I.V. Kulakovskiy</u>, V.J. Makeev; Identification of composite elements in eukaryotic transcription regulatory regions using protein-protein interaction data. *New Biotechnology*, Volume 27, Supplement 1, P1.66, S47

    24.2. <u>I.V. Kulakovskiy</u>, V.A. Boeva, A.V. Favorov, V.J. Makeev; Motif discovery for transcription factor binding sites using a priori information on potential similarity regions at different resolution scales. *New Biotechnology*, Volume 27, Supplement 1, P1.52, S41

25. (2009) July 20-23, The 4th International Moscow Conference on Computational Molecular Biology, MCCMB'09, Moscow, Russia

    25.1. R.T. Boekhorst, I. Abnizova, F. Naumenko, <u>I. V. Kulakovskiy</u>, W. Lorenz; Using SVM and a measure of motif 'surprise' to distinguish regulatory DNA. p.46-47

    25.2. **[talk]** <u>I.V. Kulakovskiy</u>, V.A. Boeva, A.V. Favorov, V.J. Makeev; ChIPMunk: a fast DNA motif finder for ChIP data and its application to data integration from different experimental sources. p.194-196

    25.3. S. Rahmanov, <u>I. V. Kulakovskiy</u>, V. Makeev; Predicting binding sites of ions in protein structures. p.305-306

26. (2008) September 29 -October 3, Information Technologies and Systems Conference, ITAS-2008, Gelendzhik, Russia; Y.A. Medvedeva, M.V. Fridman, N.J. Oparina, D.B.

Malko, E.O. Ermakova, <u>I.V. Kulakovskiy</u>, V.J. Makeev; Non-5' CpG islands in the human genome: probable involvement in transcription regulation. p.298-299

27. (2008) June 22-28, The Sixth International Conference on Bioinformatics of Genome Regulation and Structure, BGRS'2008, Novosibirsk, Russia

    27.1. A. Heinzel, <u>I.V. Kulakovskiy</u>, V.J. Makeev; Comparison of ChIP-chip Sp1 binding location data for human chromosome 21, 22 with PWM hits. p.97

    27.2. **[talk]** <u>I.V. Kulakovskiy</u>, A.V. Favorov, V.J. Makeev; Incorporating different types of experimental data on DNA-protein binding into the single in silico model. p.129

28. (2008) February 27-29 , Helmholtz Russian German Workshop on Systems Biology, Moscow, Russia; <u>I.V. Kulakovskiy</u>; Integrated tool for analysis of DNA-protein binding data. p.45

29. (2007) July 27-31, The 3-rd Moscow Conference on Computational Molecular Biology, MCCMB'07, Moscow, Russia; <u>I.V. Kulakovskiy</u>, V.J. Makeev; Constructing PWM from unaligned TFBS footprints. p.167-168

Conference abstracts [In Russian]

1. (2016) 4-8 октября, V съезд физиологов снг, V съезд биохимиков россии, конференция adflim, Сочи-Дагомыс, Россия; <u>И.В. Кулаковский</u>, И.Е. Воронцов, А.С. Ландо. В.Ю. Макеев; Полиморфизмы и соматические мутации в регуляторных сегментах днк и тканеспецифическая экспрессия генов. *Acta Naturae*, Спецвыпуск том 2, 2016, стр.116

2. (2011) 14-17 ноября, II международная научно-практическая конференция «Постгеномные методы анализа в биологии, лабораторной и клинической медицине: геномика, протеомика, биоинформатика», Новосибирск, Академгородок, Россия; Д.Ю. Ощепков, В.Г. Левицкий, И.В. Кулаковский, Н.И. Ершов, Г.В. Васильев, Т.И. Меркулова; Анализ данных массовой иммунопреципитации хроматина с помощью экспериментально верифицированных методов распознавания сайтов связывания транскрипционных факторов FoxA. Том 2, стр 187.

3. (2011) 11 мая, Официальное открытие центра коллективного пользования (ЦКП) «Биоинформатика», Новосибирск, Академгородок, Россия; <u>И.В. Кулаковский</u>, А.С. Касьянов, В.Ю. Макеев; Алгоритмические проблемы анализа данных ChIP-Seq.

4. (2009) 30 ноября, Всероссийская конференция с элементами научной школы для молодежи «Проведение научных исследований под руководством приглашенных исследователей», Москва, Россия; А.С. Касьянов, Е.Ю. Климова, А.А. Белостоцкий, <u>И.В. Кулаковский</u>, Д.Б. Малько, Д.Г. Наумов, М.В. Фридман, Е.А. Пермина, В. Ю. Макеев; Автоматическая структурной и функциональной аннотации нуклеотидных последовательностей геномов, используемых в биотехнологии, полученных с помощью секвенаторов нового поколения.

5. (2008) 11-15 мая, IV съезд Российского общества биохимиков и молекулярных биологов, Новосибирск, Академгородок, Россия; <u>И.В. Кулаковский</u>, А.А. Белостоцкий, А.В. Фаворов, В.А. Боева, Д.Б. Малько, В.Ю. Макеев; Интеграция различных типов экспериментальных данных для анализа последовательностей регуляторных районов эукариот. стр.278

6. (2007) 18-21 сентября, Информационные технологии и системы, ИтиС'07, Звенигород, Россия; А.В. Фаворов, М.С. Гельфанд, А. Герасимова, Д.А. Равчеев, <u>И.В. Кулаковский</u>, А.А. Миронов, В.Ю. Макеев; Алгоритм SeSiMCMC для поиска участков специфического связывания белков-регуляторов транскрипции. стр.334-337

Additional education

(2008) June, The BGRS'2008 Summer School "Evolution, Systems Biology and High Performance Computing Bioinformatics", Institute of Cytology and Genetics, Novosibirsk, Akademgorodok, Russia

(2007) October, short-term internship, Project ALGO, INRIA Rocquencourt, France

Software tools and web-resources

1. http://autosome.ru/ and http://opera.autosome.ru/

   Hub and web-interface for various bioinformatics software developed by our team.

2. http://hocomoco.autosome.ru/

   HOmo sapiens COmprehensive MOdel COllection (HOCOMOCO) contains transcription factor (TF) binding models obtained by careful integration of data from different sources. In the current release (v10) models for 601 human TFs are accompanied by a separate set of models for 396 mouse TFs.

3. http://autosome.ru/ChIPMunk/

   ChIPMunk is a fast heuristic DNA motif digger based on a greedy approach accompanied by subsampling. ChIPMunk identifies the strong motif with the maximum Discrete Information Content in a set of DNA sequences. diChIPMunk is a "dinucleotide offspring" of ChIPMunk and accounts for dinucleotide composition.

Awards and fellowships

(2016) Academia Europaea prize for young russian scientists

(2015) Medal "The Phenomenon of Life" in memory of V.I. Korogodin

(2015) Certificate of Merit from Russian Academy of Sciences for series of publications on transcription factors of higher eukaryotes

(2014) 1st prize at young scientists research contest, Engelhardt Institute of Molecular Biology, Moscow, Russia

(2011, 2013) Young scientists stipend of Engelhardt Institute of Molecular Biology, Moscow, Russia

(2012) Dynasty Foundation Postdoctoral fellowship, Moscow, Russia

(2012) 11th European Conference on Computational Biology travel fellowship; Basel, Switzerland

(2011) Russian Fund for Basic Research travel grant to participate in "Albany 2011: The 17th Conversation", Albany NY, USA

(2010) 9th European Conference on Computational Biology travel fellowship; Ghent, Belgium

(2010) Russian Fund for Basic Research travel grant to participate in the 4th ESF Conference on Functional Genomics and Disease, Dresden, Germany

(2008) The BGRS'2008 Summer School "Evolution, Systems Biology and High Performance Computing Bioinformatics" travel fellowship; Novosibirsk, Akademgorodok, Russia

(2004) Mytischi's award for excellent study (Mytischi, Russia)

Grants

(2015) Russian Fund for Basic Research grant 15-34-20423-mol_ved "Advanced sequence motifs to study DNA-protein recognition for regulatory genomics of

higher eukaryotes", Moscow, Russia

(2014) Russian Fund for Basic Research grant 14-04-01838_a "Regulatory interplay between transcription and translation in cell response to growth stimulus", Moscow, Russia

(2012) Russian Fund for Basic Research grant 12-04-32082-mol_a "In silico prediction of putative single-nucleotide genome variations effecting transcription in human", Moscow, Russia

Educational Activities

Invited lecture @Big data analysis in bioinformatics and applications, 2016, Moscow, Russia   http://bioinformatics2016.fbras.ru/conference/school

ChIP-Seq analysis @NGS bioinformatics course, Bioinformatics School, 2015, Moscow, Russia   http://bioinfschool.ru/ngs [In Russian]

ChIP-Seq analysis @NGS data analysis course 2014,2015, FBB MSU, Moscow, Russia   http://bioinf.fbb.msu.ru/wiki/index.php/NgsCourse [In Russian]

Guest lecture in "BIOINFORMATICS, COMPARATIVE GENOMICS AND SYSTEMS BIOLOGY" (course by Mikhail Gelfand), 2015 @Skoltech, Skolkovo, Russia

Invited lecture @Omics data analysis course 2015, @Skolkovo, Russia
http://biologica.org/omics-data-program/

Invited lecture @Bioinformatics Summer school, Moscow region, Russia
http://bioinformaticsinstitute.ru/summer2015 [In Russian]

Invited lecture @Next-generation sequencing data analysis course 2016,

Peter the Great Saint-Petersburg Polytechnic University

School of Molecular and Theoretical Biology 2012-2015 (Project of The Dynasty / Zimin Foundation), Pushchino, Russia   http://molbioschool.com/en/

Membership

(2014-2016) BIOSTEC Bioinformatics conference, Program Committee member

(2010-2016) Member of the International Society for Computational Biology (ISCB)