Kulakovskiy Ivan Vladimirovich

Publications in peer-reviewed journals

1. (2022) M. Kuiper, J. Bonello, J.T. Fernández-Breis, P. Bucher, M.E. Futschik, P. Gaudet, I.V. Kulakovskiy, L. Licata, C. Logie, R.C. Lovering, V.J. Makeev, S. Orchard, S. Panni, L. Perfetto, D. Sant, S. Schulz, S. Vercruysse, D.R. Zerbino, A. Lægreid. The gene regulation knowledge commons: the action area of GREEKC. *BBA - Gene Regulatory Mechanisms*, 1865(1):194768, doi:10.1016/j.bbagrm.2021.194768
2. (2022) V.V. Smirnova, E.D. Shestakova, D.S. Nogina, P.A. Mishchenko, T.A. Prikazchikova, T.S. Zatsepin, I.V. Kulakovskiy, I.N. Shatsky, I.M. Terenin. Ribosomal leaky scanning through a translated uORF requires eIF4G2. *Nucleic Acids Research*, gkab1286, doi:10.1093/nar/gkab1286
3. (2021) A.S. Ershova, I.A. Eliseeva, O.S. Nikonov, A.D. Fedorova, I.E. Vorontsov, D. Papatsenko, I.V. Kulakovskiy. Enhanced C/EBP binding to G·T mismatches facilitates fixation of CpG mutations in cancer and adult stem cells. *Cell Reports*, 35(10):109221, doi:10.1016/j.celrep.2021.109221
4. (2021) S.Abramov, A. Boytsov, D. Bykova, D.D. Penzar, I. Yevshin, S.K. Kolmykov, M.V. Fridman, A.V. Favorov, I.E. Vorontsov, E. Baulin, F. Kolpakov, V.J. Makeev, I.V. Kulakovskiy. Landscape of allele-specific transcription factor binding in the human genome. *Nature Communications*, 12:2751, doi:10.1038/s41467-021-23007-0
5. (2021) R.C. Lovering, P. Gaudet, M.L. Acencio, A. Ignatchenko, A. Jolma, O. Fornes, M. Kuiper, I.V. Kulakovskiy, A. Lægreid, M.J. Martin, C. Logie. A GO catalogue of human DNA-binding transcription factors. *BBA - Gene Regulatory Mechanisms*, 1864(11-12):194765, doi:10.1016/j.bbagrm.2021.194765
6. (2021) A.A. Shalybkova, D.S. Mikhailova, I.V. Kulakovskiy, L.I. Fakhranurova, E.F. Baulin. Annotation of the local context of the RNA secondary structure improves the classification and prediction of A-minors. *RNA*, 27:907-919, doi:10.1261/rna.078535.120
7. (2021) A.A. Egorov, D.S. Makeeva, N.E. Makarova, D.A. Bykov, Y.S. Hrytseniuk, O.V. Mitkevich, V.N. Urakov, A.I. Alexandrov, I.V. Kulakovskiy, S.E. Dmitriev. Ribo-Seq and RNA-Seq of TMA46 (DFRP1) and GIR2 (DFRP2) knockout yeast strains. *F1000Res*, 10:1162, doi:10.12688/f1000research.74727.1
8. (2021) A.A. Egorov, A.I. Alexandrov, V.N. Urakov, D.S. Makeeva, R.O. Edakin, A.S. Kushchenko, V.N. Gladyshev, I.V. Kulakovskiy, S.E. Dmitriev. A standard knockout procedure alters expression of adjacent loci at the translational level. *Nucleic Acids Research*, 49(19):11134-11144, doi:10.1093/nar/gkab872
9. (2021) A. Tomashevsky, E. Kulakovskaya, L. Trilisenko, I.V. Kulakovskiy, T. Kulakovskaya, A. Fedorov, M. Eldarov. VTC4 Polyphosphate Polymerase Knockout Increases Stress Resistance of Saccharomyces cerevisiae Cells. *Biology*, 10(6):487, 10.3390/biology10060487
10. (2021) S. Kolmykov, I. Yevshin, M. Kulyashov, R. Sharipov, Y. Kondrakhin, V.J. Makeev, I.V. Kulakovskiy, A. Kel, F. Kolpakov. GTRD: an integrated view of

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11. (2020) J.A. Ramilowski, C.W. Yip, S. Agrawal, J.-C. Chang, Y. Ciani, I.V. Kulakovskiy *et al*. Functional annotation of human long noncoding RNAs via molecular phenotyping. *Genome Res*, 30:1060-1072, doi:10.1101/gr.254219.119
12. (2020) G. Ambrosini, I. Vorontsov, D. Penzar, R. Groux, O. Fornes, D.D. Nikolaeva, B. Ballester, J. Grau, I. Grosse, V. Makeev, I. Kulakovskiy, P. Bucher. Insights gained from a comprehensive all-against-all transcription factor binding motif benchmarking study. *Genome Biol*, 21:114, doi:10.1186/s13059-020-01996-3
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15. (2020) D.N. Lyabin, I.A. Eliseeva, E.A. Smolin, A.N. Doronin, K.S. Budkina, I.V. Kulakovskiy, L.P. Ovchinnikov. YB-3 substitutes YB-1 in global mRNA binding. *RNA Biology*, 17(4), 487-499, doi:10.1080/15476286.2019.1710050
16. (2020) K.V. Korneev, E.N. Sviriaeva, N.A.Mitkin, A.M. Gorbacheva, A.N. Uvarova, A.S. Ustiugova, O.L. Polanovsky, I.V. Kulakovskiy, M.A. Afanasyeva, A.M. Schwartz, D.V. Kuprash. Minor C allele of the SNP rs7873784 associated with rheumatoid arthritis and type-2 diabetes mellitus binds PU.1 and enhances TLR4 expression. *Biochimica et Biophysica Acta (BBA) - Molecular Basis of Disease*, 1866(3):165626, doi:10.1016/j.bbadis.2019.165626
17. (2019) D.D. Penzar, A.O. Zinkevich, I.E. Vorontsov, V.V. Sitnik, A.V. Favorov, V.J. Makeev, I.V. Kulakovskiy. What Do Neighbors Tell About You: The Local Context of Cis-Regulatory Modules Complicates Prediction of Regulatory Variants. *Frontiers in Genetics*, 10:1078, doi:10.3389/fgene.2019.01078
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25. (2018) I.E. Vorontsov, A.D. Fedorova, I.S. Yevshin, R.N. Sharipov, F.A. Kolpakov, V.J. Makeev, I.V. Kulakovskiy; Genome-wide map of human and mouse transcription factor binding sites aggregated from ChIP-Seq data. *BMC Research Notes*, 11(1): 756, doi:10.1186/s13104-018-3856-x

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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

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Book chapters

1. (2021) I.E. Vorontsov, A.A. Egorov, A.S. Anisimova, I.A. Eliseeva, V.J. Makeev, V.N. Gladyshev, S.E. Dmitriev, I.V. Kulakovskiy. Assessing Ribosome Distribution Along Transcripts with Polarity Scores and Regression Slope Estimates. *Methods in Molecular Biology* (Clifton, NJ), 2252, 269-294, doi:10.1007/978-1-0716-1150-0_13. Chapter in *Ribosome Profiling* (Methods and Protocols), edited by Vyacheslav M. Labunskyy, Humana (New York, NY), ISBN 978-1-0716-1152-4 / 978-1-0716-1150-0, doi:10.1007/978-1-0716-1150-0
2. (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 T. Kulakovskaya, E. Pavlov, Dedkova E.N., Springer International Publishing, 15-33. ISBN 978-3-319-41073-9, doi:10.1007/978-3-319-41073-9

3. (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
4. (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 (Elsevier Inc), 135-171. ISBN 978-0-12-411637-5

Invited talks

1. (2021) [In Russian] April 8, QIAGEN Day 2021, Moscow, Russia; Regulatory sequence variants as genetic determinants of disease: meta-analysis of allele-specific transcription factor binding.
2. (2020) [In Russian] December 10, Bioinformatics Seminar @ITMO, St. Petersburg, Russia; Landscape of allele-specific transcription factor binding.
3. (2017) [In Russian] April 17-21, 21 International Young Scientists Conference "Biology – science of the 21st century", Pushchino, Russia; **[plenary talk]** Nucleotide-level genetic code of non-coding sequences: analysis of sequence patterns in regulatory regions.
4. (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.
5. (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]** Is there a nucleotide-level genetic code for gene expression control?
6. (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.
7. (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.
8. (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.
9. (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.
10. (2010) November 8-10, LIX Bioinformatics Colloquium, Paris, France; Deep and

wide digging for binding motifs in ChIP-Seq data.

11. (2010) June 15-17, Bioinformatics after Next Generation Sequencing, Zvenigorod, Russia; ChIPMunk: digging for transcription factor binding motifs in ChIP-Seq data.
12. (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. (2021) July 30-August 2, MCCMB 2021: Moscow Conference on Computational Molecular Biology, Moscow, Russia; **[talk]** Peeking inside the clockworks of regulatory single-nucleotide variants with ADASTRA and ANANASTRA.
2. (2020) July 6-10, BGRS/SB-2020: 12th International Multiconference "Bioinformatics of Genome Regulation and Structure/Systems Biology", Section "Genomics, transcriptomics and bioinformatics", Novosibirsk, Russia; **[talk]** S. Abramov, E. Baulin, V.J. Makeev, A. Boytsov, I. Yevshin, I. Kulakovskiy, D. Bykova, F. Kolpakov; AD ASTRA: the database of Allelic Dosage-corrected Allele-Specific TRAnscription factor binding suggests causal regulatory sequence variants of pathologies. p. 2, doi:10.18699/BGRS/SB-2020-001
3. (2019) March 19-20, GREEKC 'The nucleotide sequence recognition level' Workshop, Lausanne, Switzerland; **[talk]** I.V. Kulakovskiy; TF specificity models: GRECO TFBS models open benchmarking initiative.
4. (2018) February 12-14, GREEKC 'Representing and Assessing Transcription Factor Binding Specificity (RATFBS)' Workshop, Ljubljana, Slovenia; **[talk]** I.V. Kulakovskiy; Renovating transcription factor binding consensus statements by merging up-to-date binding profiles.
5. (2017) October 23-24, GREEKC Lisbon Workshop, Lisbon, Portugal; **[talk]** I.V. Kulakovskiy; Sequence motifs: tilting bricks of the yellow brick road to gene regulation knowledge.
6. (2017) August 31-September 1, FANTOM6 First General Meeting "Natsu", RIKEN Yokohama, Japan; **[talk]** I.V.Kulakovskiy; Systematic ChIP-Seq-based cistrome and motif analysis to unravel transcriptional control of lncRNA-KD response.
7. (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.
8. (2016) September 3-7, 15th European Conference on Computational Biology, ECCB 2016, The Hague, Netherlands
    8.1. I.A. Eliseeva, I.E. Vorontsov, I.V. Kulakovskiy; Can transcription determine mRNA translation in mammals? Digging evidence with sequence analysis.
    8.2. I.V. Kulakovskiy, 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.

9. (2016) August 29-September 2, 10th anniversary International Multiconference "Bioinformatics of Genome Regulation and Structure\Systems Biology" (BGRS\SB-2016), Novosibirsk, Russia

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

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

10. (2016) June 14-16, SocBiN Bioinformatics 2016, Moscow, Russia

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

   10.2. 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

   10.3. 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

11. (2015) July 16-19, Moscow Conference on Computational Molecular Biology (MCCMB'15); **[talk]** I.E. Vorontsov, I.V. Kulakovskiy, G.N. Khimulya, D.D. Nikolaeva, V.J. Makeev; Selection pressure on breast cancer somatic mutations revealed by bioinformatics sequence analysis.

12. (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, I.V. Kulakovskiy, G. Khimulya, D. Nikolaeva, V.J. Makeev; Sequence analysis of regulatory variants reveals selection pressure on somatic mutations in breast cancer.

13. (2015) January 12-15, 6th International Conference on Bioinformatics Models, Methods and Algorithms, BIOINFORMATICS 2015, Lisbon, Portugal; I.E. Vorontsov, I.V. Kulakovskiy, 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

14. (2014) June 23-28, The ninth international conference on bioinformatics of genome regulation and structure\systems biology, BGRS\SB-2014, Novosibirsk, Russia

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

   14.2. D.Y. Oshchepkov, V.G. Levitsky, I.V. Kulakovskiy, 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

15. (2014) March 27-28, Integrative and Computational Biology, V IMPPC Annual Conference and 4DCellFate Workshop, Barcelona, Spain

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

    15.2. I.E. Vorontsov, I.V. Kulakovskiy, V.J. Makeev; Large non-redundant collection of binding motifs for human transcription factors.

    15.3. Y.A. Medvedeva, A. Khamis, I.V. Kulakovskiy, 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.

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

16. (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

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

    16.2. I. Vorontsov, I. Kulakovskiy, V. Makeev; Jaccard Index to Compare Position Weight Matrices of Transcription Factor Binding Sites.

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

17. (2013) July 25-28, Moscow Conference on Computational Molecular Biology, MCCMB'13, Moscow, Russia; **[talk]** I.V. Kulakovskiy, V.G. Levitsky, D.G. Oshchepkov, I.E. Vorontsov, V.J. Makeev; From ChIP-Seq data to improved transcription factor binding sites models.

18. (2013) July 6-11, 38th FEBS Congress, Saint Petersburg, Russia; M. Fridman, I. Kulakovskiy, D. Lvovs, N. Oparina, V. Makeev; Distribution of tandem repeats in human genome. *FEBS Journal*, Volume 20 Supplement 1, p. 20

19. (2013) February 11-14, 4th International Conference on Bioinformatics Models, Methods and Algorithms, BIOINFORMATICS 2013, Barcelona, Spain; **[talk]** I.V. Kulakovskiy, 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

20. (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, I.V. Kulakovskiy, V.J. Makeev; Comparing DNA motifs specifically recognized by transcription factors.

21. (2012) October 29 - November 2, FANTOM5 Timecourses meeting, Workshop: Motifs

and composite elements for time-courses, RIKEN Yokohama Institute, Tsurumi, Japan

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

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

22. (2012) September 9-12, 11th European Conference on Computational Biology, ECCB'12, Basel, Switzerland; I.V. Kulakovskiy, 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).

23. (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, I.V. Kulakovskiy, V.J. Makeev; In silico verification of TFBS in ChIP-Seq data. p. 43

24. (2012) June 25–29, The Eighth International Conference on Bioinformatics of Genome Regulation and Structure/Systems Biology, BGRS\SB’12, Novosibirsk, Russia

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

24.2. N.Y. Oparina, M. Fridman, I.V. Kulakovskiy, 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

25. (2011) July 21-24, The International Moscow Conference on Computational Molecular Biology, MCCMB'11, Moscow, Russia

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

25.2. I.V. Kulakovskiy, 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

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

25.4. L. Uroshlev, S. Rakhmanov, I. Kulakovskiy, V. Makeev; GPGPU-assisted prediction of ion binding sites in proteins; p.375

26. (2011) July 15-19, 19th Annual International Conference on Intelligent Systems for Molecular Biology & 10th European Conference on Computational Biology, ISMB/ECCB 2011, Vienna, Austria **[talk** @BioREG SIG, Bioinformatics for Regulatory Genomics Special Interest Group**]** I.V. Kulakovskiy, A.A. Belostotsky, A.S. Kasianov, I.A. Eliseeva, V.J. Makeev; Preferred Pair Distance Templates reveal functional transcription factor binding sites.

27. (2011) June 14-18, Albany 2011: The 17th conversation, Albany, NY, USA

27.1. I.V. Kulakovskiy, 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

27.2. **[talk]** I.V. Kulakovskiy, 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

28. (2010) September 26-29, 9th European Conference on Computational Biology, ECCB'10, Ghent, Belgium; I.V. Kulakovskiy, V.A. Boeva, A.V. Favorov, V.J. Makeev; Fast and accurate digging for binding motifs in ChIP-Seq data using ChIPMunk software.

29. (2010) June 20-27, The 7th International Conference on Bioinformatics of Genome Regulation and Structure\Systems Biology, BGRS\SB'10, Novosibirsk, Russia

29.1. A.A. Belostotsky, I.V. Kulakovskiy, V.J. Makeev; Identification of eukaryotic transcription regulatory regions using protein-protein interaction data. p.41

29.2. M.V. Fridman, I.V. Kulakovskiy, N.J. Oparina, V.J. Makeev; Frequent repeats in mammal genomes and active retroposones. p.74

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

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

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

30. (2010) April 14-17, The 4th ESF Conference on Functional Genomics & Disease, Dresden, Germany

30.1. A.A. Belostotsky, I.V. Kulakovskiy, 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

30.2. I.V. Kulakovskiy, 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

31. (2009) July 20-23, The 4th International Moscow Conference on Computational Molecular Biology, MCCMB'09, Moscow, Russia

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

31.2. **[talk]** I.V. Kulakovskiy, 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

31.3. S. Rahmanov, I. V. Kulakovskiy, V. Makeev; Predicting binding sites of ions in protein structures. p.305-306

32. (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, I.V. Kulakovskiy, V.J. Makeev; Non-5' CpG islands in the human genome: probable involvement in transcription regulation. p.298-299

33. (2008) June 22-28, The Sixth International Conference on Bioinformatics of Genome Regulation and Structure, BGRS'2008, Novosibirsk, Russia

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

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

34. (2008) February 27-29 , Helmholtz Russian German Workshop on Systems Biology, Moscow, Russia; I.V. Kulakovskiy; Integrated tool for analysis of DNA-protein binding data. p.45

35. (2007) July 27-31, The 3-rd Moscow Conference on Computational Molecular Biology, MCCMB'07, Moscow, Russia; I.V. Kulakovskiy, V.J. Makeev; Constructing PWM from unaligned TFBS footprints. p.167-168