

# Fedor A Kolpakov

## List of Publications by Year in descending order

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Version: 2024-02-01

41  
papers

4,513  
citations

516710

16  
h-index

330143

37  
g-index

44  
all docs

44  
docs citations

44  
times ranked

8034  
citing authors

#	ARTICLE	IF	CITATIONS
1	Modular Representation of Physiologically Based Pharmacokinetic Models: Nanoparticle Delivery to Solid Tumors in Mice as an Example. <i>Mathematics</i> , 2022, 10, 1176.	2.2	1
2	BioUML – towards a universal research platform. <i>Nucleic Acids Research</i> , 2022, 50, W124-W131.	14.5	10
3	ANANASTRA: annotation and enrichment analysis of allele-specific transcription factor binding at SNPs. <i>Nucleic Acids Research</i> , 2022, 50, W51-W56.	14.5	7
4	Multicompartmental Mathematical Model of SARS-CoV-2 Distribution in Human Organs and Their Treatment. <i>Mathematics</i> , 2022, 10, 1925.	2.2	5
5	GTRD: an integrated view of transcription regulation. <i>Nucleic Acids Research</i> , 2021, 49, D104-D111.	14.5	137
6	Landscape of allele-specific transcription factor binding in the human genome. <i>Nature Communications</i> , 2021, 12, 2751.	12.8	55
7	Genome-Wide Atlas of Promoter Expression Reveals Contribution of Transcribed Regulatory Elements to Genetic Control of Disuse-Mediated Atrophy of Skeletal Muscle. <i>Biology</i> , 2021, 10, 557.	2.8	2
8	A Modular Mathematical Model of Exercise-Induced Changes in Metabolism, Signaling, and Gene Expression in Human Skeletal Muscle. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10353.	4.1	8
9	Thoroughly Calibrated Modular Agent-Based Model of the Human Cardiovascular and Renal Systems for Blood Pressure Regulation in Health and Disease. <i>Frontiers in Physiology</i> , 2021, 12, 746300.	2.8	6
10	Advanced data curation in GTRD database: hierarchical dictionaries of cell types and experimental factors. , 2020, , .		0
11	Meta-analysis of ChIP-seq Datasets Through the Rank Aggregation Approach. , 2020, , .		1
12	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , 2020, 16, e9110.	7.2	178
13	Assessment of transcriptional importance of cell line-specific features based on GTRD and FANTOM5 data. <i>PLoS ONE</i> , 2020, 15, e0243332.	2.5	0
14	BioUML: an integrated environment for systems biology and collaborative analysis of biomedical data. <i>Nucleic Acids Research</i> , 2019, 47, W225-W233.	14.5	32
15	Walking pathways with positive feedback loops reveal DNA methylation biomarkers of colorectal cancer. <i>BMC Bioinformatics</i> , 2019, 20, 119.	2.6	37
16	Population size estimation for quality control of ChIP-Seq datasets. <i>PLoS ONE</i> , 2019, 14, e0221760.	2.5	4
17	GTRD: a database on gene transcription regulation – 2019 update. <i>Nucleic Acids Research</i> , 2019, 47, D100-D105.	14.5	181
18	HOCOMOCO: towards a complete collection of transcription factor binding models for human and mouse via large-scale ChIP-Seq analysis. <i>Nucleic Acids Research</i> , 2018, 46, D252-D259.	14.5	660

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19	Computational master-regulator search reveals mTOR and PI3K pathways responsible for low sensitivity of NCI-H292 and A427 lung cancer cell lines to cytotoxic action of p53 activator Nutlin-3. BMC Medical Genomics, 2018, 11, 12.	1.5	11
20	Genome-wide map of human and mouse transcription factor binding sites aggregated from CHIP-Seq data. BMC Research Notes, 2018, 11, 756.	1.4	19
21	GTRD: a database of transcription factor binding sites identified by CHIP-seq experiments. Nucleic Acids Research, 2017, 45, D61-D67.	14.5	206
22	Prediction of protein-DNA interactions of transcription factors linking proteomics and transcriptomics data. EuPA Open Proteomics, 2016, 13, 14-23.	2.5	4
23	HOCOMOCO: expansion and enhancement of the collection of transcription factor binding sites models. Nucleic Acids Research, 2016, 44, D116-D125.	14.5	215
24	Patient-specific 1D model of the human cardiovascular system. , 2015, , .		1
25	Transcriptome Characteristics and X-Chromosome Inactivation Status in Cultured Rat Pluripotent Stem Cells. Stem Cells and Development, 2015, 24, 2912-2924.	2.1	18
26	BioUML: plugin for population-based modeling. Virtual Biology, 2014, 1, 7.	0.2	2
27	Toolkit for CHIP-Seq based comparative analysis of the PWM methods for prediction of transcription factor binding sites. Virtual Biology, 2014, 1, 19.	0.2	0
28	Model composition through model reduction: a combined model of CD95 and NF- $\kappa$ B signaling pathways. BMC Systems Biology, 2013, 7, 13.	3.0	17
29	MicroRNA Expression Profile in Human Macrophages in Response to Leishmania major Infection. PLoS Neglected Tropical Diseases, 2013, 7, e2478.	3.0	125
30	BioUML plug-in for nonlinear parameter estimation using multiple experimental data. Virtual Biology, 2013, 1, 47.	0.2	2
31	BioUML Genome Browser. Virtual Biology, 2013, 1, 15.	0.2	5
32	Modular Modeling of Biological Systems. Virtual Biology, 2013, 1, 30.	0.2	2
33	A Modular Model of the Apoptosis Machinery. Advances in Experimental Medicine and Biology, 2012, 736, 235-245.	1.6	12
34	Prediction of nonsmall cell lung cancer sensitivity to cisplatin and paclitaxel based on marker gene expression. Molecular Biology, 2011, 45, 600-607.	1.3	2
35	Reproducible computational biology experiments with SED-ML - The Simulation Experiment Description Markup Language. BMC Systems Biology, 2011, 5, 198.	3.0	211
36	The Systems Biology Graphical Notation. Nature Biotechnology, 2009, 27, 735-741.	17.5	828

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37	CYCLONET—an integrated database on cell cycle regulation and carcinogenesis. Nucleic Acids Research, 2007, 35, D550-D556.	14.5	16
38	Transcription Regulatory Regions Database (TRRD): its status in 2000. Nucleic Acids Research, 2000, 28, 298-301.	14.5	47
39	Transcription Regulatory Regions Database (TRRD): its status in 1999. Nucleic Acids Research, 1999, 27, 303-306.	14.5	27
40	Databases on transcriptional regulation: TRANSFAC, TRRD and COMPEL. Nucleic Acids Research, 1998, 26, 362-367.	14.5	1,345
41	GeneNet: a gene network database and its automated visualization. Bioinformatics, 1998, 14, 529-537.	4.1	65