Olga A Tarasova

List of Publications by Year in Descending Order

27 papers	278 citations	10 h-index	16 g-index
34 ext. papers	383 ext. citations	4.1 avg, IF	3.35 L-index

#	Paper	IF	Citations
27	Spectrum of Atazanavir-Selected Protease Inhibitor-Resistance Mutations. *Pathogens*, **2022**, 11, 546	4.5	0
26	Machine Learning Methods in Antiviral Drug Discovery. *Topics in Medicinal Chemistry*, **2021**, 245-279	0.4	0
25	Extraction of Data on Parent Compounds and Their Metabolites from Texts of Scientific Abstracts. *Journal of Chemical Information and Modeling*, **2021**, 61, 1683-1690	6.1	0
24	RHIVDB: A Freely Accessible Database of HIV Amino Acid Sequences and Clinical Data of Infected Patients. *Frontiers in Genetics*, **2021**, 12, 679029	4.5	2
23	A computational analysis of transcriptional profiles from CD8(+) T lymphocytes reveals potential mechanisms of HIV/AIDS control and progression. *Computational and Structural Biotechnology Journal*, **2021**, 19, 2447-2459	6.8	0
22	Network-Based Analysis of OMICs Data to Understand the HIV-Host Interaction. *Frontiers in Microbiology*, **2020**, 11, 1314	5.7	8
21	Data and Text Mining Help Identify Key Proteins Involved in the Molecular Mechanisms Shared by SARS-CoV-2 and HIV-1. *Molecules*, **2020**, 25,	4.8	6
20	A Computational Approach for the Prediction of Treatment History and the Effectiveness or Failure of Antiretroviral Therapy. *International Journal of Molecular Sciences*, **2020**, 21,	6.3	6
19	Automatic Recognition of Chemical Entity Mentions in Texts of Scientific Publications. *Automatic Documentation and Mathematical Linguistics*, **2020**, 54, 306-315	0.6	
18	Automated Extraction of Information From Texts of Scientific Publications: Insights Into HIV Treatment Strategies. *Frontiers in Genetics*, **2020**, 11, 618862	4.5	0
17	Data Mining Approach for Extraction of Useful Information About Biologically Active Compounds from Publications. *Journal of Chemical Information and Modeling*, **2019**, 59, 3635-3644	6.1	8
16	HIV Resistance Prediction to Reverse Transcriptase Inhibitors: Focus on Open Data. *Molecules*, **2018** , 23,	4.8	9
15	Molecular Docking Studies of HIV-1 Resistance to Reverse Transcriptase Inhibitors: Mini-Review. *Molecules*, **2018**, 23,	4.8	15
14	A Computational Approach for the Prediction of HIV Resistance Based on Amino Acid and Nucleotide Descriptors. *Molecules*, **2018**, 23,	4.8	12
13	PASS-based approach to predict HIV-1 reverse transcriptase resistance. *Journal of Bioinformatics and Computational Biology*, **2017**, 15, 1650040	1	7
12	QNA-Based Prediction of Sites of Metabolism. *Molecules*, **2017**, 22,	4.8	5
11	Computational platform Way2Drug: from the prediction of biological activity to drug repurposing. *Russian Chemical Bulletin*, **2017**, 66, 1832-1841	1.7	21

List of Publications

10	Integral estimation of xenobiotics□toxicity with regard to their metabolism in human organism. *Pure and Applied Chemistry*, **2017**, 89, 1449-1458	2.1	7
9	Computer-aided prediction of xenobiotic metabolism in the human body. *Russian Chemical Reviews*, **2016**, 85, 854-879	6.8	17
8	Novel HIV-1 Integrase Inhibitor Development by Virtual Screening Based on QSAR Models. *Current Topics in Medicinal Chemistry*, **2016**, 16, 441-8	3	11
7	Synthesis and chemoinformatics analysis of N-aryl-□alanine derivatives. *Research on Chemical Intermediates*, **2015**, 41, 7517-7540	2.8	11
6	QSAR Modeling Using Large-Scale Databases: Case Study for HIV-1 Reverse Transcriptase Inhibitors. *Journal of Chemical Information and Modeling*, **2015**, 55, 1388-99	6.1	26
5	Virtual Screening for Potential Substances for the Prophylaxis of HIV Infection in Libraries of Commercially Available Organic Compounds. *Pharmaceutical Chemistry Journal*, **2013**, 47, 343-360	0.9	3
4	Fragment-based design, docking, synthesis, biological evaluation and structure-activity relationships of 2-benzo/benzisothiazolimino-5-aryliden-4-thiazolidinones as cycloxygenase/lipoxygenase inhibitors. *European Journal of Medicinal Chemistry*, **2012**, 47, 111-24	6.8	61
3	Fragment-based lead design. *Russian Chemical Reviews*, **2012**, 81, 158-174	6.8	16
2	In silico fragment-based drug design using a PASS approach. *SAR and QSAR in Environmental Research*, **2012**, 23, 279-96	3.5	4
1	Computer-aided prediction of QT-prolongation. *SAR and QSAR in Environmental Research*, **2008**, 19, 81-90	3.5	17