

Olga A Tarasova

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Fragment-based design, docking, synthesis, biological evaluation and structure-activity relationships of 2-benzo/benzisothiazolimino-5-arylidene-4-thiazolidinones as cyclooxygenase/lipoxygenase inhibitors. <i>European Journal of Medicinal Chemistry</i> , 2012 , 47, 111-24	6.8	61
26	QSAR Modeling Using Large-Scale Databases: Case Study for HIV-1 Reverse Transcriptase Inhibitors. <i>Journal of Chemical Information and Modeling</i> , 2015 , 55, 1388-99	6.1	26
25	Computational platform Way2Drug: from the prediction of biological activity to drug repurposing. <i>Russian Chemical Bulletin</i> , 2017 , 66, 1832-1841	1.7	21
24	Computer-aided prediction of xenobiotic metabolism in the human body. <i>Russian Chemical Reviews</i> , 2016 , 85, 854-879	6.8	17
23	Computer-aided prediction of QT-prolongation. <i>SAR and QSAR in Environmental Research</i> , 2008 , 19, 81-90	9.5	17
22	Fragment-based lead design. <i>Russian Chemical Reviews</i> , 2012 , 81, 158-174	6.8	16
21	Molecular Docking Studies of HIV-1 Resistance to Reverse Transcriptase Inhibitors: Mini-Review. <i>Molecules</i> , 2018 , 23,	4.8	15
20	A Computational Approach for the Prediction of HIV Resistance Based on Amino Acid and Nucleotide Descriptors. <i>Molecules</i> , 2018 , 23,	4.8	12
19	Synthesis and chemoinformatics analysis of N-aryl-β-alanine derivatives. <i>Research on Chemical Intermediates</i> , 2015 , 41, 7517-7540	2.8	11
18	Novel HIV-1 Integrase Inhibitor Development by Virtual Screening Based on QSAR Models. <i>Current Topics in Medicinal Chemistry</i> , 2016 , 16, 441-8	3	11
17	HIV Resistance Prediction to Reverse Transcriptase Inhibitors: Focus on Open Data. <i>Molecules</i> , 2018 , 23,	4.8	9
16	Data Mining Approach for Extraction of Useful Information About Biologically Active Compounds from Publications. <i>Journal of Chemical Information and Modeling</i> , 2019 , 59, 3635-3644	6.1	8
15	Network-Based Analysis of OMICs Data to Understand the HIV-Host Interaction. <i>Frontiers in Microbiology</i> , 2020 , 11, 1314	5.7	8
14	PASS-based approach to predict HIV-1 reverse transcriptase resistance. <i>Journal of Bioinformatics and Computational Biology</i> , 2017 , 15, 1650040	1	7
13	Integral estimation of xenobiotics toxicity with regard to their metabolism in human organism. <i>Pure and Applied Chemistry</i> , 2017 , 89, 1449-1458	2.1	7
12	Data and Text Mining Help Identify Key Proteins Involved in the Molecular Mechanisms Shared by SARS-CoV-2 and HIV-1. <i>Molecules</i> , 2020 , 25,	4.8	6
11	A Computational Approach for the Prediction of Treatment History and the Effectiveness or Failure of Antiretroviral Therapy. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	6

10	QNA-Based Prediction of Sites of Metabolism. <i>Molecules</i> , 2017 , 22,	4.8	5
9	In silico fragment-based drug design using a PASS approach. <i>SAR and QSAR in Environmental Research</i> , 2012 , 23, 279-96	3.5	4
8	Virtual Screening for Potential Substances for the Prophylaxis of HIV Infection in Libraries of Commercially Available Organic Compounds. <i>Pharmaceutical Chemistry Journal</i> , 2013 , 47, 343-360	0.9	3
7	RHIVDB: A Freely Accessible Database of HIV Amino Acid Sequences and Clinical Data of Infected Patients. <i>Frontiers in Genetics</i> , 2021 , 12, 679029	4.5	2
6	Machine Learning Methods in Antiviral Drug Discovery. <i>Topics in Medicinal Chemistry</i> , 2021 , 245-279	0.4	0
5	Automated Extraction of Information From Texts of Scientific Publications: Insights Into HIV Treatment Strategies. <i>Frontiers in Genetics</i> , 2020 , 11, 618862	4.5	0
4	Extraction of Data on Parent Compounds and Their Metabolites from Texts of Scientific Abstracts. <i>Journal of Chemical Information and Modeling</i> , 2021 , 61, 1683-1690	6.1	0
3	A computational analysis of transcriptional profiles from CD8(+) T lymphocytes reveals potential mechanisms of HIV/AIDS control and progression. <i>Computational and Structural Biotechnology Journal</i> , 2021 , 19, 2447-2459	6.8	0
2	Spectrum of Atazanavir-Selected Protease Inhibitor-Resistance Mutations. <i>Pathogens</i> , 2022 , 11, 546	4.5	0
1	Automatic Recognition of Chemical Entity Mentions in Texts of Scientific Publications. <i>Automatic Documentation and Mathematical Linguistics</i> , 2020 , 54, 306-315	0.6	