Olga A Tarasova

List of Publications by Year in descending order

28	484	686830 13	713013 21
papers	citations	h-index	g-index

34	34	34	557
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Fragment-based design, docking, synthesis, biological evaluation and structureâ€“activity relationships of 2-benzo/benzisothiazolimino-5-aryliden-4-thiazolidinones as cycloxygenase/lipoxygenase inhibitors. European Journal of Medicinal Chemistry, 2012, 47, 111-124.	2.6	72
2	Computational platform Way2Drug: from the prediction of biological activity to drug repurposing. Russian Chemical Bulletin, 2017, 66, 1832-1841.	0.4	60
3	Molecular Docking Studies of HIV-1 Resistance to Reverse Transcriptase Inhibitors: Mini-Review. Molecules, 2018, 23, 1233.	1.7	37
4	QSAR Modeling Using Large-Scale Databases: Case Study for HIV-1 Reverse Transcriptase Inhibitors. Journal of Chemical Information and Modeling, 2015, 55, 1388-1399.	2.5	34
5	Computer-aided prediction of QT-prolongation. SAR and QSAR in Environmental Research, 2008, 19, 81-90.	1.0	27
6	A Computational Approach for the Prediction of HIV Resistance Based on Amino Acid and Nucleotide Descriptors. Molecules, 2018, 23, 2751.	1.7	25
7	Computer-aided prediction of xenobiotic metabolism in the human body. Russian Chemical Reviews, 2016, 85, 854-879.	2.5	22
8	Fragment-based lead design. Russian Chemical Reviews, 2012, 81, 158-174.	2.5	19
9	Synthesis and chemoinformatics analysis of N-aryl-Î²-alanine derivatives. Research on Chemical Intermediates, 2015, 41, 7517-7540.	1.3	18
10	HIV Resistance Prediction to Reverse Transcriptase Inhibitors: Focus on Open Data. Molecules, 2018, 23, 956.	1.7	18
11	Data Mining Approach for Extraction of Useful Information About Biologically Active Compounds from Publications. Journal of Chemical Information and Modeling, 2019, 59, 3635-3644.	2.5	16
12	PASS-based approach to predict HIV-1 reverse transcriptase resistance. Journal of Bioinformatics and Computational Biology, 2017, 15, 1650040.	0.3	15
13	Novel HIV-1 Integrase Inhibitor Development by Virtual Screening Based on QSAR Models. Current Topics in Medicinal Chemistry, 2015, 16, 441-448.	1.0	14
14	Network-Based Analysis of OMICs Data to Understand the HIVâ€“Host Interaction. Frontiers in Microbiology, 2020, 11, 1314.	1.5	14
15	A Computational Approach for the Prediction of Treatment History and the Effectiveness or Failure of Antiretroviral Therapy. International Journal of Molecular Sciences, 2020, 21, 748.	1.8	13
16	Data and Text Mining Help Identify Key Proteins Involved in the Molecular Mechanisms Shared by SARS-CoV-2 and HIV-1. Molecules, 2020, 25, 2944.	1.7	12
17	QNA-Based Prediction of Sites of Metabolism. Molecules, 2017, 22, 2123.	1.7	8
18	Integral estimation of xenobioticsâ€™ toxicity with regard to their metabolism in human organism. Pure and Applied Chemistry, 2017, 89, 1449-1458.	0.9	8

#	Article	IF	Citations
19	In Silico fragment-based drug design using a PASS approach. SAR and QSAR in Environmental Research, 2012, 23, 279-296.	1.0	7
20	Extraction of Data on Parent Compounds and Their Metabolites from Texts of Scientific Abstracts. Journal of Chemical Information and Modeling, 2021, 61, 1683-1690.	2.5	7
21	HIV-1 drug resistance profiling using amino acid sequence space cartography. Bioinformatics, 2022, 38, 2307-2314.	1.8	5
22	Automated Extraction of Information From Texts of Scientific Publications: Insights Into HIV Treatment Strategies. Frontiers in Genetics, 2020, 11, 618862.	1.1	4
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.	1.9	4
24	Machine Learning in Discovery of New Antivirals and Optimization of Viral Infections Therapy. Current Medicinal Chemistry, 2021, 28, .	1.2	4
25	RHIVDB: A Freely Accessible Database of HIV Amino Acid Sequences and Clinical Data of Infected Patients. Frontiers in Genetics, 2021, 12, 679029.	1.1	4
26	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.	0.3	3
27	Spectrum of Atazanavir-Selected Protease Inhibitor-Resistance Mutations. Pathogens, 2022, 11, 546.	1.2	3
28	Automatic Recognition of Chemical Entity Mentions in Texts of Scientific Publications. Automatic Documentation and Mathematical Linguistics, 2020, 54, 306-315.	0.2	1