Danil Kutov

List of Publications by Year in descending order

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23 papers	381 citations	840585 11 h-index	794469 19 g-index
26 all docs	26 docs citations	26 times ranked	244 citing authors

#	Article	IF	Citations
1	Quantum-Chemical Quasi-Docking for Molecular Dynamics Calculations. Nanomaterials, 2022, 12, 274.	1.9	4
2	New Blood Coagulation Factor XIIa Inhibitors: Molecular Modeling, Synthesis, and Experimental Confirmation. Molecules, 2022, 27, 1234.	1.7	11
3	Novel Inhibitors of 2â€²-O-Methyltransferase of the SARS-CoV-2 Coronavirus. Molecules, 2022, 27, 2721.	1.7	6
4	Advances in Docking. Current Medicinal Chemistry, 2020, 26, 7555-7580.	1.2	66
5	Synthesis, Docking, and In Vitro Anticoagulant Activity Assay of Hybrid Derivatives of Pyrrolo[3,2,1-ij]Quinolin-2(1H)-one as New Inhibitors of Factor Xa and Factor XIa. Molecules, 2020, 25, 1889.	1.7	21
6	Development of docking programs for Lomonosov supercomputer. Journal of the Turkish Chemical Society, Section A: Chemistry, 2020, 7, 259-276.	0.4	11
7	Supercomputer docking with a large number of degrees of freedom. SAR and QSAR in Environmental Research, 2019, 30, 733-749.	1.0	4
8	Docking of oligopeptides. Russian Chemical Bulletin, 2019, 68, 1780-1786.	0.4	4
9	New factor Xa inhibitors based on 1,2,3,4-tetrahydroquinoline developed by molecular modelling. Journal of Molecular Graphics and Modelling, 2019, 89, 215-224.	1.3	19
10	Parallel Supercomputer Docking Program of the New Generation: Finding Low Energy Minima Spectrum. Communications in Computer and Information Science, 2019, , 314-330.	0.4	6
11	Search for Approaches to Supercomputer Quantum-Chemical Docking. Communications in Computer and Information Science, 2019, , 363-378.	0.4	6
12	Supercomputer Docking. Supercomputing Frontiers and Innovations, 2019, 6, .	0.5	3
13	Supercomputer Docking: Investigation of Low Energy Minima of Protein-Ligand Complexes. Supercomputing Frontiers and Innovations, 2018, 5, .	0.5	3
14	Evaluation of the novel algorithm of flexible ligand docking with moveable target-protein atoms. Computational and Structural Biotechnology Journal, 2017, 15, 275-285.	1.9	17
15	New generation of docking programs: Supercomputer validation of force fields and quantum-chemical methods for docking. Journal of Molecular Graphics and Modelling, 2017, 78, 139-147.	1.3	37
16	Search for approaches to improving the calculation accuracy of the proteinâ€”ligand binding energy by docking. Russian Chemical Bulletin, 2017, 66, 1913-1924.	0.4	13
17	Combined Docking with Classical Force Field and Quantum Chemical Semiempirical Method PM7. Advances in Bioinformatics, 2017, 2017, 1-6.	5.7	39
18	Tensor Train Global Optimization: Application to Docking in the Configuration Space with a Large Number of Dimensions. Communications in Computer and Information Science, 2017, , 151-167.	0.4	6

#	Article	IF	Citations
19	Influence of the Method of Hydrogen Atoms Incorporation Into the Target Protein on the Protein-Ligand Binding Energy. Bulletin of the South Ural State University, Series: Mathematical Modelling, Programming and Computer Software, 2017, 10, 94-107.	0.1	9
20	Evaluation of Docking Target Functions by the Comprehensive Investigation of Protein-Ligand Energy Minima. Advances in Bioinformatics, 2015, 2015, 1-12.	5.7	38
21	Application of Molecular Modeling to Development of New Factor Xa Inhibitors. BioMed Research International, 2015, 2015, 1-15.	0.9	33
22	Genome-Wide Analysis of Genetic Associations for Prediction of Polygenic Hypercholesterolemia with Bayesian Networks. Journal of Computational and Engineering Mathematics, 2015, 2, 11-26.	0.4	7
23	Evaluation of the Docking Algorithm Based on Tensor Train Global Pptimization. Bulletin of the South Ural State University, Series: Mathematical Modelling, Programming and Computer Software, 2015, 8, 83-99.	0.1	9