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	Advances in Docking. Current Medicinal Chemistry, 2020, 26, 7555-7580.	1.2	66
2	Combined Docking with Classical Force Field and Quantum Chemical Semiempirical Method PM7. Advances in Bioinformatics, 2017, 2017, 1-6.	5.7	39
3	Evaluation of Docking Target Functions by the Comprehensive Investigation of Protein-Ligand Energy Minima. Advances in Bioinformatics, 2015, 2015, 1-12.	5.7	38
4	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
5	Application of Molecular Modeling to Development of New Factor Xa Inhibitors. BioMed Research International, 2015, 2015, 1-15.	0.9	33
6	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
7	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
8	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
9	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
10	Development of docking programs for Lomonosov supercomputer. Journal of the Turkish Chemical Society, Section A: Chemistry, 2020, 7, 259-276.	0.4	11
11	New Blood Coagulation Factor XIIa Inhibitors: Molecular Modeling, Synthesis, and Experimental Confirmation. Molecules, 2022, 27, 1234.	1.7	11
12	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
13	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
14	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
15	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
16	Search for Approaches to Supercomputer Quantum-Chemical Docking. Communications in Computer and Information Science, 2019, , 363-378.	0.4	6
17	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
18	Novel Inhibitors of 2â€²-O-Methyltransferase of the SARS-CoV-2 Coronavirus. Molecules, 2022, 27, 2721.	1.7	6

#	Article	IF	Citations
19	Supercomputer docking with a large number of degrees of freedom. SAR and QSAR in Environmental Research, 2019, 30, 733-749.	1.0	4
20	Docking of oligopeptides. Russian Chemical Bulletin, 2019, 68, 1780-1786.	0.4	4
21	Quantum-Chemical Quasi-Docking for Molecular Dynamics Calculations. Nanomaterials, 2022, 12, 274.	1.9	4
22	Supercomputer Docking. Supercomputing Frontiers and Innovations, 2019, 6, .	0.5	3
23	Supercomputer Docking: Investigation of Low Energy Minima of Protein-Ligand Complexes. Supercomputing Frontiers and Innovations, 2018, 5, .	0.5	3