Artur Gieldon

List of Publications by Year
in descending order

53	861	471371	580701
papers	citations	17 h-index	25 g-index

53	53	53	1097
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Prediction of protein assemblies, the next frontier: The <scp>CASP14â€CAPRI</scp> experiment. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1800-1823.	1.5	73
2	Structural insights into the activation mechanisms of human HtrA serine proteases. Archives of Biochemistry and Biophysics, 2017, 621, 6-23.	1.4	53
3	Performance of protein-structure predictions with the physics-based UNRES force field in CASP11. Bioinformatics, 2016, 32, 3270-3278.	1.8	44
4	Analysis of interactions responsible for vasopressin binding to human neurohypophyseal hormone receptorsâ€"molecular dynamics study of the activated receptorâ€"vasopressinâ€"Gİ± systems. Journal of Peptide Science, 2006, 12, 180-189.	0.8	33
5	Temperature-induced changes of HtrA2(Omi) protease activity and structure. Cell Stress and Chaperones, 2013, 18, 35-51.	1.2	33
6	Preliminary studies on trigonelline as potential anti-Alzheimer disease agent: Determination by hydrophilic interaction liquid chromatography and modeling of interactions with beta-amyloid. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2014, 968, 101-104.	1.2	33
7	Temperature-dependent structure-property modeling of viscosity for ionic liquids. Fluid Phase Equilibria, 2016, 427, 9-17.	1.4	32
8	3-[2-(8-Quinolinyl)benzoxazol-5-yl]alanine derivativeâ€"a specific fluorophore for transition and rare-earth metal ion detection. Tetrahedron, 2004, 60, 11889-11894.	1.0	27
9	Prediction of protein structure with the coarseâ€grained UNRES force field assisted by small Xâ€ray scattering data and knowledgeâ€based information. Proteins: Structure, Function and Bioinformatics, 2018, 86, 228-239.	1.5	26
10	Theoretical Study of Polymerization Mechanism of p-Xylylene Based Polymers. Journal of Physical Chemistry A, 2010, 114, 4296-4303.	1.1	25
11	Crystal structure of a low molecular weight activator Blm-pep with yeast 20S proteasome â€“ insights into the enzyme activation mechanism. Scientific Reports, 2017, 7, 6177.	1.6	23
12	Molecular modeling of interactions of the non-peptide antagonist YM087 with the human vasopressin V1a, V2 receptors and with oxytocin receptors. Journal of Computer-Aided Molecular Design, 2001, 15, 1085-1104.	1.3	22
13	The LA Loop as an Important Regulatory Element of the HtrA (DegP) Protease from Escherichia coli. Journal of Biological Chemistry, 2014, 289, 15880-15893.	1.6	22
14	Structure-based design and in vivo anti-arthritic activity evaluation of a potent dipeptidyl cyclopropyl nitrile inhibitor of cathepsin C. Biochemical Pharmacology, 2019, 164, 349-367.	2.0	21
15	Scale-consistent approach to the derivation of coarse-grained force fields for simulating structure, dynamics, and thermodynamics of biopolymers. Progress in Molecular Biology and Translational Science, 2020, 170, 73-122.	0.9	20
16	Temperature-induced conformational changes within the regulatory loops L1â€"L2â€"LA of the HtrA heat-shock protease from Escherichia coli. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2009, 1794, 1573-1582.	1.1	19
17	Use of the UNRES force field in template-assisted prediction of protein structures and the refinement of server models: Test with CASP12 targets. Journal of Molecular Graphics and Modelling, 2018, 83, 92-99.	1.3	19
18	An analysis and evaluation of the WeFold collaborative for protein structure prediction and its pipelines in CASP11 and CASP12. Scientific Reports, 2018, 8, 9939.	1.6	19

#	Article	IF	Citations
19	Evaluation of the scale-consistent UNRES force field in template-free prediction of protein structures in the CASP13 experiment. Journal of Molecular Graphics and Modelling, 2019, 92, 154-166.	1.3	19
20	An enormously active and selective azapeptide inhibitor of cathepsin B. Journal of Peptide Science, 2007, 13, 536-543.	0.8	18
21	Anti-inflammatory effect of novel analogs of natural enkephalinase inhibitors in a mouse model of experimental colitis. Future Medicinal Chemistry, 2016, 8, 2231-2243.	1.1	17
22	Theoretical calculation of the physico-chemical properties of 1-butyl-4-methylpyridinium based ionic liquids. Journal of Molecular Liquids, 2017, 225, 467-474.	2.3	17
23	Modeling protein structures with the coarse-grained UNRES force field in the CASP14 experiment. Journal of Molecular Graphics and Modelling, 2021, 108, 108008.	1.3	17
24	Cathepsin C inhibition as a potential treatment strategy in cancer. Biochemical Pharmacology, 2021, 194, 114803.	2.0	17
25	A new protein nucleicâ€acid coarseâ€grained force field based on the UNRES and NARESâ€2P force fields. Journal of Computational Chemistry, 2018, 39, 2360-2370.	1.5	16
26	Theoretical Calculations of Heteroconjugation Equilibrium Constants in Systems Modeling Acidâ^'Base Interactions in Side Chains of Biomolecules Using the Potential of Mean Force. Journal of Physical Chemistry B, 2004, 108, 12222-12230.	1.2	15
27	RASMOL AB - New functionalities in the program for structure analysis. Acta Biochimica Polonica, 2015, 62, 629-631.	0.3	14
28	Distinct 3D Architecture and Dynamics of the Human HtrA2(Omi) Protease and Its Mutated Variants. PLoS ONE, 2016, 11, e0161526.	1.1	14
29	Study of New Oxytocin Antagonist Barusiban (Fe200 440) Affinity Toward Human Oxytocin Receptor Versus Vasopressin V1a and V2 Receptors - Molecular Dynamics Simulation in POPC Bilayer. QSAR and Combinatorial Science, 2005, 24, 603-610.	1.5	12
30	Biochemical properties of the HtrA homolog from bacterium Stenotrophomonas maltophilia. International Journal of Biological Macromolecules, 2018, 109, 992-1005.	3.6	12
31	Processing and Maturation of Cathepsin C Zymogen: A Biochemical and Molecular Modeling Analysis. International Journal of Molecular Sciences, 2019, 20, 4747.	1.8	12
32	Improved Consensus-Fragment Selection in Template-Assisted Prediction of Protein Structures with the UNRES Force Field in CASP13. Journal of Chemical Information and Modeling, 2020, 60, 1844-1864.	2.5	11
33	Theoretical Study of the Human Bradykininâ€“Bradykinin B2 Receptor Complex. ChemBioChem, 2008, 9, 2487-2497.	1.3	10
34	Molecular dynamics of protein A and a WW domain with a united-residue model including hydrodynamic interaction. Journal of Chemical Physics, 2016, 144, 184110.	1.2	10
35	PEGylated substrates of NSP4 protease: A tool to study protease specificity. Scientific Reports, 2016, 6, 22856.	1.6	10
36	Introduction of Phosphorylated Residues into the UNRES Coarse-Grained Model: Toward Modeling of Signaling Processes. Journal of Physical Chemistry B, 2019, 123, 5721-5729.	1.2	10

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37	Alanine scan of sialorphin and its hybrids with opiorphin: synthesis, molecular modelling and effect on enkephalins degradation. Amino Acids, 2018, 50, 1083-1088.	1.2	9
38	The <scp>LD</scp> loop as an important structural element required for transmission of the allosteric signal in the HtrA (DegP) protease from Escherichia coli. FEBS Journal, 2016, 283, 3471-3487.	2.2	8
39	Molecular dynamics study of 4-OH-phenylacetyl- D -Y(Me)FQNRPR-NH 2 selectivity to V1a receptor. Journal of Molecular Modeling, 2003, 9, 372-378.	0.8	7
40	Theoretical study on binding of S100B protein. Journal of Molecular Modeling, 2007, 13, 1123-1131.	0.8	7
41	1-Substituted sialorphin analoguesâ€"synthesis, molecular modelling and in vitro effect on enkephalins degradation by NEP. Amino Acids, 2019, 51, 1201-1207.	1.2	6
42	The role of the L2 loop in the regulation and maintaining the proteolytic activity of HtrA (DegP) protein from Escherichia coli. Archives of Biochemistry and Biophysics, 2010, 500, 123-130.	1.4	5
43	Impact of selected amino acids of HP0377 (Helicobacter pylori thiol oxidoreductase) on its functioning as a CcmG (cytochrome c maturation) protein and Dsb (disulfide bond) isomerase. PLoS ONE, 2018, 13, e0195358.	1.1	5
44	Molecular dynamics simulations of the growth of poly(chloro-para-xylylene) films. Journal of Molecular Modeling, 2011, 17, 2725-2733.	0.8	4
45	A Peptidomimetic Fluorescent Probe to Detect the Trypsin Î²2 Subunit of the Human 20S Proteasome. International Journal of Molecular Sciences, 2020, 21, 2396.	1.8	4
46	Polymerization of chloro-p-xylylenes, quantum-chemical study. Journal of Molecular Modeling, 2017, 23, 40.	0.8	2
47	Influence of Temperature and Salt Concentration on the Hydrophobic Interactions of Adamantane and Hexane. Journal of Physical Chemistry B, 2022, 126, 634-642.	1.2	2
48	Theoretical Investigation of the Coronavirus SARS-CoV-2 (COVID-19) Infection Mechanism and Selectivity. Molecules, 2022, 27, 2080.	1.7	2
49	Low-Molecular Pyrazine-Based DNA Binders: Physicochemical and Antimicrobial Properties. Molecules, 2022, 27, 3704.	1.7	2
50	Molecular dynamics simulation of polymerization of p-xylylene. , 2012, , .		1
51	Selection of Effective HTRA3 Activators Using Combinatorial Chemistry. ACS Combinatorial Science, 2017, 19, 565-573.	3.8	1
52	Peptidomimetics Based on C-Terminus of Blm10 Stimulate Human 20S Proteasome Activity and Promote Degradation of Proteins. Biomolecules, 2022, 12, 777.	1.8	1
53	Determination of the Binding Sites of Activators within the Proteasome Structure. Proceedings (mdpi), 2019, 22, .	0.2	0