Athanassios Stavrakoudis

List of Publications by Year
in descending order

45	519	758635	713013
papers	citations	12 h-index	21 g-index

47	47	47	576
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	On locating all roots of systems of nonlinear equations inside bounded domain using global optimization methods. Nonlinear Analysis: Real World Applications, 2010, 11, 2465-2471.	0.9	68
2	Enhancing PSO methods for global optimization. Applied Mathematics and Computation, 2010, 216, 2988-3001.	1.4	55
3	Synthesis of a proline-rich [60]fullerene peptide with potential biological activity. Tetrahedron, 2004, 60, 2823-2828.	1.0	46
4	Molecular dynamics simulation of antimicrobial peptide arenicinâ€2: Î²â€Hairpin stabilization by noncovalent interactions. Biopolymers, 2009, 92, 143-155.	1.2	40
5	The relative orientation of the Arg and Asp side chains defined by a pseudodihedral angle as a key criterion for evaluating the structureâ€“activity relationship of RGD peptides. Journal of Peptide Science, 2004, 10, 494-509.	0.8	23
6	Biometric Digital Health Technology for Measuring Motor Function in Parkinsonâ€™s Disease: Results from a Feasibility and Patient Satisfaction Study. Frontiers in Neurology, 2017, 8, 273.	1.1	23
7	Application of Machine Learning in a Parkinson's Disease Digital Biomarker Dataset Using Neural Network Construction (NNC) Methodology Discriminates Patient Motor Status. Frontiers in ICT, 2019, 6, .	3.6	22
8	Tablet-Based Application for Objective Measurement of Motor Fluctuations in Parkinson Disease. Digital Biomarkers, 2018, 1, 126-135.	2.2	21
9	Eucb: A C++ program for molecular dynamics trajectory analysis. Computer Physics Communications, 2011, 182, 834-841.	3.0	19
10	Computational screening of branched cyclic peptide motifs as potential enzyme mimetics. Journal of Peptide Science, 2003, 9, 145-155.	0.8	18
11	A three-residue cyclic scaffold of non-RGD containing peptide analogues as platelet aggregation inhibitors: Design, synthesis, and structure-function relationships. Biopolymers, 2000, 56, 20-26.	1.2	15
12	T-cell epitopes of the La/SSB autoantigen: Prediction based on the homology modeling of HLA-DQ2/DQ7 with the insulin-B peptide/HLA-DQ8 complex. Journal of Computational Chemistry, 2006, 27, 1033-1044.	1.5	12
13	Conformational Flexibility in Designing Peptides for Immunology: The Molecular Dynamics Approach. Current Computer-Aided Drug Design, 2010, 6, 207-222.	0.8	12
14	Insights into the structure of the LC13 TCR/HLA-B8-EBV peptide complex with molecular dynamics simulations. Cell Biochemistry and Biophysics, 2011, 60, 283-295.	0.9	11
15	The Ac-RGD-NH2 peptide as a probe of slow conformational exchange of short linear peptides in DMSO. Biopolymers, 2003, 69, 72-86.	1.2	10
16	Molecular Dynamics as a pattern recognition tool: An automated process detects peptides that preserve the 3D arrangement of Trypsin's Active Site. Biophysical Chemistry, 2008, 133, 36-44.	1.5	9
17	A disulfide linked model of the complement protein C8Î³ complexed with C8Î± indel peptide. Journal of Molecular Modeling, 2009, 15, 165-171.	0.8	9
18	Molecular Dynamics Simulations of BcZBP, A Deacetylase from Bacillus cereus: Active Site Loops Determine Substrate Accessibility and Specificity. Journal of Chemical Theory and Computation, 2009, 5, 3299-3311.	2.3	9

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19	Molecular dynamics simulations of an apoliprotein Aâ€“I derived peptide in explicit water. Chemical Physics Letters, 2008, 461, 294-299.	1.2	7
20	Molecular Dynamics Simulations of the TSSPSAD Peptide Antigen in Free and Bound with CAMPATH-1H Fab Antibody States: The Importance of the Î²-Turn Conformation. International Journal of Peptide Research and Therapeutics, 2009, 15, 1-9.	0.9	7
21	Computational modelling and molecular dynamics simulations of a cyclic peptide mimotope of the CD52 antigen complexed with CAMPATH-1H antibody. Molecular Simulation, 2010, 36, 127-137.	0.9	7
22	Cis-transisomerization of the Epstein-Barr virus determinant peptide EENLLDFVRF after the DM1 TCR recognition of the HLA-B*4405/peptide complex. FEBS Letters, 2011, 585, 485-491.	1.3	7
23	Design, synthesis and catalytic activity of a serine protease synthetic model. International Journal of Peptide Research and Therapeutics, 1997, 4, 481-487.	0.1	6
24	LysinebasedTrypsinActSite(LysTAS): A configurational tool of the TINKER software to evaluate Lysine based branched cyclic peptides as potential chymotrypsin-mimetics. Molecular Simulation, 2006, 32, 643-644.	0.9	6
25	Computational studies on the backboneâ€dependent sideâ€chain orientation induced by the (S,S)â€CXC motif. Journal of Peptide Science, 2008, 14, 1259-1270.	0.8	6
26	Price asymmetry between different pork cuts in the USA: a copula approach. Agricultural and Food Economics, 2015, 3, .	1.3	6
27	A Stochastic Production Frontier Estimator of the Degree of Oligopsony Power in the U.S. Cattle Industry. Journal of Industry, Competition and Trade, 2017, 17, 121-133.	0.2	6
28	Okun's law: Copula-based evidence from G7 countries. Quarterly Review of Economics and Finance, 2022, 84, 478-491.	1.5	5
29	Influence of sequential oligopeptide carriers on the bioactive structure of conjugated epitopes: Comparative study of the conformation of aHerpes simplex virus glycoprotein gD-1 epitope in the free and conjugated form, and protein â€œbuilt-inâ€•crystal structure. Biopolymers, 2006, 84, 383-399.	1.2	4
30	Insights into the structure of the PmrD protein with molecular dynamics simulations. International Journal of Biological Macromolecules, 2009, 44, 393-399.	3.6	4
31	Vertical price relationships between different cuts and quality grades in the U.S. beef marketing channel: AÂwholesale-retail analysis. Journal of Economic Asymmetries, 2017, 16, 53-63.	1.6	4
32	A stochastic frontier estimator of the aggregate degree of market power exerted by the US meat packing industry. Journal of Industrial and Business Economics, 2018, 45, 387-401.	0.8	4
33	Empirical size and power of some diagnostic tests applied to a distributed lag model. Empirical Economics, 2006, 31, 631-643.	1.5	3
34	Conformational Studies of the 313-320 and 313-332 Peptide Fragments Derived from the Î±IIb Subunit of Integrin Receptor with Molecular Dynamics Simulations. International Journal of Peptide Research and Therapeutics, 2009, 15, 263-272.	0.9	3
35	Homology modeling and molecular dynamics simulations of MUC1-9/H-2Kb complex suggest novel binding interactions. Journal of Molecular Modeling, 2011, 17, 1817-1829.	0.8	3
36	A Stochastic Frontier Analysis Approach for Estimating Market Power in the Major US Meat Export Markets. Journal of Industry, Competition and Trade, 2020, 20, 569-586.	0.2	3

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37	Configurational Entropy Reallocation and Complex Loop Dynamics of the Mosquito-Stage Pvs25 Protein Complexed with the Fab Fragment of the Malaria Transmission Blocking Antibody 2A8. Journal of Chemical Theory and Computation, 2011, 7, 515-524.	2.3	2
38	Price Dependence between Different Beef Cuts and Quality Grades: A Copula Approach at the Retail Level for the U.S. Beef Industry. Journal of Agricultural and Food Industrial Organization, 2016, 14, 121-131.	0.9	2
39	Free-on-board and uniform delivered pricing strategies in pure and mixed spatial duopolies: The strategic role of cooperatives. Journal of Economic Asymmetries, 2018, 18, e00109.	1.6	2
40	Design, synthesis and catalytic activity of a serine protease synthetic model. International Journal of Peptide Research and Therapeutics, 1997, 4, 481-487.	0.1	0
41	Molecular dynamics study of the human insulin B peptide SHLVEALYLVCGERGG complexed with HLA-DQ8 reveals important hydrogen bond interactions. Molecular Simulation, 2011, 37, 837-845.	0.9	0
42	EDITORIAL (Hot Topic: Biomolecular Simulations and Applications). Current Physical Chemistry, 2012, 2, 313-313.	0.1	0
43	EDITORIAL (Hot Topic: Biomolecular Simulations and Applications). Current Physical Chemistry, 2012, 2, 313-313.	0.1	0
44	Price Dependence between Different Beef Cuts and Quality Grades: A Copula Approach at the Retail Level for the U.S. Beef Industry. SSRN Electronic Journal, 0, , .	0.4	0
45	Price Dependence between Coffee Qualities: A Copula Model to Evaluate Asymmetric Responses. SSRN Electronic Journal, 0, , .	0.4	0