

Csaba Magyar

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

565
citations

759233

12
h-index

677142

22
g-index

24
all docs

24
docs citations

24
times ranked

724
citing authors

#	ARTICLE	IF	CITATIONS
1	SRide: a server for identifying stabilizing residues in proteins. <i>Nucleic Acids Research</i> , 2005, 33, W303-W305.	14.5	107
2	SCide: identification of stabilization centers in proteins. <i>Bioinformatics</i> , 2003, 19, 899-900.	4.1	99
3	Locating the stabilizing residues in (β/β) ₈ barrel proteins based on hydrophobicity, long-range interactions, and sequence conservation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 55, 316-329.	2.6	73
4	Vibrational analysis for short carbon chains with alternating and cumulenenic structure. <i>Synthetic Metals</i> , 1995, 71, 1865-1866.	3.9	43
5	Impact of Ligand Protonation on Virtual Screening against β -Secretase (BACE1). <i>Journal of Chemical Information and Modeling</i> , 2007, 47, 2366-2373.	5.4	37
6	Phosphorylation-induced transient intrinsic structure in the kinase-inducible domain of CREB facilitates its recognition by the KIX domain of CBP. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 749-757.	2.6	31
7	Increasing the thermal stability of cellulase C using rules learned from thermophilic proteins: a pilot study. <i>Biophysical Chemistry</i> , 2002, 96, 229-241.	2.8	22
8	Combination of 2D/3D Ligand-Based Similarity Search in Rapid Virtual Screening from Multimillion Compound Repositories. Selection and Biological Evaluation of Potential PDE4 and PDE5 Inhibitors. <i>Molecules</i> , 2014, 19, 7008-7039.	3.8	22
9	Mirror image mutations reveal the significance of an intersubunit ion cluster in the stability of 3-isopropylmalate dehydrogenase. <i>FEBS Letters</i> , 2000, 468, 48-52.	2.8	15
10	Access Path to the Ligand Binding Pocket May Play a Role in Xenobiotics Selection by AhR. <i>PLoS ONE</i> , 2016, 11, e0146066.	2.5	15
11	Identification of potential glutaminyl cyclase inhibitors from lead-like libraries by in silico and in vitro fragment-based screening. <i>Molecular Diversity</i> , 2017, 21, 175-186.	3.9	13
12	Relationship between thermal stability and 3-D structure in a homology model of 3-isopropylmalate dehydrogenase from <i>Escherichia coli</i> . <i>Protein Engineering, Design and Selection</i> , 1996, 9, 663-670.	2.1	12
13	Stabilization centers and protein stability. <i>Theoretical Chemistry Accounts</i> , 2001, 106, 121-127.	1.4	12
14	Servers for sequence-structure relationship analysis and prediction. <i>Nucleic Acids Research</i> , 2003, 31, 3359-3363.	14.5	12
15	The role of stabilization centers in protein thermal stability. <i>Biochemical and Biophysical Research Communications</i> , 2016, 471, 57-62.	2.1	9
16	Functionally and structurally relevant residues of enzymes: are they segregated or overlapping?. <i>FEBS Letters</i> , 2004, 567, 239-242.	2.8	8
17	Noncovalent Cross-links in Context with Other Structural and Functional Elements of Proteins. <i>Journal of Chemical Information and Computer Sciences</i> , 2004, 44, 347-351.	2.8	7
18	Analysis of Heterodimeric α -Mutual Synergistic Folding-Complexes. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5136.	4.1	7

#	ARTICLE	IF	CITATIONS
19	Peptide Binding Sites of Connexin Proteins. Chemistry, 2020, 2, 662-673.	2.2	7
20	Combination of Pharmacophore Matching, 2D Similarity Search, and <i>In Vitro</i> Biological Assays in the Selection of Potential 5-HT ₆ Antagonists from Large Commercial Repositories. Chemical Biology and Drug Design, 2015, 86, 864-880.	3.2	6
21	Physical Background of the Disordered Nature of α -Mutual Synergetic Folding Proteins. International Journal of Molecular Sciences, 2018, 19, 3340.	4.1	6
22	Origin of Increased Solvent Accessibility of Peptide Bonds in Mutual Synergetic Folding Proteins. International Journal of Molecular Sciences, 2021, 22, 13404.	4.1	2
23	Noncovalent Cross-Links in Context with Other Structural and Functional Elements of Proteins.. ChemInform, 2004, 35, no.	0.0	0
24	Assortment of Frontiers in Protein Science. International Journal of Molecular Sciences, 2022, 23, 3685.	4.1	0