

Andrea Scir`

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6361886/publications.pdf>

Version: 2024-02-01

43
papers

860
citations

394421

19
h-index

526287

27
g-index

43
all docs

43
docs citations

43
times ranked

1176
citing authors

#	ARTICLE	IF	CITATIONS
1	Glutathione compartmentalization and its role in glutathionylation and other regulatory processes of cellular pathways. <i>BioFactors</i> , 2019, 45, 152-168.	5.4	79
2	Side Effects of Curcumin: Epigenetic and Antiproliferative Implications for Normal Dermal Fibroblast and Breast Cancer Cells. <i>Antioxidants</i> , 2019, 8, 382.	5.1	52
3	The N-terminal region of HtrA heat shock protease from <i>Escherichia coli</i> is essential for stabilization of HtrA primary structure and maintaining of its oligomeric structure. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2003, 1649, 171-182.	2.3	51
4	Structural and thermal stability analysis of <i>Escherichia coli</i> and <i>Alicyclobacillus acidocaldarius</i> thioredoxin revealed a molten globule-like state in thermal denaturation pathway of the proteins: an infrared spectroscopic study. <i>Biochemical Journal</i> , 2003, 373, 875-883.	3.7	37
5	Thermal Stability and Aggregation of <i>Sulfolobus solfataricus</i> β -Glycosidase Are Dependent upon the N ⁶ -Methylation of Specific Lysyl Residues. <i>Journal of Biological Chemistry</i> , 2004, 279, 10185-10194.	3.4	36
6	Interplay among Oxidative Stress, Methylglyoxal Pathway and S-Glutathionylation. <i>Antioxidants</i> , 2021, 10, 19.	5.1	32
7	Temperature-Induced Molten Globule-like State in Human β 1-Acid Glycoprotein: An Infrared Spectroscopic Study. <i>Biochemistry</i> , 2005, 44, 15997-16006.	2.5	31
8	Binding of glutamine to glutamine-binding protein from <i>Escherichia coli</i> induces changes in protein structure and increases protein stability. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 58, 80-87.	2.6	30
9	Stability and conformational dynamics of metallothioneins from the antarctic fish <i>Notothenia coriiceps</i> and mouse. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 46, 259-267.	2.6	27
10	Structure-activity relationship on fungal laccase from <i>Rigidoporus lignosus</i> : a Fourier-transform infrared spectroscopic study. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2002, 1601, 155-162.	2.3	26
11	Characterization of Thymoquinone Binding to Human β 1-Acid Glycoprotein. <i>Journal of Pharmaceutical Sciences</i> , 2012, 101, 2564-2573.	3.3	26
12	A possible S-glutathionylation of specific proteins by glyoxalase II: An in vitro and in silico study. <i>Cell Biochemistry and Function</i> , 2016, 34, 620-627.	2.9	26
13	Protein-protein interactions of human glyoxalase II: findings of a reliable docking protocol. <i>Organic and Biomolecular Chemistry</i> , 2018, 16, 5167-5177.	2.8	26
14	Two-dimensional IR correlation spectroscopy of mutants of the β -glycosidase from the hyperthermophilic archaeon <i>Sulfolobus solfataricus</i> identifies the mechanism of quaternary structure stabilization and unravels the sequence of thermal unfolding events. <i>Biochemical Journal</i> , 2004, 384, 69-78.	3.7	24
15	Structural and Thermal Stability Characterization of <i>Escherichia coli</i> -Galactose/d-Glucose-Binding Protein. <i>Biotechnology Progress</i> , 2008, 20, 330-337.	2.6	24
16	Specific interaction of cytosolic and mitochondrial glyoxalase II with acidic phospholipids in form of liposomes results in the inhibition of the cytosolic enzyme only. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000, 41, 33-39.	2.6	22
17	Nitroxides are more efficient inhibitors of oxidative damage to calf skin collagen than antioxidant vitamins. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2008, 1780, 58-68.	2.4	21
18	D-Trehalose/D-maltose-binding protein from the hyperthermophilic archaeon <i>Thermococcus litoralis</i> : The binding of trehalose and maltose results in different protein conformational states. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 754-767.	2.6	20

#	ARTICLE	IF	CITATIONS
19	Amino acid transport in thermophiles: characterization of an arginine-binding protein in <i>Thermotoga maritima</i> . 2. Molecular organization and structural stability. <i>Molecular BioSystems</i> , 2010, 6, 687.	2.9	20
20	A comparative infrared spectroscopic study of glycoside hydrolases from extremophilic archaea revealed different molecular mechanisms of adaptation to high temperatures. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 67, 991-1001.	2.6	19
21	Temperature-induced conformational changes within the regulatory loops L1 and L2 of the HtrA heat-shock protease from <i>Escherichia coli</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2009, 1794, 1573-1582.	2.3	19
22	Structure and Stability of a Rat Odorant-Binding Protein: Another Brick in the Wall. <i>Journal of Proteome Research</i> , 2009, 8, 4005-4013.	3.7	17
23	Temperature-, SDS-, and pH-Induced Conformational Changes in Protein Disulfide Oxidoreductase from the Archaeon <i>Pyrococcus furiosus</i> : A Dynamic Simulation and Fourier Transform Infrared Spectroscopic Study. <i>Journal of Proteome Research</i> , 2005, 4, 1972-1980.	3.7	16
24	A Strategic Fluorescence Labeling of d-Galactose/d-Glucose-Binding Protein from <i>Escherichia coli</i> Helps to Shed Light on the Protein Structural Stability and Dynamics. <i>Journal of Proteome Research</i> , 2007, 6, 4119-4126.	3.7	16
25	Wild-Type and Mutant Bovine Odorant-Binding Proteins To Probe the Role of the Quaternary Structure Organization in the Protein Thermal Stability. <i>Journal of Proteome Research</i> , 2008, 7, 5221-5229.	3.7	16
26	The belonging of gpMuc, a glycoprotein from <i>Mucuna pruriens</i> seeds, to the Kunitz-type trypsin inhibitor family explains its direct anti-snake venom activity. <i>Phytomedicine</i> , 2011, 18, 887-895.	5.3	16
27	The thermal unfolding of the ribosome-inactivating protein saporin-S6 characterized by infrared spectroscopy. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 1357-1364.	2.3	16
28	The Role of Artificial Intelligence in the Diagnosis and Prognosis of Renal Cell Tumors. <i>Diagnostics</i> , 2021, 11, 206.	2.6	15
29	Fibrillation properties of human α 1-acid glycoprotein. <i>Biochimie</i> , 2013, 95, 158-166.	2.6	14
30	Salts Induce Structural Changes in Elongation Factor β from the Hyperthermophilic Archaeon <i>Sulfolobus solfataricus</i> : A Fourier Transform Infrared Spectroscopic Study. <i>Biochemistry</i> , 2001, 40, 13143-13148.	2.5	11
31	Pressure Affects the Structure and the Dynamics of the d-Galactose/d-Glucose-Binding Protein from <i>Escherichia coli</i> by Perturbing the C-Terminal Domain of the Protein. <i>Biochemistry</i> , 2006, 45, 11885-11894.	2.5	10
32	Analysis of the Link between the Redox State and Enzymatic Activity of the HtrA (DegP) Protein from <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2015, 10, e0117413.	2.5	10
33	Mink Growth Hormone Structural-Functional Relationships: Effects of Renaturing and Storage Conditions. <i>Protein Journal</i> , 2008, 27, 170-180.	1.6	9
34	Molecular strategies for protein stabilization: The case of a trehalose/maltose-binding protein from <i>Thermus thermophilus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 73, 839-850.	2.6	8
35	Effect of acidic phospholipids on the structural properties of recombinant cytosolic human glyoxalase II. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 48, 126-133.	2.6	7
36	Interaction of β -conglutin from <i>Lupinus albus</i> with model phospholipid membranes: Investigations on structure, thermal stability and oligomerization status. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2018, 1866, 1242-1248.	2.3	6

#	ARTICLE	IF	CITATIONS
37	Mutagenesis of the Dimer Interface Region of <i>Corynebacterium callunae</i> Starch Phosphorylase Perturbs the Phosphate-Dependent Conformational Relay that Enhances Oligomeric Stability of the Enzyme. <i>Journal of Biochemistry</i> , 2003, 134, 599-606.	1.7	5
38	Effects induced by mono- and divalent cations on protein regions responsible for thermal adaptation in α -D-glucosidase from <i>Sulfolobus solfataricus</i> . <i>European Biophysics Journal</i> , 2004, 33, 38-49.	2.2	5
39	The role of the L2 loop in the regulation and maintaining the proteolytic activity of HtrA (DegP) protein from <i>Escherichia coli</i> . <i>Archives of Biochemistry and Biophysics</i> , 2010, 500, 123-130.	3.0	5
40	A Spectroscopic Study on Secondary Structure and Thermal Unfolding of the Plant Toxin Gelonin Confirms Some Typical Structural Characteristics and Unravels the Sequence of Thermal Unfolding Events. <i>Toxins</i> , 2019, 11, 483.	3.4	5
41	Effects of Fe(III) binding to the nucleotide-independent site of F1-ATPase: enzyme thermostability and response to activating anions. <i>FEBS Letters</i> , 2001, 506, 221-224.	2.8	3
42	Computational, spectroscopic, and resonant mirror biosensor analysis of the interaction of adrenodoxin with native and tryptophan-modified NADPH-adrenodoxin reductase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 57, 302-310.	2.6	2
43	Protein-Protein Interaction between Glyoxalase II and Specific Redox Dependent Proteins through S-Glutathionylation Modification. <i>Medical Sciences Forum</i> , 2020, 2, .	0.5	0