

Gabriel Zoldak

List of Publications by Year in descending order

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48
papers

1,198
citations

361413

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1533
citing authors

#	ARTICLE	IF	CITATIONS
1	Allosteric Inter-Domain Contacts in Bacterial Hsp70 Are Located in Regions That Avoid Insertion and Deletion Events. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2788.	4.1	1
2	Single-Molecule Mechanics of Protein Nanomachines. , 2022, , 67-79.		0
3	Nanoimpact in Plants: Lessons from the Transcriptome. <i>Plants</i> , 2021, 10, 751.	3.5	11
4	SlyD Accelerates <i>cis</i> -to- <i>trans</i> Prolyl Isomerization in a Mechanosignaling Protein under Load. <i>Journal of Physical Chemistry B</i> , 2021, 125, 8712-8721.	2.6	3
5	Power Spectral Density Analysis of Nanowire-Anchored Fluctuating Microbead Reveals a Double Lorentzian Distribution. <i>Mathematics</i> , 2021, 9, 1748.	2.2	2
6	Salt-dependent passive adsorption of IgG1 ^h -type monoclonal antibodies on hydrophobic microparticles. <i>Biophysical Chemistry</i> , 2021, 275, 106609.	2.8	4
7	Classifying Residues in Mechanically Stable and Unstable Substructures Based on a Protein Sequence: The Case Study of the DnaK Hsp70 Chaperone. <i>Nanomaterials</i> , 2021, 11, 2198.	4.1	3
8	Interpretation of Single-Molecule Force Experiments on Proteins Using Normal Mode Analysis. <i>Nanomaterials</i> , 2021, 11, 2795.	4.1	1
9	Assessing the Viscoelasticity of Photopolymer Nanowires Using a Three-Parameter Solid Model for Bending Recovery Motion. <i>Nanomaterials</i> , 2021, 11, 2961.	4.1	3
10	A kinetic coupling between protein unfolding and aggregation controls time-dependent solubility of the human myeloma antibody light chain. <i>Protein Science</i> , 2020, 29, 2408-2421.	7.6	2
11	Entropy-Based Strategies for Rapid Pre-Processing and Classification of Time Series Data from Single-Molecule Force Experiments. <i>Entropy</i> , 2020, 22, 701.	2.2	1
12	Bending dynamics of viscoelastic photopolymer nanowires. <i>Applied Physics Letters</i> , 2020, 117, .	3.3	4
13	Ion-Specific Protein/Water Interface Determines the Hofmeister Effect on the Kinetic Stability of Glucose Oxidase. <i>Journal of Physical Chemistry B</i> , 2019, 123, 7965-7973.	2.6	12
14	An Active, Ligand-Responsive Pulling Geometry Reports on Internal Signaling between Subdomains of the DnaK Nucleotide-Binding Domain in Single-Molecule Mechanical Experiments. <i>Biochemistry</i> , 2019, 58, 4744-4750.	2.5	10
15	Stable Substructures in Proteins and How to Find Them Using Single-Molecule Force Spectroscopy. <i>Methods in Molecular Biology</i> , 2019, 1958, 263-282.	0.9	4
16	A folding nucleus and minimal ATP binding domain of Hsp70 identified by single-molecule force spectroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4666-4671.	7.1	38
17	Synergistic Effects of Copper Sites on Apparent Stability of Multicopper Oxidase, Fet3p. <i>International Journal of Molecular Sciences</i> , 2018, 19, 269.	4.1	3
18	Nanomechanics of the substrate binding domain of Hsp70 determine its allosteric ATP-induced conformational change. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 6040-6045.	7.1	28

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19	The fluorescence intensities ratio is not a reliable parameter for evaluation of protein unfolding transitions. <i>Protein Science</i> , 2017, 26, 1236-1239.	7.6	22
20	Analysis of IgG kinetic stability by differential scanning calorimetry, probe fluorescence and light scattering. <i>Protein Science</i> , 2017, 26, 2229-2239.	7.6	14
21	The molten-globule residual structure is critical for refluination of glucose oxidase. <i>Biophysical Chemistry</i> , 2017, 230, 74-83.	2.8	9
22	Subnanometre enzyme mechanics probed by single-molecule force spectroscopy. <i>Nature Communications</i> , 2016, 7, 10848.	12.8	58
23	A Compact Native 24-Residue Supersecondary Structure Derived from the Villin Headpiece Subdomain. <i>Biophysical Journal</i> , 2015, 108, 678-686.	0.5	7
24	Nucleotides regulate the mechanical hierarchy between subdomains of the nucleotide binding domain of the Hsp70 chaperone DnaK. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 10389-10394.	7.1	41
25	Force-dependent isomerization kinetics of a highly conserved proline switch modulates the mechanosensing region of filamin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5568-5573.	7.1	45
26	Force as a single molecule probe of multidimensional protein energy landscapes. <i>Current Opinion in Structural Biology</i> , 2013, 23, 48-57.	5.7	117
27	Unique Proline-Rich Domain Regulates the Chaperone Function of AIPL1. <i>Biochemistry</i> , 2013, 52, 2089-2096.	2.5	20
28	The Prolyl Isomerase SlyD Is a Highly Efficient Enzyme but Decelerates the Conformational Folding of a Client Protein. <i>Journal of the American Chemical Society</i> , 2013, 135, 4372-4379.	13.7	5
29	Ultrafast folding kinetics and cooperativity of villin headpiece in single-molecule force spectroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 18156-18161.	7.1	73
30	Folding Mechanism of an Extremely Thermostable (β -Barrel Enzyme: A High Kinetic Barrier Protects the Protein from Denaturation. <i>Biochemistry</i> , 2012, 51, 3420-3432.	2.5	10
31	Cooperation of the Prolyl Isomerase and Chaperone Activities of the Protein Folding Catalyst SlyD. <i>Journal of Molecular Biology</i> , 2011, 406, 176-194.	4.2	21
32	Activity of NADH oxidase from <i>Thermus thermophilus</i> in water/alcohol binary mixtures is limited by the stability of quaternary structure. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2010, 64, 60-67.	1.8	8
33	Chaperone domains convert prolyl isomerases into generic catalysts of protein folding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 20282-20287.	7.1	58
34	A Library of Fluorescent Peptides for Exploring the Substrate Specificities of Prolyl Isomerases. <i>Biochemistry</i> , 2009, 48, 10423-10436.	2.5	56
35	Consequences of Domain Insertion on the Stability and Folding Mechanism of a Protein. <i>Journal of Molecular Biology</i> , 2009, 386, 1138-1152.	4.2	23
36	NMR Solution Structure of SlyD from <i>Escherichia coli</i> : Spatial Separation of Prolyl Isomerase and Chaperone Function. <i>Journal of Molecular Biology</i> , 2009, 387, 295-305.	4.2	70

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37	Flexibility and enzyme activity of NADH oxidase from <i>Thermus thermophilus</i> in the presence of monovalent cations of Hofmeister series. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2008, 1784, 789-795.	2.3	41
38	Role of Copper in Thermal Stability of Human Ceruloplasmin. <i>Biophysical Journal</i> , 2008, 94, 1384-1391.	0.5	42
39	Multidomain Initiation Factor 2 from <i>Thermus thermophilus</i> Consists of the Individual Autonomous Domains. <i>Biochemistry</i> , 2008, 47, 4992-5005.	2.5	5
40	Release Factors 2 from <i>Escherichia coli</i> and <i>Thermus thermophilus</i> : structural, spectroscopic and microcalorimetric studies. <i>Nucleic Acids Research</i> , 2007, 35, 1343-1353.	14.5	43
41	Conformational stability and dynamics of cytochrome c affect its alkaline isomerization. <i>Journal of Biological Inorganic Chemistry</i> , 2007, 12, 257-266.	2.6	23
42	Cofactor assisted gating mechanism in the active site of NADH oxidase from <i>Thermus thermophilus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 465-476.	2.6	11
43	Unusual effect of salts on the homodimeric structure of NADH oxidase from <i>Thermus thermophilus</i> in acidic pH. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2006, 1764, 129-137.	2.3	11
44	Irreversible thermal denaturation of elongation factor Ts from <i>Thermus thermophilus</i> effect of the residual structure and intermonomer disulfide bond. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2006, 1764, 1277-1285.	2.3	5
45	Irreversible Thermal Denaturation of Glucose Oxidase from <i>Aspergillus niger</i> Is the Transition to the Denatured State with Residual Structure. <i>Journal of Biological Chemistry</i> , 2004, 279, 47601-47609.	3.4	122
46	Modulation of activity of NADH oxidase from <i>Thermus thermophilus</i> through change in flexibility in the enzyme active site induced by Hofmeister series anions. <i>FEBS Journal</i> , 2004, 271, 48-57.	0.2	69
47	Role of conformational flexibility for enzymatic activity in NADH oxidase from <i>Thermus thermophilus</i> . <i>FEBS Journal</i> , 2003, 270, 4887-4897.	0.2	34
48	Thermodynamic properties of nucleotide-free EF-Tu from <i>Thermus thermophilus</i> in the presence of low-molecular weight effectors of its GTPase activity. <i>BBA - Proteins and Proteomics</i> , 2002, 1597, 22-27.	2.1	5