

JÃ³zsef Kardos

List of Publications by Year in descending order

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Version: 2024-02-01

89
papers

5,125
citations

136740

32
h-index

95083

68
g-index

92
all docs

92
docs citations

92
times ranked

7292
citing authors

#	ARTICLE	IF	CITATIONS
1	Disorderedâ€œOrdered Protein Binary Classification by Circular Dichroism Spectroscopy. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 863141.	1.6	18
2	BeStSel: webserver for secondary structure and fold prediction for protein CD spectroscopy. <i>Nucleic Acids Research</i> , 2022, 50, W90-W98.	6.5	103
3	Competitive inhibition of the classical complement pathway using exogenous single-chain C1q recognition proteins. <i>Journal of Biological Chemistry</i> , 2022, 298, 102113.	1.6	5
4	Breakdown of supersaturation barrier links protein folding to amyloid formation. <i>Communications Biology</i> , 2021, 4, 120.	2.0	39
5	Cellular Chaperone Function of Intrinsically Disordered Dehydrin ERD14. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6190.	1.8	11
6	The C-terminal tail extension of myosin 16 acts as a molten globule, including intrinsically disordered regions, and interacts with the N-terminal ankyrin. <i>Journal of Biological Chemistry</i> , 2021, 297, 100716.	1.6	3
7	BeStSel: From Secondary Structure Analysis to Protein Fold Prediction by Circular Dichroism Spectroscopy. <i>Methods in Molecular Biology</i> , 2021, 2199, 175-189.	0.4	53
8	The Single-Cell Transcriptomic Analysis of Prefrontal Pyramidal Cells and Interneurons Reveals the Neuronal Expression of Genes Encoding Antimicrobial Peptides and Immune Proteins. <i>Frontiers in Immunology</i> , 2021, 12, 749433.	2.2	1
9	Pathogenic D76N Variant of Î²2-Microglobulin: Synergy of Diverse Effects in Both the Native and Amyloid States. <i>Biology</i> , 2021, 10, 1197.	1.3	3
10	Highâ€œthroughput competitive fluorescence polarization assay reveals functional redundancy in the S100 protein family. <i>FEBS Journal</i> , 2020, 287, 2834-2846.	2.2	25
11	Chronic stepwise cerebral hypoperfusion differentially induces synaptic proteome changes in the frontal cortex, occipital cortex, and hippocampus in rats. <i>Scientific Reports</i> , 2020, 10, 15999.	1.6	8
12	Membrane Active Peptides Remove Surface Adsorbed Protein Corona From Extracellular Vesicles of Red Blood Cells. <i>Frontiers in Chemistry</i> , 2020, 8, 703.	1.8	10
13	Interplay of Structural Disorder and Short Binding Elements in the Cellular Chaperone Function of Plant Dehydrin ERD14. <i>Cells</i> , 2020, 9, 1856.	1.8	12
14	Comparison of ligand binding and conformational stability of human calmodulin with its homolog from the malaria parasite<i>Plasmodium falciparum</i>. <i>FASEB BioAdvances</i> , 2020, 2, 489-505.	1.3	4
15	Genetic deletion of TRPA1 receptor attenuates amyloid beta- 1-42 (AÎ²1-42)-induced neurotoxicity in the mouse basal forebrain in vivo. <i>Mechanisms of Ageing and Development</i> , 2020, 189, 111268.	2.2	10
16	Isoelectric point-amyloid formation of Î±-synuclein extends the generality of the solubility and supersaturation-limited mechanism. <i>Current Research in Structural Biology</i> , 2020, 2, 35-44.	1.1	17
17	Synaptic mitochondrial dysfunction and septin accumulation are linked to complement-mediated synapse loss in an Alzheimerâ€œs disease animal model. <i>Cellular and Molecular Life Sciences</i> , 2020, 77, 5243-5258.	2.4	39
18	Identification of Neuronal Pentraxins as Synaptic Binding Partners of C1q and the Involvement of NP1 in Synaptic Pruning in Adult Mice. <i>Frontiers in Immunology</i> , 2020, 11, 599771.	2.2	21

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19	Impact of the Conformational Variability of Oligopeptides on the Computational Prediction of Their CD Spectra. <i>Journal of Physical Chemistry B</i> , 2019, 123, 6694-6704.	1.2	7
20	Amyloid Formation under Complicated Conditions in Which Î ² -Microglobulin Coexists with Its Proteolytic Fragments. <i>Biochemistry</i> , 2019, 58, 4925-4934.	1.2	3
21	Heating during agitation of Î ² -microglobulin reveals that supersaturation breakdown is required for amyloid fibril formation at neutral pH. <i>Journal of Biological Chemistry</i> , 2019, 294, 15826-15835.	1.6	20
22	Possible mechanisms of polyphosphate-induced amyloid fibril formation of Î ² -microglobulin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 12833-12838.	3.3	35
23	Ligand entry in human ileal bile acid-binding protein is mediated by histidine protonation. <i>Scientific Reports</i> , 2019, 9, 4825.	1.6	3
24	Directed Evolution of Canonical Loops and Their Swapping between Unrelated Serine Proteinase Inhibitors Disprove the Interscaffolding Additivity Model. <i>Journal of Molecular Biology</i> , 2019, 431, 557-575.	2.0	11
25	Improved Structural Estimation of Disordered Proteins by CD Spectroscopy: Method Development and Application. <i>Biophysical Journal</i> , 2018, 114, 587a.	0.2	0
26	Protein Fold Recognition by Circular Dichroism Spectroscopy. <i>Biophysical Journal</i> , 2018, 114, 174a.	0.2	3
27	Disordered Regions of Mixed Lineage Leukemia 4 (MLL4) Protein Are Capable of RNA Binding. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3478.	1.8	9
28	Atomistic Details of Chymotrypsin Conformational Changes upon Adsorption on Silica. <i>ACS Biomaterials Science and Engineering</i> , 2018, 4, 4036-4050.	2.6	15
29	Local apoptotic-like mechanisms underlie complement-mediated synaptic pruning. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 6303-6308.	3.3	133
30	Aggregation-phase diagrams of Î ² -microglobulin reveal temperature and salt effects on competitive formation of amyloids versus amorphous aggregates. <i>Journal of Biological Chemistry</i> , 2018, 293, 14775-14785.	1.6	32
31	BeStSel: a web server for accurate protein secondary structure prediction and fold recognition from the circular dichroism spectra. <i>Nucleic Acids Research</i> , 2018, 46, W315-W322.	6.5	771
32	Inhibition of the LOX enzyme family members with old and new ligands. Selectivity analysis revisited. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2018, 28, 3113-3118.	1.0	38
33	Structural insight into a partially unfolded state preceding aggregation in an intracellular lipid-binding protein. <i>FEBS Journal</i> , 2017, 284, 3637-3661.	2.2	9
34	Nuclease activity gives an edge to host defense peptide piscidin 3 over piscidin 1, rendering it more effective against persisters and biofilms. <i>FEBS Journal</i> , 2017, 284, 3662-3683.	2.2	86
35	Structural plasticity of the <i>Salmonella</i> FljS flagellar export chaperone. <i>FEBS Letters</i> , 2016, 590, 1103-1113.	1.3	5
36	Widespread alterations in the synaptic proteome of the adolescent cerebral cortex following prenatal immune activation in rats. <i>Brain, Behavior, and Immunity</i> , 2016, 56, 289-309.	2.0	17

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37	Thioflavin T-Silent Denaturation Intermediates Support the Main-Chain-Dominated Architecture of Amyloid Fibrils. <i>Biochemistry</i> , 2016, 55, 3937-3948.	1.2	8
38	Amorphous Aggregation of Cytochrome <i>c</i> with Inherently Low Amyloidogenicity Is Characterized by the Metastability of Supersaturation and the Phase Diagram. <i>Langmuir</i> , 2016, 32, 2010-2022.	1.6	22
39	Amorphous Aggregation of Cytochrome C with Inherently low Amyloidogenicity is Characterized by the Metastability of Supersaturation and the Phase Diagram. <i>Biophysical Journal</i> , 2016, 110, 399a.	0.2	0
40	Without Binding ATP, Human Rad51 Does Not Form Helical Filaments on ssDNA. <i>Journal of Physical Chemistry B</i> , 2016, 120, 2165-2178.	1.2	4
41	ATP Binding is Prerequisite to the Helical Structure of Human Rad51 Presynaptic Filament. <i>Biophysical Journal</i> , 2015, 108, 222a.	0.2	0
42	Evidence-Based Structural Model of the Staphylococcal Repressor Protein: Separation of Functions into Different Domains. <i>PLoS ONE</i> , 2015, 10, e0139086.	1.1	16
43	Accurate secondary structure prediction and fold recognition for circular dichroism spectroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E3095-103.	3.3	1,215
44	Phosphorylation as Conformational Switch from the Native to Amyloid State: Trp-Cage as a Protein Aggregation Model. <i>Journal of Physical Chemistry B</i> , 2015, 119, 2946-2955.	1.2	14
45	A multi-pathway perspective on protein aggregation: Implications for control of the rate and extent of amyloid formation. <i>FEBS Letters</i> , 2015, 589, 672-679.	1.3	38
46	Effects of a reduced disulfide bond on aggregation properties of the human IgG1 CH3 domain. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 1526-1535.	1.1	7
47	Supersaturation-limited and Unlimited Phase Transitions Compete to Produce the Pathway Complexity in Amyloid Fibrillation. <i>Journal of Biological Chemistry</i> , 2015, 290, 18134-18145.	1.6	58
48	The Role of Structural Flexibility and Stability in the Interaction of Serine Proteases with their Inhibitors. <i>Current Protein and Peptide Science</i> , 2015, 16, 521-531.	0.7	5
49	Heat of supersaturation-limited amyloid burst directly monitored by isothermal titration calorimetry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6654-6659.	3.3	82
50	Cold Denaturation of Î±-Synuclein Amyloid Fibrils. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 7799-7804.	7.2	72
51	Supersaturation-limited Amyloid Fibrillation of Insulin Revealed by Ultrasonication. <i>Journal of Biological Chemistry</i> , 2014, 289, 18228-18238.	1.6	45
52	Improved Secondary Structure Determination and Fold Prediction by Circular Dichroism Spectroscopy. <i>Biophysical Journal</i> , 2013, 104, 567a.	0.2	0
53	Comparison of complexes formed by a crustacean and a vertebrate trypsin with bovine pancreatic trypsin inhibitor – the key to achieving extreme stability?. <i>FEBS Journal</i> , 2013, 280, 5750-5763.	2.2	11
54	Structural Stability of Rad51 Filaments of Self-Aggregates and of Presynaptic Complexes Studied by Electron Microscopy and Pressure Tuning Fluorescence Spectroscopy. <i>Biophysical Journal</i> , 2013, 104, 422a.	0.2	0

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55	Self-Association and DNA Binding of hsRad51 Studied by Pressure Perturbation Spectroscopy. <i>Biophysical Journal</i> , 2012, 102, 282a.	0.2	0
56	Single-Molecule Studies of Amyloidogenic Proteins. , 2012, , 169-210.		1
57	The Catalytic Aspartate Is Protonated in the Michaelis Complex Formed between Trypsin and an in Vitro Evolved Substrate-like Inhibitor. <i>Journal of Biological Chemistry</i> , 2011, 286, 3587-3596.	1.6	23
58	Reversible Heat-Induced Dissociation of Î ² -Microglobulin Amyloid Fibrils. <i>Biochemistry</i> , 2011, 50, 3211-3220.	1.2	52
59	Myosin cleft closure determines the energetics of the actomyosin interaction. <i>FASEB Journal</i> , 2011, 25, 111-121.	0.2	19
60	Effects of Estrogen on Beta-Amyloid-Induced Cholinergic Cell Death in the Nucleus Basalis Magnocellularis. <i>Neuroendocrinology</i> , 2011, 93, 90-105.	1.2	20
61	Different electrophysiological actions of 24- and 72-hour aggregated amyloid-beta oligomers on hippocampal field population spike in both anesthetized and awake rats. <i>Brain Research</i> , 2010, 1354, 227-235.	1.1	20
62	The amyloid fibrils of the constant domain of immunoglobulin light chain. <i>FEBS Letters</i> , 2010, 584, 3348-3353.	1.3	20
63	Calcium-dependent Conformational Flexibility of a CLUB Domain Controls Activation of the Complement Serine Protease C1r. <i>Journal of Biological Chemistry</i> , 2010, 285, 11863-11869.	1.6	15
64	Affinity, Avidity, and Kinetics of Target Sequence Binding to LC8 Dynein Light Chain Isoforms*. <i>Journal of Biological Chemistry</i> , 2010, 285, 38649-38657.	1.6	32
65	New Aspects of Lipid-Protein Interactions Revealed by Calmodulin Binding to the Lipid Mediator Sphingosylphosphorylcholine. <i>Biophysical Journal</i> , 2010, 98, 675a.	0.2	0
66	Structure and mechanism of calmodulin binding to a signaling sphingolipid reveal new aspects of lipidâ€protein interactions. <i>FASEB Journal</i> , 2010, 24, 3829-3839.	0.2	8
67	Mechanism of Lysophosphatidic Acid-Induced Amyloid Fibril Formation of Î ² -Microglobulin <i>in Vitro</i> under Physiological Conditions. <i>Biochemistry</i> , 2009, 48, 5689-5699.	1.2	29
68	A Link between Hinge-Bending Domain Motions and the Temperature Dependence of Catalysis in 3-Isopropylmalate Dehydrogenase. <i>Biophysical Journal</i> , 2009, 96, 5003-5012.	0.2	11
69	Adjustment of conformational flexibility of glyceraldehyde-3-phosphate dehydrogenase as a means of thermal adaptation and allosteric regulation. <i>European Biophysics Journal</i> , 2008, 37, 1139-1144.	1.2	8
70	An Unstable Headâ€Rod Junction May Promote Folding into the Compact Off-State Conformation of Regulated Myosins. <i>Journal of Molecular Biology</i> , 2008, 375, 1434-1443.	2.0	15
71	Revisiting the mechanism of the autoactivation of the complement protease C1r in the C1 complex: Structure of the active catalytic region of C1r. <i>Molecular Immunology</i> , 2008, 45, 1752-1760.	1.0	41
72	Probing Conformational Plasticity of the Activation Domain of Trypsin:â€ The Role of Glycine Hinges. <i>Biochemistry</i> , 2008, 47, 1675-1684.	1.2	40

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73	The effect of solvent environment on the conformation and stability of human polyclonal IgG in solution. <i>Biologicals</i> , 2006, 34, 5-14.	0.5	64
74	Structural studies reveal that the diverse morphology of Î²2-microglobulin aggregates is a reflection of different molecular architectures. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2005, 1753, 108-120.	1.1	39
75	Extended Intermolecular Interactions in a Serine Proteaseâ€™Canonical Inhibitor Complex Account for Strong and Highly Specific Inhibition. <i>Journal of Molecular Biology</i> , 2005, 350, 156-169.	2.0	43
76	Direct Measurement of the Thermodynamic Parameters of Amyloid Formation by Isothermal Titration Calorimetry. <i>Journal of Biological Chemistry</i> , 2004, 279, 55308-55314.	1.6	131
77	Increase in the conformational flexibility of Î²2-microglobulin upon copper binding: A possible role for copper in dialysis-related amyloidosis. <i>Protein Science</i> , 2004, 13, 797-809.	3.1	78
78	Low Concentrations of Sodium Dodecyl Sulfate Induce the Extension of Î²2-Microglobulin-Related Amyloid Fibrils at a Neutral pHâ€™. <i>Biochemistry</i> , 2004, 43, 11075-11082.	1.2	185
79	The Structure of MBL-associated Serine Protease-2 Reveals that Identical Substrate Specificities of C1s and MASP-2 are Realized Through Different Sets of Enzymeâ€™Substrate Interactions. <i>Journal of Molecular Biology</i> , 2004, 342, 1533-1546.	2.0	74
80	Protein folding: could hydrophobic collapse be coupled with hydrogen-bond formation?. <i>FEBS Letters</i> , 2003, 536, 187-192.	1.3	46
81	Structural defects and the diagnosis of amyloidogenic propensity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 6446-6451.	3.3	86
82	Remarkable Phylum Selectivity of a <i>Schistocerca gregaria</i> Trypsin Inhibitor: The Possible Role of Enzymeâ€™Inhibitor Flexibility. <i>Archives of Biochemistry and Biophysics</i> , 2002, 398, 179-187.	1.4	26
83	Assembly and Enzymatic Properties of the Catalytic Domain of Human Complement Protease C1r. <i>Journal of Biological Chemistry</i> , 2001, 276, 36233-36240.	1.6	40
84	The Role of the Individual Domains in the Structure and Function of the Catalytic Region of a Modular Serine Protease, C1r. <i>Journal of Immunology</i> , 2001, 167, 5202-5208.	0.4	43
85	A Better Enzyme to Cope with Cold. <i>Journal of Biological Chemistry</i> , 2001, 276, 28121-28125.	1.6	58
86	Serum Albuminâ€™Lipid Membrane Interaction Influencing the Uptake of Porphyrins. <i>Archives of Biochemistry and Biophysics</i> , 2000, 373, 261-270.	1.4	25
87	Disulfide-Linked Propeptides Stabilize the Structure of Zymogen and Mature Pancreatic Serine Proteasesâ€™. <i>Biochemistry</i> , 1999, 38, 12248-12257.	1.2	20
88	Adjustment of conformational flexibility is a key event in the thermal adaptation of proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 7406-7411.	3.3	524
89	Effects of Serpin Binding on the Target Proteinase:â€™ Global Stabilization, Localized Increased Structural Flexibility, and Conserved Hydrogen Bonding at the Active Siteâ€™. <i>Biochemistry</i> , 1997, 36, 5455-5464.	1.2	104