JÃ³zsef Kardos

List of Publications by Year
in descending order

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89	5,125	136740	95083
papers	citations	32 h-index	68 g-index

92	92	92	7292
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Accurate secondary structure prediction and fold recognition for circular dichroism spectroscopy. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E3095-103.	3.3	1,215
2	BeStSel: a web server for accurate protein secondary structure prediction and fold recognition from the circular dichroism spectra. Nucleic Acids Research, 2018, 46, W315-W322.	6.5	771
3	Adjustment of conformational flexibility is a key event in the thermal adaptation of proteins. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 7406-7411.	3.3	524
4	Low Concentrations of Sodium Dodecyl Sulfate Induce the Extension of Î²2-Microglobulin-Related Amyloid Fibrils at a Neutral pHâ€. Biochemistry, 2004, 43, 11075-11082.	1.2	185
5	Local apoptotic-like mechanisms underlie complement-mediated synaptic pruning. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 6303-6308.	3.3	133
6	Direct Measurement of the Thermodynamic Parameters of Amyloid Formation by Isothermal Titration Calorimetry. Journal of Biological Chemistry, 2004, 279, 55308-55314.	1.6	131
7	Effects of Serpin Binding on the Target Proteinase:Â Global Stabilization, Localized Increased Structural Flexibility, and Conserved Hydrogen Bonding at the Active Siteâ€. Biochemistry, 1997, 36, 5455-5464.	1.2	104
8	BeStSel: webserver for secondary structure and fold prediction for protein CD spectroscopy. Nucleic Acids Research, 2022, 50, W90-W98.	6.5	103
9	Structural defects and the diagnosis of amyloidogenic propensity. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 6446-6451.	3.3	86
10	Nuclease activity gives an edge to hostâ€defense peptide piscidin 3 over piscidin 1, rendering it more effective against persisters and biofilms. FEBS Journal, 2017, 284, 3662-3683.	2.2	86
11	Heat of supersaturation-limited amyloid burst directly monitored by isothermal titration calorimetry. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6654-6659.	3.3	82
12	Increase in the conformational flexibility of Â2-microglobulin upon copper binding: A possible role for copper in dialysis-related amyloidosis. Protein Science, 2004, 13, 797-809.	3.1	78
13	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. Journal of Molecular Biology, 2004, 342, 1533-1546.	2.0	74
14	Cold Denaturation of Î±â€Synuclein Amyloid Fibrils. Angewandte Chemie - International Edition, 2014, 53, 7799-7804.	7.2	72
15	The effect of solvent environment on the conformation and stability of human polyclonal IgG in solution. Biologicals, 2006, 34, 5-14.	0.5	64
16	A Better Enzyme to Cope with Cold. Journal of Biological Chemistry, 2001, 276, 28121-28125.	1.6	58
17	Supersaturation-limited and Unlimited Phase Transitions Compete to Produce the Pathway Complexity in Amyloid Fibrillation. Journal of Biological Chemistry, 2015, 290, 18134-18145.	1.6	58
18	BeStSel: From Secondary Structure Analysis to Protein Fold Prediction by Circular Dichroism Spectroscopy. Methods in Molecular Biology, 2021, 2199, 175-189.	0.4	53

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19	Reversible Heat-Induced Dissociation of Î²₂-Microglobulin Amyloid Fibrils. Biochemistry, 2011, 50, 3211-3220.	1.2	52
20	Protein folding: could hydrophobic collapse be coupled with hydrogen-bond formation?. FEBS Letters, 2003, 536, 187-192.	1.3	46
21	Supersaturation-limited Amyloid Fibrillation of Insulin Revealed by Ultrasonication. Journal of Biological Chemistry, 2014, 289, 18228-18238.	1.6	45
22	The Role of the Individual Domains in the Structure and Function of the Catalytic Region of a Modular Serine Protease, C1r. Journal of Immunology, 2001, 167, 5202-5208.	0.4	43
23	Extended Intermolecular Interactions in a Serine Proteaseâ€“Canonical Inhibitor Complex Account for Strong and Highly Specific Inhibition. Journal of Molecular Biology, 2005, 350, 156-169.	2.0	43
24	Revisiting the mechanism of the autoactivation of the complement protease C1r in the C1 complex: Structure of the active catalytic region of C1r. Molecular Immunology, 2008, 45, 1752-1760.	1.0	41
25	Assembly and Enzymatic Properties of the Catalytic Domain of Human Complement Protease C1r. Journal of Biological Chemistry, 2001, 276, 36233-36240.	1.6	40
26	Probing Conformational Plasticity of the Activation Domain of Trypsin:â€‰ The Role of Glycine Hinges. Biochemistry, 2008, 47, 1675-1684.	1.2	40
27	Structural studies reveal that the diverse morphology of Î²2-microglobulin aggregates is a reflection of different molecular architectures. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2005, 1753, 108-120.	1.1	39
28	Synaptic mitochondrial dysfunction and septin accumulation are linked to complement-mediated synapse loss in an Alzheimerâ€™s disease animal model. Cellular and Molecular Life Sciences, 2020, 77, 5243-5258.	2.4	39
29	Breakdown of supersaturation barrier links protein folding to amyloid formation. Communications Biology, 2021, 4, 120.	2.0	39
30	A multiâ€pathway perspective on protein aggregation: Implications for control of the rate and extent of amyloid formation. FEBS Letters, 2015, 589, 672-679.	1.3	38
31	Inhibition of the LOX enzyme family members with old and new ligands. Selectivity analysis revisited. Bioorganic and Medicinal Chemistry Letters, 2018, 28, 3113-3118.	1.0	38
32	Possible mechanisms of polyphosphate-induced amyloid fibril formation of Î² ₂ -microglobulin. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 12833-12838.	3.3	35
33	Affinity, Avidity, and Kinetics of Target Sequence Binding to LC8 Dynein Light Chain Isoforms*. Journal of Biological Chemistry, 2010, 285, 38649-38657.	1.6	32
34	Aggregation-phase diagrams of Î²2-microglobulin reveal temperature and salt effects on competitive formation of amyloids versus amorphous aggregates. Journal of Biological Chemistry, 2018, 293, 14775-14785.	1.6	32
35	Mechanism of Lysophosphatidic Acid-Induced Amyloid Fibril Formation of Î²₂-Microglobulin in Vitro under Physiological Conditions. Biochemistry, 2009, 48, 5689-5699.	1.2	29
36	Remarkable Phylum Selectivity of a Schistocerca gregaria Trypsin Inhibitor: The Possible Role of Enzymeâ€“Inhibitor Flexibility. Archives of Biochemistry and Biophysics, 2002, 398, 179-187.	1.4	26

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37	Serum Albuminâ€“Lipid Membrane Interaction Influencing the Uptake of Porphyrins. Archives of Biochemistry and Biophysics, 2000, 373, 261-270.	1.4	25
38	Highâ€throughput competitive fluorescence polarization assay reveals functional redundancy in the S100 protein family. FEBS Journal, 2020, 287, 2834-2846.	2.2	25
39	The Catalytic Aspartate Is Protonated in the Michaelis Complex Formed between Trypsin and an in Vitro Evolved Substrate-like Inhibitor. Journal of Biological Chemistry, 2011, 286, 3587-3596.	1.6	23
40	Amorphous Aggregation of Cytochrome c with Inherently Low Amyloidogenicity Is Characterized by the Metastability of Supersaturation and the Phase Diagram. Langmuir, 2016, 32, 2010-2022.	1.6	22
41	Identification of Neuronal Pentraxins as Synaptic Binding Partners of C1q and the Involvement of NP1 in Synaptic Pruning in Adult Mice. Frontiers in Immunology, 2020, 11, 599771.	2.2	21
42	Disulfide-Linked Propeptides Stabilize the Structure of Zymogen and Mature Pancreatic Serine Proteasesâ€. Biochemistry, 1999, 38, 12248-12257.	1.2	20
43	Different electrophysiological actions of 24- and 72-hour aggregated amyloid-beta oligomers on hippocampal field population spike in both anesthetized and awake rats. Brain Research, 2010, 1354, 227-235.	1.1	20
44	The amyloid fibrils of the constant domain of immunoglobulin light chain. FEBS Letters, 2010, 584, 3348-3353.	1.3	20
45	Effects of Estrogen on Beta-Amyloid-Induced Cholinergic Cell Death in the Nucleus Basalis Magnocellularis. Neuroendocrinology, 2011, 93, 90-105.	1.2	20
46	Heating during agitation of Î²2-microglobulin reveals that supersaturation breakdown is required for amyloid fibril formation at neutral pH. Journal of Biological Chemistry, 2019, 294, 15826-15835.	1.6	20
47	Myosin cleft closure determines the energetics of the actomyosin interaction. FASEB Journal, 2011, 25, 111-121.	0.2	19
48	Disorderedâ€“Ordered Protein Binary Classification by Circular Dichroism Spectroscopy. Frontiers in Molecular Biosciences, 2022, 9, 863141.	1.6	18
49	Widespread alterations in the synaptic proteome of the adolescent cerebral cortex following prenatal immune activation in rats. Brain, Behavior, and Immunity, 2016, 56, 289-309.	2.0	17
50	Isoelectric point-amyloid formation of Î±-synuclein extends the generality of the solubility and supersaturation-limited mechanism. Current Research in Structural Biology, 2020, 2, 35-44.	1.1	17
51	Evidence-Based Structural Model of the Staphylococcal Repressor Protein: Separation of Functions into Different Domains. PLoS ONE, 2015, 10, e0139086.	1.1	16
52	An Unstable Headâ€“Rod Junction May Promote Folding into the Compact Off-State Conformation of Regulated Myosins. Journal of Molecular Biology, 2008, 375, 1434-1443.	2.0	15
53	Calcium-dependent Conformational Flexibility of a CUB Domain Controls Activation of the Complement Serine Protease C1r. Journal of Biological Chemistry, 2010, 285, 11863-11869.	1.6	15
54	Atomistic Details of Chymotrypsin Conformational Changes upon Adsorption on Silica. ACS Biomaterials Science and Engineering, 2018, 4, 4036-4050.	2.6	15

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55	Phosphorylation as Conformational Switch from the Native to Amyloid State: Trp-Cage as a Protein Aggregation Model. Journal of Physical Chemistry B, 2015, 119, 2946-2955.	1.2	14
56	Interplay of Structural Disorder and Short Binding Elements in the Cellular Chaperone Function of Plant Dehydrin ERD14. Cells, 2020, 9, 1856.	1.8	12
57	A Link between Hinge-Bending Domain Motions and the Temperature Dependence of Catalysis in 3-Isopropylmalate Dehydrogenase. Biophysical Journal, 2009, 96, 5003-5012.	0.2	11
58	Comparison of complexes formed by a crustacean and a vertebrate trypsin with bovine pancreatic trypsin inhibitor â€“ the key to achieving extreme stability?. FEBS Journal, 2013, 280, 5750-5763.	2.2	11
59	Directed Evolution of Canonical Loops and Their Swapping between Unrelated Serine Proteinase Inhibitors Disprove the Interscaffolding Additivity Model. Journal of Molecular Biology, 2019, 431, 557-575.	2.0	11
60	Cellular Chaperone Function of Intrinsically Disordered Dehydrin ERD14. International Journal of Molecular Sciences, 2021, 22, 6190.	1.8	11
61	Membrane Active Peptides Remove Surface Adsorbed Protein Corona From Extracellular Vesicles of Red Blood Cells. Frontiers in Chemistry, 2020, 8, 703.	1.8	10
62	Genetic deletion of TRPA1 receptor attenuates amyloid beta- 1-42 (AÎ²1-42)-induced neurotoxicity in the mouse basal forebrain in vivo. Mechanisms of Ageing and Development, 2020, 189, 111268.	2.2	10
63	Structural insight into a partially unfolded state preceding aggregation in an intracellular lipidâ€binding protein. FEBS Journal, 2017, 284, 3637-3661.	2.2	9
64	Disordered Regions of Mixed Lineage Leukemia 4 (MLL4) Protein Are Capable of RNA Binding. International Journal of Molecular Sciences, 2018, 19, 3478.	1.8	9
65	Adjustment of conformational flexibility of glyceraldehyde-3-phosphate dehydrogenase as a means of thermal adaptation and allosteric regulation. European Biophysics Journal, 2008, 37, 1139-1144.	1.2	8
66	Structure and mechanism of calmodulin binding to a signaling sphingolipid reveal new aspects of lipidâ€protein interactions. FASEB Journal, 2010, 24, 3829-3839.	0.2	8
67	Thioflavin T-Silent Denaturation Intermediates Support the Main-Chain-Dominated Architecture of Amyloid Fibrils. Biochemistry, 2016, 55, 3937-3948.	1.2	8
68	Chronic stepwise cerebral hypoperfusion differentially induces synaptic proteome changes in the frontal cortex, occipital cortex, and hippocampus in rats. Scientific Reports, 2020, 10, 15999.	1.6	8
69	Effects of a reduced disulfide bond on aggregation properties of the human IgG1 CH3 domain. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2015, 1854, 1526-1535.	1.1	7
70	Impact of the Conformational Variability of Oligopeptides on the Computational Prediction of Their CD Spectra. Journal of Physical Chemistry B, 2019, 123, 6694-6704.	1.2	7
71	Structural plasticity of the Salmonella FliS flagellar export chaperone. FEBS Letters, 2016, 590, 1103-1113.	1.3	5
72	The Role of Structural Flexibility and Stability in the Interaction of Serine Proteases with their Inhibitors. Current Protein and Peptide Science, 2015, 16, 521-531.	0.7	5

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73	Competitive inhibition of the classical complement pathway using exogenous single-chain C1q recognition proteins. Journal of Biological Chemistry, 2022, 298, 102113.	1.6	5
74	Without Binding ATP, Human Rad51 Does Not Form Helical Filaments on ssDNA. Journal of Physical Chemistry B, 2016, 120, 2165-2178.	1.2	4
75	Comparison of ligand binding and conformational stability of human calmodulin with its homolog from the malaria parasitePlasmodium falciparum. FASEB BioAdvances, 2020, 2, 489-505.	1.3	4
76	Protein Fold Recognition by Circular Dichroism Spectroscopy. Biophysical Journal, 2018, 114, 174a.	0.2	3
77	Amyloid Formation under Complicated Conditions in Which Î²₂-Microglobulin Coexists with Its Proteolytic Fragments. Biochemistry, 2019, 58, 4925-4934.	1.2	3
78	Ligand entry in human ileal bile acid-binding protein is mediated by histidine protonation. Scientific Reports, 2019, 9, 4825.	1.6	3
79	The C-terminal tail extension of myosin 16 acts as a molten globule, including intrinsically disordered regions, and interacts with the N-terminal ankyrin. Journal of Biological Chemistry, 2021, 297, 100716.	1.6	3
80	Pathogenic D76N Variant of Î²2-Microglobulin: Synergy of Diverse Effects in Both the Native and Amyloid States. Biology, 2021, 10, 1197.	1.3	3
81	Single-Molecule Studies of Amyloidogenic Proteins. , 2012, , 169-210.		1
82	The Single-Cell Transcriptomic Analysis of Prefrontal Pyramidal Cells and Interneurons Reveals the Neuronal Expression of Genes Encoding Antimicrobial Peptides and Immune Proteins. Frontiers in Immunology, 2021, 12, 749433.	2.2	1
83	New Aspects of Lipid-Protein Interactions Revealed by Calmodulin Binding to the Lipid Mediator Sphingosylphosphorylcholine. Biophysical Journal, 2010, 98, 675a.	0.2	0
84	Self-Association and DNA Binding of hsRad51 Studied by Pressure Perturbation Spectroscopy. Biophysical Journal, 2012, 102, 282a.	0.2	0
85	Improved Secondary Structure Determination and Fold Prediction by Circular Dichroism Spectroscopy. Biophysical Journal, 2013, 104, 567a.	0.2	0
86	Structural Stability of Rad51 Filaments of Self-Aggregates and of Presynaptic Complexes Studied by Electron Microscopy and Pressure Tuning Fluorescence Spectroscopy. Biophysical Journal, 2013, 104, 422a.	0.2	0
87	ATP Binding is Prerequisite to the Helical Structure of Human Rad51 Presynaptic Filament. Biophysical Journal, 2015, 108, 222a.	0.2	0
88	Amorphous Aggregation of Cytochrome C with Inherently low Amyloidogenicity is Characterized by the Metastability of Supersaturation and the Phase Diagram. Biophysical Journal, 2016, 110, 399a.	0.2	0
89	Improved Structural Estimation of Disordered Proteins by CD Spectroscopy: Method Development and Application. Biophysical Journal, 2018, 114, 587a.	0.2	0