Krishna M G Mallela

List of Publications by Year
in descending order

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32	751	516215 16	552369 26
papers	citations	h-index	g-index

35	35	35	808
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Manufacturing Challenges and Rational Formulation Development for AAV Viral Vectors. Journal of Pharmaceutical Sciences, 2021, 110, 2609-2624.	1.6	103
2	Effect of Polysorbate 20 and Polysorbate 80 on the Higher-Order Structure of a Monoclonal Antibody and Its Fab and Fc Fragments Probed Using 2D Nuclear Magnetic Resonance Spectroscopy. Journal of Pharmaceutical Sciences, 2017, 106, 3486-3498.	1.6	86
3	Missense mutations in dystrophin that trigger muscular dystrophy decrease protein stability and lead to cross-Î² aggregates. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 15069-15074.	3.3	68
4	Effect of photo-degradation on the structure, stability, aggregation, and function of an IgG1 monoclonal antibody. International Journal of Pharmaceutics, 2018, 547, 438-449.	2.6	45
5	Role of partial protein unfolding in alcoholâ€induced protein aggregation. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2625-2637.	1.5	41
6	Receptor binding, immune escape, and protein stability direct the natural selection of SARS-CoV-2 variants. Journal of Biological Chemistry, 2021, 297, 101208.	1.6	37
7	Effect of Peroxide- Versus Alkoxyl-Induced Chemical Oxidation on the Structure, Stability, Aggregation, and Function of a Therapeutic Monoclonal Antibody. Journal of Pharmaceutical Sciences, 2018, 107, 2789-2803.	1.6	30
8	Mechanisms of m-cresol-induced Protein Aggregation Studied Using a Model Protein Cytochrome c. Journal of Pharmaceutical Sciences, 2011, 100, 1679-1689.	1.6	29
9	Effect of Antimicrobial Preservatives on Partial Protein Unfolding and Aggregation. Journal of Pharmaceutical Sciences, 2013, 102, 365-376.	1.6	26
10	The N-Terminal Actin-Binding Tandem Calponin-Homology (CH) Domain ofÂDystrophin Is in a Closed Conformation in Solution and When Bound toÂF-actin. Biophysical Journal, 2012, 103, 1970-1978.	0.2	22
11	Antimicrobial preservatives induce aggregation of interferon alpha-2a: The order in which preservatives induce protein aggregation is independent of the protein. International Journal of Pharmaceutics, 2014, 472, 356-361.	2.6	21
12	The N-Terminal Flanking Region Modulates the Actin Binding Affinity of the Utrophin Tandem Calponin-Homology Domain. Biochemistry, 2017, 56, 2627-2636.	1.2	21
13	High yield soluble bacterial expression and streamlined purification of recombinant human interferon Î±-2a. Protein Expression and Purification, 2014, 99, 138-146.	0.6	20
14	The Actin Binding Affinity of the Utrophin Tandem Calponin-Homology Domain Is Primarily Determined by Its N-Terminal Domain. Biochemistry, 2014, 53, 1801-1809.	1.2	20
15	Role of Benzyl Alcohol in the Unfolding and Aggregation of Interferon Î±-2a. Journal of Pharmaceutical Sciences, 2015, 104, 407-415.	1.6	18
16	Effects of Tubing Type, Operating Parameters, and Surfactants on Particle Formation During Peristaltic Filling Pump Processing of a mAb Formulation. Journal of Pharmaceutical Sciences, 2020, 109, 1439-1448.	1.6	18
17	Sevoflurane-Induced Structural Changes in a Four-Î±-Helix Bundle Protein. Biochemistry, 2005, 44, 12128-12135.	1.2	14
18	Thermodynamic stability, unfolding kinetics, and aggregation of the Nâ€terminal actinâ€binding domains of utrophin and dystrophin. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1377-1392.	1.5	14

#	Article	IF	Citations
19	Effect of Chemical Oxidation on the Higher Order Structure, Stability, Aggregation, and Biological Function of Interferon Alpha-2a: Role of Local Structural Changes Detected by 2D NMR. Pharmaceutical Research, 2018, 35, 232.	1.7	14
20	The C-Terminal Domain of the Utrophin Tandem Calponin-Homology Domain Appears To Be Thermodynamically and Kinetically More Stable Than the Full-Length Protein. Biochemistry, 2014, 53, 2209-2211.	1.2	13
21	Interdomain Linker Determines Primarily the Structural Stability of Dystrophin and Utrophin Tandem Calponin-Homology Domains Rather than Their Actin-Binding Affinity. Biochemistry, 2015, 54, 5480-5488.	1.2	13
22	Missense Mutation Lys18Asn in Dystrophin that Triggers X-Linked Dilated Cardiomyopathy Decreases Protein Stability, Increases Protein Unfolding, and Perturbs Protein Structure, but Does Not Affect Protein Function. PLoS ONE, 2014, 9, e110439.	1.1	13
23	Expression and Characterization of a Four-Î±-Helix Bundle Protein That Binds the Volatile General Anesthetic Halothane. Biomacromolecules, 2005, 6, 1516-1523.	2.6	12
24	Convergent Evolution of Multiple Mutations Improves the Viral Fitness of SARS-CoV-2 Variants by Balancing Positive and Negative Selection. Biochemistry, 2022, 61, 963-980.	1.2	12
25	2D NMR Analysis of the Effect of Asparagine Deamidation Versus Methionine Oxidation on the Structure, Stability, Aggregation, and Function of a Therapeutic Protein. Molecular Pharmaceutics, 2019, 16, 4621-4635.	2.3	10
26	Antibody-Dependent Complement Responses toward SARS-CoV-2 Receptor-Binding Domain Immobilized on â€œPseudovirus-likeâ€•Nanoparticles. ACS Nano, 2022, , .	7.3	7
27	The N- and C-Terminal Domains Differentially Contribute to the Structure and Function of Dystrophin and Utrophin Tandem Calponin-Homology Domains. Biochemistry, 2015, 54, 6942-6950.	1.2	5
28	Tissue-Specificity of Dystrophinâ€“Actin Interactions: Isoform-Specific Thermodynamic Stability and Actin-Binding Function of Tandem Calponin-Homology Domains. ACS Omega, 2020, 5, 2159-2168.	1.6	4
29	Biophysical analysis of the effect of chemical modification by 4-oxononenal on the structure, stability, and function of binding immunoglobulin protein (BiP). PLoS ONE, 2017, 12, e0183975.	1.1	4
30	Biophysical Fitness Landscape of the SARS-CoV-2 Delta Variant Receptor Binding Domain. Journal of Molecular Biology, 2022, 434, 167622.	2.0	3
31	Structural changes in a four-alpha-helix bundle protein following sevoflurane binding. International Congress Series, 2005, 1283, 155-159.	0.2	1
32	The Nâ€terminal actin binding domain (ABD1) of dystrophin is in a closed conformation in solution and undergoes a conformational transition upon binding to Fâ€actin. FASEB Journal, 2012, 26, 773.5.	0.2	0