Tapan K Das

List of Publications by Year
in descending order

65 papers	2,021 citations	331670 21 h-index	243625 44 g-index
70 all docs	70 docs citations	70 times ranked	2000 citing authors

#	Article	IF	Citations
1	Stress Factors in Protein Drug Product Manufacturing and Their Impact on Product Quality. Journal of Pharmaceutical Sciences, 2022, 111, 868-886.	3.3	12
2	An Interlaboratory Comparison on the Characterization of a Sub-micrometer Polydisperse Particle Dispersion. Journal of Pharmaceutical Sciences, 2022, 111, 699-709.	3.3	6
3	Stress Factors in Primary Packaging, Transportation and Handling of Protein Drug Products and Their Impact on Product Quality. Journal of Pharmaceutical Sciences, 2022, 111, 887-902.	3.3	12
4	Nucleation in Protein Aggregation in Biotherapeutic Development: A look into the Heart of the Event. Journal of Pharmaceutical Sciences, 2022, 111, 951-959.	3.3	8
5	Emerging Challenges and Innovations in Surfactant-mediated Stabilization of Biologic Formulations. Journal of Pharmaceutical Sciences, 2022, 111, 919-932.	3.3	14
6	A Cluster of Articles in Memory of Wim Jiskoot, Ph.D.. Journal of Pharmaceutical Sciences, 2022, 111, 859-860.	3.3	0
7	A Detailed Protocol for Generation of Therapeutic Antibodies with Galactosylated Glycovariants at Laboratory Scale Using In-Vitro Glycoengineering Technology. Journal of Pharmaceutical Sciences, 2021, 110, 935-945.	3.3	1
8	Mimicking Low pH Virus Inactivation Used in Antibody Manufacturing Processes: Effect of Processing Conditions and Biophysical Properties on Antibody Aggregation and Particle Formation. Journal of Pharmaceutical Sciences, 2021, 110, 3188-3199.	3.3	4
9	Structure-Function Assessment and High-Throughput Quantification of Site-Specific Aspartate Isomerization in Monoclonal Antibody Using a Novel Analytical Tool Kit. Journal of Pharmaceutical Sciences, 2020, 109, 422-428.	3.3	7
10	Stress Factors in mAb Drug Substance Production Processes: Critical Assessment of Impact on Product Quality and Control Strategy. Journal of Pharmaceutical Sciences, 2020, 109, 116-133.	3.3	41
11	A Multicompany Assessment of Submicron Particle Levels by NTA and RMM in a Wide Range of Late-Phase Clinical and Commercial Biotechnology-Derived Protein Products. Journal of Pharmaceutical Sciences, 2020, 109, 830-844.	3.3	17
12	Unique Impacts of Methionine Oxidation, Tryptophan Oxidation, and Asparagine Deamidation on Antibody Stability and Aggregation. Journal of Pharmaceutical Sciences, 2020, 109, 656-669.	3.3	35
13	Bridging size and charge variants of a therapeutic monoclonal antibody by two-dimensional liquid chromatography. Journal of Pharmaceutical and Biomedical Analysis, 2020, 183, 113178.	2.8	10
14	Characterization of therapeutic antibody fragmentation using automated capillary western blotting as an orthogonal analytical technique. Electrophoresis, 2019, 40, 2888-2898.	2.4	4
15	Quadrupole Dalton-Based Controlled Proteolysis Method for Characterization of Higher Order Protein Structure. Analytical Chemistry, 2019, 91, 5339-5345.	6.5	6
16	Deamidation Can Compromise Antibody Colloidal Stability and Enhance Aggregation in a pH-Dependent Manner. Molecular Pharmaceutics, 2019, 16, 1939-1949.	4.6	21
17	Probing the Tryptophan Environment in Therapeutic Proteins: Implications for Higher Order Structure on Tryptophan Oxidation. Journal of Pharmaceutical Sciences, 2019, 108, 1944-1952.	3.3	20
18	Impact of Tryptophan Oxidation in Complementarity-Determining Regions of Two Monoclonal Antibodies on Structure-Function Characterized by Hydrogen-Deuterium Exchange Mass Spectrometry and Surface Plasmon Resonance. Pharmaceutical Research, 2019, 36, 24.	3.5	21

#	Article	IF	Citations
19	Submicron Protein Particle Characterization using Resistive Pulse Sensing and Conventional Light Scattering Based Approaches. Pharmaceutical Research, 2018, 35, 58.	3.5	10
20	Challenges and new frontiers in analytical characterization of antibody-drug conjugates. MAbs, 2018, 10, 222-243.	5.2	79
21	A three-point identity criteria tool for establishing product identity using icIEF method. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2018, 1083, 271-277.	2.3	3
22	Enhanced Precision of Circular Dichroism Spectral Measurements Permits Detection of Subtle Higher Order Structural Changes in Therapeutic Proteins. Journal of Pharmaceutical Sciences, 2018, 107, 2559-2569.	3.3	15
23	Detection and Identification of the Vibrational Markers for the Quantification of Methionine Oxidation in Therapeutic Proteins. Analytical Chemistry, 2018, 90, 6959-6966.	6.5	19
24	Comparative study of therapeutic antibody candidates derived from miniâ€pool and clonal cell lines. Biotechnology Progress, 2017, 33, 1456-1462.	2.6	26
25	Interference from Proteins and Surfactants on Particle Size Distributions Measured by Nanoparticle Tracking Analysis (NTA). Pharmaceutical Research, 2017, 34, 800-808.	3.5	27
26	Codon-Directed Determination of the Biological Causes of Sequence Variants in Therapeutic Proteins. Analytical Chemistry, 2017, 89, 12749-12755.	6.5	2
27	Identification and quantification of signal peptide variants in an IgG1 monoclonal antibody produced in mammalian cell lines. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2017, 1068-1069, 193-200.	2.3	12
28	Mapping the Binding Interface in a Noncovalent Size Variant of a Monoclonal Antibody Using Native Mass Spectrometry, Hydrogenâ€"Deuterium Exchange Mass Spectrometry, and Computational Analysis. Journal of Pharmaceutical Sciences, 2017, 106, 3222-3229.	3.3	10
29	Characterization of Aggregation Propensity of a Human Fc-Fusion Protein Therapeutic by Hydrogen/Deuterium Exchange Mass Spectrometry. Journal of the American Society for Mass Spectrometry, 2017, 28, 795-802.	2.8	20
30	A Biopharmaceutical Industry Perspective on the Control of Visible Particles in Biotechnology-Derived Injectable Drug Products. PDA Journal of Pharmaceutical Science and Technology, 2016, 70, 392-408.	0.5	37
31	Technical Decision Making With Higher Order Structure Data: Perspectives on Higher Order Structure Characterization From the Biopharmaceutical Industry. Journal of Pharmaceutical Sciences, 2016, 105, 3465-3470.	3.3	26
32	Isomerization and Oxidation in the Complementarity-Determining Regions of a Monoclonal Antibody: A Study of the Modificationâ€"Structureâ€"Function Correlations by Hydrogenâ€"Deuterium Exchange Mass Spectrometry. Analytical Chemistry, 2016, 88, 2041-2050.	6.5	66
33	Investigation of Color in a Fusion Protein Using Advanced Analytical Techniques: Delineating Contributions from Oxidation Products and Process Related Impurities. Pharmaceutical Research, 2016, 33, 932-941.	3.5	22
34	Heterogeneous glycoform separation by process chromatography: I. Journal of Chromatography A, 2015, 1404, 51-59.	3.7	4
35	Protein Particulate Detection Issues in Biotherapeutics Developmentâ€"Current Status. AAPS PharmSciTech, 2012, 13, 732-746.	3.3	93
36	Aggregation and pHâ€"Temperature Phase Behavior for Aggregates of an IgG2 Antibody. Journal of Pharmaceutical Sciences, 2012, 101, 1678-1687.	3.3	54

#	Article	IF	Citations
37	Predicting solution aggregation rates for therapeutic proteins: Approaches and challenges. International Journal of Pharmaceutics, 2011, 418, 318-333.	5.2	128
38	Investigation of PEG Crystallization in Frozen and Freezeâ€Dried PEGylated Recombinant Human Growth Hormoneâ€"Sucrose Systems: Implications on Storage Stability. Journal of Pharmaceutical Sciences, 2011, 100, 3062-3075.	3.3	14
39	Modulation of the active site conformation by site-directed mutagenesis in cytochrome c oxidase from Paracoccus denitrificans. Journal of Inorganic Biochemistry, 2010, 104, 318-323.	3.5	9
40	Ultrafiltration of a highly self-associating protein. Journal of Membrane Science, 2010, 353, 41-50.	8.2	6
41	Modulation Of The Conformation Of Cytochrome C Oxidase From Paracoccus Denitrificans By Active-Site Mutations. , 2010, , .		0
42	Potential aggregation prone regions in biotherapeutics. MAbs, 2009, 1, 254-267.	5.2	173
43	Impact of denaturation with urea on recombinant apolipoprotein A-IMilano ion-exchange adsorption: Equilibrium uptake behavior and protein mass transfer kinetics. Biotechnology Journal, 2007, 2, 110-120.	3.5	9
44	Multiple Active Site Conformers in the Carbon Monoxide Complexes of Trematode Hemoglobins. Journal of Biological Chemistry, 2006, 281, 11471-11479.	3.4	6
45	Distal Heme Pocket Conformers of Carbonmonoxy Derivatives of Ascaris Hemoglobin. Journal of Biological Chemistry, 2004, 279, 10433-10441.	3.4	10
46	NMR studies on interaction of lauryl maltoside with cytochrome c oxidase: a model for surfactant interaction with the membrane protein. Journal of Inorganic Biochemistry, 2002, 91, 116-124.	3.5	17
47	pH-Dependent Structural Changes at the Heme-Copper Binuclear Center of Cytochrome c Oxidase. Biophysical Journal, 2001, 80, 2039-2045.	0.5	33
48	Simultaneous observation of the O--O and Fe--O2 stretching modes in oxyhemoglobins. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 479-484.	7.1	141
49	Structural investigations of the hemoglobin of the cyanobacterium Synechocystis PCC6803 reveal a unique distal heme pocket. FEBS Journal, 2000, 267, 4770-4780.	0.2	96
50	Effect of Adriamycin on the boundary lipid structure of cytochrome c oxidase: pico-second time-resolved fluorescence depolarization studies. Biophysical Chemistry, 2000, 86, 15-28.	2.8	13
51	Chlamydomonas Chloroplast Ferrous Hemoglobin. Journal of Biological Chemistry, 1999, 274, 6898-6910.	3.4	106
52	Hydroxide Rather Than Histidine Is Coordinated to the Heme in Five-coordinate Ferric Scapharca inaequivalvisHemoglobin. Journal of Biological Chemistry, 1999, 274, 2916-2919.	3.4	18
53	The Heme Environment in Barley Hemoglobin. Journal of Biological Chemistry, 1999, 274, 4207-4212.	3.4	45
54	Pentacoordinate Hemin Derivatives in Sodium Dodecyl Sulfate Micelles: Model Systems for the Assignment of the Fifth Ligand in Ferric Heme Proteins. Biophysical Journal, 1999, 77, 1143-1149.	0.5	96

#	Article	IF	Citations
55	Preservation of the Native Structure in Myoglobin at Low pH by Solâˆ’Gel Encapsulation. Journal of the American Chemical Society, 1998, 120, 10268-10269.	13.7	56
56	Folding of cytochrome c initiated by submillisecond mixing. Nature Structural and Molecular Biology, 1997, 4, 44-50.	8.2	218
57	Rotational dynamics of lipidâ€“detergent mixtures probed by a cyanine dye: a mechanism for vesicle formation. Journal of the Chemical Society, Faraday Transactions, 1996, 92, 4279-4283.	1.7	3
58	Protein-surfactant interaction: Selective unfolding in hemeproteins. Journal of Chemical Sciences, 1996, 108, 313-313.	1.5	0
59	Time-resolved fluorescence study of the single tryptophan in thiocyanate and azide derivatives of horseradish peroxidase: Implication for apH-induced conformational change in the heme cavity. Journal of Chemical Sciences, 1995, 107, 505-518.	1.5	1
60	Heme CD as a probe for monitoring local structural changes in hemeproteins: Alkaline transition in hemeproteins. Journal of Chemical Sciences, 1995, 107, 497-503.	1.5	4
61	Miceile-induced release of heme-NO from nitric oxide complex of myogiobin. Journal of Chemical Sciences, 1994, 106, 763-763.	1.5	0
62	Picosecond fluorescence decay of tryptophan in bovine cytochrome-c oxidase. Journal of Chemical Sciences, 1994, 106, 766-766.	1.5	0
63	Time-resolved study of tryptophan fluorescence in vesicle reconstituted cytochrome oxidase. FEBS Letters, 1993, 336, 211-214.	2.8	11
64	Mechanism of response of potential-sensitive dyes studied by time-resolved fluorescence. Biophysical Journal, 1993, 64, 1122-1132.	0.5	35
65	Dualâ€detection approach for charge variant analysis of monoclonal antibody combination products using imaged capillary isoelectric focusing. Electrophoresis, 0, , .	2.4	3