Salvador Ventura

List of Publications by Year
in descending order

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256 papers	15,351 citations	31902 53 h-index	21474 114 g-index

269 all docs	269 docs citations	269 times ranked	23294 citing authors

#	Article	IF	Citations
1	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). Autophagy, 2016, 12, 1-222.	4.3	4,701
2	AGGRESCAN: a server for the prediction and evaluation of "hot spots" of aggregation in polypeptides. BMC Bioinformatics, 2007, 8, 65.	1.2	845
3	Protein quality in bacterial inclusion bodies. Trends in Biotechnology, 2006, 24, 179-185.	4.9	310
4	Aggregation as bacterial inclusion bodies does not imply inactivation of enzymes and fluorescent proteins. Microbial Cell Factories, 2005, 4, 27.	1.9	266
5	DisProt 7.0: a major update of the database of disordered proteins. Nucleic Acids Research, 2017, 45, D219-D227.	6.5	242
6	Short amino acid stretches can mediate amyloid formation in globular proteins: The Src homology 3 (SH3) case. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 7258-7263.	3.3	241
7	Amyloid-like Properties of Bacterial Inclusion Bodies. Journal of Molecular Biology, 2005, 347, 1025-1037.	2.0	217
8	Amyloid Fibril Formation by a Partially Structured Intermediate State of Î±-Chymotrypsin. Journal of Molecular Biology, 2004, 342, 321-331.	2.0	206
9	AGGRESCAN3D (A3D): server for prediction of aggregation properties of protein structures. Nucleic Acids Research, 2015, 43, W306-W313.	6.5	201
10	Design, Selection, and Characterization of Thioflavin-Based Intercalation Compounds with Metal Chelating Properties for Application in Alzheimerâ€™s Disease. Journal of the American Chemical Society, 2009, 131, 1436-1451.	6.6	196
11	Critical assessment of protein intrinsic disorder prediction. Nature Methods, 2021, 18, 472-481.	9.0	187
12	Prediction of "hot spots" of aggregation in disease-linked polypeptides. BMC Structural Biology, 2005, 5, 18.	2.3	173
13	Small molecule inhibits Î±-synuclein aggregation, disrupts amyloid fibrils, and prevents degeneration of dopaminergic neurons. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 10481-10486.	3.3	166
14	Mutagenesis of the central hydrophobic cluster in Abeta42 Alzheimer's peptide. Side-chain properties correlate with aggregation propensities. FEBS Journal, 2006, 273, 658-668.	2.2	164
15	Folding of small disulfide-rich proteins: clarifying the puzzle. Trends in Biochemical Sciences, 2006, 31, 292-301.	3.7	154
16	DisProt: intrinsic protein disorder annotation in 2020. Nucleic Acids Research, 2020, 48, D269-D276.	6.5	141
17	Protein aggregation: Mechanisms and functional consequences. International Journal of Biochemistry and Cell Biology, 2012, 44, 1541-1554.	1.2	139
18	Repositioning tolcapone as a potent inhibitor of transthyretin amyloidogenesis and associated cellular toxicity. Nature Communications, 2016, 7, 10787.	5.8	139

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19	Amyloids in bacterial inclusion bodies. Trends in Biochemical Sciences, 2009, 34, 408-416.	3.7	137
20	Staphylococcal Bap Proteins Build Amyloid Scaffold Biofilm Matrices in Response to Environmental Signals. PLoS Pathogens, 2016, 12, e1005711.	2.1	135
21	Effect of temperature on protein quality in bacterial inclusion bodies. FEBS Letters, 2006, 580, 6471-6476.	1.3	133
22	Inclusion bodies: Specificity in their aggregation process and amyloid-like structure. Biochimica Et Biophysica Acta - Molecular Cell Research, 2008, 1783, 1815-1825.	1.9	131
23	Ile-Phe Dipeptide Self-Assembly: Clues to Amyloid Formation. Biophysical Journal, 2007, 92, 1732-1741.	0.2	129
24	DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. Nucleic Acids Research, 2022, 50, D480-D487.	6.5	117
25	Conformational strain in the hydrophobic core and its implications for protein folding and design. Nature Structural Biology, 2002, 9, 485-493.	9.7	100
26	Specific Hsp100 Chaperones Determine the Fate of the First Enzyme of the Plastidial Isoprenoid Pathway for Either Refolding or Degradation by the Stromal Clp Protease in Arabidopsis. PLoS Genetics, 2016, 12, e1005824.	1.5	100
27	Aggrescan3D (A3D) 2.0: prediction and engineering of protein solubility. Nucleic Acids Research, 2019, 47, W300-W307.	6.5	91
28	Bacterial Inclusion Bodies of Alzheimer's Disease Î²â€Amyloid Peptides Can Be Employed To Study Nativeâ€Like Aggregation Intermediate States. ChemBioChem, 2011, 12, 407-423.	1.3	90
29	Structure of human carboxypeptidase A4 with its endogenous protein inhibitor, latexin. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 3978-3983.	3.3	89
30	What Makes a Protein Sequence a Prion?. PLoS Computational Biology, 2015, 11, e1004013.	1.5	88
31	Sequence determinants of protein aggregation: tools to increase protein solubility. Microbial Cell Factories, 2005, 4, 11.	1.9	87
32	Detection of transient proteinâ€“protein interactions by bimolecular fluorescence complementation: The Abl-SH3 case. Proteomics, 2007, 7, 1023-1036.	1.3	85
33	Protein folding and aggregation in bacteria. Cellular and Molecular Life Sciences, 2010, 67, 2695-2715.	2.4	76
34	Environmental and genetic factors support the dissociation between Î±-synuclein aggregation and toxicity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E6506-E6515.	3.3	75
35	PrionW: a server to identify proteins containing glutamine/asparagine rich prion-like domains and their amyloid cores. Nucleic Acids Research, 2015, 43, W331-W337.	6.5	74
36	Discovering putative prion sequences in complete proteomes using probabilistic representations of Q/N-rich domains. BMC Genomics, 2013, 14, 316.	1.2	73

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37	The small GTPase Rab11 co-localizes with Â-synuclein in intracellular inclusions and modulates its aggregation, secretion and toxicity. Human Molecular Genetics, 2014, 23, 6732-6745.	1.4	73
38	Sulfated Polysaccharides Promote the Assembly of Amyloid Î²1â€“42 Peptide into Stable Fibrils of Reduced Cytotoxicity. Journal of Biological Chemistry, 2008, 283, 32471-32483.	1.6	70
39	Amyloidogenic Regions and Interaction Surfaces Overlap in Globular Proteins Related to Conformational Diseases. PLoS Computational Biology, 2009, 5, e1000476.	1.5	70
40	Prion and Non-prion Amyloids of the HET-s Prion forming Domain. Journal of Molecular Biology, 2007, 370, 768-783.	2.0	68
41	Biological role of bacterial inclusion bodies: a model for amyloid aggregation. FEBS Journal, 2011, 278, 2419-2427.	2.2	68
42	Prediction of the aggregation propensity of proteins from the primary sequence: Aggregation properties of proteomes. Biotechnology Journal, 2011, 6, 674-685.	1.8	68
43	Modulation of AÎ² ₄₂ fÃ¬brillogenesis by glycosaminoglycan structure. FASEB Journal, 2010, 24, 4250-4261.	0.2	66
44	High-Throughput Screening Methodology to Identify Alpha-Synuclein Aggregation Inhibitors. International Journal of Molecular Sciences, 2017, 18, 478.	1.8	66
45	Protein activity in bacterial inclusion bodies correlates with predicted aggregation rates. Journal of Biotechnology, 2006, 125, 110-113.	1.9	64
46	AGGRESCAN: Method, Application, and Perspectives for Drug Design. Methods in Molecular Biology, 2012, 819, 199-220.	0.4	64
47	Human kallikrein 6 activity is regulated via an autoproteolytic mechanism of activation/inactivation. Biological Chemistry, 2004, 385, 517-24.	1.2	62
48	Recent Structural and Computational Insights into Conformational Diseases. Current Medicinal Chemistry, 2008, 15, 1336-1349.	1.2	62
49	C-mannosylation supports folding and enhances stability of thrombospondin repeats. ELife, 2019, 8, .	2.8	62
50	Protein complementation assays: Approaches for the in vivo analysis of protein interactions. FEBS Letters, 2009, 583, 1684-1691.	1.3	60
51	Dissecting the contribution of Staphylococcus aureus Î±-phenol-soluble modulins to biofilm amyloid structure. Scientific Reports, 2016, 6, 34552.	1.6	57
52	The in Vivo and in Vitro Aggregation Properties of Globular Proteins Correlate With Their Conformational Stability: The SH3 Case. Journal of Molecular Biology, 2008, 378, 1116-1131.	2.0	56
53	Thioflavin-T excimer formation upon interaction with amyloid fibers. Chemical Communications, 2013, 49, 5745.	2.2	56
54	Characterization of Amyloid Cores in Prion Domains. Scientific Reports, 2016, 6, 34274.	1.6	56

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55	Protein Aggregation Profile of the Bacterial Cytosol. PLoS ONE, 2010, 5, e9383.	1.1	53
56	Overexpression of Human Procarboxypeptidase A2 in Pichia pastoris and Detailed Characterization of Its Activation Pathway. Journal of Biological Chemistry, 1998, 273, 3535-3541.	1.6	52
57	Study and selection of in vivo protein interactions by coupling bimolecular fluorescence complementation and flow cytometry. Nature Protocols, 2008, 3, 22-33.	5.5	51
58	pH-Responsive Self-Assembly of Amyloid Fibrils for Dual Hydrolase-Oxidase Reactions. ACS Catalysis, 2021, 11, 595-607.	5.5	49
59	Thioflavin-S staining coupled to flow cytometry. A screening tool to detect in vivo protein aggregation. Molecular BioSystems, 2012, 8, 2839.	2.9	47
60	Amyloids or prions? That is the question. Prion, 2015, 9, 200-206.	0.9	47
61	hnRNPDL Phase Separation Is Regulated by Alternative Splicing and Disease-Causing Mutations Accelerate Its Aggregation. Cell Reports, 2020, 30, 1117-1128.e5.	2.9	47
62	Fluorescent dye ProteoStat to detect and discriminate intracellular amyloidâ€like aggregates in Escherichia coli. Biotechnology Journal, 2014, 9, 1259-1266.	1.8	46
63	Mapping the Pro-region of Carboxypeptidase B by Protein Engineering. Journal of Biological Chemistry, 1999, 274, 19925-19933.	1.6	45
64	Combining Structural Aggregation Propensity and Stability Predictions To Redesign Protein Solubility. Molecular Pharmaceutics, 2018, 15, 3846-3859.	2.3	45
65	Computational prediction of protein aggregation: Advances in proteomics, conformation-specific algorithms and biotechnological applications. Computational and Structural Biotechnology Journal, 2020, 18, 1403-1413.	1.9	45
66	Amyloid-Like Protein Inclusions in Tobacco Transgenic Plants. PLoS ONE, 2010, 5, e13625.	1.1	44
67	The Rho Termination Factor of Clostridium botulinum Contains a Prion-Like Domain with a Highly Amyloidogenic Core. Frontiers in Microbiology, 2015, 6, 1516.	1.5	44
68	Thioflavin-S Staining of Bacterial Inclusion Bodies for the Fast, Simple, and Inexpensive Screening of Amyloid Aggregation Inhibitors. Current Medicinal Chemistry, 2014, 21, 1152-1159.	1.2	44
69	Chemical Chaperones as Novel Drugs for Parkinsonâ€™s Disease. Trends in Molecular Medicine, 2020, 26, 408-421.	3.5	43
70	PrionScan: an online database of predicted prion domains in complete proteomes. BMC Genomics, 2014, 15, 102.	1.2	42
71	Discovering Putative Prion-Like Proteins in Plasmodium falciparum: A Computational and Experimental Analysis. Frontiers in Microbiology, 2018, 9, 1737.	1.5	42
72	AlphaFold and the amyloid landscape. Journal of Molecular Biology, 2021, 433, 167059.	2.0	42

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73	Insights into the Origin of the Tendency of the PI3-SH3 Domain to form Amyloid Fibrils. Journal of Molecular Biology, 2002, 322, 1147-1158.	2.0	40
74	Effect of the surface charge of artificial model membranes on the aggregation of amyloid Î²-peptide. Biochimie, 2012, 94, 1730-1738.	1.3	40
75	The biofilm-associated surface protein Esp of Enterococcus faecalis forms amyloid-like fibers. Npj Biofilms and Microbiomes, 2020, 6, 15.	2.9	40
76	Î±-Helical peptidic scaffolds to target Î±-synuclein toxic species with nanomolar affinity. Nature Communications, 2021, 12, 3752.	5.8	40
77	Discovery of Novel Inhibitors of Amyloid Î²-Peptide 1â€“42 Aggregation. Journal of Medicinal Chemistry, 2012, 55, 9521-9530.	2.9	39
78	The chaperone DnaK controls the fractioning of functional protein between soluble and insoluble cell fractions in inclusion body-forming cells. Microbial Cell Factories, 2006, 5, 26.	1.9	38
79	The Role of Protein Sequence and Amino Acid Composition in Amyloid Formation: Scrambling and Backward Reading of IAPP Amyloid Fibrils. Journal of Molecular Biology, 2010, 404, 337-352.	2.0	38
80	Benzbromarone, Quercetin, and Folic Acid Inhibit Amylin Aggregation. International Journal of Molecular Sciences, 2016, 17, 964.	1.8	38
81	Characterization of Soft Amyloid Cores in Human Prion-Like Proteins. Scientific Reports, 2017, 7, 12134.	1.6	38
82	Designing proteins from the inside out. Proteins: Structure, Function and Bioinformatics, 2004, 56, 1-10.	1.5	37
83	Characterization of the amyloid bacterial inclusion bodies of the HET-s fungal prion. Microbial Cell Factories, 2009, 8, 56.	1.9	37
84	Computational analysis of candidate prion-like proteins in bacteria and their role. Frontiers in Microbiology, 2015, 6, 1123.	1.5	37
85	Minimalist Prion-Inspired Polar Self-Assembling Peptides. ACS Nano, 2018, 12, 5394-5407.	7.3	37
86	pH-Dependent Aggregation in Intrinsically Disordered Proteins Is Determined by Charge and Lipophilicity. Cells, 2020, 9, 145.	1.8	37
87	Tolcapone, a potent aggregation inhibitor for the treatment of familial leptomeningeal amyloidosis. FEBS Journal, 2021, 288, 310-324.	2.2	37
88	The Importance of a Gatekeeper Residue on the Aggregation of Transthyretin. Journal of Biological Chemistry, 2014, 289, 28324-28337.	1.6	35
89	The effects of the novel A53E alpha-synuclein mutation on its oligomerization and aggregation. Acta Neuropathologica Communications, 2016, 4, 128.	2.4	35
90	Studies on bacterial inclusion bodies. Future Microbiology, 2008, 3, 423-435.	1.0	34

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91	Biasing the native Î±-synuclein conformational ensemble towards compact states abolishes aggregation and neurotoxicity. Redox Biology, 2019, 22, 101135.	3.9	34
92	Using bacterial inclusion bodies to screen for amyloid aggregation inhibitors. Microbial Cell Factories, 2012, 11, 55.	1.9	33
93	Contribution of Disulfide Bonds to Stability, Folding, and Amyloid Fibril Formation: The PI3-SH3 Domain Case. Antioxidants and Redox Signaling, 2012, 16, 1-15.	2.5	32
94	Evolutionary selection for protein aggregation. Biochemical Society Transactions, 2012, 40, 1032-1037.	1.6	32
95	N-Terminal Protein Tails Act as Aggregation Protective Entropic Bristles: The SUMO Case. Biomacromolecules, 2014, 15, 1194-1203.	2.6	32
96	Protein aggregation into insoluble deposits protects from oxidative stress. Redox Biology, 2017, 12, 699-711.	3.9	32
97	ZPD-2, a Small Compound That Inhibits Î±-Synuclein Amyloid Aggregation and Its Seeded Polymerization. Frontiers in Molecular Neuroscience, 2019, 12, 306.	1.4	32
98	The aggregation properties of Escherichia coli proteins associated with their cellular abundance. Biotechnology Journal, 2011, 6, 752-760.	1.8	30
99	Dual Binding Mode of Metallacarborane Produces a Robust Shield on Proteins. Chemistry - A European Journal, 2019, 25, 12820-12829.	1.7	29
100	Insight into the specificity and severity of pathogenic mechanisms associated with missense mutations through experimental and structural perturbation analyses. Human Molecular Genetics, 2019, 28, 1-15.	1.4	29
101	Crystal structure of an oligomer of proteolytic zymogens: detailed conformational analysis of the bovine ternary complex and implications for their activation 1 1Edited by I. A. Wilson. Journal of Molecular Biology, 1997, 269, 861-880.	2.0	28
102	Amyloid fibril formation by bovine cytochromec. Spectroscopy, 2005, 19, 199-205.	0.8	28
103	Native Structure Protects SUMO Proteins from Aggregation into Amyloid Fibrils. Biomacromolecules, 2012, 13, 1916-1926.	2.6	28
104	Monitoring the interference of proteinâ€protein interactions in vivo by bimolecular fluorescence complementation: the DnaK case. Proteomics, 2008, 8, 3433-3442.	1.3	27
105	The Effect of Amyloidogenic Peptides on Bacterial Aging Correlates with Their Intrinsic Aggregation Propensity. Journal of Molecular Biology, 2012, 421, 270-281.	2.0	27
106	Role of Kinetic Intermediates in the Folding of Leech Carboxypeptidase Inhibitor. Journal of Biological Chemistry, 2004, 279, 37261-37270.	1.6	26
107	Linking amyloid protein aggregation and yeast survival. Molecular BioSystems, 2011, 7, 1121.	2.9	26
108	Yeast prions form infectious amyloid inclusion bodies in bacteria. Microbial Cell Factories, 2012, 11, 89.	1.9	26

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109	Association Between Foldability and Aggregation Propensity in Small Disulfide-Rich Proteins. Antioxidants and Redox Signaling, 2014, 21, 368-383.	2.5	25
110	Understanding and predicting protein misfolding and aggregation: Insights from proteomics. Proteomics, 2016, 16, 2570-2581.	1.3	25
111	A single cysteine post-translational oxidation suffices to compromise globular proteins kinetic stability and promote amyloid formation. Redox Biology, 2018, 14, 566-575.	3.9	25
112	Advances in the Prediction of Protein Aggregation Propensity. Current Medicinal Chemistry, 2019, 26, 3911-3920.	1.2	25
113	Kinetic and thermodynamic stability of bacterial intracellular aggregates. FEBS Letters, 2008, 582, 3669-3673.	1.3	24
114	Modeling amyloids in bacteria. Microbial Cell Factories, 2012, 11, 166.	1.9	24
115	Prion-like proteins and their computational identification in proteomes. Expert Review of Proteomics, 2017, 14, 335-350.	1.3	24
116	The Transcription Terminator Rho: A First Bacterial Prion. Trends in Microbiology, 2017, 25, 434-437.	3.5	24
117	AMYCO: evaluation of mutational impact on prion-like proteins aggregation propensity. BMC Bioinformatics, 2019, 20, 24.	1.2	24
118	Computational methods to predict protein aggregation. Current Opinion in Structural Biology, 2022, 73, 102343.	2.6	24
119	Energy barriers for HETâ€s prion forming domain amyloid formation. FEBS Journal, 2009, 276, 5053-5064.	2.2	23
120	Deciphering the role of the thermodynamic and kinetic stabilities of SH3 domains on their aggregation inside bacteria. Proteomics, 2010, 10, 4172-4185.	1.3	23
121	Procarboxypeptidase in rat pancreas Overall characterization and comparison of the activation processes. FEBS Journal, 1994, 222, 55-64.	0.2	22
122	Copper(II) and the pathological H50Q Î±-synuclein mutant: Environment meets genetics. Communicative and Integrative Biology, 2017, 10, e1270484.	0.6	22
123	Aggrescan3D standalone package for structure-based prediction of protein aggregation properties. Bioinformatics, 2019, 35, 3834-3835.	1.8	22
124	Scrambled Isomers as Key Intermediates in the Oxidative Folding of Ligand Binding Module 5 of the Low Density Lipoprotein Receptor. Journal of Biological Chemistry, 2008, 283, 13627-13637.	1.6	21
125	Prion-based nanomaterials and their emerging applications. Prion, 2018, 12, 266-272.	0.9	21
126	Cross-Î²-Sheet Supersecondary Structure in Amyloid Folds: Techniques for Detection and Characterization. Methods in Molecular Biology, 2012, 932, 237-257.	0.4	20

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127	Amyloid cores in prion domains: Key regulators for prion conformational conversion. Prion, 2017, 11, 31-39.	0.9	20
128	Rational design of small molecules able to inhibit Î±-synuclein amyloid aggregation for the treatment of Parkinsonâ€™s disease. Journal of Enzyme Inhibition and Medicinal Chemistry, 2020, 35, 1727-1735.	2.5	20
129	Structure and dynamics of the potato carboxypeptidase inhibitor by 1H and 15N NMR. Proteins: Structure, Function and Bioinformatics, 2003, 50, 410-422.	1.5	19
130	Detailed molecular comparison between the inhibition mode of A/B-type carboxypeptidases in the zymogen state and by the endogenous inhibitor latexin. Cellular and Molecular Life Sciences, 2005, 62, 1996-2014.	2.4	19
131	MIRRAGGE â€“ Minimum Information Required for Reproducible AGGregation Experiments. Frontiers in Molecular Neuroscience, 2020, 13, 582488.	1.4	19
132	Secondary Binding Site of the Potato Carboxypeptidase Inhibitor. Contribution to Its Structure, Folding, and Biological Properties. Biochemistry, 2004, 43, 7973-7982.	1.2	18
133	NMR Structural Characterization and Computational Predictions of the Major Intermediate in Oxidative Folding of Leech Carboxypeptidase Inhibitor. Structure, 2005, 13, 1193-1202.	1.6	18
134	Temperature Dependence of the Aggregation Kinetics of Sup35 and Ure2p Yeast Prions. Biomacromolecules, 2012, 13, 474-483.	2.6	18
135	Amyloid Formation by Human Carboxypeptidase D Transthyretin-like Domain under Physiological Conditions. Journal of Biological Chemistry, 2014, 289, 33783-33796.	1.6	18
136	Mammalian prion protein (PrP) forms conformationally different amyloid intracellular aggregates in bacteria. Microbial Cell Factories, 2015, 14, 174.	1.9	18
137	One ring is sufficient to inhibit Î±-synuclein aggregation. Neural Regeneration Research, 2022, 17, 508.	1.6	18
138	Study of a Major Intermediate in the Oxidative Folding of Leech Carboxypeptidase Inhibitor: Contribution of the Fourth Disulfide Bond. Journal of Molecular Biology, 2005, 352, 961-975.	2.0	17
139	Characterizing the Tick Carboxypeptidase Inhibitor. Journal of Biological Chemistry, 2006, 281, 22906-22916.	1.6	17
140	Protein aggregation propensity is a crucial determinant of intracellular inclusion formation and quality control degradation. Biochimica Et Biophysica Acta - Molecular Cell Research, 2013, 1833, 2714-2724.	1.9	17
141	Inhibition of Human Transthyretin Aggregation by Non-Steroidal Anti-Inflammatory Compounds: A Structural and Thermodynamic Analysis. International Journal of Molecular Sciences, 2013, 14, 5284-5311.	1.8	17
142	Molecular and Clinical Aspects of Protein Aggregation Assays in Neurodegenerative Diseases. Molecular Neurobiology, 2018, 55, 7588-7605.	1.9	17
143	In silico Characterization of Human Prion-Like Proteins: Beyond Neurological Diseases. Frontiers in Physiology, 2019, 10, 314.	1.3	17
144	Prionâ€like proteins: from computational approaches to proteomeâ€wide analysis. FEBS Open Bio, 2021, 11, 2400-2417.	1.0	17

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145	Designing Out Disulfide Bonds of Leech Carboxypeptidase Inhibitor: Implications for Its Folding, Stability and Function. Journal of Molecular Biology, 2009, 392, 529-546.	2.0	16
146	The Mitochondrial Intermembrane Space Oxireductase Mia40 Funnels the Oxidative Folding Pathway of the Cytochrome c Oxidase Assembly Protein Cox19. Journal of Biological Chemistry, 2014, 289, 9852-9864.	1.6	16
147	Selection against toxic aggregation-prone protein sequences in bacteria. Biochimica Et Biophysica Acta - Molecular Cell Research, 2014, 1843, 866-874.	1.9	16
148	Cavity filling mutations at the thyroxine-binding site dramatically increase transthyretin stability and prevent its aggregation. Scientific Reports, 2017, 7, 44709.	1.6	16
149	Prion soft amyloid core driven self-assembly of globular proteins into bioactive nanofibrils. Nanoscale, 2019, 11, 12680-12694.	2.8	16
150	The N-terminal Helix Controls the Transition between the Soluble and Amyloid States of an FF Domain. PLoS ONE, 2013, 8, e58297.	1.1	16
151	Design and NMR conformational study of a Î²-sheet peptide based on Betanova and WW domains. Protein Science, 2006, 15, 2278-2289.	3.1	15
152	Deciphering the Structural Basis That Guides the Oxidative Folding of Leech-derived Tryptase Inhibitor. Journal of Biological Chemistry, 2009, 284, 35612-35620.	1.6	15
153	Human Stefin B Role in Cell's Response to Misfolded Proteins and Autophagy. PLoS ONE, 2014, 9, e102500.	1.1	15
154	DispHred: A Server to Predict pH-Dependent Orderâ€“Disorder Transitions in Intrinsically Disordered Proteins. International Journal of Molecular Sciences, 2020, 21, 5814.	1.8	15
155	Coiled-coil inspired functional inclusion bodies. Microbial Cell Factories, 2020, 19, 117.	1.9	15
156	Direct interaction between a human digestive protease and the mucoadhesive poly(acrylic acid). Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 784-791.	2.5	14
157	Bimolecular Fluorescence Complementation: Illuminating Cellular Protein Interactions. Current Molecular Medicine, 2011, 11, 582-598.	0.6	14
158	In vivo amyloid aggregation kinetics tracked by timeâ€lapse confocal microscopy in realâ€time. Biotechnology Journal, 2016, 11, 172-177.	1.8	14
159	Disulfide driven folding for a conditionally disordered protein. Scientific Reports, 2017, 7, 16994.	1.6	14
160	AGGRESCAN3D: Toward the Prediction of the Aggregation Propensities of Protein Structures. Methods in Molecular Biology, 2018, 1762, 427-443.	0.4	14
161	Computational re-design of protein structures to improve solubility. Expert Opinion on Drug Discovery, 2019, 14, 1077-1088.	2.5	14
162	Histone H1 Favors Folding and Parallel Fibrillar Aggregation of the 1â€“42 Amyloid-Î² Peptide. Langmuir, 2015, 31, 6782-6790.	1.6	13

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163	Perfecting prediction of mutational impact on the aggregation propensity of the <scp>ALS</scp>â€associated hn<scp>RNPA</scp>2 prionâ€like protein. FEBS Letters, 2017, 591, 1966-1971.	1.3	13
164	Inhibition of Î±-Synuclein Aggregation and Mature Fibril Disassembling With a Minimalistic Compound, ZPDm. Frontiers in Bioengineering and Biotechnology, 2020, 8, 588947.	2.0	13
165	The prion-like RNA-processing protein HNRPDL forms inherently toxic amyloid-like inclusion bodies in bacteria. Microbial Cell Factories, 2015, 14, 102.	1.9	12
166	MED15 prion-like domain forms a coiled-coil responsible for its amyloid conversion and propagation. Communications Biology, 2021, 4, 414.	2.0	12
167	Functionalized Prion-Inspired Amyloids for Biosensor Applications. Biomacromolecules, 2021, 22, 2822-2833.	2.6	12
168	Multifunctional antibody-conjugated coiled-coil protein nanoparticles for selective cell targeting. Acta Biomaterialia, 2021, 131, 472-482.	4.1	12
169	Small molecules to prevent the neurodegeneration caused by Î±-synuclein aggregation. Neural Regeneration Research, 2020, 15, 2260.	1.6	12
170	Oxidative Folding of Leech-Derived Tryptase Inhibitor Via Native Disulfide-Bonded Intermediates. Antioxidants and Redox Signaling, 2008, 10, 77-86.	2.5	11
171	Zinc induced folding is essential for TIM15 activity as an mtHsp70 chaperone. Biochimica Et Biophysica Acta - General Subjects, 2013, 1830, 2139-2149.	1.1	11
172	Amyloid properties of the leader peptide of variant B cystatin C: implications for Alzheimer and macular degeneration. FEBS Letters, 2016, 590, 644-654.	1.3	11
173	Functional Amyloids Germinate in Plants. Trends in Plant Science, 2021, 26, 7-10.	4.3	11
174	Design, synthesis and structure-activity evaluation of novel 2-pyridone-based inhibitors of Î±-synuclein aggregation with potentially improved BBB permeability. Bioorganic Chemistry, 2021, 117, 105472.	2.0	11
175	Global Protein Stabilization Does Not Suffice to Prevent Amyloid Fibril Formation. ACS Chemical Biology, 2018, 13, 2094-2105.	1.6	10
176	The fitness cost and benefit of phaseâ€separated protein deposits. Molecular Systems Biology, 2019, 15, e8075.	3.2	10
177	Computational prediction and redesign of aberrant protein oligomerization. Progress in Molecular Biology and Translational Science, 2020, 169, 43-83.	0.9	10
178	SolupHred: a server to predict the pH-dependent aggregation of intrinsically disordered proteins. Bioinformatics, 2021, 37, 1602-1603.	1.8	10
179	Multifunctional Amyloid Oligomeric Nanoparticles for Specific Cell Targeting and Drug Delivery. Biomacromolecules, 2020, 21, 4302-4312.	2.6	10
180	Soluble Assemblies in the Fibrillation Pathway of Prion-Inspired Artificial Functional Amyloids are Highly Cytotoxic. Biomacromolecules, 2020, 21, 2334-2345.	2.6	10

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181	The NMR Structures of the Major Intermediates of the Two-domain Tick Carboxypeptidase Inhibitor Reveal Symmetry in Its Folding and Unfolding Pathways. Journal of Biological Chemistry, 2008, 283, 27110-27120.	1.6	9
182	Protease Inhibitors as Models for the Study of Oxidative Folding. Antioxidants and Redox Signaling, 2011, 14, 97-112.	2.5	9
183	Trifluoroethanol Modulates Amyloid Formation by the All Î±-Helical URN1 FF Domain. International Journal of Molecular Sciences, 2013, 14, 17830-17844.	1.8	9
184	Proteome response at the edge of protein aggregation. Open Biology, 2015, 5, 140221.	1.5	9
185	A fast and specific method to screen for intracellular amyloid inhibitors using bacterial model systems. European Journal of Medicinal Chemistry, 2016, 121, 785-792.	2.6	9
186	Computational Assessment of Bacterial Protein Structures Indicates a Selection Against Aggregation. Cells, 2019, 8, 856.	1.8	9
187	Atomistic fibrillar architectures of polar prion-inspired heptapeptides. Chemical Science, 2020, 11, 13143-13151.	3.7	9
188	Cryptic amyloidogenic regions in intrinsically disordered proteins: Function and disease association. Computational and Structural Biotechnology Journal, 2021, 19, 4192-4206.	1.9	9
189	Screening for Amyloid Aggregation: In-Silico, In-Vitro and In-Vivo Detection. Current Protein and Peptide Science, 2014, 15, 477-489.	0.7	9
190	Discovery of Neuroprotective Agents Based on a 5-(4-Pyridinyl)-1,2,4-triazole Scaffold. ACS Chemical Neuroscience, 2022, 13, 581-586.	1.7	9
191	Folding specificity induced by loop stiffness. Protein Science, 2003, 12, 1473-1482.	3.1	8
192	Detecting and Interfering Protein Interactions: Towards the Control of Biochemical Pathways. Current Medicinal Chemistry, 2009, 16, 362-379.	1.2	8
193	Dual Antibody-Conjugated Amyloid Nanorods to Promote Selective Cellâ€“Cell Interactions. ACS Applied Materials & Interfaces, 2021, 13, 14875-14884.	4.0	8
194	SGnn: A Web Server for the Prediction of Prion-Like Domains Recruitment to Stress Granules Upon Heat Stress. Frontiers in Molecular Biosciences, 2021, 8, 718301.	1.6	8
195	Disease-associated mutations impacting BC-loop flexibility trigger long-range transthyretin tetramer destabilization and aggregation. Journal of Biological Chemistry, 2021, 297, 101039.	1.6	8
196	Inducing Î±-synuclein compaction: a new strategy for inhibiting Î±-synuclein aggregation?. Neural Regeneration Research, 2019, 14, 1897.	1.6	8
197	In-Silico Analysis of pH-Dependent Liquid-Liquid Phase Separation in Intrinsically Disordered Proteins. Biomolecules, 2022, 12, 974.	1.8	8
198	Cutting at the right place. The importance of selective limited proteolysis in the activation of proproteinase E. FEBS Journal, 1998, 251, 839-844.	0.2	7

#	Article	IF	Citations
199	Oxidative Folding in the Mitochondrial Intermembrane Space in Human Health and Disease. International Journal of Molecular Sciences, 2013, 14, 2916-2927.	1.8	7
200	The Disordered C-Terminus of Yeast Hsf1 Contains a Cryptic Low-Complexity Amyloidogenic Region. International Journal of Molecular Sciences, 2018, 19, 1384.	1.8	7
201	A3D 2.0 Update for the Prediction and Optimization of Protein Solubility. Methods in Molecular Biology, 2022, 2406, 65-84.	0.4	7
202	Is a cure for Parkinsonâ€™s disease hiding inside us?. Trends in Biochemical Sciences, 2022, 47, 641-644.	3.7	7
203	Self-assembly of human latexin into amyloid-like oligomers. BMC Structural Biology, 2007, 7, 75.	2.3	6
204	Protein aggregation profile of the human kinome. Frontiers in Physiology, 2012, 3, 438.	1.3	6
205	Structure-Based Analysis of A19D, a Variant of Transthyretin Involved in Familial Amyloid Cardiomyopathy. PLoS ONE, 2013, 8, e82484.	1.1	6
206	Protein misfolding diseases. Future Science OA, 2015, 1, FSO38.	0.9	6
207	Detection of Protein Aggregation in Live Plasmodium Parasites. Antimicrobial Agents and Chemotherapy, 2020, 64, .	1.4	6
208	Prion domains as a driving force for the assembly of functional nanomaterials. Prion, 2020, 14, 170-179.	0.9	6
209	Pathological ATX3 Expression Induces Cell Perturbations in E. coli as Revealed by Biochemical and Biophysical Investigations. International Journal of Molecular Sciences, 2021, 22, 943.	1.8	6
210	Prion-like domain disease-causing mutations and misregulation of alternative splicing relevance in limb-girdle muscular dystrophy (LGMD) 1G. Neural Regeneration Research, 2020, 15, 2239.	1.6	6
211	The small aromatic compound SynuClean-D inhibits theÂaggregation and seeded polymerization of multiple Î±-synuclein strains. Journal of Biological Chemistry, 2022, 298, 101902.	1.6	6
212	Molecular dynamics study of amyloid formation of two Abl-SH3 domain peptides. Journal of Peptide Science, 2006, 12, 780-789.	0.8	5
213	Folding of Disulfide Proteins. , 2011, , .		5
214	Aggregation of the neuroblastoma-associated mutant (S120G) of the human nucleoside diphosphate kinase-A/NM23-H1 into amyloid fibrils. Naunyn-Schmiedeberg's Archives of Pharmacology, 2011, 384, 373-381.	1.4	5
215	Self-assembly of human amylin-derived peptides studied by atomic force microscopy and single molecule force spectroscopy. Soft Matter, 2012, 8, 1234-1242.	1.2	5
216	Curing bacterial infections with protein aggregates. Molecular Microbiology, 2016, 99, 827-830.	1.2	5

#	Article	IF	Citations
217	Plasticity in the Oxidative Folding Pathway of the High Affinity Nerita Versicolor Carboxypeptidase Inhibitor (NvCI). Scientific Reports, 2017, 7, 5457.	1.6	5
218	Decoding the role of coiled-coil motifs in human prion-like proteins. Prion, 2021, 15, 143-154.	0.9	5
219	Coiled-Coil Based Inclusion Bodies and Their Potential Applications. Frontiers in Bioengineering and Biotechnology, 2021, 9, 734068.	2.0	5
220	Spectroscopic Analysis of Amyloid Fibril Formation in SH3-Domains. Spectroscopy, 2003, 17, 647-652.	0.8	4
221	Protein Aggregation Acts as Strong Constraint During Evolution. , 2012, , 103-120.		4
222	Possible roles of amyloids in malaria pathophysiology. Future Science OA, 2015, 1, FSO43.	0.9	4
223	SOM0226, a repositioned compound for the treatment of TTR amyloidosis. Orphanet Journal of Rare Diseases, 2015, 10, .	1.2	4
224	Prediction of Protein Aggregation and Amyloid Formation. , 2017, , 205-263.		4
225	Characterization of Amyloid-Like Properties in Bacterial Intracellular Aggregates. Methods in Molecular Biology, 2015, 1258, 99-122.	0.4	4
226	DispHScan: A Multi-Sequence Web Tool for Predicting Protein Disorder as a Function of pH. Biomolecules, 2021, 11, 1596.	1.8	4
227	A3D database: structure-based predictions of protein aggregation for the human proteome. Bioinformatics, 2022, 38, 3121-3123.	1.8	4
228	CARs-DB: A Database of Cryptic Amyloidogenic Regions in Intrinsically Disordered Proteins. Frontiers in Molecular Biosciences, 0, 9, .	1.6	4
229	Oxidative Protein Folding: From the Test Tube to In Vivo Insights. Antioxidants and Redox Signaling, 2008, 10, 51-54.	2.5	3
230	Does Stoichiometry Drive Protein Folding?. Journal of Biomolecular Structure and Dynamics, 2011, 28, 655-656.	2.0	3
231	Protein Oxidative Folding in the Intermembrane Mitochondrial Space: More than Protein Trafficking. Current Protein and Peptide Science, 2012, 13, 224-231.	0.7	3
232	Multiple Î²â€sheet molecular dynamics of amyloid formation from two ABlâ€SH3 domain peptides. Biopolymers, 2012, 98, 557-566.	1.2	3
233	Intradomain Confinement of Disulfides in the Folding of Two Consecutive Modules of the LDL Receptor. PLoS ONE, 2015, 10, e0132141.	1.1	3
234	Editorial: Protein Solubility and Aggregation in Bacteria. Frontiers in Microbiology, 2016, 7, 1178.	1.5	3

#	Article	IF	Citations
235	Protein Environment: A Crucial Triggering Factor in Josephin Domain Aggregation: The Role of 2,2,2-Trifluoroethanol. International Journal of Molecular Sciences, 2018, 19, 2151.	1.8	3
236	Screening Protein Aggregation in Cells Using Fluorescent Labels Coupled to Flow Cytometry. Methods in Molecular Biology, 2019, 1873, 195-212.	0.4	3
237	Amyloidogenicity as a driving force for the formation of functional oligomers. Journal of Structural Biology, 2020, 212, 107604.	1.3	3
238	Oxidative Folding: Coupling Conformational Folding and Disulfide Formation. , 2011, , 1-22.		3
239	Influence of Cytoplasmatic Folding on Mitochondrial Import. Current Medicinal Chemistry, 2015, 22, 2349-2359.	1.2	3
240	Prediction of the Effect of pH on the Aggregation and Conditional Folding of Intrinsically Disordered Proteins with SolupHred and DispHred. Methods in Molecular Biology, 2022, 2449, 197-211.	0.4	3
241	Mammalian prion amyloid formation in bacteria. Prion, 2016, 10, 112-118.	0.9	2
242	A pyrene-inhibitor fluorescent probe with large Stokes shift for the staining of AÎ²1â€“42, Î±-synuclein, and amylin amyloid fibrils as well as amyloid-containing Staphylococcus aureus biofilms. Analytical and Bioanalytical Chemistry, 2019, 411, 251-265.	1.9	2
243	Crystallization and preliminary X-ray analysis of the ternary complex of procarboxypeptidase A from bovine pancreas. FEBS Letters, 1995, 367, 211-213.	1.3	1
244	About targets and causes in protein folding. Journal of Biomolecular Structure and Dynamics, 2013, 31, 970-972.	2.0	1
245	Aggregation propensity of neuronal receptors: potential implications in neurodegenerative disorders. Future Science OA, 2015, 1, FSO39.	0.9	1
246	Data on correlation between AÎ²42 structural aggregation propensity and toxicity in bacteria. Data in Brief, 2016, 7, 143-147.	0.5	1
247	Formation of Cross-Beta Supersecondary Structure by Soft-Amyloid Cores: Strategies for Their Prediction and Characterization. Methods in Molecular Biology, 2019, 1958, 237-261.	0.4	1
248	Editorial: Protein Aggregation and Solubility in Microorganisms (Archaea, Bacteria and Unicellular) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.5	1
249	Protein Aggregation and Its Prediction. NATO Science for Peace and Security Series A: Chemistry and Biology, 2015, , 115-127.	0.5	1
250	Protein aggregation into bacterial inclusion bodies is a specific kinetically driven process. Microbial Cell Factories, 2006, 5, S9.	1.9	0
251	Evaluation of the Impact of Protein Aggregation on Cellular Oxidative Stress in Yeast. Journal of Visualized Experiments, 2018, , .	0.2	0
252	Reply to Comment on â€œN-terminal Protein Tail Acts as Aggregation Protective Entropic Bristles: The SUMO Caseâ€• Biomacromolecules, 2020, 21, 3483-3484.	2.6	0

#	Article	IF	Citations
253	Dynamics study on single and multiple Î²-sheets. Advances in Experimental Medicine and Biology, 2009, 611, 293-294.	0.8	0
254	Structural and Computational Insights into Conformational Diseases: A Review. , 2015, , 134-182.		0
255	Amyloid Formation in Bacteria. , 2018, , 1-3.		0
256	Protocols for Rational Design of Protein Solubility and Aggregation Properties Using Aggrescan3D Standalone. Methods in Molecular Biology, 2022, 2340, 17-40.	0.4	0