

# 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	One ring is sufficient to inhibit $\hat{\alpha}$ -synuclein aggregation. <i>Neural Regeneration Research</i> , 2022, 17, 508.	1.6	18
2	DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. <i>Nucleic Acids Research</i> , 2022, 50, D480-D487.	6.5	117
3	A3D 2.0 Update for the Prediction and Optimization of Protein Solubility. <i>Methods in Molecular Biology</i> , 2022, 2406, 65-84.	0.4	7
4	Protocols for Rational Design of Protein Solubility and Aggregation Properties Using Aggrescan3D Standalone. <i>Methods in Molecular Biology</i> , 2022, 2340, 17-40.	0.4	0
5	Discovery of Neuroprotective Agents Based on a 5-(4-Pyridinyl)-1,2,4-triazole Scaffold. <i>ACS Chemical Neuroscience</i> , 2022, 13, 581-586.	1.7	9
6	Is a cure for Parkinson's disease hiding inside us?. <i>Trends in Biochemical Sciences</i> , 2022, 47, 641-644.	3.7	7
7	The small aromatic compound SynuClean-D inhibits the aggregation and seeded polymerization of multiple $\hat{\alpha}$ -synuclein strains. <i>Journal of Biological Chemistry</i> , 2022, 298, 101902.	1.6	6
8	Computational methods to predict protein aggregation. <i>Current Opinion in Structural Biology</i> , 2022, 73, 102343.	2.6	24
9	A3D database: structure-based predictions of protein aggregation for the human proteome. <i>Bioinformatics</i> , 2022, 38, 3121-3123.	1.8	4
10	Prediction of the Effect of pH on the Aggregation and Conditional Folding of Intrinsically Disordered Proteins with SolupHred and DispHred. <i>Methods in Molecular Biology</i> , 2022, 2449, 197-211.	0.4	3
11	In-Silico Analysis of pH-Dependent Liquid-Liquid Phase Separation in Intrinsically Disordered Proteins. <i>Biomolecules</i> , 2022, 12, 974.	1.8	8
12	SolupHred: a server to predict the pH-dependent aggregation of intrinsically disordered proteins. <i>Bioinformatics</i> , 2021, 37, 1602-1603.	1.8	10
13	Tolcapone, a potent aggregation inhibitor for the treatment of familial leptomeningeal amyloidosis. <i>FEBS Journal</i> , 2021, 288, 310-324.	2.2	37
14	Functional Amyloids Germinate in Plants. <i>Trends in Plant Science</i> , 2021, 26, 7-10.	4.3	11
15	Decoding the role of coiled-coil motifs in human prion-like proteins. <i>Prion</i> , 2021, 15, 143-154.	0.9	5
16	Pathological ATX3 Expression Induces Cell Perturbations in <i>E. coli</i> as Revealed by Biochemical and Biophysical Investigations. <i>International Journal of Molecular Sciences</i> , 2021, 22, 943.	1.8	6
17	MED15 prion-like domain forms a coiled-coil responsible for its amyloid conversion and propagation. <i>Communications Biology</i> , 2021, 4, 414.	2.0	12
18	Dual Antibody-Conjugated Amyloid Nanorods to Promote Selective Cell-Cell Interactions. <i>ACS Applied Materials &amp; Interfaces</i> , 2021, 13, 14875-14884.	4.0	8

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19	Critical assessment of protein intrinsic disorder prediction. <i>Nature Methods</i> , 2021, 18, 472-481.	9.0	187
20	AlphaFold and the amyloid landscape. <i>Journal of Molecular Biology</i> , 2021, 433, 167059.	2.0	42
21	Î±-Helical peptidic scaffolds to target Î±-synuclein toxic species with nanomolar affinity. <i>Nature Communications</i> , 2021, 12, 3752.	5.8	40
22	Prion-like proteins: from computational approaches to proteome-wide analysis. <i>FEBS Open Bio</i> , 2021, 11, 2400-2417.	1.0	17
23	Functionalized Prion-Inspired Amyloids for Biosensor Applications. <i>Biomacromolecules</i> , 2021, 22, 2822-2833.	2.6	12
24	SGnn: A Web Server for the Prediction of Prion-Like Domains Recruitment to Stress Granules Upon Heat Stress. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 718301.	1.6	8
25	Coiled-Coil Based Inclusion Bodies and Their Potential Applications. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 734068.	2.0	5
26	Disease-associated mutations impacting BC-loop flexibility trigger long-range transthyretin tetramer destabilization and aggregation. <i>Journal of Biological Chemistry</i> , 2021, 297, 101039.	1.6	8
27	Multifunctional antibody-conjugated coiled-coil protein nanoparticles for selective cell targeting. <i>Acta Biomaterialia</i> , 2021, 131, 472-482.	4.1	12
28	Cryptic amyloidogenic regions in intrinsically disordered proteins: Function and disease association. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 4192-4206.	1.9	9
29	pH-Responsive Self-Assembly of Amyloid Fibrils for Dual Hydrolase-Oxidase Reactions. <i>ACS Catalysis</i> , 2021, 11, 595-607.	5.5	49
30	DispHScan: A Multi-Sequence Web Tool for Predicting Protein Disorder as a Function of pH. <i>Biomolecules</i> , 2021, 11, 1596.	1.8	4
31	Design, synthesis and structure-activity evaluation of novel 2-pyridone-based inhibitors of Î±-synuclein aggregation with potentially improved BBB permeability. <i>Bioorganic Chemistry</i> , 2021, 117, 105472.	2.0	11
32	DisProt: intrinsic protein disorder annotation in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D269-D276.	6.5	141
33	Computational prediction and redesign of aberrant protein oligomerization. <i>Progress in Molecular Biology and Translational Science</i> , 2020, 169, 43-83.	0.9	10
34	MIRRAGGE “ Minimum Information Required for Reproducible AGGregation Experiments. <i>Frontiers in Molecular Neuroscience</i> , 2020, 13, 582488.	1.4	19
35	Inhibition of Î±-Synuclein Aggregation and Mature Fibril Disassembling With a Minimalistic Compound, ZPDm. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 588947.	2.0	13
36	Reply to Comment on “N-terminal Protein Tail Acts as Aggregation Protective Entropic Bristles: The SUMO Case”. <i>Biomacromolecules</i> , 2020, 21, 3483-3484.	2.6	0

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37	Amyloidogenicity as a driving force for the formation of functional oligomers. <i>Journal of Structural Biology</i> , 2020, 212, 107604.	1.3	3
38	DispHred: A Server to Predict pH-Dependent Order→Disorder Transitions in Intrinsically Disordered Proteins. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5814.	1.8	15
39	Multifunctional Amyloid Oligomeric Nanoparticles for Specific Cell Targeting and Drug Delivery. <i>Biomacromolecules</i> , 2020, 21, 4302-4312.	2.6	10
40	Rational design of small molecules able to inhibit $\alpha$ -synuclein amyloid aggregation for the treatment of Parkinson's disease. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 2020, 35, 1727-1735.	2.5	20
41	Editorial: Protein Aggregation and Solubility in Microorganisms (Archaea, Bacteria and Unicellular) <i>Trends in Microbiology</i> , 2020, 28, 100001.	1.5	1
42	Atomistic fibrillar architectures of polar prion-inspired heptapeptides. <i>Chemical Science</i> , 2020, 11, 13143-13151.	3.7	9
43	Detection of Protein Aggregation in Live <i>Plasmodium</i> Parasites. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	6
44	Coiled-coil inspired functional inclusion bodies. <i>Microbial Cell Factories</i> , 2020, 19, 117.	1.9	15
45	Soluble Assemblies in the Fibrillation Pathway of Prion-Inspired Artificial Functional Amyloids are Highly Cytotoxic. <i>Biomacromolecules</i> , 2020, 21, 2334-2345.	2.6	10
46	Prion domains as a driving force for the assembly of functional nanomaterials. <i>Prion</i> , 2020, 14, 170-179.	0.9	6
47	Computational prediction of protein aggregation: Advances in proteomics, conformation-specific algorithms and biotechnological applications. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1403-1413.	1.9	45
48	Chemical Chaperones as Novel Drugs for Parkinson's Disease. <i>Trends in Molecular Medicine</i> , 2020, 26, 408-421.	3.5	43
49	pH-Dependent Aggregation in Intrinsically Disordered Proteins Is Determined by Charge and Lipophilicity. <i>Cells</i> , 2020, 9, 145.	1.8	37
50	hnRNPDL Phase Separation Is Regulated by Alternative Splicing and Disease-Causing Mutations Accelerate Its Aggregation. <i>Cell Reports</i> , 2020, 30, 1117-1128.e5.	2.9	47
51	The biofilm-associated surface protein Esp of <i>Enterococcus faecalis</i> forms amyloid-like fibers. <i>Npj Biofilms and Microbiomes</i> , 2020, 6, 15.	2.9	40
52	Small molecules to prevent the neurodegeneration caused by $\alpha$ -synuclein aggregation. <i>Neural Regeneration Research</i> , 2020, 15, 2260.	1.6	12
53	Prion-like domain disease-causing mutations and misregulation of alternative splicing relevance in limb-girdle muscular dystrophy (LGMD) 1G. <i>Neural Regeneration Research</i> , 2020, 15, 2239.	1.6	6
54	Dual Binding Mode of Metallacarborane Produces a Robust Shield on Proteins. <i>Chemistry - A European Journal</i> , 2019, 25, 12820-12829.	1.7	29

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55	Computational Assessment of Bacterial Protein Structures Indicates a Selection Against Aggregation. <i>Cells</i> , 2019, 8, 856.	1.8	9
56	Computational re-design of protein structures to improve solubility. <i>Expert Opinion on Drug Discovery</i> , 2019, 14, 1077-1088.	2.5	14
57	AMYCO: evaluation of mutational impact on prion-like proteins aggregation propensity. <i>BMC Bioinformatics</i> , 2019, 20, 24.	1.2	24
58	Aggrescan3D (A3D) 2.0: prediction and engineering of protein solubility. <i>Nucleic Acids Research</i> , 2019, 47, W300-W307.	6.5	91
59	Prion soft amyloid core driven self-assembly of globular proteins into bioactive nanofibrils. <i>Nanoscale</i> , 2019, 11, 12680-12694.	2.8	16
60	Aggrescan3D standalone package for structure-based prediction of protein aggregation properties. <i>Bioinformatics</i> , 2019, 35, 3834-3835.	1.8	22
61	In silico Characterization of Human Prion-Like Proteins: Beyond Neurological Diseases. <i>Frontiers in Physiology</i> , 2019, 10, 314.	1.3	17
62	The fitness cost and benefit of phase-separated protein deposits. <i>Molecular Systems Biology</i> , 2019, 15, e8075.	3.2	10
63	Formation of Cross-Beta Supersecondary Structure by Soft-Amyloid Cores: Strategies for Their Prediction and Characterization. <i>Methods in Molecular Biology</i> , 2019, 1958, 237-261.	0.4	1
64	Biasing the native $\alpha$ -synuclein conformational ensemble towards compact states abolishes aggregation and neurotoxicity. <i>Redox Biology</i> , 2019, 22, 101135.	3.9	34
65	ZPD-2, a Small Compound That Inhibits $\alpha$ -Synuclein Amyloid Aggregation and Its Seeded Polymerization. <i>Frontiers in Molecular Neuroscience</i> , 2019, 12, 306.	1.4	32
66	Insight into the specificity and severity of pathogenic mechanisms associated with missense mutations through experimental and structural perturbation analyses. <i>Human Molecular Genetics</i> , 2019, 28, 1-15.	1.4	29
67	A pyrene-inhibitor fluorescent probe with large Stokes shift for the staining of $A\beta^{1-42}$ , $\alpha$ -synuclein, and amylin amyloid fibrils as well as amyloid-containing <i>Staphylococcus aureus</i> biofilms. <i>Analytical and Bioanalytical Chemistry</i> , 2019, 411, 251-265.	1.9	2
68	Screening Protein Aggregation in Cells Using Fluorescent Labels Coupled to Flow Cytometry. <i>Methods in Molecular Biology</i> , 2019, 1873, 195-212.	0.4	3
69	Advances in the Prediction of Protein Aggregation Propensity. <i>Current Medicinal Chemistry</i> , 2019, 26, 3911-3920.	1.2	25
70	Inducing $\alpha$ -synuclein compaction: a new strategy for inhibiting $\alpha$ -synuclein aggregation?. <i>Neural Regeneration Research</i> , 2019, 14, 1897.	1.6	8
71	C-mannosylation supports folding and enhances stability of thrombospondin repeats. <i>ELife</i> , 2019, 8, .	2.8	62
72	AGGRESKAN3D: Toward the Prediction of the Aggregation Propensities of Protein Structures. <i>Methods in Molecular Biology</i> , 2018, 1762, 427-443.	0.4	14

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73	Molecular and Clinical Aspects of Protein Aggregation Assays in Neurodegenerative Diseases. <i>Molecular Neurobiology</i> , 2018, 55, 7588-7605.	1.9	17
74	A single cysteine post-translational oxidation suffices to compromise globular proteins kinetic stability and promote amyloid formation. <i>Redox Biology</i> , 2018, 14, 566-575.	3.9	25
75	Small molecule inhibits $\alpha$ -synuclein aggregation, disrupts amyloid fibrils, and prevents degeneration of dopaminergic neurons. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 10481-10486.	3.3	166
76	Prion-based nanomaterials and their emerging applications. <i>Prion</i> , 2018, 12, 266-272.	0.9	21
77	Minimalist Prion-Inspired Polar Self-Assembling Peptides. <i>ACS Nano</i> , 2018, 12, 5394-5407.	7.3	37
78	Evaluation of the Impact of Protein Aggregation on Cellular Oxidative Stress in Yeast. <i>Journal of Visualized Experiments</i> , 2018, , .	0.2	0
79	Global Protein Stabilization Does Not Suffice to Prevent Amyloid Fibril Formation. <i>ACS Chemical Biology</i> , 2018, 13, 2094-2105.	1.6	10
80	Combining Structural Aggregation Propensity and Stability Predictions To Redesign Protein Solubility. <i>Molecular Pharmaceutics</i> , 2018, 15, 3846-3859.	2.3	45
81	The Disordered C-Terminus of Yeast Hsf1 Contains a Cryptic Low-Complexity Amyloidogenic Region. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1384.	1.8	7
82	Discovering Putative Prion-Like Proteins in <i>Plasmodium falciparum</i> : A Computational and Experimental Analysis. <i>Frontiers in Microbiology</i> , 2018, 9, 1737.	1.5	42
83	Protein Environment: A Crucial Triggering Factor in Josephin Domain Aggregation: The Role of 2,2,2-Trifluoroethanol. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2151.	1.8	3
84	Amyloid Formation in Bacteria. , 2018, , 1-3.		0
85	Prion-like proteins and their computational identification in proteomes. <i>Expert Review of Proteomics</i> , 2017, 14, 335-350.	1.3	24
86	Amyloid cores in prion domains: Key regulators for prion conformational conversion. <i>Prion</i> , 2017, 11, 31-39.	0.9	20
87	Prediction of Protein Aggregation and Amyloid Formation. , 2017, , 205-263.		4
88	DisProt 7.0: a major update of the database of disordered proteins. <i>Nucleic Acids Research</i> , 2017, 45, D219-D227.	6.5	242
89	Perfecting prediction of mutational impact on the aggregation propensity of the $\alpha$ -synuclein-associated hnRNP A2 prion-like protein. <i>FEBS Letters</i> , 2017, 591, 1966-1971.	1.3	13
90	Cavity filling mutations at the thyroxine-binding site dramatically increase transthyretin stability and prevent its aggregation. <i>Scientific Reports</i> , 2017, 7, 44709.	1.6	16

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91	Protein aggregation into insoluble deposits protects from oxidative stress. <i>Redox Biology</i> , 2017, 12, 699-711.	3.9	32
92	The Transcription Terminator Rho: A First Bacterial Prion. <i>Trends in Microbiology</i> , 2017, 25, 434-437.	3.5	24
93	Copper(II) and the pathological H50Q $\beta$ -synuclein mutant: Environment meets genetics. <i>Communicative and Integrative Biology</i> , 2017, 10, e1270484.	0.6	22
94	Characterization of Soft Amyloid Cores in Human Prion-Like Proteins. <i>Scientific Reports</i> , 2017, 7, 12134.	1.6	38
95	Plasticity in the Oxidative Folding Pathway of the High Affinity Nerita Versicolor Carboxypeptidase Inhibitor (NvCI). <i>Scientific Reports</i> , 2017, 7, 5457.	1.6	5
96	Disulfide driven folding for a conditionally disordered protein. <i>Scientific Reports</i> , 2017, 7, 16994.	1.6	14
97	High-Throughput Screening Methodology to Identify Alpha-Synuclein Aggregation Inhibitors. <i>International Journal of Molecular Sciences</i> , 2017, 18, 478.	1.8	66
98	Editorial: Protein Solubility and Aggregation in Bacteria. <i>Frontiers in Microbiology</i> , 2016, 7, 1178.	1.5	3
99	Benzbromarone, Quercetin, and Folic Acid Inhibit Amylin Aggregation. <i>International Journal of Molecular Sciences</i> , 2016, 17, 964.	1.8	38
100	Amyloid properties of the leader peptide of variant B cystatin C: implications for Alzheimer and macular degeneration. <i>FEBS Letters</i> , 2016, 590, 644-654.	1.3	11
101	Repositioning tolcapone as a potent inhibitor of transthyretin amyloidogenesis and associated cellular toxicity. <i>Nature Communications</i> , 2016, 7, 10787.	5.8	139
102	Curing bacterial infections with protein aggregates. <i>Molecular Microbiology</i> , 2016, 99, 827-830.	1.2	5
103	Environmental and genetic factors support the dissociation between $\beta$ -synuclein aggregation and toxicity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E6506-E6515.	3.3	75
104	Understanding and predicting protein misfolding and aggregation: Insights from proteomics. <i>Proteomics</i> , 2016, 16, 2570-2581.	1.3	25
105	In vivo amyloid aggregation kinetics tracked by time-lapse confocal microscopy in real-time. <i>Biotechnology Journal</i> , 2016, 11, 172-177.	1.8	14
106	Characterization of Amyloid Cores in Prion Domains. <i>Scientific Reports</i> , 2016, 6, 34274.	1.6	56
107	Dissecting the contribution of <i>Staphylococcus aureus</i> $\beta$ -phenol-soluble modulins to biofilm amyloid structure. <i>Scientific Reports</i> , 2016, 6, 34552.	1.6	57
108	The effects of the novel A53E alpha-synuclein mutation on its oligomerization and aggregation. <i>Acta Neuropathologica Communications</i> , 2016, 4, 128.	2.4	35

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109	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). <i>Autophagy</i> , 2016, 12, 1-222.	4.3	4,701
110	Data on correlation between A $\beta$ 42 structural aggregation propensity and toxicity in bacteria. <i>Data in Brief</i> , 2016, 7, 143-147.	0.5	1
111	Mammalian prion amyloid formation in bacteria. <i>Prion</i> , 2016, 10, 112-118.	0.9	2
112	A fast and specific method to screen for intracellular amyloid inhibitors using bacterial model systems. <i>European Journal of Medicinal Chemistry</i> , 2016, 121, 785-792.	2.6	9
113	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. <i>PLoS Genetics</i> , 2016, 12, e1005824.	1.5	100
114	Staphylococcal Bap Proteins Build Amyloid Scaffold Biofilm Matrices in Response to Environmental Signals. <i>PLoS Pathogens</i> , 2016, 12, e1005711.	2.1	135
115	The prion-like RNA-processing protein HNRPDL forms inherently toxic amyloid-like inclusion bodies in bacteria. <i>Microbial Cell Factories</i> , 2015, 14, 102.	1.9	12
116	Mammalian prion protein (PrP) forms conformationally different amyloid intracellular aggregates in bacteria. <i>Microbial Cell Factories</i> , 2015, 14, 174.	1.9	18
117	Aggregation propensity of neuronal receptors: potential implications in neurodegenerative disorders. <i>Future Science OA</i> , 2015, 1, FSO39.	0.9	1
118	Possible roles of amyloids in malaria pathophysiology. <i>Future Science OA</i> , 2015, 1, FSO43.	0.9	4
119	Protein misfolding diseases. <i>Future Science OA</i> , 2015, 1, FSO38.	0.9	6
120	Computational analysis of candidate prion-like proteins in bacteria and their role. <i>Frontiers in Microbiology</i> , 2015, 6, 1123.	1.5	37
121	SOM0226, a repositioned compound for the treatment of TTR amyloidosis. <i>Orphanet Journal of Rare Diseases</i> , 2015, 10, .	1.2	4
122	Intradomain Confinement of Disulfides in the Folding of Two Consecutive Modules of the LDL Receptor. <i>PLoS ONE</i> , 2015, 10, e0132141.	1.1	3
123	Histone H1 Favors Folding and Parallel Fibrillar Aggregation of the A $\beta$ 42 Amyloid- $\beta$ Peptide. <i>Langmuir</i> , 2015, 31, 6782-6790.	1.6	13
124	Amyloids or prions? That is the question. <i>Prion</i> , 2015, 9, 200-206.	0.9	47
125	What Makes a Protein Sequence a Prion?. <i>PLoS Computational Biology</i> , 2015, 11, e1004013.	1.5	88
126	PrionW: a server to identify proteins containing glutamine/asparagine rich prion-like domains and their amyloid cores. <i>Nucleic Acids Research</i> , 2015, 43, W331-W337.	6.5	74



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127	Proteome response at the edge of protein aggregation. <i>Open Biology</i> , 2015, 5, 140221.	1.5	9
128	AGGRESCAN3D (A3D): server for prediction of aggregation properties of protein structures. <i>Nucleic Acids Research</i> , 2015, 43, W306-W313.	6.5	201
129	The Rho Termination Factor of <i>Clostridium botulinum</i> Contains a Prion-Like Domain with a Highly Amyloidogenic Core. <i>Frontiers in Microbiology</i> , 2015, 6, 1516.	1.5	44
130	Characterization of Amyloid-Like Properties in Bacterial Intracellular Aggregates. <i>Methods in Molecular Biology</i> , 2015, 1258, 99-122.	0.4	4
131	Protein Aggregation and Its Prediction. <i>NATO Science for Peace and Security Series A: Chemistry and Biology</i> , 2015, , 115-127.	0.5	1
132	Influence of Cytoplasmatic Folding on Mitochondrial Import. <i>Current Medicinal Chemistry</i> , 2015, 22, 2349-2359.	1.2	3
133	Structural and Computational Insights into Conformational Diseases: A Review. , 2015, , 134-182.		0
134	Human Stefin B Role in Cell's Response to Misfolded Proteins and Autophagy. <i>PLoS ONE</i> , 2014, 9, e102500.	1.1	15
135	The Importance of a Gatekeeper Residue on the Aggregation of Transthyretin. <i>Journal of Biological Chemistry</i> , 2014, 289, 28324-28337.	1.6	35
136	The Mitochondrial Intermembrane Space Oxidoreductase Mia40 Funnels the Oxidative Folding Pathway of the Cytochrome c Oxidase Assembly Protein Cox19. <i>Journal of Biological Chemistry</i> , 2014, 289, 9852-9864.	1.6	16
137	Amyloid Formation by Human Carboxypeptidase D Transthyretin-like Domain under Physiological Conditions. <i>Journal of Biological Chemistry</i> , 2014, 289, 33783-33796.	1.6	18
138	PrionScan: an online database of predicted prion domains in complete proteomes. <i>BMC Genomics</i> , 2014, 15, 102.	1.2	42
139	Selection against toxic aggregation-prone protein sequences in bacteria. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2014, 1843, 866-874.	1.9	16
140	Fluorescent dye ProteoStat to detect and discriminate intracellular amyloid-like aggregates in <i>Escherichia coli</i> . <i>Biotechnology Journal</i> , 2014, 9, 1259-1266.	1.8	46
141	The small GTPase Rab11 co-localizes with $\alpha$ -synuclein in intracellular inclusions and modulates its aggregation, secretion and toxicity. <i>Human Molecular Genetics</i> , 2014, 23, 6732-6745.	1.4	73
142	N-Terminal Protein Tails Act as Aggregation Protective Entropic Bristles: The SUMO Case. <i>Biomacromolecules</i> , 2014, 15, 1194-1203.	2.6	32
143	Association Between Foldability and Aggregation Propensity in Small Disulfide-Rich Proteins. <i>Antioxidants and Redox Signaling</i> , 2014, 21, 368-383.	2.5	25
144	Thioflavin-S Staining of Bacterial Inclusion Bodies for the Fast, Simple, and Inexpensive Screening of Amyloid Aggregation Inhibitors. <i>Current Medicinal Chemistry</i> , 2014, 21, 1152-1159.	1.2	44

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145	Screening for Amyloid Aggregation: In-Silico, In-Vitro and In-Vivo Detection. <i>Current Protein and Peptide Science</i> , 2014, 15, 477-489.	0.7	9
146	Discovering putative prion sequences in complete proteomes using probabilistic representations of Q/N-rich domains. <i>BMC Genomics</i> , 2013, 14, 316.	1.2	73
147	Protein aggregation propensity is a crucial determinant of intracellular inclusion formation and quality control degradation. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2013, 1833, 2714-2724.	1.9	17
148	Thioflavin-T excimer formation upon interaction with amyloid fibers. <i>Chemical Communications</i> , 2013, 49, 5745.	2.2	56
149	Zinc induced folding is essential for TIM15 activity as an mtHsp70 chaperone. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2013, 1830, 2139-2149.	1.1	11
150	Oxidative Folding in the Mitochondrial Intermembrane Space in Human Health and Disease. <i>International Journal of Molecular Sciences</i> , 2013, 14, 2916-2927.	1.8	7
151	Inhibition of Human Transthyretin Aggregation by Non-Steroidal Anti-Inflammatory Compounds: A Structural and Thermodynamic Analysis. <i>International Journal of Molecular Sciences</i> , 2013, 14, 5284-5311.	1.8	17
152	Trifluoroethanol Modulates Amyloid Formation by the All $\beta$ -Helical URN1 FF Domain. <i>International Journal of Molecular Sciences</i> , 2013, 14, 17830-17844.	1.8	9
153	About targets and causes in protein folding. <i>Journal of Biomolecular Structure and Dynamics</i> , 2013, 31, 970-972.	2.0	1
154	Structure-Based Analysis of A19D, a Variant of Transthyretin Involved in Familial Amyloid Cardiomyopathy. <i>PLoS ONE</i> , 2013, 8, e82484.	1.1	6
155	The N-terminal Helix Controls the Transition between the Soluble and Amyloid States of an FF Domain. <i>PLoS ONE</i> , 2013, 8, e58297.	1.1	16
156	Protein aggregation profile of the human kinome. <i>Frontiers in Physiology</i> , 2012, 3, 438.	1.3	6
157	Contribution of Disulfide Bonds to Stability, Folding, and Amyloid Fibril Formation: The PI3-SH3 Domain Case. <i>Antioxidants and Redox Signaling</i> , 2012, 16, 1-15.	2.5	32
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