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List of Publications by Year in descending order

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36
papers

774
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471509
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all docs

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docs citations

40
times ranked

847
citing authors

#	ARTICLE	IF	CITATIONS
1	WALTZ-DB 2.0: an updated database containing structural information of experimentally determined amyloid-forming peptides. <i>Nucleic Acids Research</i> , 2020, 48, D389-D393.	14.5	64
2	Structure-based machine-guided mapping of amyloid sequence space reveals uncharted sequence clusters with higher solubilities. <i>Nature Communications</i> , 2020, 11, 3314.	12.8	54
3	Aggregating sequences that occur in many proteins constitute weak spots of bacterial proteostasis. <i>Nature Communications</i> , 2018, 9, 866.	12.8	53
4	Bcl-xL acts as an inhibitor of IP3R channels, thereby antagonizing Ca ²⁺ -driven apoptosis. <i>Cell Death and Differentiation</i> , 2022, 29, 788-805.	11.2	41
5	Thermodynamic and Evolutionary Coupling between the Native and Amyloid State of Globular Proteins. <i>Cell Reports</i> , 2020, 31, 107512.	6.4	34
6	Processing Induced Changes in Food Proteins: Amyloid Formation during Boiling of Hen Egg White. <i>Biomacromolecules</i> , 2020, 21, 2218-2228.	5.4	34
7	Structural Analysis of Peptide-Analogues of Human Zona Pellucida ZP1 Protein with Amyloidogenic Properties: Insights into Mammalian Zona Pellucida Formation. <i>PLoS ONE</i> , 2013, 8, e73258.	2.5	33
8	Autonomous aggregation suppression by acidic residues explains why chaperones favour basic residues. <i>EMBO Journal</i> , 2020, 39, e102864.	7.8	33
9	Repurposing the Antidepressant Sertraline as SHMT Inhibitor to Suppress Serine/Glycine Synthesis-Addicted Breast Tumor Growth. <i>Molecular Cancer Therapeutics</i> , 2021, 20, 50-63.	4.1	31
10	A common "aggregation-prone" interface possibly participates in the self-assembly of human zona pellucida proteins. <i>FEBS Letters</i> , 2016, 590, 619-630.	2.8	30
11	Chameleon "aggregation-prone" segments of apoA-I: A model of amyloid fibrils formed in apoA-I amyloidosis. <i>International Journal of Biological Macromolecules</i> , 2015, 79, 711-718.	7.5	29
12	Exploring the "aggregation-prone" core of human Cystatin C: A structural study. <i>Journal of Structural Biology</i> , 2015, 191, 272-280.	2.8	26
13	An N-terminal pro-atrial natriuretic peptide (NT-proANP) "aggregation-prone" segment involved in isolated atrial amyloidosis. <i>FEBS Letters</i> , 2014, 588, 52-57.	2.8	25
14	Reverse engineering synthetic antiviral amyloids. <i>Nature Communications</i> , 2020, 11, 2832.	12.8	25
15	Structural studies and cytotoxicity assays of "aggregation-prone" Aβ ¹⁻⁴² and its non-amyloidogenic variants suggest its important role in fibrillogenesis and cytotoxicity of human amylin. <i>Biopolymers</i> , 2015, 104, 196-205.	2.4	19
16	Heterotypic Amyloid I ² interactions facilitate amyloid assembly and modify amyloid structure. <i>EMBO Journal</i> , 2022, 41, e108591.	7.8	19
17	Intrinsic aggregation propensity of the CsgB nucleator protein is crucial for curli fiber formation. <i>Journal of Structural Biology</i> , 2016, 195, 179-189.	2.8	18
18	Heating Wheat Gluten Promotes the Formation of Amyloid-like Fibrils. <i>ACS Omega</i> , 2021, 6, 1823-1833.	3.5	18

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19	Heterotypic interactions in amyloid function and disease. FEBS Journal, 2022, 289, 2025-2046.	4.7	18
20	A β -solenoid model of the Pmel17 repeat domain: insights to the formation of functional amyloid fibrils. Journal of Computer-Aided Molecular Design, 2016, 30, 153-164.	2.9	17
21	The structural basis for an on/off switch controlling $G\beta$ -mediated inhibition of TRPM3 channels. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 29090-29100.	7.1	17
22	Structural studies of aggregation-prone peptide analogues of teleostean egg chorion ZPB proteins. Biopolymers, 2014, 102, 427-436.	2.4	16
23	Identification of an amyloid fibril forming segment of human Pmel17 repeat domain (<sc>RPT</sc>) Tj ETQq1 1 0.784314 pgBT /Overl	2.4	15
24	Entropic Bristles Tune the Seeding Efficiency of Prion-Nucleating Fragments. Cell Reports, 2020, 30, 2834-2845.e3.	6.4	12
25	Mapping the sequence specificity of heterotypic amyloid interactions enables the identification of aggregation modifiers. Nature Communications, 2022, 13, 1351.	12.8	11
26	Thermodynamic analysis of amyloid fibril structures reveals a common framework for stability in amyloid polymorphs. Structure, 2022, 30, 1178-1189.e3.	3.3	11
27	Hexapeptide Tandem Repeats Dictate the Formation of Silkmoth Chorion, a Natural Protective Amyloid. Journal of Molecular Biology, 2018, 430, 3774-3783.	4.2	10
28	Tracking the amyloidogenic core of IAPP amyloid fibrils: Insights from micro-Raman spectroscopy. Journal of Structural Biology, 2017, 199, 140-152.	2.8	9
29	Hidden Aggregation Hot-Spots on Human Apolipoprotein E: A Structural Study. International Journal of Molecular Sciences, 2019, 20, 2274.	4.1	9
30	StAMP-DB: a platform for structures of polymorphic amyloid fibril cores. Bioinformatics, 2022, 38, 2636-2638.	4.1	8
31	Heterotypic amyloid interactions: Clues to polymorphic bias and selective cellular vulnerability?. Current Opinion in Structural Biology, 2022, 72, 176-186.	5.7	7
32	β -CGRP, another amyloidogenic member of the CGRP family. Journal of Structural Biology, 2018, 203, 27-36.	2.8	6
33	Exposure of a cryptic Hsp70 binding site determines the cytotoxicity of the ALS-associated SOD1-mutant A4V. Protein Engineering, Design and Selection, 2019, 32, 443-457.	2.1	6
34	Unraveling the aggregation propensity of human insulin C-peptide. Biopolymers, 2017, 108, e22882.	2.4	3
35	Exploring Amyloidogenicity of Clusterin: A Structural and Bioinformatics Analysis. Advances in Experimental Medicine and Biology, 2017, 989, 93-107.	1.6	3
36	Arabidopsis thaliana Plant Natriuretic Peptide Active Domain Forms Amyloid-like Fibrils in a pH-Dependent Manner. Plants, 2022, 11, 9.	3.5	2