Nikolaos N Louros

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4325325/publications.pdf

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36	774	535685	651938
papers	citations	17 h-index	25 g-index

40	40	40	925
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Heterotypic interactions in amyloid function and disease. FEBS Journal, 2022, 289, 2025-2046.	2.2	18
2	Bcl-xL acts as an inhibitor of IP3R channels, thereby antagonizing Ca2+-driven apoptosis. Cell Death and Differentiation, 2022, 29, 788-805.	5.0	41
3	Heterotypic Amyloid Î² interactions facilitate amyloid assembly and modify amyloid structure. EMBO Journal, 2022, 41, e108591.	3.5	19
4	Heterotypic amyloid interactions: Clues to polymorphic bias and selective cellular vulnerability?. Current Opinion in Structural Biology, 2022, 72, 176-186.	2.6	7
5	StAmP-DB: a platform for structures of polymorphic amyloid fibril cores. Bioinformatics, 2022, 38, 2636-2638.	1.8	8
6	Mapping the sequence specificity of heterotypic amyloid interactions enables the identification of aggregation modifiers. Nature Communications, 2022, 13, 1351.	5.8	11
7	Arabidopsis thaliana Plant Natriuretic Peptide Active Domain Forms Amyloid-like Fibrils in a pH-Dependent Manner. Plants, 2022, 11, 9.	1.6	2
8	Thermodynamic analysis of amyloid fibril structures reveals a common framework for stability in amyloid polymorphs. Structure, 2022, 30, 1178-1189.e3.	1.6	11
9	Heating Wheat Gluten Promotes the Formation of Amyloid-like Fibrils. ACS Omega, 2021, 6, 1823-1833.	1.6	18
10	Repurposing the Antidepressant Sertraline as SHMT Inhibitor to Suppress Serine/Glycine Synthesisâ€“Addicted Breast Tumor Growth. Molecular Cancer Therapeutics, 2021, 20, 50-63.	1.9	31
11	WALTZ-DB 2.0: an updated database containing structural information of experimentally determined amyloid-forming peptides. Nucleic Acids Research, 2020, 48, D389-D393.	6.5	64
12	Thermodynamic and Evolutionary Coupling between the Native and Amyloid State of Globular Proteins. Cell Reports, 2020, 31, 107512.	2.9	34
13	Reverse engineering synthetic antiviral amyloids. Nature Communications, 2020, 11, 2832.	5.8	25
14	Processing Induced Changes in Food Proteins: Amyloid Formation during Boiling of Hen Egg White. Biomacromolecules, 2020, 21, 2218-2228.	2.6	34
15	Structure-based machine-guided mapping of amyloid sequence space reveals uncharted sequence clusters with higher solubilities. Nature Communications, 2020, 11, 3314.	5.8	54
16	Entropic Bristles Tune the Seeding Efficiency of Prion-Nucleating Fragments. Cell Reports, 2020, 30, 2834-2845.e3.	2.9	12
17	The structural basis for an onâ€“off switch controlling GÎ²Î³-mediated inhibition of TRPM3 channels. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 29090-29100.	3.3	17
18	Autonomous aggregation suppression by acidic residues explains why chaperones favour basic residues. EMBO Journal, 2020, 39, e102864.	3.5	33

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19	Hidden Aggregation Hot-Spots on Human Apolipoprotein E: A Structural Study. International Journal of Molecular Sciences, 2019, 20, 2274.	1.8	9
20	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.	1.0	6
21	Aggregating sequences that occur in many proteins constitute weak spots of bacterial proteostasis. Nature Communications, 2018, 9, 866.	5.8	53
22	Î±CGRP, another amyloidogenic member of the CGRP family. Journal of Structural Biology, 2018, 203, 27-36.	1.3	6
23	Hexapeptide Tandem Repeats Dictate the Formation of Silkmoth Chorion, a Natural Protective Amyloid. Journal of Molecular Biology, 2018, 430, 3774-3783.	2.0	10
24	Unraveling the aggregation propensity of human insulin Câ€peptide. Biopolymers, 2017, 108, e22882.	1.2	3
25	Tracking the amyloidogenic core of IAPP amyloid fibrils: Insights from micro-Raman spectroscopy. Journal of Structural Biology, 2017, 199, 140-152.	1.3	9
26	Exploring Amyloidogenicity of Clusterin: A Structural and Bioinformatics Analysis. Advances in Experimental Medicine and Biology, 2017, 989, 93-107.	0.8	3
27	Identification of an amyloid fibril forming segment of human Pmel17 repeat domain (<scp>RPT</scp>) Tj ETQq1 1 0.784314 rgBT /Ov	1.2	18
28	Intrinsic aggregation propensity of the CsgB nucleator protein is crucial for curli fiber formation. Journal of Structural Biology, 2016, 195, 179-189.	1.3	18
29	A common â€˜aggregationâ€proneâ€™ interface possibly participates in the selfâ€assembly of human zona pellucida proteins. FEBS Letters, 2016, 590, 619-630.	1.3	30
30	A Î²-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.	1.3	17
31	Chameleon â€˜aggregation-proneâ€™ segments of apoA-I: A model of amyloid fibrils formed in apoA-I amyloidosis. International Journal of Biological Macromolecules, 2015, 79, 711-718.	3.6	29
32	Exploring the â€˜aggregation-proneâ€™ core of human Cystatin C: A structural study. Journal of Structural Biology, 2015, 191, 272-280.	1.3	26
33	Structural studies and cytotoxicity assays of â€œaggregationâ€proneâ€•IAPP_{8â€“16} and its nonâ€amyloidogenic variants suggest its important role in fibrillogenesis and cytotoxicity of human amylin. Biopolymers, 2015, 104, 196-205.	1.2	19
34	Structural studies of â€œaggregationâ€proneâ€•peptideâ€analogues of teleostean egg chorion ZPB proteins. Biopolymers, 2014, 102, 427-436.	1.2	16
35	An Nâ€terminal proâ€atrial natriuretic peptide (NTâ€proANP) â€˜aggregationâ€proneâ€™ segment involved in isolated atrial amyloidosis. FEBS Letters, 2014, 588, 52-57.	1.3	25
36	Structural Analysis of Peptide-Analogues of Human Zona Pellucida ZP1 Protein with Amyloidogenic Properties: Insights into Mammalian Zona Pellucida Formation. PLoS ONE, 2013, 8, e73258.	1.1	33