Natalia Sanchez de Groot

List of Publications by Year
in descending order

52 papers	4,369 citations	126708 33 h-index	214527 47 g-index
58 all docs	58 docs citations	58 times ranked	5977 citing authors

#	Article	IF	Citations
1	AGGRESCAN: a server for the prediction and evaluation of "hot spots" of aggregation in polypeptides. BMC Bioinformatics, 2007, 8, 65.	1.2	845
2	Intrinsically disordered proteins: regulation and disease. Current Opinion in Structural Biology, 2011, 21, 432-440.	2.6	518
3	Cells alter their tRNA abundance to selectively regulate protein synthesis during stress conditions. Science Signaling, 2018, 11, .	1.6	201
4	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
5	Intrinsically Disordered Segments Affect Protein Half-Life in the Cell and during Evolution. Cell Reports, 2014, 8, 1832-1844.	2.9	192
6	Prediction of "hot spots" of aggregation in disease-linked polypeptides. BMC Structural Biology, 2005, 5, 18.	2.3	173
7	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
8	Amyloids in bacterial inclusion bodies. Trends in Biochemical Sciences, 2009, 34, 408-416.	3.7	137
9	Effect of temperature on protein quality in bacterial inclusion bodies. FEBS Letters, 2006, 580, 6471-6476.	1.3	133
10	Ile-Phe Dipeptide Self-Assembly: Clues to Amyloid Formation. Biophysical Journal, 2007, 92, 1732-1741.	0.2	129
11	RNA structure drives interaction with proteins. Nature Communications, 2019, 10, 3246.	5.8	123
12	Advances in the characterization of RNAâ€binding proteins. Wiley Interdisciplinary Reviews RNA, 2016, 7, 793-810.	3.2	89
13	Protein folding and aggregation in bacteria. Cellular and Molecular Life Sciences, 2010, 67, 2695-2715.	2.4	76
14	Prion and Non-prion Amyloids of the HET-s Prion forming Domain. Journal of Molecular Biology, 2007, 370, 768-783.	2.0	68
15	Biological role of bacterial inclusion bodies: a model for amyloid aggregation. FEBS Journal, 2011, 278, 2419-2427.	2.2	68
16	Modulation of AÎ² ₄₂ fÃ¬brillogenesis by glycosaminoglycan structure. FASEB Journal, 2010, 24, 4250-4261.	0.2	66
17	RNA as a key factor in driving or preventing self-assembly of the TAR DNA-binding protein 43. Journal of Molecular Biology, 2019, 431, 1671-1688.	2.0	65
18	Protein activity in bacterial inclusion bodies correlates with predicted aggregation rates. Journal of Biotechnology, 2006, 125, 110-113.	1.9	64

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19	AGGRESCAN: Method, Application, and Perspectives for Drug Design. Methods in Molecular Biology, 2012, 819, 199-220.	0.4	64
20	Recent Structural and Computational Insights into Conformational Diseases. Current Medicinal Chemistry, 2008, 15, 1336-1349.	1.2	62
21	Centrality in the hostâ€"pathogen interactome is associated with pathogen fitness during infection. Nature Communications, 2017, 8, 14092.	5.8	62
22	RNA-binding and prion domains: the Yin and Yang of phase separation. Nucleic Acids Research, 2020, 48, 9491-9504.	6.5	57
23	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
24	Characterization of Amyloid Cores in Prion Domains. Scientific Reports, 2016, 6, 34274.	1.6	56
25	Affinity and competition for TBP are molecular determinants of gene expression noise. Nature Communications, 2016, 7, 10417.	5.8	55
26	Protein Aggregation Profile of the Bacterial Cytosol. PLoS ONE, 2010, 5, e9383.	1.1	53
27	Constraints and consequences of the emergence of amino acid repeats in eukaryotic proteins. Nature Structural and Molecular Biology, 2017, 24, 765-777.	3.6	53
28	Discovering Putative Prion-Like Proteins in Plasmodium falciparum: A Computational and Experimental Analysis. Frontiers in Microbiology, 2018, 9, 1737.	1.5	42
29	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
30	Benzbromarone, Quercetin, and Folic Acid Inhibit Amylin Aggregation. International Journal of Molecular Sciences, 2016, 17, 964.	1.8	38
31	Characterization of Soft Amyloid Cores in Human Prion-Like Proteins. Scientific Reports, 2017, 7, 12134.	1.6	38
32	Computational analysis of candidate prion-like proteins in bacteria and their role. Frontiers in Microbiology, 2015, 6, 1123.	1.5	37
33	Studies on bacterial inclusion bodies. Future Microbiology, 2008, 3, 423-435.	1.0	34
34	Using bacterial inclusion bodies to screen for amyloid aggregation inhibitors. Microbial Cell Factories, 2012, 11, 55.	1.9	33
35	Is membrane homeostasis the missing link between inflammation and neurodegenerative diseases?. Cellular and Molecular Life Sciences, 2015, 72, 4795-4805.	2.4	33
36	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

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37	Evolutionary selection for protein aggregation. Biochemical Society Transactions, 2012, 40, 1032-1037.	1.6	32
38	Protein aggregation into insoluble deposits protects from oxidative stress. Redox Biology, 2017, 12, 699-711.	3.9	32
39	Amyloid fibril formation by bovine cytochrome<i>c</i>. Spectroscopy, 2005, 19, 199-205.	0.8	28
40	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
41	Linking amyloid protein aggregation and yeast survival. Molecular BioSystems, 2011, 7, 1121.	2.9	26
42	RNAâ€protein interactions: Central players in coordination of regulatory networks. BioEssays, 2021, 43, e2000118.	1.2	17
43	The Interplay Between Disordered Regions in RNAs and Proteins Modulates Interactions Within Stress Granules and Processing Bodies. Journal of Molecular Biology, 2022, 434, 167159.	2.0	15
44	The fitness cost and benefit of phaseâ€separated protein deposits. Molecular Systems Biology, 2019, 15, e8075.	3.2	10
45	Proteome response at the edge of protein aggregation. Open Biology, 2015, 5, 140221.	1.5	9
46	Bacteria use structural imperfect mimicry to hijack the host interactome. PLoS Computational Biology, 2020, 16, e1008395.	1.5	9
47	A Coordinated Response at The Transcriptome and Interactome Level is Required to Ensure Uropathogenic Escherichia coli Survival during Bacteremia. Microorganisms, 2019, 7, 292.	1.6	5
48	Microbiome Impact on Amyloidogenesis. Frontiers in Molecular Biosciences, 0, 9, .	1.6	3
49	Protein aggregation into bacterial inclusion bodies is a specific kinetically driven process. Microbial Cell Factories, 2006, 5, S9.	1.9	0
50	INTRINSICALLY DISORDERED PROTEINS: REGULATION AND DISEASE. , 2013, , 346-361.		0
51	Frontiers in Medicinal Chemistry. , 2015, , .		0
52	Structural and Computational Insights into Conformational Diseases: A Review. , 2015, , 134-182.		0