Zhefeng Guo

List of Publications by Year
in descending order

31 papers	1,567 citations	516710 16 h-index	434195 31 g-index
31 all docs	31 docs citations	31 times ranked	2199 citing authors

#	Article	IF	Citations
1	Static and dynamic disorder in AÎ²40 fibrils. Biochemical and Biophysical Research Communications, 2022, 610, 107-112.	2.1	1
2	Alzheimerâ€™s AÎ²42 and AÎ²40 form mixed oligomers with direct molecular interactions. Biochemical and Biophysical Research Communications, 2021, 534, 292-296.	2.1	17
3	Amyloid hypothesis through the lens of AÎ² supersaturation. Neural Regeneration Research, 2021, 16, 1562.	3.0	7
4	Effect of spin labelling on the aggregation kinetics of yeast prion protein Ure2. Royal Society Open Science, 2021, 8, 201747.	2.4	1
5	Segmental structural dynamics in AÎ²42 globulomers. Biochemical and Biophysical Research Communications, 2021, 545, 119-124.	2.1	6
6	Lipid membranes induce structural conversion from amyloid oligomers to fibrils. Biochemical and Biophysical Research Communications, 2021, 557, 122-126.	2.1	8
7	Distinguishing the Effect on the Rate and Yield of AÎ²42 Aggregation by Green Tea Polyphenol EGCG. ACS Omega, 2020, 5, 21497-21505.	3.5	10
8	Spin Label Scanning Reveals Likely Locations of Î²-Strands in the Amyloid Fibrils of the Ure2 Prion Domain. ACS Omega, 2020, 5, 5984-5993.	3.5	10
9	Polymorphic AÎ²42 fibrils adopt similar secondary structure but differ in cross-strand side chain stacking interactions within the same Î²-sheet. Scientific Reports, 2020, 10, 5720.	3.3	13
10	AÎ²42 fibril formation from predominantly oligomeric samples suggests a link between oligomer heterogeneity and fibril polymorphism. Royal Society Open Science, 2019, 6, 190179.	2.4	17
11	Site-specific structural order in Alzheimer's AÎ²42 fibrils. Royal Society Open Science, 2018, 5, 180166.	2.4	11
12	Key Residues for the Formation of AÎ²42 Amyloid Fibrils. ACS Omega, 2018, 3, 8401-8407.	3.5	26
13	Thioflavin T as an amyloid dye: fibril quantification, optimal concentration and effect on aggregation. Royal Society Open Science, 2017, 4, 160696.	2.4	475
14	Crossâ€seeding between AÎ²40 and AÎ²42 in Alzheimer's disease. FEBS Letters, 2017, 591, 177-185.	2.8	42
15	A mix-and-click method to measure amyloid-Î² concentration with sub-micromolar sensitivity. Royal Society Open Science, 2017, 4, 170325.	2.4	11
16	A new structural model of Alzheimerâ€™s AÎ²42 fibrils based on electron paramagnetic resonance data and Rosetta modeling. Journal of Structural Biology, 2016, 194, 61-67.	2.8	50
17	Antiparallel Triple-strand Architecture for Prefibrillar AÎ²42 Oligomers. Journal of Biological Chemistry, 2014, 289, 27300-27313.	3.4	60
18	Alzheimer's AÎ²42 and AÎ²40 peptides form interlaced amyloid fibrils. Journal of Neurochemistry, 2013, 126, 305-311.	3.9	175

#	Article	IF	Citations
19	Structural Insights into AÎ²42 Oligomers Using Site-directed Spin Labeling. Journal of Biological Chemistry, 2013, 288, 18673-18683.	3.4	70
20	Solid-support Electron Paramagnetic Resonance (EPR) Studies of AÎ²40 Monomers Reveal a Structured State with Three Ordered Segments. Journal of Biological Chemistry, 2012, 287, 9081-9089.	3.4	15
21	Quantitative analysis of spin exchange interactions to identify Î² strand and turn regions in Ure2 prion domain fibrils with site-directed spin labeling. Journal of Structural Biology, 2012, 180, 374-381.	2.8	17
22	Structural origin of polymorphism of Alzheimer's amyloid Î²-fibrils. Biochemical Journal, 2012, 447, 43-50.	3.7	31
23	Prion Domain of Yeast Ure2 Protein Adopts a Completely Disordered Structure: A Solid-Support EPR Study. PLoS ONE, 2012, 7, e47248.	2.5	11
24	Key residues for the oligomerization of AÎ²42 protein in Alzheimerâ€™s disease. Biochemical and Biophysical Research Communications, 2011, 414, 512-516.	2.1	28
25	Hierarchical Organization in the Amyloid Core of Yeast Prion Protein Ure2. Journal of Biological Chemistry, 2011, 286, 29691-29699.	3.4	29
26	Osmolyte perturbation reveals conformational equilibria in spinâ€labeled proteins. Protein Science, 2009, 18, 1637-1652.	7.6	99
27	Structural determinants of nitroxide motion in spinâ€labeled proteins: Solventâ€exposed sites in helix B of T4 lysozyme. Protein Science, 2008, 17, 228-239.	7.6	111
28	The structure of a fibrilâ€forming sequence, NNQQNY, in the context of a globular fold. Protein Science, 2008, 17, 1617-1623.	7.6	20
29	The Mechanism of the Amyloidogenic Conversion of T7 Endonuclease I. Journal of Biological Chemistry, 2007, 282, 14968-14974.	3.4	7
30	Structural determinants of nitroxide motion in spin-labeled proteins: Tertiary contact and solvent-inaccessible sites in helix G of T4 lysozyme. Protein Science, 2007, 16, 1069-1086.	7.6	101
31	Runaway domain swapping in amyloid-like fibrils of T7 endonuclease I. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 8042-8047.	7.1	88