Johnny Habchi

List of Publications by Year
in descending order

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52 papers	3,281 citations	159358 30 h-index	174990 52 g-index
55 all docs	55 docs citations	55 times ranked	3835 citing authors

#	Article	IF	Citations
1	Structural and dynamics analysis of intrinsically disordered proteins by high-speed atomic force microscopy. Nature Nanotechnology, 2021, 16, 181-189.	15.6	69
2	Infrared nanospectroscopy reveals the molecular interaction fingerprint of an aggregation inhibitor with single AÎ²42 oligomers. Nature Communications, 2021, 12, 688.	5.8	52
3	Quantifying misfolded protein oligomers as drug targets and biomarkers in Alzheimer and Parkinson diseases. Nature Reviews Chemistry, 2021, 5, 277-294.	13.8	56
4	Squalamine and Its Derivatives Modulate the Aggregation of Amyloid-Î² and Î±-Synuclein and Suppress the Toxicity of Their Oligomers. Frontiers in Neuroscience, 2021, 15, 680026.	1.4	34
5	Two human metabolites rescue a C. elegans model of Alzheimerâ€™s disease via a cytosolic unfolded protein response. Communications Biology, 2021, 4, 843.	2.0	6
6	A dopamine metabolite stabilizes neurotoxic amyloid-Î² oligomers. Communications Biology, 2021, 4, 19.	2.0	25
7	Proliferation of Tau 304â€“380 Fragment Aggregates through Autocatalytic Secondary Nucleation. ACS Chemical Neuroscience, 2021, 12, 4406-4415.	1.7	19
8	Trodusquemine displaces protein misfolded oligomers from cell membranes and abrogates their cytotoxicity through a generic mechanism. Communications Biology, 2020, 3, 435.	2.0	44
9	Rational design of a conformation-specific antibody for the quantification of AÎ² oligomers. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 13509-13518.	3.3	61
10	Complexity in Lipid Membrane Composition Induces Resilience to AÎ²₄₂ Aggregation. ACS Chemical Neuroscience, 2020, 11, 1347-1352.	1.7	22
11	Rationally Designed Antibodies as Research Tools to Study the Structureâ€“Toxicity Relationship of Amyloid-Î² Oligomers. International Journal of Molecular Sciences, 2020, 21, 4542.	1.8	12
12	Transthyretin Inhibits Primary and Secondary Nucleations of Amyloid-Î² Peptide Aggregation and Reduces the Toxicity of Its Oligomers. Biomacromolecules, 2020, 21, 1112-1125.	2.6	59
13	Screening of small molecules using the inhibition of oligomer formation in Î±-synuclein aggregation as a selection parameter. Communications Chemistry, 2020, 3, .	2.0	27
14	Bacterial production and direct functional screening of expanded molecular libraries for discovering inhibitors of protein aggregation. Science Advances, 2019, 5, eaax5108.	4.7	12
15	Chemical and mechanistic analysis of photodynamic inhibition of Alzheimer's Î²-amyloid aggregation. Chemical Communications, 2019, 55, 1152-1155.	2.2	19
16	Trodusquemine enhances AÎ²42 aggregation but suppresses its toxicity by displacing oligomers from cell membranes. Nature Communications, 2019, 10, 225.	5.8	111
17	Chemical Kinetics for Bridging Molecular Mechanisms and Macroscopic Measurements of Amyloid Fibril Formation. Annual Review of Physical Chemistry, 2018, 69, 273-298.	4.8	161
18	Massively parallel C. elegans tracking provides multi-dimensional fingerprints for phenotypic discovery. Journal of Neuroscience Methods, 2018, 306, 57-67.	1.3	52

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19	Microfluidic deposition for resolving single-molecule protein architecture and heterogeneity. Nature Communications, 2018, 9, 3890.	5.8	40
20	SAR by kinetics for drug discovery in protein misfolding diseases. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 10245-10250.	3.3	54
21	Stabilization and Characterization of Cytotoxic AÎ²₄₀ Oligomers Isolated from an Aggregation Reaction in the Presence of Zinc Ions. ACS Chemical Neuroscience, 2018, 9, 2959-2971.	1.7	42
22	Structure-based design of allosteric calpain-1 inhibitors populating a novel bioactivity space. European Journal of Medicinal Chemistry, 2018, 157, 1264-1275.	2.6	8
23	Cholesterol catalyses AÎ²42 aggregation through a heterogeneous nucleation pathway in the presence of lipid membranes. Nature Chemistry, 2018, 10, 673-683.	6.6	186
24	Systematic development of small molecules to inhibit specific microscopic steps of AÎ²42 aggregation in Alzheimerâ€™s disease. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E200-E208.	3.3	180
25	Monomeric and fibrillar Î±-synuclein exert opposite effects on the catalytic cycle that promotes the proliferation of AÎ²42 aggregates. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 8005-8010.	3.3	45
26	Interfacial Properties of NTAIL, an Intrinsically Disordered Protein. Biophysical Journal, 2017, 113, 2723-2735.	0.2	8
27	AFM-Based Single Molecule Techniques: Unraveling the Amyloid Pathogenic Species. Current Pharmaceutical Design, 2016, 22, 3950-3970.	0.9	75
28	An anticancer drug suppresses the primary nucleation reaction that initiates the production of the toxic AÎ²42 aggregates linked with Alzheimerâ€™s disease. Science Advances, 2016, 2, e1501244.	4.7	180
29	A Fragment-Based Method of Creating Small-Molecule Libraries to Target the Aggregation of Intrinsically Disordered Proteins. ACS Combinatorial Science, 2016, 18, 144-153.	3.8	35
30	The inverted free energy landscape of an intrinsically disordered peptide by simulations and experiments. Scientific Reports, 2015, 5, 15449.	1.6	118
31	Structural Disorder within Paramyxoviral Nucleoproteins and Phosphoproteins in Their Free and Bound Forms: From Predictions to Experimental Assessment. International Journal of Molecular Sciences, 2015, 16, 15688-15726.	1.8	19
32	Order and Disorder in the Replicative Complex of Paramyxoviruses. Advances in Experimental Medicine and Biology, 2015, 870, 351-381.	0.8	10
33	Dynamics of the Intrinsically Disordered Câ€Terminal Domain of the Nipah Virus Nucleoprotein and Interaction with the X Domain of the Phosphoprotein as Unveiled by NMR Spectroscopy. ChemBioChem, 2015, 16, 268-276.	1.3	31
34	Molecular Basis for Structural Heterogeneity of an Intrinsically Disordered Protein Bound to a Partner by Combined ESI-IM-MS and Modeling. Journal of the American Society for Mass Spectrometry, 2015, 26, 472-481.	1.2	45
35	Neuronal Cx3cr1 Deficiency Protects against Amyloid Î²-Induced Neurotoxicity. PLoS ONE, 2015, 10, e0127730.	1.1	26
36	Structural Disorder in Viral Proteins. Chemical Reviews, 2014, 114, 6880-6911.	23.0	181

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37	Introducing Protein Intrinsic Disorder. Chemical Reviews, 2014, 114, 6561-6588.	23.0	628
38	Diversification of EPR signatures in site directed spin labeling using a Î²-phosphorylated nitroxide. Physical Chemistry Chemical Physics, 2014, 16, 4202.	1.3	13
39	Coiled-coil deformations in crystal structures: themeasles virusphosphoprotein multimerization domain as an illustrative example. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1589-1603.	2.5	29
40	Assessing induced folding within the intrinsically disordered C-terminal domain of theHenipavirusnucleoproteins by site-directed spin labeling EPR spectroscopy. Journal of Biomolecular Structure and Dynamics, 2013, 31, 453-471.	2.0	38
41	Atomic Resolution Description of the Interaction between the Nucleoprotein and Phosphoprotein of Hendra Virus. PLoS Pathogens, 2013, 9, e1003631.	2.1	68
42	Extracting structural information from charge-state distributions of intrinsically disordered proteins by non-denaturing electrospray-ionization mass spectrometry. Intrinsically Disordered Proteins, 2013, 1, e25068.	1.9	33
43	Plasticity in Structural and Functional Interactions between the Phosphoprotein and Nucleoprotein of Measles Virus. Journal of Biological Chemistry, 2012, 287, 11951-11967.	1.6	36
44	Compaction and binding properties of the intrinsically disordered C-terminal domain of Henipavirus nucleoprotein as unveiled by deletion studies. Molecular BioSystems, 2012, 8, 392-410.	2.9	43
45	Interaction between the Câ€terminal domains of measles virus nucleoprotein and phosphoprotein: A tight complex implying one binding site. Protein Science, 2012, 21, 1577-1585.	3.1	15
46	Monitoring Structural Transitions in IDPs by Vibrational Spectroscopy of Cyanylated Cysteine. Methods in Molecular Biology, 2012, 895, 245-270.	0.4	3
47	Monitoring Structural Transitions in IDPs by Site-Directed Spin Labeling EPR Spectroscopy. Methods in Molecular Biology, 2012, 895, 361-386.	0.4	13
48	Structural disorder within paramyxovirus nucleoproteins and phosphoproteins. Molecular BioSystems, 2012, 8, 69-81.	2.9	62
49	Transcription et rÃ©plication des MononegaviralesÂ: une machine molÃ©culaire originale. Virologie, 2012, 16, 225-257.	0.1	17
50	Dividing To Unveil Protein Microheterogeneities: Traveling Wave Ion Mobility Study. Analytical Chemistry, 2011, 83, 7306-7315.	3.2	10
51	Characterization of the Interactions between the Nucleoprotein and the Phosphoprotein of Henipavirus. Journal of Biological Chemistry, 2011, 286, 13583-13602.	1.6	65
52	Structural Disorder within Henipavirus Nucleoprotein and Phosphoprotein: From Predictions to Experimental Assessment. PLoS ONE, 2010, 5, e11684.	1.1	78