

# Elodie Monsellier

## List of Publications by Year in descending order

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Version: 2024-02-01

14  
papers

839  
citations

840776

11  
h-index

1058476

14  
g-index

15  
all docs

15  
docs citations

15  
times ranked

1391  
citing authors

#	ARTICLE	IF	CITATIONS
1	Polypeptides derived from $\hat{\text{I}}\pm$ -Synuclein binding partners to prevent $\hat{\text{I}}\pm$ -Synuclein fibrils interaction with and take-up by cells. PLoS ONE, 2020, 15, e0237328.	2.5	3
2	Interaction of the chaperones alpha B-crystallin and CHIP with fibrillar alpha-synuclein: Effects on internalization by cells and identification of interacting interfaces. Biochemical and Biophysical Research Communications, 2020, 527, 760-769.	2.1	8
3	$\hat{\text{I}}\pm$ -Synuclein and huntingtin exon 1 amyloid fibrils bind laterally to the cellular membrane. Scientific Reports, 2016, 6, 19180.	3.3	35
4	Molecular Interaction between the Chaperone Hsc70 and the N-terminal Flank of Huntingtin Exon 1 Modulates Aggregation. Journal of Biological Chemistry, 2015, 290, 2560-2576.	3.4	73
5	DNAJB6 is a peptide-binding chaperone which can suppress amyloid fibrillation of polyglutamine peptides at substoichiometric molar ratios. Cell Stress and Chaperones, 2014, 19, 227-239.	2.9	98
6	Polyglutamine Repeats Are Associated to Specific Sequence Biases That Are Conserved among Eukaryotes. PLoS ONE, 2012, 7, e30824.	2.5	32
7	A Computational Approach for Identifying the Chemical Factors Involved in the Glycosaminoglycans-Mediated Acceleration of Amyloid Fibril Formation. PLoS ONE, 2010, 5, e11363.	2.5	9
8	Kinetic Analysis of Amyloid Formation in the Presence of Heparan Sulfate. Journal of Biological Chemistry, 2009, 284, 29921-29934.	3.4	58
9	Amyloid Formation by the Model Protein Muscle Acylphosphatase is Accelerated by Heparin and Heparan Sulphate Through a Scaffolding-based Mechanism. Journal of Biochemistry, 2009, 146, 805-814.	1.7	53
10	Aggregation Propensity of the Human Proteome. PLoS Computational Biology, 2008, 4, e1000199.	3.2	81
11	The Distribution of Residues in a Polypeptide Sequence Is a Determinant of Aggregation Optimized by Evolution. Biophysical Journal, 2007, 93, 4382-4391.	0.5	55
12	Prevention of amyloid-like aggregation as a driving force of protein evolution. EMBO Reports, 2007, 8, 737-742.	4.5	238
13	Improving the Stability of an Antibody Variable Fragment by a Combination of Knowledge-based Approaches: Validation and Mechanisms. Journal of Molecular Biology, 2006, 362, 580-593.	4.2	48
14	Quantitative measurement of protein stability from unfolding equilibria monitored with the fluorescence maximum wavelength. Protein Engineering, Design and Selection, 2005, 18, 445-456.	2.1	48