## Francesco Bemporad

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2702825/publications.pdf

Version: 2024-02-01

39 papers 1,436 citations

394421 19 h-index 315739 38 g-index

42 all docs 42 docs citations

times ranked

42

2057 citing authors

| #  | Article  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | Protein Misfolded Oligomers: Experimental Approaches, Mechanism of Formation, and Structure-Toxicity Relationships. Chemistry and Biology, 2012, 19, 315-327.  | 6.0  | 239       |
| 2  | Protein folding: Defining a "standard―set of experimental conditions and a preliminary kinetic data set of two-state proteins. Protein Science, 2005, 14, 602-616.   | 7.6  | 207       |
| 3  | Evidence for a Mechanism of Amyloid Formation Involving Molecular Reorganisation within<br>Native-like Precursor Aggregates. Journal of Molecular Biology, 2005, 351, 910-922.                                     | 4.2  | 129       |
| 4  | Assessing the role of aromatic residues in the amyloid aggregation of human muscle acylphosphatase. Protein Science, 2006, 15, 862-870.  | 7.6  | 107       |
| 5  | Sequence and Structural Determinants of Amyloid Fibril Formation. Accounts of Chemical Research, 2006, 39, 620-627.  | 15.6 | 102       |
| 6  | Amyloid Formation of a Protein in the Absence of Initial Unfolding and Destabilization of the Native State. Biophysical Journal, 2005, 89, 4234-4244.  | 0.5  | 67        |
| 7  | Transthyretin Inhibits Primary and Secondary Nucleations of Amyloid- $\hat{l}^2$ Peptide Aggregation and Reduces the Toxicity of Its Oligomers. Biomacromolecules, 2020, 21, 1112-1125.                            | 5.4  | 59        |
| 8  | Structure, conformational stability, and enzymatic properties of acylphosphatase from the hyperthermophile Sulfolobus solfataricus. Proteins: Structure, Function and Bioinformatics, 2005, 62, 64-79.             | 2.6  | 43        |
| 9  | Exploring the Mechanism of Formation of Native-like and Precursor Amyloid Oligomers for the Native Acylphosphatase from Sulfolobus solfataricus. Structure, 2006, 14, 993-1001.                                    | 3.3  | 36        |
| 10 | Biological function in a non-native partially folded state of a protein. EMBO Journal, 2008, 27, 1525-35.  | 7.8  | 32        |
| 11 | "Nativeâ€like aggregationâ€of the acylphosphatase from <i>Sulfolobus solfataricus</i> and its biological implications. FEBS Letters, 2009, 583, 2630-2638.   | 2.8  | 32        |
| 12 | Rapid oligomer formation of human muscle acylphosphatase induced by heparan sulfate. Nature Structural and Molecular Biology, 2012, 19, 547-554.   | 8.2  | 28        |
| 13 | The Degree of Structural Protection at the Edge $\hat{l}^2$ -Strands Determines the Pathway of Amyloid Formation in Globular Proteins. Journal of the American Chemical Society, 2008, 130, 4295-4302.             | 13.7 | 26        |
| 14 | Characterizing Intermolecular Interactions That Initiate Native-Like Protein Aggregation. Biophysical Journal, 2012, 102, 2595-2604.   | 0.5  | 26        |
| 15 | Structural and Dynamics Characteristics of Acylphosphatase from Sulfolobus solfataricus in the Monomeric State and in the Initial Native-like Aggregates. Journal of Biological Chemistry, 2010, 285, 14689-14700. | 3.4  | 23        |
| 16 | Mutations of Profilin-1 Associated with Amyotrophic Lateral Sclerosis Promote Aggregation Due to Structural Changes of Its Native State. ACS Chemical Biology, 2015, 10, 2553-2563.                                | 3.4  | 23        |
| 17 | Molecular insights into cell toxicity of a novel familial amyloidogenic variant of β2â€microglobulin.<br>Journal of Cellular and Molecular Medicine, 2016, 20, 1443-1456.  | 3.6  | 23        |
| 18 | A model for the aggregation of the acylphosphatase from Sulfolobus solfataricus in its native-like state. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2008, 1784, 1986-1996.                          | 2.3  | 20        |

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|----|--|-----|-----------|
| 19 | Studying the Folding Process of the Acylphosphatase fromSulfolobus solfataricus. A Comparative Analysis with Other Proteins from the Same Superfamilyâ€. Biochemistry, 2004, 43, 9116-9126.  | 2.5 | 19        |
| 20 | 1H, 13C and 15N resonance assignments of human muscle acylphosphatase. Biomolecular NMR Assignments, 2012, 6, 27-29.   | 0.8 | 16        |
| 21 | Structure and Dynamics of the Integrin LFA-1 I-Domain in the Inactive State Underlie its Inside-Out/Outside-In Signaling and Allosteric Mechanisms. Structure, 2015, 23, 745-753.  | 3.3 | 15        |
| 22 | The Folding Process of Acylphosphatase from Escherichia coli is Remarkably Accelerated by the Presence of a Disulfide Bond. Journal of Molecular Biology, 2008, 379, 1107-1118.  | 4.2 | 14        |
| 23 | The Folding process of Human Profilin-1, a novel protein associated with familial amyotrophic lateral sclerosis. Scientific Reports, 2015, 5, 12332.   | 3.3 | 14        |
| 24 | Probing conformational changes of monomeric transthyretin with second derivative fluorescence. Scientific Reports, 2019, 9, 10988.   | 3.3 | 14        |
| 25 | A single amino acid mutation affects elicitor and expansins-like activities of cerato-platanin, a non-catalytic fungal protein. PLoS ONE, 2017, 12, e0178337.  | 2.5 | 14        |
| 26 | Edge strand engineering prevents nativeâ€like aggregation in <i><scp>S</scp>ulfolobusÂsolfataricus</i> acylphosphatase. FEBS Journal, 2014, 281, 4072-4084.  | 4.7 | 13        |
| 27 | From the Evolution of Protein Sequences Able to Resist Self-Assembly to the Prediction of Aggregation Propensity. International Review of Cell and Molecular Biology, 2017, 329, 1-47.   | 3.2 | 13        |
| 28 | Insight into the Folding and Dimerization Mechanisms of the N-Terminal Domain from Human TDP-43. International Journal of Molecular Sciences, 2020, 21, 6259.  | 4.1 | 13        |
| 29 | A Complex Equilibrium among Partially Unfolded Conformations in Monomeric Transthyretin.<br>Biochemistry, 2014, 53, 4381-4392.   | 2.5 | 12        |
| 30 | Stability of an aggregation-prone partially folded state of human profilin-1 correlates with aggregation propensity. Journal of Biological Chemistry, 2018, 293, 10303-10313.  | 3.4 | 10        |
| 31 | Direct Conversion of an Enzyme from Native-like to Amyloid-like Aggregates within Inclusion Bodies.<br>Biophysical Journal, 2017, 112, 2540-2551.  | 0.5 | 9         |
| 32 | NMR characterization of the conformational fluctuations of the human lymphocyte functionâ€associated antigenâ€1 lâ€domain. Protein Science, 2014, 23, 1596-1606.   | 7.6 | 8         |
| 33 | FRET studies of various conformational states adopted by transthyretin. Cellular and Molecular Life Sciences, 2017, 74, 3577-3598.   | 5.4 | 7         |
| 34 | Amyloid fibril formation by a normally folded protein in the absence of denaturants and agitation. Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis, 2013, 20, 226-232. | 3.0 | 6         |
| 35 | Identification of Novel 1,3,5-Triphenylbenzene Derivative Compounds as Inhibitors of Hen Lysozyme Amyloid Fibril Formation. International Journal of Molecular Sciences, 2019, 20, 5558.   | 4.1 | 6         |
| 36 | Preliminary characterization of two different crystal forms of acylphosphatase from the hyperthermophile archaeonSulfolobus solfataricus. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 144-146.                                      | 0.7 | 3         |

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|----|--|-----|-----------|
| 37 | The Transthyretin/Oleuropein Aglycone Complex: A New Tool against TTR Amyloidosis.<br>Pharmaceuticals, 2022, 15, 277.                                | 3.8 | 3         |
| 38 | Conversion of the Native N-Terminal Domain of TDP-43 into a Monomeric Alternative Fold with Lower Aggregation Propensity. Molecules, 2022, 27, 4309. | 3.8 | 3         |
| 39 | Capturing A $\hat{I}^2$ 42 aggregation in the cell. Journal of Biological Chemistry, 2019, 294, 1488-1489.   | 3.4 | 1         |