

Carlo Pm Van Mierlo

List of Publications by Year in descending order

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59
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2,111
citations

218677

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59
all docs

59
docs citations

59
times ranked

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citing authors

#	ARTICLE	IF	CITATIONS
1	Multiple Steps during the Formation of \hat{I}^2 -Lactoglobulin Fibrils. <i>Biomacromolecules</i> , 2003, 4, 1614-1622.	5.4	161
2	Local Structure Due to an Aromatic-Amide Interaction Observed by ^1H -Nuclear Magnetic Resonance Spectroscopy in Peptides Related to the N Terminus of Bovine Pancreatic Trypsin Inhibitor. <i>Journal of Molecular Biology</i> , 1993, 230, 312-322.	4.2	121
3	Partially Folded Conformation of the (30-51) Intermediate in the Disulphide Folding Pathway of Bovine Pancreatic Trypsin Inhibitor. <i>Journal of Molecular Biology</i> , 1993, 229, 1125-1146.	4.2	120
4	Conformation and orientation of a protein folding intermediate trapped by adsorption. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 11316-11321.	7.1	94
5	Kinetic and Structural Characterization of Adsorption-induced Unfolding of Bovine \hat{I}^\pm -Lactalbumin. <i>Journal of Biological Chemistry</i> , 2002, 277, 10922-10930.	3.4	87
6	Two-dimensional ^1H nuclear magnetic resonance study of the ($5\hat{\alpha}^{\epsilon}55$) single-disulphide folding intermediate of bovine pancreatic trypsin inhibitor. <i>Journal of Molecular Biology</i> , 1991, 222, 373-390.	4.2	86
7	($14\hat{\alpha}^{\epsilon}38, 30\hat{\alpha}^{\epsilon}51$) Double-disulphide intermediate in folding of bovine pancreatic trypsin inhibitor: A two-dimensional ^1H nuclear magnetic resonance study. <i>Journal of Molecular Biology</i> , 1991, 222, 353-371.	4.2	82
8	Structural characterisation of apoflavodoxin shows that the location of the stable nucleus differs among proteins with a flavodoxin-like topology 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1998, 282, 653-666.	4.2	80
9	In vivo uniform ^{15}N -isotope labelling of plants: Using the greenhouse for structural proteomics. <i>Proteomics</i> , 2004, 4, 226-234.	2.2	79
10	Formation of On- and Off-Pathway Intermediates in the Folding Kinetics of <i>Azotobacter vinelandii</i> Apoflavodoxin. <i>Biochemistry</i> , 2004, 43, 10475-10489.	2.5	68
11	Macromolecular Crowding Compacts Unfolded Apoflavodoxin and Causes Severe Aggregation of the Off-pathway Intermediate during Apoflavodoxin Folding. <i>Journal of Biological Chemistry</i> , 2008, 283, 27383-27394.	3.4	65
12	The equilibrium unfolding of <i>Azotobacter vinelandii</i> apoflavodoxin II occurs via a relatively stable folding intermediate. <i>Protein Science</i> , 1998, 7, 2331-2344.	7.6	64
13	The folding energy landscape of apoflavodoxin is rugged: Hydrogen exchange reveals nonproductive misfolded intermediates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 4095-4100.	7.1	63
14	Protein folding and stability investigated by fluorescence, circular dichroism (CD), and nuclear magnetic resonance (NMR) spectroscopy: the flavodoxin story. <i>Journal of Biotechnology</i> , 2000, 79, 281-298.	3.8	58
15	Last In, First Out. <i>Journal of Biological Chemistry</i> , 2005, 280, 7836-7844.	3.4	55
16	^1H NMR Analysis of the Partly-folded Non-native Two-disulphide Intermediates (30-51,5-14) and (30-51,5-38) in the Folding Pathway of Bovine Pancreatic Trypsin Inhibitor. <i>Journal of Molecular Biology</i> , 1994, 235, 1044-1061.	4.2	50
17	A crystallographic study of Cys69Ala flavodoxin II from <i>Azotobacter vinelandii</i> : Structural determinants of redox potential. <i>Protein Science</i> , 2005, 14, 2284-2295.	7.6	48
18	Protein topology affects the appearance of intermediates during the folding of proteins with a flavodoxin-like fold. <i>Biophysical Chemistry</i> , 2005, 114, 181-189.	2.8	42

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19	Redox Properties of Wild-Type, Cys69Ala, and Cys69Ser <i>Azotobacter Vinelandii</i> Flavodoxin II as Measured by Cyclic Voltammetry and EPR Spectroscopy. <i>FEBS Journal</i> , 1996, 235, 167-172.	0.2	36
20	Apoflavodoxin (un) folding followed at the residue level by NMR. <i>Protein Science</i> , 2000, 9, 145-157.	7.6	35
21	Extensive Formation of Off-Pathway Species during Folding of an α - β Parallel Protein Is Due to Docking of (Non)native Structure Elements in Unfolded Molecules. <i>Journal of the American Chemical Society</i> , 2008, 130, 16914-16920.	13.7	33
22	Distant residues mediate picomolar binding affinity of a protein cofactor. <i>Nature Communications</i> , 2012, 3, 1010.	12.8	33
23	Kinetic roles and conformational properties of the non-native two-disulphide intermediates in the refolding of bovine pancreatic trypsin inhibitor. <i>Journal of Molecular Biology</i> , 1992, 224, 905-911.	4.2	31
24	Tryptophan-Tryptophan Energy Migration as a Tool to Follow Apoflavodoxin Folding. <i>Biophysical Journal</i> , 2008, 95, 2462-2469.	0.5	31
25	Apparent local stability of the secondary structure of <i>Azotobacter vinelandii</i> holoflavodoxin II as probed by hydrogen exchange: Implications for redox potential regulation and flavodoxin folding. <i>Protein Science</i> , 1998, 7, 306-317.	7.6	29
26	Reversible Temperature-Switching of Hydrogel Stiffness of Coassembled, Silk-Collagen-Like Hydrogels. <i>Biomacromolecules</i> , 2015, 16, 2506-2513.	5.4	28
27	Molecular Dynamics Study of the Solvation of an α -Helical Transmembrane Peptide by DMSO. <i>Journal of Physical Chemistry B</i> , 2008, 112, 8664-8671.	2.6	27
28	Noncooperative Formation of the Off-Pathway Molten Globule during Folding of the α - β Parallel Protein Apoflavodoxin. <i>Journal of the American Chemical Society</i> , 2009, 131, 2739-2746.	13.7	26
29	A General Approach for Detecting Folding Intermediates from Steady-State and Time-Resolved Fluorescence of Single-Tryptophan-Containing Proteins. <i>Biochemistry</i> , 2011, 50, 3441-3450.	2.5	26
30	Fluorescence of Alexa Fluor Dye Tracks Protein Folding. <i>PLoS ONE</i> , 2012, 7, e46838.	2.5	24
31	Rise-Time of FRET-Acceptor Fluorescence Tracks Protein Folding. <i>International Journal of Molecular Sciences</i> , 2014, 15, 23836-23850.	4.1	24
32	Three-dimensional correlated NMR study of <i>Megasphaera elsdenii</i> flavodoxin in the oxidized state. <i>FEBS Journal</i> , 1991, 195, 807-822.	0.2	21
33	Solution conformation of a peptide fragment representing a proposed RNA-binding site of a viral coat protein studied by two-dimensional NMR. <i>Biochemistry</i> , 1991, 30, 5722-5727.	2.5	20
34	Interrupted Hydrogen/Deuterium Exchange Reveals the Stable Core of the Remarkably Helical Molten Globule of α - β Parallel Protein Flavodoxin. <i>Journal of Biological Chemistry</i> , 2010, 285, 4165-4172.	3.4	20
35	Mechanism of the small ATP-independent chaperone Spy is substrate specific. <i>Nature Communications</i> , 2021, 12, 851.	12.8	20
36	Structure and localization of an essential transmembrane segment of the proton translocation channel of yeast H ⁺ -V-ATPase. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2007, 1768, 218-227.	2.6	18

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37	Non-native hydrophobic interactions detected in unfolded apoflavodoxin by paramagnetic relaxation enhancement. <i>European Biophysics Journal</i> , 2010, 39, 689-698.	2.2	17
38	Gradual Folding of an Off-Pathway Molten Globule Detected at the Single-Molecule Level. <i>Journal of Molecular Biology</i> , 2015, 427, 3148-3157.	4.2	17
39	Doubly sensitivity-enhanced 3D TOCSY-HSQC. <i>Journal of Biomolecular NMR</i> , 1996, 8, 319-330.	2.8	16
40	Segment TM7 from the cytoplasmic hemi-channel from VO-H ⁺ -V-ATPase includes a flexible region that has a potential role in proton translocation. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2007, 1768, 2263-2270.	2.6	16
41	Refolding of Adsorbed Bovine β -Lactalbumin during Surfactant Induced Displacement from a Hydrophobic Interface. <i>Langmuir</i> , 2003, 19, 2929-2937.	3.5	15
42	Topological Switching between an β -Sheet Parallel Protein and a Remarkably Helical Molten Globule. <i>Journal of the American Chemical Society</i> , 2009, 131, 8290-8295.	13.7	14
43	Adsorption of Bovine β -Lactalbumin on Suspended Solid Nanospheres and Its Subsequent Displacement Studied by NMR Spectroscopy. <i>Langmuir</i> , 2004, 20, 5530-5538.	3.5	13
44	Secondary and tertiary structure characteristics of <i>Megasphaera elsdenii</i> flavodoxin in the reduced state as determined by two-dimensional 1H NMR. <i>FEBS Journal</i> , 1990, 189, 589-600.	0.2	12
45	Folding of proteins with a flavodoxin-like architecture. <i>FEBS Journal</i> , 2017, 284, 3145-3167.	4.7	11
46	Doubly Sensitivity-Enhanced 3D HCCH-TOCSY of ¹³ C-Labeled Proteins in H ₂ O Using Heteronuclear Cross Polarization and Pulsed Field Gradients. <i>Journal of Magnetic Resonance</i> , 1997, 124, 459-467.	2.1	10
47	Illuminating the Off-Pathway Nature of the Molten Globule Folding Intermediate of an β -Sheet Parallel Protein. <i>PLoS ONE</i> , 2012, 7, e45746.	2.5	10
48	Cofactor Binding Protects Flavodoxin against Oxidative Stress. <i>PLoS ONE</i> , 2012, 7, e41363.	2.5	9
49	The <i>Arabidopsis thaliana</i> SERK1 Kinase Domain Spontaneously Refolds to an Active State In Vitro. <i>PLoS ONE</i> , 2012, 7, e50907.	2.5	9
50	Functional and Structural Characterization of a Synthetic Peptide Representing the N-Terminal Domain of Prokaryotic Pyruvate Dehydrogenase. <i>Biochemistry</i> , 2002, 41, 7490-7500.	2.5	5
51	The Ribosome Restrains Molten Globule Formation in Stalled Nascent Flavodoxin. <i>Journal of Biological Chemistry</i> , 2016, 291, 25911-25920.	3.4	5
52	Stabilisation centres differ between structurally homologous proteins as shown by NMR spectroscopy. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 1999, 7, 147-156.	1.8	4
53	Ligand binding and conformational states of the photoprotein obelin. <i>FEBS Letters</i> , 2012, 586, 4173-4179.	2.8	4
54	Stalled flavodoxin binds its cofactor while fully exposed outside the ribosome. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 1317-1324.	2.3	4

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55	Concurrent presence of on- and off-pathway folding intermediates of apoflavodoxin at physiological ionic strength. <i>Physical Chemistry Chemical Physics</i> , 2018, 20, 7059-7072.	2.8	4
56	NMR characterization of a 264-residue hyperthermostable endo- β -1,3-glucanase. <i>Biochemical and Biophysical Research Communications</i> , 2010, 391, 370-375.	2.1	3
57	Double Electronâ€“Electron Spin Resonance Tracks Flavodoxin Folding. <i>Journal of Physical Chemistry B</i> , 2015, 119, 13507-13514.	2.6	3
58	Chaotropic heat treatment resolves nativeâ€“like aggregation of a heterologously produced hyperthermostable laminarinase. <i>Biotechnology Journal</i> , 2017, 12, 1700007.	3.5	3
59	Measurement of heteronuclear NOE enhancements in biological macromolecules. A convenient pulse sequence for use with aqueous solutions. <i>Journal of Magnetic Resonance</i> , 1992, 100, 221-228.	0.5	2