

Carlo Pm Van Mierlo

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4961513/publications.pdf>

Version: 2024-02-01

59
papers

2,111
citations

218677

26
h-index

233421

45
g-index

59
all docs

59
docs citations

59
times ranked

2042
citing authors

#	ARTICLE	IF	CITATIONS
1	Mechanism of the small ATP-independent chaperone Spy is substrate specific. <i>Nature Communications</i> , 2021, 12, 851.	12.8	20
2	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
3	Chaotropic heat treatment resolves native-like aggregation of a heterologously produced hyperthermostable laminarinase. <i>Biotechnology Journal</i> , 2017, 12, 1700007.	3.5	3
4	Folding of proteins with a flavodoxin-like architecture. <i>FEBS Journal</i> , 2017, 284, 3145-3167.	4.7	11
5	The Ribosome Restrains Molten Globule Formation in Stalled Nascent Flavodoxin. <i>Journal of Biological Chemistry</i> , 2016, 291, 25911-25920.	3.4	5
6	Reversible Temperature-Switching of Hydrogel Stiffness of Coassembled, Silk-Collagen-Like Hydrogels. <i>Biomacromolecules</i> , 2015, 16, 2506-2513.	5.4	28
7	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
8	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
9	Double Electron-Electron Spin Resonance Tracks Flavodoxin Folding. <i>Journal of Physical Chemistry B</i> , 2015, 119, 13507-13514.	2.6	3
10	Rise-Time of FRET-Acceptor Fluorescence Tracks Protein Folding. <i>International Journal of Molecular Sciences</i> , 2014, 15, 23836-23850.	4.1	24
11	Distant residues mediate picomolar binding affinity of a protein cofactor. <i>Nature Communications</i> , 2012, 3, 1010.	12.8	33
12	Ligand binding and conformational states of the photoprotein obelin. <i>FEBS Letters</i> , 2012, 586, 4173-4179.	2.8	4
13	Fluorescence of Alexa Fluor Dye Tracks Protein Folding. <i>PLoS ONE</i> , 2012, 7, e46838.	2.5	24
14	Cofactor Binding Protects Flavodoxin against Oxidative Stress. <i>PLoS ONE</i> , 2012, 7, e41363.	2.5	9
15	Illuminating the Off-Pathway Nature of the Molten Globule Folding Intermediate of an $\hat{I}\pm\hat{I}^2$ Parallel Protein. <i>PLoS ONE</i> , 2012, 7, e45746.	2.5	10
16	The Arabidopsis thaliana SERK1 Kinase Domain Spontaneously Refolds to an Active State In Vitro. <i>PLoS ONE</i> , 2012, 7, e50907.	2.5	9
17	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
18	Non-native hydrophobic interactions detected in unfolded apoflavodoxin by paramagnetic relaxation enhancement. <i>European Biophysics Journal</i> , 2010, 39, 689-698.	2.2	17

#	ARTICLE	IF	CITATIONS
19	Interrupted Hydrogen/Deuterium Exchange Reveals the Stable Core of the Remarkably Helical Molten Globule of β -Parallel Protein Flavodoxin. <i>Journal of Biological Chemistry</i> , 2010, 285, 4165-4172.	3.4	20
20	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
21	Topological Switching between an α -Parallel Protein and a Remarkably Helical Molten Globule. <i>Journal of the American Chemical Society</i> , 2009, 131, 8290-8295.	13.7	14
22	Noncooperative Formation of the Off-Pathway Molten Globule during Folding of the β -Parallel Protein Apoflavodoxin. <i>Journal of the American Chemical Society</i> , 2009, 131, 2739-2746.	13.7	26
23	Tryptophan-Tryptophan Energy Migration as a Tool to Follow Apoflavodoxin Folding. <i>Biophysical Journal</i> , 2008, 95, 2462-2469.	0.5	31
24	Extensive Formation of Off-Pathway Species during Folding of an α -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
25	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
26	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
27	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
28	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
29	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
30	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
31	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
32	Last In, First Out. <i>Journal of Biological Chemistry</i> , 2005, 280, 7836-7844.	3.4	55
33	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
34	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
35	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
36	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

#	ARTICLE	IF	CITATIONS
37	Multiple Steps during the Formation of Î²-Lactoglobulin Fibrils. <i>Biomacromolecules</i> , 2003, 4, 1614-1622.	5.4	161
38	Refolding of Adsorbed Bovine Î²-Lactalbumin during Surfactant Induced Displacement from a Hydrophobic Interface. <i>Langmuir</i> , 2003, 19, 2929-2937.	3.5	15
39	Kinetic and Structural Characterization of Adsorption-induced Unfolding of Bovine Î²-Lactalbumin. <i>Journal of Biological Chemistry</i> , 2002, 277, 10922-10930.	3.4	87
40	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
41	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
42	Apoflavodoxin (un) folding followed at the residue level by NMR. <i>Protein Science</i> , 2000, 9, 145-157.	7.6	35
43	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
44	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
45	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
46	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
47	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
48	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
49	Doubly sensitivity-enhanced 3D TOCSY-HSQC. <i>Journal of Biomolecular NMR</i> , 1996, 8, 319-330.	2.8	16
50	¹ H 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
51	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
52	Local Structure Due to an Aromatic-Amide Interaction Observed by ¹ H-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
53	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
54	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

#	ARTICLE	IF	CITATIONS
55	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
56	(14â€“38, 30â€“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
57	Two-dimensional 1H nuclear magnetic resonance study of the (5â€“55) single-disulphide folding intermediate of bovine pancreatic trypsin inhibitor. <i>Journal of Molecular Biology</i> , 1991, 222, 373-390.	4.2	86
58	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
59	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