Eva Meirovitch

List of Publications by Year
in descending order

65 papers	2,024 citations	279487 23 h-index	243296 44 g-index
67 all docs	67 docs citations	67 times ranked	1158 citing authors

#	Article	IF	Citations
1	The N-Terminal Domain of AÎ²₄₀-Amyloid Fibril: The MOMD Perspective of its Dynamic Structure from NMR Lineshape Analysis. Journal of Physical Chemistry B, 2022, 126, 1202-1211.	1.2	2
2	Structural Dynamics by NMR in the Solid State: II. The MOMD Perspective of the Dynamic Structure of Metalâ€“Organic Frameworks Comprising Several Mobile Components. Journal of Physical Chemistry B, 2022, 126, 2452-2465.	1.2	4
3	SRLS Analysis of 15Nâ€“1H NMR Relaxation from the Protein S100A1: Dynamic Structure, Calcium Binding, and Related Changes in Conformational Entropy. Journal of Physical Chemistry B, 2021, 125, 805-816.	1.2	5
4	Structural Dynamics from NMR Relaxation by SRLS Analysis: Local Geometry, Potential Energy Landscapes, and Spectral Densities. Journal of Physical Chemistry B, 2021, 125, 6130-6143.	1.2	4
5	Local ordering and dynamics in anisotropic media by magnetic resonance: from liquid crystals to proteins. Liquid Crystals, 2020, 47, 1926-1954.	0.9	4
6	Conformational Entropy from Mobile Bond Vectors in Proteins: A Viewpoint that Unifies NMR Relaxation Theory and Molecular Dynamics Simulation Approaches. Journal of Physical Chemistry B, 2020, 124, 9323-9334.	1.2	9
7	Structural Dynamics by NMR in the Solid State: The Unified MOMD Perspective Applied to Organic Frameworks with Interlocked Molecules. Journal of Physical Chemistry B, 2020, 124, 6225-6235.	1.2	4
8	Conformational Entropy from Restricted Bond-Vector Motion in Proteins: The Symmetry of the Local Restrictions and Relation to NMR Relaxation. Journal of Physical Chemistry B, 2020, 124, 4284-4292.	1.2	0
9	Local Ordering at the Nâ€“H Sites of the Rho GTPase Binding Domain of Plexin-B1: Impact of Dimerization. Journal of Physical Chemistry B, 2019, 123, 8019-8033.	1.2	6
10	Local Ordering at Mobile Sites in Proteins: Combining Perspectives from NMR Relaxation and Molecular Dynamics. Journal of Physical Chemistry B, 2019, 123, 2745-2755.	1.2	10
11	Comment on â€œDistinct Populations in Spin-Label EPR Spectra from Nitroxidesâ€• Journal of Physical Chemistry B, 2019, 123, 2454-2456.	1.2	1
12	MOMD Analysis of NMR Line Shapes from AÎ²-Amyloid Fibrils: A New Tool for Characterizing Molecular Environments in Protein Aggregates. Journal of Physical Chemistry B, 2018, 122, 4793-4801.	1.2	7
13	Phenyl-Ring Dynamics in Amyloid Fibrils and Proteins: The Microscopic-Order-Macroscopic-Disorder Perspective. Journal of Physical Chemistry B, 2018, 122, 8675-8684.	1.2	6
14	Protein dynamics in the solid-state from 2H NMR lineshape analysis. III. MOMD in the presence of Magic Angle Spinning. Solid State Nuclear Magnetic Resonance, 2018, 89, 35-44.	1.5	10
15	Conformational Entropy from NMR Relaxation in Proteins: The SRLS Perspective. Journal of Physical Chemistry B, 2017, 121, 758-768.	1.2	6
16	¹⁵Nâ€“H-Related Conformational Entropy Changes Entailed By Plexin-B1 RBD Dimerization: Combined Molecular Dynamics/NMR Relaxation Approach. Journal of Physical Chemistry B, 2017, 121, 3007-3015.	1.2	8
17	Conformational Entropy from Slowly Relaxing Local Structure Analysis of 15Nâ€“H Relaxation in Proteins: Application to Pheromone Binding to MUP-I in the 283â€“308 K Temperature Range. Journal of Physical Chemistry B, 2017, 121, 8684-8692.	1.2	4
18	An SRLS Study of ²H Methyl-Moiety Relaxation and Related Conformational Entropy in Free and Peptide-Bound PLC_{Î³}1C SH2. Journal of Physical Chemistry B, 2016, 120, 10695-10705.	1.2	8

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19	Polar Versus Non-polar Local Ordering at Mobile Sites in Proteins: Slowly Relaxing Local Structure Analysis of ¹⁵N Relaxation in the Third Immunoglobulin-Binding Domain of Streptococcal Protein G. Journal of Physical Chemistry B, 2016, 120, 386-395.	1.2	5
20	Local Ordering at Mobile Sites in Proteins from Nuclear Magnetic Resonance Relaxation: The Role of Site Symmetry. Journal of Physical Chemistry B, 2016, 120, 2886-2898.	1.2	16
21	Protein Dynamics in the Solid State from2H NMR Line Shape Analysis. II. MOMD Applied to Câ€“D and Câ€“CD3Probes. Journal of Physical Chemistry B, 2015, 119, 14022-14032.	1.2	11
22	Structural Dynamics of the Potassium Channel Blocker ShK: SRLS Analysis of ¹⁵N Relaxation. Journal of Physical Chemistry B, 2015, 119, 15130-15137.	1.2	9
23	Protein Dynamics in the Solid State from ²H NMR Line Shape Analysis: A Consistent Perspective. Journal of Physical Chemistry B, 2015, 119, 2857-2868.	1.2	25
24	The Slowly Relaxing Local Structure Perspective of Protein Dynamics by NMR Relaxation. Israel Journal of Chemistry, 2014, 54, 47-59.	1.0	3
25	The time correlation function perspective of NMR relaxation in proteins. Journal of Chemical Physics, 2013, 139, 084107.	1.2	4
26	Analysis of ¹⁵Nâ€“¹H NMR Relaxation in Proteins by a Combined Experimental and Molecular Dynamics Simulation Approach: Picosecondâ€“Nanosecond Dynamics of the Rho GTPase Binding Domain of Plexin-B1 in the Dimeric State Indicates Allosteric Pathways. Journal of Physical Chemistry B, 2013, 117, 174-184.	1.2	28
27	The eigenmode perspective of NMR spin relaxation in proteins. Journal of Chemical Physics, 2013, 139, 225104.	1.2	1
28	SRLS Analysis of ¹⁵N Relaxation from Bacteriophage T4 Lysozyme: a Tensorial Perspective That Features Domain Motion. Journal of Physical Chemistry B, 2012, 116, 6118-6127.	1.2	7
29	SRLS Analysis of ¹⁵N Spin Relaxation from E. coli Ribonuclease HI: The Tensorial Perspective. Journal of Physical Chemistry B, 2012, 116, 886-894.	1.2	15
30	Standard Tensorial Analysis of Local Ordering in Proteins from Residual Dipolar Couplings. Journal of Physical Chemistry B, 2012, 116, 6106-6117.	1.2	4
31	Slowly Relaxing Local Structure (SRLS) Analysis of ¹⁵Nâ€“H Relaxation from the Prototypical Small Proteins GB1 and GB3. Journal of Physical Chemistry B, 2012, 116, 4056-4068.	1.2	19
32	Methyl Dynamics of a Ca²⁺â^'Calmodulinâ^'Peptide Complex from NMR/SRLS. Journal of Physical Chemistry B, 2011, 115, 354-365.	1.2	15
33	Backbone Dynamics of Deoxy and Carbonmonoxy Hemoglobin by NMR/SRLS. Journal of Physical Chemistry B, 2011, 115, 143-157.	1.2	13
34	Integrated Computational Approach to the Analysis of NMR Relaxation in Proteins: Application to psâ^'ns Main Chain ¹⁵Nâ^'¹H and Global Dynamics of the Rho GTPase Binding Domain of Plexin-B1. Journal of Physical Chemistry B, 2011, 115, 376-388.	1.2	32
35	Structural dynamics of bio-macromolecules by NMR: The slowly relaxing local structure approach. Progress in Nuclear Magnetic Resonance Spectroscopy, 2010, 56, 360-405.	3.9	86
36	C++OPPS, a new software for the interpretation of protein dynamics from nuclear magnetic resonance measurements. International Journal of Quantum Chemistry, 2010, 110, 387-405.	1.0	9

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37	Comment on â€œThe physical basis of model-free analysis of NMR relaxation data from proteins and complex fluidsâ€•[J. Chem. Phys. 131, 224507 (2009)]. Journal of Chemical Physics, 2010, 132, 207101.	1.2	11
38	Domain Mobility in Proteins from NMR/SRLS. Journal of Physical Chemistry B, 2009, 113, 12050-12060.	1.2	19
39	Evidence for Domain Motion in Proteins Affecting Global Diffusion Properties: a Nuclear Magnetic Resonance Study. Journal of Physical Chemistry B, 2009, 113, 7003-7011.	1.2	12
40	An integrated approach to NMR spin relaxation in flexible biomolecules: Application to Î²-D-glucopyranosyl-(1â†'6)-Î±-D-mannopyranosyl-OMe. Journal of Chemical Physics, 2009, 131, 234501.	1.2	27
41	General Theoretical/Computational Tool for Interpreting NMR Spin Relaxation in Proteins. Journal of Physical Chemistry B, 2009, 113, 13613-13625.	1.2	50
42	NMR studies of a channel protein without membranes: Structure and dynamics of water-solubilized KcsA. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 16537-16542.	3.3	41
43	Measurement of bond vector orientations in invisible excited states of proteins. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 18473-18477.	3.3	172
44	An Improved Picture of Methyl Dynamics in Proteins from Slowly Relaxing Local Structure Analysis of ²H Spin Relaxation. Journal of Physical Chemistry B, 2007, 111, 12865-12875.	1.2	23
45	Methyl Dynamics in Proteins from NMR Slowly Relaxing Local Structure Spin Relaxation Analysis:Â A New Perspective. Journal of Physical Chemistry B, 2006, 110, 20615-20628.	1.2	22
46	Protein Dynamics from NMR:Â The Slowly Relaxing Local Structure Analysis Compared with Model-Free Analysisâ€. Journal of Physical Chemistry A, 2006, 110, 8366-8396.	1.1	82
47	Activation Energy of Catalysis-Related Domain Motion inE.coliAdenylate Kinase. Journal of Physical Chemistry B, 2006, 110, 11519-11524.	1.2	39
48	Escherichia coli adenylate kinase dynamics: Comparison of elastic network model modes with mode-coupling 15N-NMR relaxation data. Proteins: Structure, Function and Bioinformatics, 2004, 57, 468-480.	1.5	88
49	Mode-Coupling SRLS versus Mode-Decoupled Model-Free Nâ^'H Bond Dynamics:Â Mode-Mixing and Renormalization. Journal of Physical Chemistry B, 2003, 107, 9898-9904.	1.2	28
50	Mode-Coupling Analysis of15N CSAâ^'15N-1H Dipolar Cross-Correlation in Proteins. Rhombic Potentials at the Nâ^'H Bond. Journal of Physical Chemistry B, 2003, 107, 9883-9897.	1.2	22
51	A novel view of domain flexibility in E. coli adenylate kinase based on structural mode-coupling 15 N NMR relaxation 1 1Edited by P. E. Wright. Journal of Molecular Biology, 2002, 315, 155-170.	2.0	62
52	Domain Flexibility in Ligand-Free and Inhibitor-BoundEscherichia coliAdenylate Kinase Based on a Mode-Coupling Analysis of15N Spin Relaxationâ€. Biochemistry, 2002, 41, 6271-6281.	1.2	74
53	A Structural Mode-Coupling Approach to15N NMR Relaxation in Proteins. Journal of the American Chemical Society, 2001, 123, 3055-3063.	6.6	146
54	Backbone Dynamics ofEscherichia coliAdenylate Kinase at the Extreme Stages of the Catalytic Cycle Studied by15N NMR Relaxationâ€. Biochemistry, 2000, 39, 6634-6644.	1.2	52

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55	Sequence-specific 1H, 15N and 13C assignment of adenylate kinase from Escherichia coli in complex with the inhibitor AP5A. Journal of Biomolecular NMR, 1999, 13, 195-196.	1.6	4
56	Theoretical modeling of a directly heated solar-driven chemical reactor. Solar Energy, 1990, 45, 139-148.	2.9	17
57	An2H N.M.R. study of solid methyl parathione-d6and parathione-d6. Molecular Physics, 1985, 56, 1129-1143.	0.8	3
58	Analysis of protein-lipid interactions based on model simulations of electron spin resonance spectra. The Journal of Physical Chemistry, 1984, 88, 3454-3465.	2.9	187
59	Electronâ€spin relaxation and ordering in smectic and supercooled nematic liquid crystals. Journal of Chemical Physics, 1982, 77, 3915-3938.	1.2	153
60	Rotational jumps of the tyrosine side chain in crystalline enkephalin. Hydrogen-2 NMR line shapes for aromatic ring motions in solids. Journal of the American Chemical Society, 1981, 103, 7707-7710.	6.6	132
61	ESR studies of low water content 1,2-dipalmitoyl-sn-glycero-3-phosphocholine in oriented multilayers. 1. Evidence for long-range cooperative chain distortions. The Journal of Physical Chemistry, 1980, 84, 3281-3295.	2.9	30
62	Electron spin resonance studies of anisotropic ordering, spin relaxation, and slow tumbling in liquid crystalline solvents. 4. Cholestane motions and surface anchoring in smectics. The Journal of Physical Chemistry, 1980, 84, 2459-2472.	2.9	37
63	Slow motional NMR lineshapes for very anisotropic diffusion: I = 1 nuclei. Chemical Physics Letters, 1979, 64, 311-316.	1.2	32
64	The structure of the smectic phases of terephthal-bis-(butylaniline) studied by electron spin resonance spectroscopy. Molecular Physics, 1975, 30, 1589-1602.	0.8	13
65	Electron spin resonance spectroscopy of single crystals of concanavalin A. Journal of the American Chemical Society, 1974, 96, 7538-7542.	6.6	42