Gianluigi Veglia

List of Publications by Year
in descending order

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199 papers	7,382 citations	46918 47 h-index	74018 75 g-index
211 all docs	211 docs citations	211 times ranked	6814 citing authors

#	Article	IF	Citations
1	Direct observation of the three regions in Î±-synuclein that determine its membrane-bound behaviour. Nature Communications, 2014, 5, 3827.	5.8	357
2	Structural basis of synaptic vesicle assembly promoted by Î±-synuclein. Nature Communications, 2016, 7, 12563.	5.8	203
3	Dynamics connect substrate recognition to catalysis in protein kinase A. Nature Chemical Biology, 2010, 6, 821-828.	3.9	182
4	Using low-E resonators to reduce RF heating in biological samples for static solid-state NMR up to 900MHz. Journal of Magnetic Resonance, 2007, 185, 77-93.	1.2	172
5	Structure and topology of monomeric phospholamban in lipid membranes determined by a hybrid solution and solid-state NMR approach. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 10165-10170.	3.3	158
6	Structure and Orientation of Pardaxin Determined by NMR Experiments in Model Membranes. Journal of Biological Chemistry, 2004, 279, 45815-45823.	1.6	157
7	Structures of the Dimeric and Monomeric Variants of Magainin Antimicrobial Peptides (MSI-78 and) Tj ETQq1 1 0.784314 rgBT /Overl	1.2	157
8	NMR Structure of the Cathelicidin-Derived Human Antimicrobial Peptide LL-37 in Dodecylphosphocholine Micelles. Biochemistry, 2008, 47, 5565-5572.	1.2	157
9	Allosteric cooperativity in protein kinase A. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 506-511.	3.3	154
10	Structural topology of phospholamban pentamer in lipid bilayers by a hybrid solution and solid-state NMR method. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 9101-9106.	3.3	154
11	NMR Solution Structure and Topological Orientation of Monomeric Phospholamban in Dodecylphosphocholine Micelles. Biophysical Journal, 2003, 85, 2589-2598.	0.2	140
12	Perturbations of Native Membrane Protein Structure in Alkyl Phosphocholine Detergents: A Critical Assessment of NMR and Biophysical Studies. Chemical Reviews, 2018, 118, 3559-3607.	23.0	132
13	Dynamically committed, uncommitted, and quenched states encoded in protein kinase A revealed by NMR spectroscopy. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 6969-6974.	3.3	129
14	Structural and Dynamic Basis of Phospholamban and Sarcolipin Inhibition of Ca²⁺-ATPase. Biochemistry, 2008, 47, 3-13.	1.2	121
15	Allosteric regulation of SERCA by phosphorylation-mediated conformational shift of phospholamban. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 17338-17343.	3.3	112
16	Dipolar Waves as NMR Maps of Protein Structure. Journal of the American Chemical Society, 2002, 124, 4206-4207.	6.6	109
17	NMR, Mass Spectrometry and Chemical Evidence Reveal a Different Chemical Structure for Methanobactin That Contains Oxazolone Rings. Journal of the American Chemical Society, 2008, 130, 12604-12605.	6.6	102
18	Spectroscopic validation of the pentameric structure of phospholamban. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 14676-14681.	3.3	101

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19	Dipolar Waves Map the Structure and Topology of Helices in Membrane Proteins. Journal of the American Chemical Society, 2003, 125, 8928-8935.	6.6	99
20	Selectivity in heavy metal- binding to peptides and proteins. Biopolymers, 2002, 64, 189-197.	1.2	96
21	A dynamic hydrophobic core orchestrates allostery in protein kinases. Science Advances, 2017, 3, e1600663.	4.7	89
22	Structure and Orientation of Sarcolipin in Lipid Environments,. Biochemistry, 2002, 41, 475-482.	1.2	83
23	Structural Ensembles of Membrane-bound Î±-Synuclein Reveal the Molecular Determinants of Synaptic Vesicle Affinity. Scientific Reports, 2016, 6, 27125.	1.6	83
24	Structure and dynamics of a primordial catalytic fold generated by in vitro evolution. Nature Chemical Biology, 2013, 9, 81-83.	3.9	80
25	Overexpression, purification, and characterization of recombinant Ca-ATPase regulators for high-resolution solution and solid-state NMR studies. Protein Expression and Purification, 2003, 30, 253-261.	0.6	79
26	Fluidic and Air-Stable Supported Lipid Bilayer and Cell-Mimicking Microarrays. Journal of the American Chemical Society, 2008, 130, 6267-6271.	6.6	78
27	Dual Acquisition Magicâ€Angle Spinning Solidâ€State NMRâ€Spectroscopy: Simultaneous Acquisition of Multidimensional Spectra of Biomacromolecules. Angewandte Chemie - International Edition, 2012, 51, 2731-2735.	7.2	76
28	Structural biology of metal-binding sequences. Current Opinion in Chemical Biology, 2002, 6, 217-223.	2.8	73
29	Serine 16 Phosphorylation Induces an Order-to-Disorder Transition in Monomeric Phospholambanâ€. Biochemistry, 2005, 44, 4386-4396.	1.2	71
30	Solid-State NMR and Rigid Body Molecular Dynamics To Determine Domain Orientations of Monomeric Phospholamban. Journal of the American Chemical Society, 2002, 124, 9392-9393.	6.6	70
31	1H/15N Heteronuclear NMR Spectroscopy Shows Four Dynamic Domains for Phospholamban Reconstituted in Dodecylphosphocholine Micelles. Biophysical Journal, 2004, 87, 1205-1214.	0.2	70
32	Lethal Arg9Cys phospholamban mutation hinders Ca ²⁺ -ATPase regulation and phosphorylation by protein kinase A. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 2735-2740.	3.3	64
33	Isotope Labeling for Solution and Solid-State NMR Spectroscopy of Membrane Proteins. Advances in Experimental Medicine and Biology, 2012, 992, 35-62.	0.8	63
34	Conformational preferences of the amylin nucleation site in SDS micelles: An NMR study. Biopolymers, 2003, 69, 29-41.	1.2	60
35	Proton-Coupled Electron Transfer in a Biomimetic Peptide as a Model of Enzyme Regulatory Mechanisms. Journal of the American Chemical Society, 2007, 129, 4393-4400.	6.6	60
36	The TLQP-21 Peptide Activates the G-Protein-Coupled Receptor C3aR1 via a Folding-upon-Binding Mechanism. Structure, 2014, 22, 1744-1753.	1.6	59

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37	cAMP-Dependent Protein Kinase A Selects the Excited State of the Membrane Substrate Phospholamban. Journal of Molecular Biology, 2011, 412, 155-164.	2.0	58
38	Activating and Deactivating Roles of Lipid Bilayers on the Ca²⁺-ATPase/Phospholamban Complex. Biochemistry, 2011, 50, 10367-10374.	1.2	57
39	15N and 13C- SOFAST-HMQC editing enhances 3D-NOESY sensitivity in highly deuterated, selectively [1H,13C]-labeled proteins. Journal of Biomolecular NMR, 2016, 66, 259-271.	1.6	56
40	Controlling the Inhibition of the Sarcoplasmic Ca2+-ATPase by Tuning Phospholamban Structural Dynamics. Journal of Biological Chemistry, 2007, 282, 37205-37214.	1.6	55
41	Synchronous Opening and Closing Motions Are Essential for cAMP-Dependent Protein Kinase A Signaling. Structure, 2014, 22, 1735-1743.	1.6	55
42	Lanthanide Ion Binding to Adventitious Sites Aligns Membrane Proteins in Micelles for Solution NMR Spectroscopy. Journal of the American Chemical Society, 2000, 122, 11733-11734.	6.6	54
43	NMR mapping of protein conformational landscapes using coordinated behavior of chemical shifts upon ligand binding. Physical Chemistry Chemical Physics, 2014, 16, 6508-6518.	1.3	54
44	Sensitivity Enhancement in Static Solid-State NMR Experiments via Single- and Multiple-Quantum Dipolar Coherences. Journal of the American Chemical Society, 2009, 131, 5754-5756.	6.6	51
45	Solution structures of the reduced and Cu(I) bound forms of the first metal binding sequence of ATP7A associated with Menkes disease. Proteins: Structure, Function and Bioinformatics, 2005, 61, 1038-1049.	1.5	50
46	Structure, Dynamics, and Membrane Topology of Stannin: A Mediator of Neuronal Cell Apoptosis Induced by Trimethyltin Chloride. Journal of Molecular Biology, 2005, 354, 652-665.	2.0	50
47	Defining the Intramembrane Binding Mechanism of Sarcolipin to Calcium ATPase Using Solution NMR Spectroscopy. Journal of Molecular Biology, 2006, 358, 420-429.	2.0	50
48	Structure and topology of a peptide segment of the 6th transmembrane domain of theSaccharomyces cerevisae ?-factor receptor in phospholipid bilayers. Biopolymers, 2001, 59, 243-256.	1.2	48
49	Deuterium/Hydrogen Exchange Factors Measured by Solution Nuclear Magnetic Resonance Spectroscopy as Indicators of the Structure and Topology of Membrane Proteins. Biophysical Journal, 2002, 82, 2176-2183.	0.2	48
50	Two-Dimensional Solid-State NMR Reveals Two Topologies of Sarcolipin in Oriented Lipid Bilayersâ€. Biochemistry, 2006, 45, 10939-10946.	1.2	48
51	A refinement protocol to determine structure, topology, and depth of insertion of membrane proteins using hybrid solution and solid-state NMR restraints. Journal of Biomolecular NMR, 2009, 44, 195-205.	1.6	48
52	Dealkylation of Organotin Compounds by Biological Dithiols:Â Toward the Chemistry of Organotin Toxicity. Journal of the American Chemical Society, 2003, 125, 13316-13317.	6.6	47
53	Lipid-Mediated Folding/Unfolding of Phospholamban as a Regulatory Mechanism for the Sarcoplasmic Reticulum Ca2+-ATPase. Journal of Molecular Biology, 2011, 408, 755-765.	2.0	47
54	Mutation of a kinase allosteric node uncouples dynamics linked to phosphotransfer. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E931-E940.	3.3	47

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55	Biological chemistry of organotin compounds: Interactions and dealkylation by dithiols. Journal of Organometallic Chemistry, 2006, 691, 1748-1755.	0.8	46
56	A Myristoyl/Phosphoserine Switch Controls cAMP-Dependent Protein Kinase Association to Membranes. Journal of Molecular Biology, 2011, 411, 823-836.	2.0	46
57	Dysfunctional conformational dynamics of protein kinase A induced by a lethal mutant of phospholamban hinder phosphorylation. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3716-3721.	3.3	43
58	Cushingâ€™s syndrome driver mutation disrupts protein kinase A allosteric network, altering both regulation and substrate specificity. Science Advances, 2019, 5, eaaw9298.	4.7	43
59	3D DUMAS: Simultaneous acquisition of three-dimensional magic angle spinning solid-state NMR experiments of proteins. Journal of Magnetic Resonance, 2012, 220, 79-84.	1.2	41
60	Probing ground and excited states of phospholamban in model and native lipid membranes by magic angle spinning NMR spectroscopy. Biochimica Et Biophysica Acta - Biomembranes, 2012, 1818, 146-153.	1.4	41
61	Allostery and Binding Cooperativity of the Catalytic Subunit of Protein Kinase A by NMR Spectroscopy and Molecular Dynamics Simulations. Advances in Protein Chemistry and Structural Biology, 2012, 87, 363-389.	1.0	41
62	Structural Dynamics and Topology of Phosphorylated Phospholamban Homopentamer Reveal Its Role in the Regulation of Calcium Transport. Structure, 2013, 21, 2119-2130.	1.6	41
63	FLAMEnGO 2.0: An enhanced fuzzy logic algorithm for structure-based assignment of methyl group resonances. Journal of Magnetic Resonance, 2014, 245, 17-23.	1.2	41
64	Globally correlated conformational entropy underlies positive and negative cooperativity in a kinaseâ€™s enzymatic cycle. Nature Communications, 2019, 10, 799.	5.8	40
65	Probing Slow Protein Dynamics by Adiabatic R_{1Ï} and R_{2Ï} NMR Experiments. Journal of the American Chemical Society, 2010, 132, 9979-9981.	6.6	39
66	Theoretical Analysis of Residual Dipolar Coupling Patterns in Regular Secondary Structures of Proteins. Journal of the American Chemical Society, 2003, 125, 12520-12526.	6.6	38
67	On the Function of Pentameric Phospholamban: Ion Channel or Storage Form?. Biophysical Journal, 2009, 96, L60-L62.	0.2	38
68	An Electrochemical Investigation of Sarcolipin Reconstituted into a Mercury-Supported Lipid Bilayer. Biophysical Journal, 2007, 93, 2678-2687.	0.2	36
69	Multidimensional oriented solid-state NMR experiments enable the sequential assignment of uniformly 15N labeled integral membrane proteins in magnetically aligned lipid bilayers. Journal of Biomolecular NMR, 2011, 51, 339-346.	1.6	36
70	Orphan spin operators enable the acquisition of multiple 2D and 3D magic angle spinning solid-state NMR spectra. Journal of Chemical Physics, 2013, 138, 184201.	1.2	36
71	Probing excited states and activation energy for the integral membrane protein phospholamban by NMR CPMG relaxation dispersion experiments. Biochimica Et Biophysica Acta - Biomembranes, 2010, 1798, 77-81.	1.4	34
72	On the Role of NMR Spectroscopy for Characterization of Antimicrobial Peptides. Methods in Molecular Biology, 2013, 1063, 159-180.	0.4	34

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73	Tilt and Azimuthal Angles of a Transmembrane Peptide: A Comparison between Molecular Dynamics Calculations and Solid-State NMR Data of Sarcolipin in Lipid Membranes. Biophysical Journal, 2009, 96, 3648-3662.	0.2	33
74	Dynamic allostery-based molecular workings of kinase:peptide complexes. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 15052-15061.	3.3	33
75	Determination of structural topology of a membrane protein in lipid bilayers using polarization optimized experiments (POE) for static and MAS solid state NMR spectroscopy. Journal of Biomolecular NMR, 2013, 57, 91-102.	1.6	32
76	Sensitivity Enhancement of Separated Local Field Experiments: Application to Membrane Proteins. Journal of Physical Chemistry B, 2010, 114, 5089-5095.	1.2	30
77	A tyrosineâ€“tryptophan dyad and radical-based charge transfer in a ribonucleotide reductase-inspired maquette. Nature Communications, 2015, 6, 10010.	5.8	30
78	Solution and Solid-State Nuclear Magnetic Resonance Structural Investigations of the Antimicrobial Designer Peptide GL13K in Membranes. Biochemistry, 2017, 56, 4269-4278.	1.2	30
79	Dynamical and allosteric regulation of photoprotection in light harvesting complex II. Science China Chemistry, 2020, 63, 1121-1133.	4.2	29
80	Probing membrane topology of the antimicrobial peptide distinctin by solid-state NMR spectroscopy in zwitterionic and charged lipid bilayers. Biochimica Et Biophysica Acta - Biomembranes, 2011, 1808, 34-40.	1.4	28
81	Simultaneous acquisition of 2D and 3D solid-state NMR experiments for sequential assignment of oriented membrane protein samples. Journal of Biomolecular NMR, 2015, 62, 53-61.	1.6	28
82	On the Performance of Spin Diffusion NMR Techniques in Oriented Solids: Prospects for Resonance Assignments and Distance Measurements from Separated Local Field Experiments. Journal of Physical Chemistry B, 2010, 114, 13872-13880.	1.2	27
83	Conformational Equilibrium of N-Myristoylated cAMP-Dependent Protein Kinase A by Molecular Dynamics Simulations. Biochemistry, 2012, 51, 10186-10196.	1.2	27
84	Nonstereogenic Î±-aminoisobutyryl-glycyl dipeptidyl unit nucleates type Iâ€² Î²-turn in linear peptides in aqueous solution. Biopolymers, 2007, 88, 746-753.	1.2	26
85	Zooming in on protons: Neutron structure of protein kinase A trapped in a product complex. Science Advances, 2019, 5, eaav0482.	4.7	26
86	Paramagnetic-Based NMR Restraints Lift Residual Dipolar Coupling Degeneracy in Multidomain Detergent-Solubilized Membrane Proteins. Journal of the American Chemical Society, 2011, 133, 2232-2241.	6.6	25
87	Sensitivity and resolution enhancement of oriented solid-state NMR: Application to membrane proteins. Progress in Nuclear Magnetic Resonance Spectroscopy, 2013, 75, 50-68.	3.9	25
88	Structures of the Excited States of Phospholamban and Shifts in Their Populations upon Phosphorylation. Biochemistry, 2013, 52, 6684-6694.	1.2	24
89	Sensitivity Enhanced Heteronuclear Correlation Spectroscopy in Multidimensional Solid-State NMR of Oriented Systems via Chemical Shift Coherences. Journal of the American Chemical Society, 2010, 132, 5357-5363.	6.6	23
90	FLAMEnGO: A fuzzy logic approach for methyl group assignment using NOESY and paramagnetic relaxation enhancement data. Journal of Magnetic Resonance, 2012, 214, 103-110.	1.2	23

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91	Conformational Landscape of the PRKACA-DNAJB1 Chimeric Kinase, the Driver for Fibrolamellar Hepatocellular Carcinoma. Scientific Reports, 2018, 8, 720.	1.6	23
92	Asymmetric Methyl Group Labeling as a Probe of Membrane Protein Homo-oligomers by NMR Spectroscopy. Journal of the American Chemical Society, 2008, 130, 2400-2401.	6.6	22
93	Multiple acquisitions via sequential transfer of orphan spin polarization (MAeSTOSO): How far can we push residual spin polarization in solid-state NMR?. Journal of Magnetic Resonance, 2016, 267, 1-8.	1.2	22
94	ALARM NMR for HTS Triage and Chemical Probe Validation. Current Protocols in Chemical Biology, 2018, 10, 91-117.	1.7	22
95	Interactions of Alkyltin Salts with Biological Dithiols:Â Dealkylation and Induction of a Regular Î²-Turn Structure in Peptides. Journal of the American Chemical Society, 2004, 126, 14400-14410.	6.6	21
96	Role of conformational entropy in the activity and regulation of the catalytic subunit of protein kinase <scp>A</scp>. FEBS Journal, 2013, 280, 5608-5615.	2.2	21
97	Defective internal allosteric network imparts dysfunctional ATP/substrate-binding cooperativity in oncogenic chimera of protein kinase A. Communications Biology, 2021, 4, 321.	2.0	21
98	Conformational Study of [Met5]Enkephalin-Arg-Phe in the Presence of Phosphatidylserine Vesicles. FEBS Journal, 1996, 240, 540-549.	0.2	20
99	Determination of helical membrane protein topology using residual dipolar couplings and exhaustive search algorithm: application to phospholamban. Chemistry and Physics of Lipids, 2004, 132, 133-144.	1.5	20
100	Structural Dynamics and Conformational Equilibria of SERCA Regulatory Proteins in Membranes by Solid-State NMR Restrained Simulations. Biophysical Journal, 2014, 106, 2566-2576.	0.2	20
101	Use of paramagnetic systems to speed-up NMR data acquisition and for structural and dynamic studies. Solid State Nuclear Magnetic Resonance, 2019, 102, 36-46.	1.5	20
102	The Role of Sarcolipin and ATP in the Transport of Phosphate Ion into the Sarcoplasmic Reticulum. Biophysical Journal, 2009, 97, 2693-2699.	0.2	19
103	Uncoupling Catalytic and Binding Functions in the Cyclic AMP-Dependent Protein Kinase A. Structure, 2016, 24, 353-363.	1.6	19
104	Multiple acquisition of magic angle spinning solid-state NMR experiments using one receiver: Application to microcrystalline and membrane protein preparations. Journal of Magnetic Resonance, 2015, 253, 143-153.	1.2	18
105	Solid-State NMR of Membrane Proteins in Lipid Bilayers: To Spin or Not To Spin?. Accounts of Chemical Research, 2021, 54, 1430-1439.	7.6	18
106	Synthesis of a-factor peptide from Saccharomyces cerevisiae and photoactive analogues via Fmoc solid phase methodology. Bioorganic and Medicinal Chemistry, 2011, 19, 490-497.	1.4	17
107	Structure and membrane interactions of chionodracine, a piscidin-like antimicrobial peptide from the icefish Chionodraco hamatus. Biochimica Et Biophysica Acta - Biomembranes, 2015, 1848, 1285-1293.	1.4	17
108	Genetic algorithm optimized triply compensated pulses in NMR spectroscopy. Journal of Magnetic Resonance, 2015, 260, 136-143.	1.2	17

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109	Clearance kinetics of the VGF-derived neuropeptide TLQP-21. Neuropeptides, 2018, 71, 97-103.	0.9	17
110	Allostery governs Cdk2 activation and differential recognition of CDK inhibitors. Nature Chemical Biology, 2021, 17, 456-464.	3.9	17
111	High-Resolution Structure and Conformational Dynamics of Rigid, Cofacially Aligned Porphyrinâ^'Bridgeâ^'Quinone Systems As Determined by NMR Spectroscopy and ab Initio Simulated Annealing Calculations. Journal of the American Chemical Society, 2001, 123, 5668-5679.	6.6	16
112	Tuning the structural coupling between the transmembrane and cytoplasmic domains of phospholamban to control sarcoplasmic reticulum Ca2+-ATPase (SERCA) function. Journal of Muscle Research and Cell Motility, 2012, 33, 485-492.	0.9	16
113	Mapping the Hydrogen Bond Networks in the Catalytic Subunit of Protein Kinase A Using H/D Fractionation Factors. Biochemistry, 2015, 54, 4042-4049.	1.2	16
114	Effects of naturally occurring arginine 14 deletion on phospholamban conformational dynamics and membrane interactions. Biochimica Et Biophysica Acta - Biomembranes, 2015, 1848, 315-322.	1.4	16
115	Probing membrane protein ground and conformationally excited states using dipolar- and J-coupling mediated MAS solid state NMR experiments. Methods, 2018, 148, 115-122.	1.9	16
116	Formalin Evokes Calcium Transients from the Endoplasmatic Reticulum. PLoS ONE, 2015, 10, e0123762.	1.1	16
117	Multi-state recognition pathway of the intrinsically disordered protein kinase inhibitor by protein kinase A. ELife, 2020, 9, .	2.8	16
118	Reversal of Phospholamban Inhibition of the Sarco(endo)plasmic Reticulum Ca2+-ATPase (SERCA) Using Short, Protein-interacting RNAs and Oligonucleotide Analogs. Journal of Biological Chemistry, 2016, 291, 21510-21518.	1.6	15
119	Probing the Conformationally Excited States of Membrane Proteins via ¹H-Detected MAS Solid-State NMR Spectroscopy. Journal of Physical Chemistry B, 2017, 121, 4456-4465.	1.2	15
120	Application of paramagnetic relaxation enhancements to accelerate the acquisition of 2D and 3D solid-state NMR spectra of oriented membrane proteins. Methods, 2018, 138-139, 54-61.	1.9	15
121	Molecular Mechanism for the Suppression of Alpha Synuclein Membrane Toxicity by an Unconventional Extracellular Chaperone. Journal of the American Chemical Society, 2020, 142, 9686-9699.	6.6	15
122	Carbonyl carbon label selective (CCLS) 1Hâ€"15N HSQC experiment for improved detection of backbone 13Câ€"15N cross peaks in larger proteins. Journal of Biomolecular NMR, 2007, 39, 177-185.	1.6	14
123	Heteronuclear Adiabatic Relaxation Dispersion (HARD) for quantitative analysis of conformational dynamics in proteins. Journal of Magnetic Resonance, 2012, 219, 75-82.	1.2	14
124	An intramembrane sensory circuit monitors sortase Aâ€"mediated processing of streptococcal adhesins. Science Signaling, 2019, 12, .	1.6	14
125	Activation mechanism of Drosophila cryptochrome through an allosteric switch. Science Advances, 2021, 7, .	4.7	14
126	1 H-detected MAS solid-state NMR experiments enable the simultaneous mapping of rigid and dynamic domains of membrane proteins. Journal of Magnetic Resonance, 2017, 285, 101-107.	1.2	14

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127	A synthetic peptide corresponding to the 550-585 region of Î±-dystroglycan binds Î²-dystroglycan as revealed by NMR spectroscopy. FEBS Letters, 2001, 499, 210-214.	1.3	13
128	Backbone NMR resonance assignment of the catalytic subunit of cAMP-dependent protein kinase A in complex with AMP-PNP. Biomolecular NMR Assignments, 2009, 3, 115-117.	0.4	13
129	Proton evolved local field solid-state nuclear magnetic resonance using Hadamard encoding: Theory and application to membrane proteins. Journal of Chemical Physics, 2011, 135, 074503.	1.2	13
130	Enhancing the sensitivity of multidimensional NMR experiments by using triply-compensated Ï€ pulses. Journal of Biomolecular NMR, 2017, 69, 237-243.	1.6	13
131	Design and characterization of chionodracine-derived antimicrobial peptides with enhanced activity against drug-resistant human pathogens. RSC Advances, 2018, 8, 41331-41346.	1.7	13
132	Hybridization of TEDOR and NCX MAS solid-state NMR experiments for simultaneous acquisition of heteronuclear correlation spectra and distance measurements. Journal of Biomolecular NMR, 2019, 73, 141-153.	1.6	13
133	Simultaneous Detection and Deconvolution of Congested NMR Spectra Containing Three Isotopically Labeled Species. Journal of the American Chemical Society, 2008, 130, 7818-7819.	6.6	12
134	NMR structure and conformational dynamics of AtPDFL2.1, a defensin-like peptide from Arabidopsis thaliana. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2016, 1864, 1739-1747.	1.1	12
135	Orphan Spin Polarization. Annual Reports on NMR Spectroscopy, 2016, 89, 103-121.	0.7	12
136	Multi-receiver solid-state NMR using polarization optimized experiments (POE) at ultrafast magic angle spinning. Journal of Biomolecular NMR, 2020, 74, 267-285.	1.6	12
137	CHESPA/CHESCA-SPARKY: automated NMR data analysis plugins for SPARKY to map protein allostery. Bioinformatics, 2021, 37, 1176-1177.	1.8	12
138	Expression and purification of isotopically labeled peptide inhibitors and substrates of cAMP-dependant protein kinase A for NMR analysis. Protein Expression and Purification, 2009, 64, 231-236.	0.6	11
139	Topology and immersion depth of an integral membrane protein by paramagnetic rates from dissolved oxygen. Journal of Biomolecular NMR, 2011, 51, 173-183.	1.6	11
140	Optimization of identity operation in NMR spectroscopy via genetic algorithm: Application to the TEDOR experiment. Journal of Magnetic Resonance, 2016, 273, 40-46.	1.2	11
141	Effects of the Arg9Cys and Arg25Cys mutations on phospholamban's conformational equilibrium in membrane bilayers. Biochimica Et Biophysica Acta - Biomembranes, 2018, 1860, 1335-1341.	1.4	11
142	Proton-detected polarization optimized experiments (POE) using ultrafast magic angle spinning solid-state NMR: Multi-acquisition of membrane protein spectra. Journal of Magnetic Resonance, 2020, 310, 106664.	1.2	11
143	Experimental Aspects of Polarization Optimized Experiments (POE) for Magic Angle Spinning Solid-State NMR of Microcrystalline and Membrane-Bound Proteins. Methods in Molecular Biology, 2018, 1688, 37-53.	0.4	11
144	Accurate Determination of Conformational Transitions in Oligomeric Membrane Proteins. Scientific Reports, 2016, 6, 23063.	1.6	10

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145	More than a Liquid Junction: Effect of Stirring, Flow Rate, and Inward and Outward Electrolyte Diffusion on Reference Electrodes with Salt Bridges Contained in Nanoporous Glass. Analytical Chemistry, 2019, 91, 7698-7704.	3.2	10
146	Structural basis for allosteric control of the SERCA-Phospholamban membrane complex by Ca2+ and phosphorylation. ELife, 2021, 10, .	2.8	10
147	Solution conformation of the Pseudomonas syringae MSU 16H phytotoxic lipodepsipeptide Pseudomycin A determined by computer simulations using distance geometry and molecular dynamics from NMR data. FEBS Journal, 1998, 257, 449-456.	0.2	9
148	One-Sample Approach to Determine the Relative Orientations of Proteins in Ternary and Binary Complexes from Residual Dipolar Coupling Measurements. Journal of the American Chemical Society, 2009, 131, 14138-14139.	6.6	9
149	Simultaneous detection of intra- and inter-molecular paramagnetic relaxation enhancements in protein complexes. Journal of Biomolecular NMR, 2018, 70, 133-140.	1.6	9
150	Probing Protein-Protein Interactions Using Asymmetric Labeling and Carbonyl-Carbon Selective Heteronuclear NMR Spectroscopy. Molecules, 2018, 23, 1937.	1.7	9
151	Structural basis for sarcolipinâ€™s regulation of muscle thermogenesis by the sarcoplasmic reticulum Ca ²⁺ -ATPase. Science Advances, 2021, 7, eabi7154.	4.7	9
152	Raf Kinase Inhibitory Protein regulates the cAMP-dependent protein kinase signaling pathway through a positive feedback loop. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	9
153	Improved resolution in dipolar NMR spectra using constant time evolution PISEMA experiment. Chemical Physics Letters, 2010, 494, 104-110.	1.2	8
154	Phospholamban and its phosphorylated form require non-physiological transmembrane potentials to translocate ions. Soft Matter, 2012, 8, 3881.	1.2	8
155	Rheostatic Regulation of the SERCA/Phospholamban Membrane Protein Complex Using Non-Coding RNA and Single-Stranded DNA oligonucleotides. Scientific Reports, 2015, 5, 13000.	1.6	8
156	Improving the quality of oriented membrane protein spectra using heat-compensated separated local field experiments. Journal of Biomolecular NMR, 2019, 73, 617-624.	1.6	8
157	Intrinsically disordered HAX-1 regulates Ca2+ cycling by interacting with lipid membranes and the phospholamban cytoplasmic region. Biochimica Et Biophysica Acta - Biomembranes, 2020, 1862, 183034.	1.4	8
158	Is Disrupted Nucleotide-Substrate Cooperativity a Common Trait for Cushing's Syndrome Driving Mutations of Protein Kinase A?. Journal of Molecular Biology, 2021, 433, 167123.	2.0	8
159	What Can We Learn from a Small Regulatory Membrane Protein?. Methods in Molecular Biology, 2010, 654, 303-319.	0.4	8
160	A kink in DWORF helical structure controls the activation of the sarcoplasmic reticulum Ca2+-ATPase. Structure, 2022, 30, 360-370.e6.	1.6	8
161	PHRONESIS: A Oneâ€Shot Approach for Sequential Assignment of Protein Resonances by Ultrafast MAS Solidâ€State NMR Spectroscopy. ChemPhysChem, 2022, 23, e202200127.	1.0	8
162	Nanosecond-Timescale Dynamics and Conformational Heterogeneity in Human GCK Regulation and Disease. Biophysical Journal, 2020, 118, 1109-1118.	0.2	7

#	Article	IF	Citations
163	PISA-SPARKY: an interactive SPARKY plugin to analyze oriented solid-state NMR spectra of helical membrane proteins. Bioinformatics, 2020, 36, 2915-2916.	1.8	7
164	Pseudoenzymatic dealkylation of alkyltins by biological dithiols. Journal of Biological Inorganic Chemistry, 2009, 14, 1219-1225.	1.1	6
165	Synthesis and characterization of the 47â€residue heterodimeric antimicrobial peptide distinctin, featuring directed disulfide bridge formation. Biopolymers, 2012, 98, 479-484.	1.2	6
166	Probing Residue-Specific Waterâ€“Protein Interactions in Oriented Lipid Membranes via Solid-State NMR Spectroscopy. Journal of Physical Chemistry B, 2016, 120, 10959-10968.	1.2	6
167	Ca²⁺ ATPase Conformational Transitions in Lipid Bilayers Mapped by Site-directed Ethylation and Solid-State NMR. ACS Chemical Biology, 2016, 11, 329-334.	1.6	6
168	Structure and Function of Tryptophanâ€“Tyrosine Dyads in Biomimetic Î² Hairpins. Journal of Physical Chemistry B, 2019, 123, 2780-2791.	1.2	6
169	Catch them if you can. Nature Chemical Biology, 2013, 9, 410-411.	3.9	5
170	T2* weighted Deconvolution of NMR Spectra: Application to 2D Homonuclear MAS Solid-State NMR of Membrane Proteins. Scientific Reports, 2019, 9, 8225.	1.6	5
171	Allosteric Regulation of the M2 Protein from Influenza A by Cholesterol. Biophysical Journal, 2016, 110, 1207-1208.	0.2	4
172	Cysteine-ethylation of tissue-extracted membrane proteins as a tool to detect conformational states by solid-state NMR spectroscopy. Methods in Enzymology, 2019, 621, 281-304.	0.4	4
173	A Theoretical Assessment of the Structure Determination of Multi-Span Membrane Proteins by Oriented Sample Solid-State NMR Spectroscopy. Australian Journal of Chemistry, 2020, 73, 246.	0.5	4
174	Simultaneous acquisition of multiple fast MAS solid-state NMR experiments via orphan spin polarization. Annual Reports on NMR Spectroscopy, 2021, , 247-268.	0.7	4
175	Templating Î±-amylase peptide inhibitors with organotin compounds. Journal of Biological Inorganic Chemistry, 2011, 16, 1197-1204.	1.1	3
176	Modeling helical proteins using residual dipolar couplings, sparse long-range distance constraints and a simple residue-based force field. Theoretical Chemistry Accounts, 2013, 132, 1388.	0.5	3
177	Special issue on â€œMembrane Protein Dynamics: Correlating Structure to Functionâ€• Biochimica Et Biophysica Acta - Biomembranes, 2010, 1798, 65-67.	1.4	2
178	A Semiautomated Assignment Protocol for Methyl Group Side Chains in Large Proteins. Methods in Enzymology, 2016, 566, 35-57.	0.4	2
179	Tunable Liaisons: eEF-2K, CaM, and Calcium. Structure, 2016, 24, 1438-1439.	1.6	2
180	Optimization of 1H decoupling eliminates sideband artifacts in 3D TROSY-based triple resonance experiments. Journal of Biomolecular NMR, 2017, 69, 45-52.	1.6	2

#	Article	IF	Citations
181	Hybridizing isotropic and anisotropic solid-state NMR restraints for membrane protein structure determination. , 0, , 12-1-12-21.		2
182	Development of a sensitive assay for SERCA activity using FRET detection of ADP. Analytical Methods, 2014, 6, 1468-1474.	1.3	1
183	Cytoplasmic nucleic acid-based XNAs directly enhance live cardiac cell function by a Ca2+ cycling-independent mechanism via the sarcomere. Journal of Molecular and Cellular Cardiology, 2019, 130, 1-9.	0.9	1
184	Met125 is essential for maintaining the structural integrity of calmodulinâ€™s C-terminal domain. Scientific Reports, 2020, 10, 21320.	1.6	1
185	Optimal Design of Offset-Specific Radio Frequency Pulses for Solution and Solid-State NMR Using a Genetic Algorithm. , 2018, , 605-615.		1
186	A Cushing Syndrome Mutation of Protein Kinase A Câ€subunit Disrupts the Internal Allosteric Network Affecting Regulation and Substrate Specificity. FASEB Journal, 2019, 33, 478.11.	0.2	1
187	Spectroscopic Design of Phospholamban Mutants to Treat Heart Failure. Biophysical Journal, 2010, 98, 246a.	0.2	0
188	Rational Structure-Based Design of PLN Mutants to Optimize Dephosphorylation and Tune Serca Function. Biophysical Journal, 2014, 106, 653a-654a.	0.2	0
189	Role of Phospholamban Mutations in Protein-Protein Interactions. Biophysical Journal, 2015, 108, 500a.	0.2	0
190	Sequence-Independent SSDNA Relieves Phospholamban Inhibition of SERCA in a Length Dependent Manner. Biophysical Journal, 2015, 108, 254a.	0.2	0
191	Phospholamban Phosphorylation Alters its Conformational Equilibrium to Regulate SERCA Activity. Biophysical Journal, 2015, 108, 131a.	0.2	0
192	Characterization of Calmodulin Binding to the Ryanodine Receptor by Solution and Solid-State NMR. Biophysical Journal, 2015, 108, 616a.	0.2	0
193	Elucidating the Role of Structural Dynamics in Ligand Selection of Human Adipocyte Fatty Acid Binding Protein By NMR Spectroscopy. Biophysical Journal, 2016, 110, 538a.	0.2	0
194	Structural Characterization of the Bacterial Succinate/Acetate Proton Symporter SatP in Lipid Bilayer Membranes. Biophysical Journal, 2016, 110, 61a.	0.2	0
195	Structure, Dynamics, and Function of the Membrane Associated SRC Family Kinase HCK. Biophysical Journal, 2017, 112, 388a-389a.	0.2	0
196	Elucidating the Uncoupling of ATP Hydrolysis and Ca 2+ Transport in SERCA by Sarcolipin. Biophysical Journal, 2017, 112, 500a.	0.2	0
197	Protein kinase A in the neutron beam: Insights for catalysis from directly observing protons. Methods in Enzymology, 2020, 634, 311-331.	0.4	0
198	Topological Allosteric Regulation of the Sarcoplasmic Reticulum Calcium Pump Phospholamban. Biophysical Journal, 2020, 118, 99a.	0.2	0

#	Article	IF	Citations
199	Optimal Design of Offset-Specific Radio Frequency Pulses for Solution and Solid-State NMR Using a Genetic Algorithm. , 2017, , 1-11.		0