

Gianluigi Veglia

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3734167/publications.pdf>

Version: 2024-02-01

199
papers

7,382
citations

47006

47
h-index

74163

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 $\hat{\text{I}}\pm$ -synuclein that determine its membrane-bound behaviour. Nature Communications, 2014, 5, 3827.	12.8	357
2	Structural basis of synaptic vesicle assembly promoted by $\hat{\text{I}}\pm$ -synuclein. Nature Communications, 2016, 7, 12563.	12.8	203
3	Dynamics connect substrate recognition to catalysis in protein kinase A. Nature Chemical Biology, 2010, 6, 821-828.	8.0	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.	2.1	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.	7.1	158
6	Structure and Orientation of Pardaxin Determined by NMR Experiments in Model Membranes. Journal of Biological Chemistry, 2004, 279, 45815-45823.	3.4	157
7	Structures of the Dimeric and Monomeric Variants of Magainin Antimicrobial Peptides (MSI-78 and) Tj ETQq1 1 0.784314 rgBT /Overl	2.5	157
8	NMR Structure of the Cathelicidin-Derived Human Antimicrobial Peptide LL-37 in Dodecylphosphocholine Micelles. Biochemistry, 2008, 47, 5565-5572.	2.5	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.	7.1	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.	7.1	154
11	NMR Solution Structure and Topological Orientation of Monomeric Phospholamban in Dodecylphosphocholine Micelles. Biophysical Journal, 2003, 85, 2589-2598.	0.5	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.	47.7	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.	7.1	129
14	Structural and Dynamic Basis of Phospholamban and Sarcolipin Inhibition of Ca ²⁺ -ATPase. Biochemistry, 2008, 47, 3-13.	2.5	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.	7.1	112
16	Dipolar Waves as NMR Maps of Protein Structure. Journal of the American Chemical Society, 2002, 124, 4206-4207.	13.7	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.	13.7	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.	7.1	101

#	ARTICLE	IF	CITATIONS
19	Dipolar Waves Map the Structure and Topology of Helices in Membrane Proteins. <i>Journal of the American Chemical Society</i> , 2003, 125, 8928-8935.	13.7	99
20	Selectivity in heavy metal-binding to peptides and proteins. <i>Biopolymers</i> , 2002, 64, 189-197.	2.4	96
21	A dynamic hydrophobic core orchestrates allostery in protein kinases. <i>Science Advances</i> , 2017, 3, e1600663.	10.3	89
22	Structure and Orientation of Sarcolipin in Lipid Environments. <i>Biochemistry</i> , 2002, 41, 475-482.	2.5	83
23	Structural Ensembles of Membrane-bound α -Synuclein Reveal the Molecular Determinants of Synaptic Vesicle Affinity. <i>Scientific Reports</i> , 2016, 6, 27125.	3.3	83
24	Structure and dynamics of a primordial catalytic fold generated by in vitro evolution. <i>Nature Chemical Biology</i> , 2013, 9, 81-83.	8.0	80
25	Overexpression, purification, and characterization of recombinant Ca-ATPase regulators for high-resolution solution and solid-state NMR studies. <i>Protein Expression and Purification</i> , 2003, 30, 253-261.	1.3	79
26	Fluidic and Air-Stable Supported Lipid Bilayer and Cell-Mimicking Microarrays. <i>Journal of the American Chemical Society</i> , 2008, 130, 6267-6271.	13.7	78
27	Dual Acquisition Magicâ€Angle Spinning Solidâ€State NMRâ€Spectroscopy: Simultaneous Acquisition of Multidimensional Spectra of Biomacromolecules. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 2731-2735.	13.8	76
28	Structural biology of metal-binding sequences. <i>Current Opinion in Chemical Biology</i> , 2002, 6, 217-223.	6.1	73
29	Serine 16 Phosphorylation Induces an Order-to-Disorder Transition in Monomeric Phospholambanâ€. <i>Biochemistry</i> , 2005, 44, 4386-4396.	2.5	71
30	Solid-State NMR and Rigid Body Molecular Dynamics To Determine Domain Orientations of Monomeric Phospholamban. <i>Journal of the American Chemical Society</i> , 2002, 124, 9392-9393.	13.7	70
31	¹ H/ ¹⁵ N Heteronuclear NMR Spectroscopy Shows Four Dynamic Domains for Phospholamban Reconstituted in Dodecylphosphocholine Micelles. <i>Biophysical Journal</i> , 2004, 87, 1205-1214.	0.5	70
32	Lethal Arg9Cys phospholamban mutation hinders Ca ²⁺ -ATPase regulation and phosphorylation by protein kinase A. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 2735-2740.	7.1	64
33	Isotope Labeling for Solution and Solid-State NMR Spectroscopy of Membrane Proteins. <i>Advances in Experimental Medicine and Biology</i> , 2012, 992, 35-62.	1.6	63
34	Conformational preferences of the amylin nucleation site in SDS micelles: An NMR study. <i>Biopolymers</i> , 2003, 69, 29-41.	2.4	60
35	Proton-Coupled Electron Transfer in a Biomimetic Peptide as a Model of Enzyme Regulatory Mechanisms. <i>Journal of the American Chemical Society</i> , 2007, 129, 4393-4400.	13.7	60
36	The TLQP-21 Peptide Activates the G-Protein-Coupled Receptor C3aR1 via a Folding-upon-Binding Mechanism. <i>Structure</i> , 2014, 22, 1744-1753.	3.3	59

#	ARTICLE	IF	CITATIONS
37	cAMP-Dependent Protein Kinase A Selects the Excited State of the Membrane Substrate Phospholamban. <i>Journal of Molecular Biology</i> , 2011, 412, 155-164.	4.2	58
38	Activating and Deactivating Roles of Lipid Bilayers on the Ca ²⁺ -ATPase/Phospholamban Complex. <i>Biochemistry</i> , 2011, 50, 10367-10374.	2.5	57
39	¹⁵ N and ¹³ C- SOFAST-HMQC editing enhances 3D-NOESY sensitivity in highly deuterated, selectively [¹ H, ¹³ C]-labeled proteins. <i>Journal of Biomolecular NMR</i> , 2016, 66, 259-271.	2.8	56
40	Controlling the Inhibition of the Sarcoplasmic Ca ²⁺ -ATPase by Tuning Phospholamban Structural Dynamics. <i>Journal of Biological Chemistry</i> , 2007, 282, 37205-37214.	3.4	55
41	Synchronous Opening and Closing Motions Are Essential for cAMP-Dependent Protein Kinase A Signaling. <i>Structure</i> , 2014, 22, 1735-1743.	3.3	55
42	Lanthanide Ion Binding to Adventitious Sites Aligns Membrane Proteins in Micelles for Solution NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2000, 122, 11733-11734.	13.7	54
43	NMR mapping of protein conformational landscapes using coordinated behavior of chemical shifts upon ligand binding. <i>Physical Chemistry Chemical Physics</i> , 2014, 16, 6508-6518.	2.8	54
44	Sensitivity Enhancement in Static Solid-State NMR Experiments via Single- and Multiple-Quantum Dipolar Coherences. <i>Journal of the American Chemical Society</i> , 2009, 131, 5754-5756.	13.7	51
45	Solution structures of the reduced and Cu(I) bound forms of the first metal binding sequence of ATP7A associated with Menkes disease. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 1038-1049.	2.6	50
46	Structure, Dynamics, and Membrane Topology of Stannin: A Mediator of Neuronal Cell Apoptosis Induced by Trimethyltin Chloride. <i>Journal of Molecular Biology</i> , 2005, 354, 652-665.	4.2	50
47	Defining the Intramembrane Binding Mechanism of Sarcolipin to Calcium ATPase Using Solution NMR Spectroscopy. <i>Journal of Molecular Biology</i> , 2006, 358, 420-429.	4.2	50
48	Structure and topology of a peptide segment of the 6th transmembrane domain of the <i>Saccharomyces cerevisiae</i> γ -factor receptor in phospholipid bilayers. <i>Biopolymers</i> , 2001, 59, 243-256.	2.4	48
49	Deuterium/Hydrogen Exchange Factors Measured by Solution Nuclear Magnetic Resonance Spectroscopy as Indicators of the Structure and Topology of Membrane Proteins. <i>Biophysical Journal</i> , 2002, 82, 2176-2183.	0.5	48
50	Two-Dimensional Solid-State NMR Reveals Two Topologies of Sarcolipin in Oriented Lipid Bilayers. <i>Biochemistry</i> , 2006, 45, 10939-10946.	2.5	48
51	A refinement protocol to determine structure, topology, and depth of insertion of membrane proteins using hybrid solution and solid-state NMR restraints. <i>Journal of Biomolecular NMR</i> , 2009, 44, 195-205.	2.8	48
52	Dealkylation of Organotin Compounds by Biological Dithiols: Toward the Chemistry of Organotin Toxicity. <i>Journal of the American Chemical Society</i> , 2003, 125, 13316-13317.	13.7	47
53	Lipid-Mediated Folding/Unfolding of Phospholamban as a Regulatory Mechanism for the Sarcoplasmic Reticulum Ca ²⁺ -ATPase. <i>Journal of Molecular Biology</i> , 2011, 408, 755-765.	4.2	47
54	Mutation of a kinase allosteric node uncouples dynamics linked to phosphotransfer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E931-E940.	7.1	47

#	ARTICLE	IF	CITATIONS
55	Biological chemistry of organotin compounds: Interactions and dealkylation by dithiols. <i>Journal of Organometallic Chemistry</i> , 2006, 691, 1748-1755.	1.8	46
56	A Myristoyl/Phosphoserine Switch Controls cAMP-Dependent Protein Kinase Association to Membranes. <i>Journal of Molecular Biology</i> , 2011, 411, 823-836.	4.2	46
57	Dysfunctional conformational dynamics of protein kinase A induced by a lethal mutant of phospholamban hinder phosphorylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3716-3721.	7.1	43
58	Cushing's syndrome driver mutation disrupts protein kinase A allosteric network, altering both regulation and substrate specificity. <i>Science Advances</i> , 2019, 5, eaaw9298.	10.3	43
59	3D DUMAS: Simultaneous acquisition of three-dimensional magic angle spinning solid-state NMR experiments of proteins. <i>Journal of Magnetic Resonance</i> , 2012, 220, 79-84.	2.1	41
60	Probing ground and excited states of phospholamban in model and native lipid membranes by magic angle spinning NMR spectroscopy. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012, 1818, 146-153.	2.6	41
61	Allostery and Binding Cooperativity of the Catalytic Subunit of Protein Kinase A by NMR Spectroscopy and Molecular Dynamics Simulations. <i>Advances in Protein Chemistry and Structural Biology</i> , 2012, 87, 363-389.	2.3	41
62	Structural Dynamics and Topology of Phosphorylated Phospholamban Homopentamer Reveal Its Role in the Regulation of Calcium Transport. <i>Structure</i> , 2013, 21, 2119-2130.	3.3	41
63	FLAMEnGO 2.0: An enhanced fuzzy logic algorithm for structure-based assignment of methyl group resonances. <i>Journal of Magnetic Resonance</i> , 2014, 245, 17-23.	2.1	41
64	Globally correlated conformational entropy underlies positive and negative cooperativity in a kinase's enzymatic cycle. <i>Nature Communications</i> , 2019, 10, 799.	12.8	40
65	Probing Slow Protein Dynamics by Adiabatic $\langle R \rangle$ and $\langle R^2 \rangle$ NMR Experiments. <i>Journal of the American Chemical Society</i> , 2010, 132, 9979-9981.	13.7	39
66	Theoretical Analysis of Residual Dipolar Coupling Patterns in Regular Secondary Structures of Proteins. <i>Journal of the American Chemical Society</i> , 2003, 125, 12520-12526.	13.7	38
67	On the Function of Pentameric Phospholamban: Ion Channel or Storage Form?. <i>Biophysical Journal</i> , 2009, 96, L60-L62.	0.5	38
68	An Electrochemical Investigation of Sarcolipin Reconstituted into a Mercury-Supported Lipid Bilayer. <i>Biophysical Journal</i> , 2007, 93, 2678-2687.	0.5	36
69	Multidimensional oriented solid-state NMR experiments enable the sequential assignment of uniformly ^{15}N labeled integral membrane proteins in magnetically aligned lipid bilayers. <i>Journal of Biomolecular NMR</i> , 2011, 51, 339-346.	2.8	36
70	Orphan spin operators enable the acquisition of multiple 2D and 3D magic angle spinning solid-state NMR spectra. <i>Journal of Chemical Physics</i> , 2013, 138, 184201.	3.0	36
71	Probing excited states and activation energy for the integral membrane protein phospholamban by NMR CPMG relaxation dispersion experiments. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2010, 1798, 77-81.	2.6	34
72	On the Role of NMR Spectroscopy for Characterization of Antimicrobial Peptides. <i>Methods in Molecular Biology</i> , 2013, 1063, 159-180.	0.9	34

#	ARTICLE	IF	CITATIONS
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. <i>Biophysical Journal</i> , 2009, 96, 3648-3662.	0.5	33
74	Dynamic allostery-based molecular workings of kinase:peptide complexes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 15052-15061.	7.1	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. <i>Journal of Biomolecular NMR</i> , 2013, 57, 91-102.	2.8	32
76	Sensitivity Enhancement of Separated Local Field Experiments: Application to Membrane Proteins. <i>Journal of Physical Chemistry B</i> , 2010, 114, 5089-5095.	2.6	30
77	A tyrosine-tryptophan dyad and radical-based charge transfer in a ribonucleotide reductase-inspired maquette. <i>Nature Communications</i> , 2015, 6, 10010.	12.8	30
78	Solution and Solid-State Nuclear Magnetic Resonance Structural Investigations of the Antimicrobial Designer Peptide GL13K in Membranes. <i>Biochemistry</i> , 2017, 56, 4269-4278.	2.5	30
79	Dynamical and allosteric regulation of photoprotection in light harvesting complex II. <i>Science China Chemistry</i> , 2020, 63, 1121-1133.	8.2	29
80	Probing membrane topology of the antimicrobial peptide distinctin by solid-state NMR spectroscopy in zwitterionic and charged lipid bilayers. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2011, 1808, 34-40.	2.6	28
81	Simultaneous acquisition of 2D and 3D solid-state NMR experiments for sequential assignment of oriented membrane protein samples. <i>Journal of Biomolecular NMR</i> , 2015, 62, 53-61.	2.8	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. <i>Journal of Physical Chemistry B</i> , 2010, 114, 13872-13880.	2.6	27
83	Conformational Equilibrium of N-Myristoylated cAMP-Dependent Protein Kinase A by Molecular Dynamics Simulations. <i>Biochemistry</i> , 2012, 51, 10186-10196.	2.5	27
84	Nonstereogenic β -aminoisobutyryl-glycyl dipeptidyl unit nucleates type I ² -turn in linear peptides in aqueous solution. <i>Biopolymers</i> , 2007, 88, 746-753.	2.4	26
85	Zooming in on protons: Neutron structure of protein kinase A trapped in a product complex. <i>Science Advances</i> , 2019, 5, eaav0482.	10.3	26
86	Paramagnetic-Based NMR Restraints Lift Residual Dipolar Coupling Degeneracy in Multidomain Detergent-Solubilized Membrane Proteins. <i>Journal of the American Chemical Society</i> , 2011, 133, 2232-2241.	13.7	25
87	Sensitivity and resolution enhancement of oriented solid-state NMR: Application to membrane proteins. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2013, 75, 50-68.	7.5	25
88	Structures of the Excited States of Phospholamban and Shifts in Their Populations upon Phosphorylation. <i>Biochemistry</i> , 2013, 52, 6684-6694.	2.5	24
89	Sensitivity Enhanced Heteronuclear Correlation Spectroscopy in Multidimensional Solid-State NMR of Oriented Systems via Chemical Shift Coherences. <i>Journal of the American Chemical Society</i> , 2010, 132, 5357-5363.	13.7	23
90	FLAMEnGO: A fuzzy logic approach for methyl group assignment using NOESY and paramagnetic relaxation enhancement data. <i>Journal of Magnetic Resonance</i> , 2012, 214, 103-110.	2.1	23

#	ARTICLE	IF	CITATIONS
91	Conformational Landscape of the PRKACA-DNAJB1 Chimeric Kinase, the Driver for Fibrolamellar Hepatocellular Carcinoma. <i>Scientific Reports</i> , 2018, 8, 720.	3.3	23
92	Asymmetric Methyl Group Labeling as a Probe of Membrane Protein Homo-oligomers by NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2008, 130, 2400-2401.	13.7	22
93	Multiple acquisitions via sequential transfer of orphan spin polarization (MAeSTOSO): How far can we push residual spin polarization in solid-state NMR?. <i>Journal of Magnetic Resonance</i> , 2016, 267, 1-8.	2.1	22
94	ALARM NMR for HTS Triage and Chemical Probe Validation. <i>Current Protocols in Chemical Biology</i> , 2018, 10, 91-117.	1.7	22
95	Interactions of Alkyltin Salts with Biological Dithiols: Dealkylation and Induction of a Regular β^2 -Turn Structure in Peptides. <i>Journal of the American Chemical Society</i> , 2004, 126, 14400-14410.	13.7	21
96	Role of conformational entropy in the activity and regulation of the catalytic subunit of protein kinase α . <i>FEBS Journal</i> , 2013, 280, 5608-5615.	4.7	21
97	Defective internal allosteric network imparts dysfunctional ATP/substrate-binding cooperativity in oncogenic chimera of protein kinase A. <i>Communications Biology</i> , 2021, 4, 321.	4.4	21
98	Conformational Study of [Met5]Enkephalin-Arg-Phe in the Presence of Phosphatidylserine Vesicles. <i>FEBS Journal</i> , 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. <i>Chemistry and Physics of Lipids</i> , 2004, 132, 133-144.	3.2	20
100	Structural Dynamics and Conformational Equilibria of SERCA Regulatory Proteins in Membranes by Solid-State NMR Restrained Simulations. <i>Biophysical Journal</i> , 2014, 106, 2566-2576.	0.5	20
101	Use of paramagnetic systems to speed-up NMR data acquisition and for structural and dynamic studies. <i>Solid State Nuclear Magnetic Resonance</i> , 2019, 102, 36-46.	2.3	20
102	The Role of Sarcolipin and ATP in the Transport of Phosphate Ion into the Sarcoplasmic Reticulum. <i>Biophysical Journal</i> , 2009, 97, 2693-2699.	0.5	19
103	Uncoupling Catalytic and Binding Functions in the Cyclic AMP-Dependent Protein Kinase A. <i>Structure</i> , 2016, 24, 353-363.	3.3	19
104	Multiple acquisition of magic angle spinning solid-state NMR experiments using one receiver: Application to microcrystalline and membrane protein preparations. <i>Journal of Magnetic Resonance</i> , 2015, 253, 143-153.	2.1	18
105	Solid-State NMR of Membrane Proteins in Lipid Bilayers: To Spin or Not To Spin?. <i>Accounts of Chemical Research</i> , 2021, 54, 1430-1439.	15.6	18
106	Synthesis of a-factor peptide from <i>Saccharomyces cerevisiae</i> and photoactive analogues via Fmoc solid phase methodology. <i>Bioorganic and Medicinal Chemistry</i> , 2011, 19, 490-497.	3.0	17
107	Structure and membrane interactions of chionodracine, a piscidin-like antimicrobial peptide from the icefish <i>Chionodraco hamatus</i> . <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2015, 1848, 1285-1293.	2.6	17
108	Genetic algorithm optimized triply compensated pulses in NMR spectroscopy. <i>Journal of Magnetic Resonance</i> , 2015, 260, 136-143.	2.1	17

#	ARTICLE	IF	CITATIONS
109	Clearance kinetics of the VGF-derived neuropeptide TLQP-21. <i>Neuropeptides</i> , 2018, 71, 97-103.	2.2	17
110	Allostery governs Cdk2 activation and differential recognition of CDK inhibitors. <i>Nature Chemical Biology</i> , 2021, 17, 456-464.	8.0	17
111	High-Resolution Structure and Conformational Dynamics of Rigid, Cofacially Aligned Porphyrin ^π -Bridge ^π -Quinone Systems As Determined by NMR Spectroscopy and ab Initio Simulated Annealing Calculations. <i>Journal of the American Chemical Society</i> , 2001, 123, 5668-5679.	13.7	16
112	Tuning the structural coupling between the transmembrane and cytoplasmic domains of phospholamban to control sarcoplasmic reticulum Ca ²⁺ -ATPase (SERCA) function. <i>Journal of Muscle Research and Cell Motility</i> , 2012, 33, 485-492.	2.0	16
113	Mapping the Hydrogen Bond Networks in the Catalytic Subunit of Protein Kinase A Using H/D Fractionation Factors. <i>Biochemistry</i> , 2015, 54, 4042-4049.	2.5	16
114	Effects of naturally occurring arginine 14 deletion on phospholamban conformational dynamics and membrane interactions. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2015, 1848, 315-322.	2.6	16
115	Probing membrane protein ground and conformationally excited states using dipolar- and J-coupling mediated MAS solid state NMR experiments. <i>Methods</i> , 2018, 148, 115-122.	3.8	16
116	Formalin Evokes Calcium Transients from the Endoplasmatic Reticulum. <i>PLoS ONE</i> , 2015, 10, e0123762.	2.5	16
117	Multi-state recognition pathway of the intrinsically disordered protein kinase inhibitor by protein kinase A. <i>ELife</i> , 2020, 9, .	6.0	16
118	Reversal of Phospholamban Inhibition of the Sarco(endo)plasmic Reticulum Ca ²⁺ -ATPase (SERCA) Using Short, Protein-interacting RNAs and Oligonucleotide Analogs. <i>Journal of Biological Chemistry</i> , 2016, 291, 21510-21518.	3.4	15
119	Probing the Conformationally Excited States of Membrane Proteins via ¹ H-Detected MAS Solid-State NMR Spectroscopy. <i>Journal of Physical Chemistry B</i> , 2017, 121, 4456-4465.	2.6	15
120	Application of paramagnetic relaxation enhancements to accelerate the acquisition of 2D and 3D solid-state NMR spectra of oriented membrane proteins. <i>Methods</i> , 2018, 138-139, 54-61.	3.8	15
121	Molecular Mechanism for the Suppression of Alpha Synuclein Membrane Toxicity by an Unconventional Extracellular Chaperone. <i>Journal of the American Chemical Society</i> , 2020, 142, 9686-9699.	13.7	15
122	Carbonyl carbon label selective (CCLS) ¹ H- ¹⁵ N HSQC experiment for improved detection of backbone ¹³ C- ¹⁵ N cross peaks in larger proteins. <i>Journal of Biomolecular NMR</i> , 2007, 39, 177-185.	2.8	14
123	Heteronuclear Adiabatic Relaxation Dispersion (HARD) for quantitative analysis of conformational dynamics in proteins. <i>Journal of Magnetic Resonance</i> , 2012, 219, 75-82.	2.1	14
124	An intramembrane sensory circuit monitors sortase A-mediated processing of streptococcal adhesins. <i>Science Signaling</i> , 2019, 12, .	3.6	14
125	Activation mechanism of <i>Drosophila</i> cryptochrome through an allosteric switch. <i>Science Advances</i> , 2021, 7, .	10.3	14
126	¹ H-detected MAS solid-state NMR experiments enable the simultaneous mapping of rigid and dynamic domains of membrane proteins. <i>Journal of Magnetic Resonance</i> , 2017, 285, 101-107.	2.1	14

#	ARTICLE	IF	CITATIONS
127	A synthetic peptide corresponding to the 550-585 region of $\hat{1}\pm$ -dystroglycan binds $\hat{1}^2$ -dystroglycan as revealed by NMR spectroscopy. <i>FEBS Letters</i> , 2001, 499, 210-214.	2.8	13
128	Backbone NMR resonance assignment of the catalytic subunit of cAMP-dependent protein kinase A in complex with AMP-PNP. <i>Biomolecular NMR Assignments</i> , 2009, 3, 115-117.	0.8	13
129	Proton evolved local field solid-state nuclear magnetic resonance using Hadamard encoding: Theory and application to membrane proteins. <i>Journal of Chemical Physics</i> , 2011, 135, 074503.	3.0	13
130	Enhancing the sensitivity of multidimensional NMR experiments by using triply-compensated $\hat{1}\epsilon$ pulses. <i>Journal of Biomolecular NMR</i> , 2017, 69, 237-243.	2.8	13
131	Design and characterization of chionodracine-derived antimicrobial peptides with enhanced activity against drug-resistant human pathogens. <i>RSC Advances</i> , 2018, 8, 41331-41346.	3.6	13
132	Hybridization of TEDOR and NCX MAS solid-state NMR experiments for simultaneous acquisition of heteronuclear correlation spectra and distance measurements. <i>Journal of Biomolecular NMR</i> , 2019, 73, 141-153.	2.8	13
133	Simultaneous Detection and Deconvolution of Congested NMR Spectra Containing Three Isotopically Labeled Species. <i>Journal of the American Chemical Society</i> , 2008, 130, 7818-7819.	13.7	12
134	NMR structure and conformational dynamics of AtPDFL2.1, a defensin-like peptide from <i>Arabidopsis thaliana</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 1739-1747.	2.3	12
135	Orphan Spin Polarization. <i>Annual Reports on NMR Spectroscopy</i> , 2016, 89, 103-121.	1.5	12
136	Multi-receiver solid-state NMR using polarization optimized experiments (POE) at ultrafast magic angle spinning. <i>Journal of Biomolecular NMR</i> , 2020, 74, 267-285.	2.8	12
137	CHESPA/CHESCA-SPARKY: automated NMR data analysis plugins for SPARKY to map protein allostery. <i>Bioinformatics</i> , 2021, 37, 1176-1177.	4.1	12
138	Expression and purification of isotopically labeled peptide inhibitors and substrates of cAMP-dependant protein kinase A for NMR analysis. <i>Protein Expression and Purification</i> , 2009, 64, 231-236.	1.3	11
139	Topology and immersion depth of an integral membrane protein by paramagnetic rates from dissolved oxygen. <i>Journal of Biomolecular NMR</i> , 2011, 51, 173-183.	2.8	11
140	Optimization of identity operation in NMR spectroscopy via genetic algorithm: Application to the TEDOR experiment. <i>Journal of Magnetic Resonance</i> , 2016, 273, 40-46.	2.1	11
141	Effects of the Arg9Cys and Arg25Cys mutations on phospholamban's conformational equilibrium in membrane bilayers. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2018, 1860, 1335-1341.	2.6	11
142	Proton-detected polarization optimized experiments (POE) using ultrafast magic angle spinning solid-state NMR: Multi-acquisition of membrane protein spectra. <i>Journal of Magnetic Resonance</i> , 2020, 310, 106664.	2.1	11
143	Experimental Aspects of Polarization Optimized Experiments (POE) for Magic Angle Spinning Solid-State NMR of Microcrystalline and Membrane-Bound Proteins. <i>Methods in Molecular Biology</i> , 2018, 1688, 37-53.	0.9	11
144	Accurate Determination of Conformational Transitions in Oligomeric Membrane Proteins. <i>Scientific Reports</i> , 2016, 6, 23063.	3.3	10

#	ARTICLE	IF	CITATIONS
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. <i>Analytical Chemistry</i> , 2019, 91, 7698-7704.	6.5	10
146	Structural basis for allosteric control of the SERCA-Phospholamban membrane complex by Ca ²⁺ and phosphorylation. <i>ELife</i> , 2021, 10, .	6.0	10
147	Solution conformation of the <i>Pseudomonas syringae</i> MSU 16H phytotoxic lipodepsipeptide Pseudomycin A determined by computer simulations using distance geometry and molecular dynamics from NMR data. <i>FEBS Journal</i> , 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. <i>Journal of the American Chemical Society</i> , 2009, 131, 14138-14139.	13.7	9
149	Simultaneous detection of intra- and inter-molecular paramagnetic relaxation enhancements in protein complexes. <i>Journal of Biomolecular NMR</i> , 2018, 70, 133-140.	2.8	9
150	Probing Protein-Protein Interactions Using Asymmetric Labeling and Carbonyl-Carbon Selective Heteronuclear NMR Spectroscopy. <i>Molecules</i> , 2018, 23, 1937.	3.8	9
151	Structural basis for sarcolipin's regulation of muscle thermogenesis by the sarcoplasmic reticulum Ca ²⁺ -ATPase. <i>Science Advances</i> , 2021, 7, eabi7154.	10.3	9
152	Raf Kinase Inhibitory Protein regulates the cAMP-dependent protein kinase signaling pathway through a positive feedback loop. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	9
153	Improved resolution in dipolar NMR spectra using constant time evolution PISEMA experiment. <i>Chemical Physics Letters</i> , 2010, 494, 104-110.	2.6	8
154	Phospholamban and its phosphorylated form require non-physiological transmembrane potentials to translocate ions. <i>Soft Matter</i> , 2012, 8, 3881.	2.7	8
155	Rheostatic Regulation of the SERCA/Phospholamban Membrane Protein Complex Using Non-Coding RNA and Single-Stranded DNA oligonucleotides. <i>Scientific Reports</i> , 2015, 5, 13000.	3.3	8
156	Improving the quality of oriented membrane protein spectra using heat-compensated separated local field experiments. <i>Journal of Biomolecular NMR</i> , 2019, 73, 617-624.	2.8	8
157	Intrinsically disordered HAX-1 regulates Ca ²⁺ cycling by interacting with lipid membranes and the phospholamban cytoplasmic region. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2020, 1862, 183034.	2.6	8
158	Is Disrupted Nucleotide-Substrate Cooperativity a Common Trait for Cushing's Syndrome Driving Mutations of Protein Kinase A?. <i>Journal of Molecular Biology</i> , 2021, 433, 167123.	4.2	8
159	What Can We Learn from a Small Regulatory Membrane Protein?. <i>Methods in Molecular Biology</i> , 2010, 654, 303-319.	0.9	8
160	A kink in DWORF helical structure controls the activation of the sarcoplasmic reticulum Ca ²⁺ -ATPase. <i>Structure</i> , 2022, 30, 360-370.e6.	3.3	8
161	PHRONESIS: A One-Shot Approach for Sequential Assignment of Protein Resonances by Ultrafast MAS Solid-State NMR Spectroscopy. <i>ChemPhysChem</i> , 2022, 23, e202200127.	2.1	8
162	Nanosecond-Timescale Dynamics and Conformational Heterogeneity in Human GCK Regulation and Disease. <i>Biophysical Journal</i> , 2020, 118, 1109-1118.	0.5	7

#	ARTICLE	IF	CITATIONS
163	PISA-SPARKY: an interactive SPARKY plugin to analyze oriented solid-state NMR spectra of helical membrane proteins. <i>Bioinformatics</i> , 2020, 36, 2915-2916.	4.1	7
164	Pseudoenzymatic dealkylation of alkyltins by biological dithiols. <i>Journal of Biological Inorganic Chemistry</i> , 2009, 14, 1219-1225.	2.6	6
165	Synthesis and characterization of the 47-residue heterodimeric antimicrobial peptide distinctin, featuring directed disulfide bridge formation. <i>Biopolymers</i> , 2012, 98, 479-484.	2.4	6
166	Probing Residue-Specific Water-Protein Interactions in Oriented Lipid Membranes via Solid-State NMR Spectroscopy. <i>Journal of Physical Chemistry B</i> , 2016, 120, 10959-10968.	2.6	6
167	Ca ²⁺ ATPase Conformational Transitions in Lipid Bilayers Mapped by Site-directed Ethylation and Solid-State NMR. <i>ACS Chemical Biology</i> , 2016, 11, 329-334.	3.4	6
168	Structure and Function of Tryptophan-Tyrosine Dyads in Biomimetic Î² Hairpins. <i>Journal of Physical Chemistry B</i> , 2019, 123, 2780-2791.	2.6	6
169	Catch them if you can. <i>Nature Chemical Biology</i> , 2013, 9, 410-411.	8.0	5
170	T2* weighted Deconvolution of NMR Spectra: Application to 2D Homonuclear MAS Solid-State NMR of Membrane Proteins. <i>Scientific Reports</i> , 2019, 9, 8225.	3.3	5
171	Allosteric Regulation of the M2 Protein from Influenza A by Cholesterol. <i>Biophysical Journal</i> , 2016, 110, 1207-1208.	0.5	4
172	Cysteine-ethylation of tissue-extracted membrane proteins as a tool to detect conformational states by solid-state NMR spectroscopy. <i>Methods in Enzymology</i> , 2019, 621, 281-304.	1.0	4
173	A Theoretical Assessment of the Structure Determination of Multi-Span Membrane Proteins by Oriented Sample Solid-State NMR Spectroscopy. <i>Australian Journal of Chemistry</i> , 2020, 73, 246.	0.9	4
174	Simultaneous acquisition of multiple fast MAS solid-state NMR experiments via orphan spin polarization. <i>Annual Reports on NMR Spectroscopy</i> , 2021, , 247-268.	1.5	4
175	Templating Î±-amylase peptide inhibitors with organotin compounds. <i>Journal of Biological Inorganic Chemistry</i> , 2011, 16, 1197-1204.	2.6	3
176	Modeling helical proteins using residual dipolar couplings, sparse long-range distance constraints and a simple residue-based force field. <i>Theoretical Chemistry Accounts</i> , 2013, 132, 1388.	1.4	3
177	Special issue on "Membrane Protein Dynamics: Correlating Structure to Function". <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2010, 1798, 65-67.	2.6	2
178	A Semiautomated Assignment Protocol for Methyl Group Side Chains in Large Proteins. <i>Methods in Enzymology</i> , 2016, 566, 35-57.	1.0	2
179	Tunable Liaisons: eEF-2K, CaM, and Calcium. <i>Structure</i> , 2016, 24, 1438-1439.	3.3	2
180	Optimization of 1H decoupling eliminates sideband artifacts in 3D TROSY-based triple resonance experiments. <i>Journal of Biomolecular NMR</i> , 2017, 69, 45-52.	2.8	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.	2.7	1
183	Cytoplasmic nucleic acid-based XNAs directly enhance live cardiac cell function by a Ca ²⁺ cycling-independent mechanism via the sarcomere. Journal of Molecular and Cellular Cardiology, 2019, 130, 1-9.	1.9	1
184	Met125 is essential for maintaining the structural integrity of calmodulin's C-terminal domain. Scientific Reports, 2020, 10, 21320.	3.3	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 α -subunit Disrupts the Internal Allosteric Network Affecting Regulation and Substrate Specificity. FASEB Journal, 2019, 33, 478.11.	0.5	1
187	Spectroscopic Design of Phospholamban Mutants to Treat Heart Failure. Biophysical Journal, 2010, 98, 246a.	0.5	0
188	Rational Structure-Based Design of PLN Mutants to Optimize Dephosphorylation and Tune Serca Function. Biophysical Journal, 2014, 106, 653a-654a.	0.5	0
189	Role of Phospholamban Mutations in Protein-Protein Interactions. Biophysical Journal, 2015, 108, 500a.	0.5	0
190	Sequence-Independent SSDNA Relieves Phospholamban Inhibition of SERCA in a Length Dependent Manner. Biophysical Journal, 2015, 108, 254a.	0.5	0
191	Phospholamban Phosphorylation Alters its Conformational Equilibrium to Regulate SERCA Activity. Biophysical Journal, 2015, 108, 131a.	0.5	0
192	Characterization of Calmodulin Binding to the Ryanodine Receptor by Solution and Solid-State NMR. Biophysical Journal, 2015, 108, 616a.	0.5	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.	0.5	0
194	Structural Characterization of the Bacterial Succinate/Acetate Proton Symporter SatP in Lipid Bilayer Membranes. Biophysical Journal, 2016, 110, 61a.	0.5	0
195	Structure, Dynamics, and Function of the Membrane Associated SRC Family Kinase HCK. Biophysical Journal, 2017, 112, 388a-389a.	0.5	0
196	Elucidating the Uncoupling of ATP Hydrolysis and Ca ²⁺ Transport in SERCA by Sarcolipin. Biophysical Journal, 2017, 112, 500a.	0.5	0
197	Protein kinase A in the neutron beam: Insights for catalysis from directly observing protons. Methods in Enzymology, 2020, 634, 311-331.	1.0	0
198	Topological Allosteric Regulation of the Sarcoplasmic Reticulum Calcium Pump Phospholamban. Biophysical Journal, 2020, 118, 99a.	0.5	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