

# Gianluigi Veglia

## List of Publications by Year in descending order

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199  
papers

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47006

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211  
docs citations

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times ranked

6814  
citing authors

#	ARTICLE	IF	CITATIONS
1	A kink in DWORF helical structure controls the activation of the sarcoplasmic reticulum Ca <sup>2+</sup> -ATPase. <i>Structure</i> , 2022, 30, 360-370.e6.	3.3	8
2	PHRONESIS: A One-Step Approach for Sequential Assignment of Protein Resonances by Ultrafast MAS Solid-State NMR Spectroscopy. <i>ChemPhysChem</i> , 2022, 23, e202200127.	2.1	8
3	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
4	CHESPA/CHESCA-SPARKY: automated NMR data analysis plugins for SPARKY to map protein allostery. <i>Bioinformatics</i> , 2021, 37, 1176-1177.	4.1	12
5	Allostery governs Cdk2 activation and differential recognition of CDK inhibitors. <i>Nature Chemical Biology</i> , 2021, 17, 456-464.	8.0	17
6	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
7	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
8	Structural basis for allosteric control of the SERCA-Phospholamban membrane complex by Ca <sup>2+</sup> and phosphorylation. <i>ELife</i> , 2021, 10, .	6.0	10
9	Activation mechanism of <i>Drosophila</i> cryptochrome through an allosteric switch. <i>Science Advances</i> , 2021, 7, .	10.3	14
10	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
11	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
12	Structural basis for sarcolipin's regulation of muscle thermogenesis by the sarcoplasmic reticulum Ca <sup>2+</sup> -ATPase. <i>Science Advances</i> , 2021, 7, eabi7154.	10.3	9
13	Intrinsically disordered HAX-1 regulates Ca <sup>2+</sup> cycling by interacting with lipid membranes and the phospholamban cytoplasmic region. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2020, 1862, 183034.	2.6	8
14	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
15	Met125 is essential for maintaining the structural integrity of calmodulin's C-terminal domain. <i>Scientific Reports</i> , 2020, 10, 21320.	3.3	1
16	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.	18.7	15
17	Dynamical and allosteric regulation of photoprotection in light harvesting complex II. <i>Science China Chemistry</i> , 2020, 63, 1121-1133.	8.2	29
18	Protein kinase A in the neutron beam: Insights for catalysis from directly observing protons. <i>Methods in Enzymology</i> , 2020, 634, 311-331.	1.0	0

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19	Topological Allosteric Regulation of the Sarcoplasmic Reticulum Calcium Pump Phospholamban. <i>Biophysical Journal</i> , 2020, 118, 99a.	0.5	0
20	Nanosecond-Timescale Dynamics and Conformational Heterogeneity in Human GCK Regulation and Disease. <i>Biophysical Journal</i> , 2020, 118, 1109-1118.	0.5	7
21	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
22	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
23	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
24	Multi-state recognition pathway of the intrinsically disordered protein kinase inhibitor by protein kinase A. <i>ELife</i> , 2020, 9, .	6.0	16
25	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
26	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
27	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
28	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
29	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
30	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
31	An intramembrane sensory circuit monitors sortase A-mediated processing of streptococcal adhesins. <i>Science Signaling</i> , 2019, 12, .	3.6	14
32	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
33	Structure and Function of Tryptophan-Tyrosine Dyads in Biomimetic $\beta^2$ Hairpins. <i>Journal of Physical Chemistry B</i> , 2019, 123, 2780-2791.	2.6	6
34	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
35	Cytoplasmic nucleic acid-based XNAs directly enhance live cardiac cell function by a Ca <sup>2+</sup> cycling-independent mechanism via the sarcomere. <i>Journal of Molecular and Cellular Cardiology</i> , 2019, 130, 1-9.	1.9	1
36	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

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37	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
38	A Cushing Syndrome Mutation of Protein Kinase A $\alpha$ -Subunit Disrupts the Internal Allosteric Network Affecting Regulation and Substrate Specificity. <i>FASEB Journal</i> , 2019, 33, 478.11.	0.5	1
39	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
40	Perturbations of Native Membrane Protein Structure in Alkyl Phosphocholine Detergents: A Critical Assessment of NMR and Biophysical Studies. <i>Chemical Reviews</i> , 2018, 118, 3559-3607.	47.7	132
41	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
42	Conformational Landscape of the PRKACA-DNAJB1 Chimeric Kinase, the Driver for Fibrolamellar Hepatocellular Carcinoma. <i>Scientific Reports</i> , 2018, 8, 720.	3.3	23
43	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
44	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
45	Probing Protein-Protein Interactions Using Asymmetric Labeling and Carbonyl-Carbon Selective Heteronuclear NMR Spectroscopy. <i>Molecules</i> , 2018, 23, 1937.	3.8	9
46	Clearance kinetics of the VGF-derived neuropeptide TLQP-21. <i>Neuropeptides</i> , 2018, 71, 97-103.	2.2	17
47	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
48	ALARM NMR for HTS Triage and Chemical Probe Validation. <i>Current Protocols in Chemical Biology</i> , 2018, 10, 91-117.	1.7	22
49	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
50	Optimal Design of Offset-Specific Radio Frequency Pulses for Solution and Solid-State NMR Using a Genetic Algorithm. , 2018, , 605-615.		1
51	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
52	Probing the Conformationally Excited States of Membrane Proteins via <sup>1</sup> H-Detected MAS Solid-State NMR Spectroscopy. <i>Journal of Physical Chemistry B</i> , 2017, 121, 4456-4465.	2.6	15
53	Structure, Dynamics, and Function of the Membrane Associated SRC Family Kinase HCK. <i>Biophysical Journal</i> , 2017, 112, 388a-389a.	0.5	0
54	Elucidating the Uncoupling of ATP Hydrolysis and Ca <sup>2+</sup> Transport in SERCA by Sarcolipin. <i>Biophysical Journal</i> , 2017, 112, 500a.	0.5	0

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55	A dynamic hydrophobic core orchestrates allostery in protein kinases. <i>Science Advances</i> , 2017, 3, e1600663.	10.3	89
56	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
57	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
58	Enhancing the sensitivity of multidimensional NMR experiments by using triply-compensated $\pi$ pulses. <i>Journal of Biomolecular NMR</i> , 2017, 69, 237-243.	2.8	13
59	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
60	Optimal Design of Offset-Specific Radio Frequency Pulses for Solution and Solid-State NMR Using a Genetic Algorithm. , 2017, , 1-11.		0
61	A Semiautomated Assignment Protocol for Methyl Group Side Chains in Large Proteins. <i>Methods in Enzymology</i> , 2016, 566, 35-57.	1.0	2
62	Accurate Determination of Conformational Transitions in Oligomeric Membrane Proteins. <i>Scientific Reports</i> , 2016, 6, 23063.	3.3	10
63	Structural basis of synaptic vesicle assembly promoted by $\alpha$ -synuclein. <i>Nature Communications</i> , 2016, 7, 12563.	12.8	203
64	Structural Ensembles of Membrane-bound $\alpha$ -Synuclein Reveal the Molecular Determinants of Synaptic Vesicle Affinity. <i>Scientific Reports</i> , 2016, 6, 27125.	3.3	83
65	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
66	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
67	Tunable Liaisons: eEF-2K, CaM, and Calcium. <i>Structure</i> , 2016, 24, 1438-1439.	3.3	2
68	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
69	Orphan Spin Polarization. <i>Annual Reports on NMR Spectroscopy</i> , 2016, 89, 103-121.	1.5	12
70	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
71	Reversal of Phospholamban Inhibition of the Sarco(endo)plasmic Reticulum Ca <sup>2+</sup> -ATPase (SERCA) Using Short, Protein-interacting RNAs and Oligonucleotide Analogs. <i>Journal of Biological Chemistry</i> , 2016, 291, 21510-21518.	3.4	15
72	15N and 13C- SOFAST-HMQC editing enhances 3D-NOESY sensitivity in highly deuterated, selectively [1H,13C]-labeled proteins. <i>Journal of Biomolecular NMR</i> , 2016, 66, 259-271.	2.8	56

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73	Elucidating the Role of Structural Dynamics in Ligand Selection of Human Adipocyte Fatty Acid Binding Protein By NMR Spectroscopy. <i>Biophysical Journal</i> , 2016, 110, 538a.	0.5	0
74	Allosteric Regulation of the M2 Protein from Influenza A by Cholesterol. <i>Biophysical Journal</i> , 2016, 110, 1207-1208.	0.5	4
75	Structural Characterization of the Bacterial Succinate/Acetate Proton Symporter SatP in Lipid Bilayer Membranes. <i>Biophysical Journal</i> , 2016, 110, 61a.	0.5	0
76	Uncoupling Catalytic and Binding Functions in the Cyclic AMP-Dependent Protein Kinase A. <i>Structure</i> , 2016, 24, 353-363.	3.3	19
77	Ca <sup>2+</sup> 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
78	Role of Phospholamban Mutations in Protein-Protein Interactions. <i>Biophysical Journal</i> , 2015, 108, 500a.	0.5	0
79	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
80	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
81	Sequence-Independent SSDNA Relieves Phospholamban Inhibition of SERCA in a Length Dependent Manner. <i>Biophysical Journal</i> , 2015, 108, 254a.	0.5	0
82	Phospholamban Phosphorylation Alters its Conformational Equilibrium to Regulate SERCA Activity. <i>Biophysical Journal</i> , 2015, 108, 131a.	0.5	0
83	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
84	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
85	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
86	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
87	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
88	Genetic algorithm optimized triply compensated pulses in NMR spectroscopy. <i>Journal of Magnetic Resonance</i> , 2015, 260, 136-143.	2.1	17
89	Characterization of Calmodulin Binding to the Ryanodine Receptor by Solution and Solid-State NMR. <i>Biophysical Journal</i> , 2015, 108, 616a.	0.5	0
90	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

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91	Formalin Evokes Calcium Transients from the Endoplasmatic Reticulum. PLoS ONE, 2015, 10, e0123762.	2.5	16
92	Synchronous Opening and Closing Motions Are Essential for cAMP-Dependent Protein Kinase A Signaling. Structure, 2014, 22, 1735-1743.	3.3	55
93	The TLQP-21 Peptide Activates the G-Protein-Coupled Receptor C3aR1 via a Folding-upon-Binding Mechanism. Structure, 2014, 22, 1744-1753.	3.3	59
94	Development of a sensitive assay for SERCA activity using FRET detection of ADP. Analytical Methods, 2014, 6, 1468-1474.	2.7	1
95	NMR mapping of protein conformational landscapes using coordinated behavior of chemical shifts upon ligand binding. Physical Chemistry Chemical Physics, 2014, 16, 6508-6518.	2.8	54
96	Direct observation of the three regions in $\hat{\alpha}$ -synuclein that determine its membrane-bound behaviour. Nature Communications, 2014, 5, 3827.	12.8	357
97	FLAMEnGO 2.0: An enhanced fuzzy logic algorithm for structure-based assignment of methyl group resonances. Journal of Magnetic Resonance, 2014, 245, 17-23.	2.1	41
98	Structural Dynamics and Conformational Equilibria of SERCA Regulatory Proteins in Membranes by Solid-State NMR Restrained Simulations. Biophysical Journal, 2014, 106, 2566-2576.	0.5	20
99	Rational Structure-Based Design of PLN Mutants to Optimize Dephosphorylation and Tune Serca Function. Biophysical Journal, 2014, 106, 653a-654a.	0.5	0
100	On the Role of NMR Spectroscopy for Characterization of Antimicrobial Peptides. Methods in Molecular Biology, 2013, 1063, 159-180.	0.9	34
101	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.	2.8	32
102	Structural Dynamics and Topology of Phosphorylated Phospholamban Homopentamer Reveal Its Role in the Regulation of Calcium Transport. Structure, 2013, 21, 2119-2130.	3.3	41
103	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
104	Structure and dynamics of a primordial catalytic fold generated by in vitro evolution. Nature Chemical Biology, 2013, 9, 81-83.	8.0	80
105	Sensitivity and resolution enhancement of oriented solid-state NMR: Application to membrane proteins. Progress in Nuclear Magnetic Resonance Spectroscopy, 2013, 75, 50-68.	7.5	25
106	Structures of the Excited States of Phospholamban and Shifts in Their Populations upon Phosphorylation. Biochemistry, 2013, 52, 6684-6694.	2.5	24
107	Catch them if you can. Nature Chemical Biology, 2013, 9, 410-411.	8.0	5
108	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.	3.0	36

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109	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
110	Role of conformational entropy in the activity and regulation of the catalytic subunit of protein kinase <sc>A</sc>. <i>FEBS Journal</i> , 2013, 280, 5608-5615.	4.7	21
111	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
112	Tuning the structural coupling between the transmembrane and cytoplasmic domains of phospholamban to control sarcoplasmic reticulum Ca <sup>2+</sup> -ATPase (SERCA) function. <i>Journal of Muscle Research and Cell Motility</i> , 2012, 33, 485-492.	2.0	16
113	Phospholamban and its phosphorylated form require non-physiological transmembrane potentials to translocate ions. <i>Soft Matter</i> , 2012, 8, 3881.	2.7	8
114	Conformational Equilibrium of N-Myristoylated cAMP-Dependent Protein Kinase A by Molecular Dynamics Simulations. <i>Biochemistry</i> , 2012, 51, 10186-10196.	2.5	27
115	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
116	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
117	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
118	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
119	Dual Acquisition Magic Angle Spinning Solid State NMR Spectroscopy: Simultaneous Acquisition of Multidimensional Spectra of Biomacromolecules. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 2731-2735.	13.8	76
120	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
121	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
122	Activating and Deactivating Roles of Lipid Bilayers on the Ca <sup>2+</sup> -ATPase/Phospholamban Complex. <i>Biochemistry</i> , 2011, 50, 10367-10374.	2.5	57
123	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
124	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
125	Lipid-Mediated Folding/Unfolding of Phospholamban as a Regulatory Mechanism for the Sarcoplasmic Reticulum Ca <sup>2+</sup> -ATPase. <i>Journal of Molecular Biology</i> , 2011, 408, 755-765.	4.2	47
126	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



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127	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
128	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
129	Multidimensional oriented solid-state NMR experiments enable the sequential assignment of uniformly <sup>15</sup> N labeled integral membrane proteins in magnetically aligned lipid bilayers. <i>Journal of Biomolecular NMR</i> , 2011, 51, 339-346.	2.8	36
130	Templating Î±-amylase peptide inhibitors with organotin compounds. <i>Journal of Biological Inorganic Chemistry</i> , 2011, 16, 1197-1204.	2.6	3
131	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
132	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
133	Structural topology of phospholamban pentamer in lipid bilayers by a hybrid solution and solid-state NMR method. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9101-9106.	7.1	154
134	Dynamically committed, uncommitted, and quenched states encoded in protein kinase A revealed by NMR spectroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 6969-6974.	7.1	129
135	Lethal Arg9Cys phospholamban mutation hinders Ca <sup>2+</sup> -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
136	Improved resolution in dipolar NMR spectra using constant time evolution PISEMA experiment. <i>Chemical Physics Letters</i> , 2010, 494, 104-110.	2.6	8
137	Dynamics connect substrate recognition to catalysis in protein kinase A. <i>Nature Chemical Biology</i> , 2010, 6, 821-828.	8.0	182
138	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
139	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
140	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
141	Probing Slow Protein Dynamics by Adiabatic <sup>1</sup> H and <sup>2</sup> D NMR Experiments. <i>Journal of the American Chemical Society</i> , 2010, 132, 9979-9981.	13.7	39
142	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
143	Special issue on Membrane Protein Dynamics: Correlating Structure to Function. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2010, 1798, 65-67.	2.6	2
144	Spectroscopic Design of Phospholamban Mutants to Treat Heart Failure. <i>Biophysical Journal</i> , 2010, 98, 246a.	0.5	0

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145	What Can We Learn from a Small Regulatory Membrane Protein?. <i>Methods in Molecular Biology</i> , 2010, 654, 303-319.	0.9	8
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