

# Junji Iwahara

## List of Publications by Year in descending order

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86  
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citations

147801

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102487

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88  
docs citations

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4213  
citing authors

#	ARTICLE	IF	CITATIONS
1	Dynamics of Cations around DNA and Protein as Revealed by <sup>23</sup> Na Diffusion NMR Spectroscopy. <i>Analytical Chemistry</i> , 2022, 94, 2444-2452.	6.5	5
2	Protein Electrostatics Investigated through Paramagnetic NMR for Nonpolar Groups. <i>Journal of Physical Chemistry B</i> , 2022, 126, 2196-2202.	2.6	15
3	Negatively Charged Disordered Regions are Prevalent and Functionally Important Across Proteomes. <i>Journal of Molecular Biology</i> , 2022, 434, 167660.	4.2	19
4	Diffusion NMR-based comparison of electrostatic influences of DNA on various monovalent cations. <i>Biophysical Journal</i> , 2022, 121, 3562-3570.	0.5	4
5	Assessment of the Components of the Electrostatic Potential of Proteins in Solution: Comparing Experiment and Theory. <i>Journal of Physical Chemistry B</i> , 2022, 126, 4543-4554.	2.6	8
6	Slow Rotational Dynamics of Cytosine NH <sub>2</sub> Groups in Double-Stranded DNA. <i>Biochemistry</i> , 2022, 61, 1415-1418.	2.5	3
7	Discrete-state stochastic kinetic models for target DNA search by proteins: Theory and experimental applications. <i>Biophysical Chemistry</i> , 2021, 269, 106521.	2.8	14
8	De novo determination of near-surface electrostatic potentials by NMR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	26
9	Dynamic Autoinhibition of the HMGB1 Protein via Electrostatic Fuzzy Interactions of Intrinsically Disordered Regions. <i>Journal of Molecular Biology</i> , 2021, 433, 167122.	4.2	18
10	Experimental approaches for investigating ion atmospheres around nucleic acids and proteins. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 2279-2285.	4.1	12
11	Quantifying and visualizing weak interactions between anions and proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	18
12	Hindered Rotations of Protein Asparagine/Glutamine Side-Chain NH <sub>2</sub> Groups: Impact of Hydrogen Bonding with DNA. <i>Journal of Physical Chemistry Letters</i> , 2021, 12, 11378-11382.	4.6	1
13	Detecting Counterion Dynamics in DNA-Protein Association. <i>Angewandte Chemie</i> , 2020, 132, 1481-1484.	2.0	1
14	Detecting Counterion Dynamics in DNA-Protein Association. <i>Angewandte Chemie - International Edition</i> , 2020, 59, 1465-1468.	13.8	14
15	Racemic phosphorothioate as a tool for NMR investigations of protein-DNA complexes. <i>Journal of Biomolecular NMR</i> , 2020, 74, 421-429.	2.8	2
16	Dynamics of Ionic Interactions at Protein-Nucleic Acid Interfaces. <i>Accounts of Chemical Research</i> , 2020, 53, 1802-1810.	15.6	36
17	Hydrogen-exchange kinetics studied through analysis of self-decoupling of nuclear magnetic resonance. <i>Journal of Magnetic Resonance</i> , 2020, 312, 106687.	2.1	3
18	NMR Observation of Intermolecular Hydrogen Bonds between Protein Tyrosine Side-Chain OH and DNA Phosphate Groups. <i>Journal of Physical Chemistry B</i> , 2020, 124, 1065-1070.	2.6	16

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19	Mobility of Histidine Side Chains Analyzed with $^{15}\text{N}$ NMR Relaxation and Cross-Correlation Data: Insight into Zinc-Finger-DNA Interactions. <i>Journal of Physical Chemistry B</i> , 2019, 123, 3706-3710.	2.6	6
20	Experimental Evidence of Solvent-Separated Ion Pairs as Metastable States in Electrostatic Interactions of Biological Macromolecules. <i>Journal of Physical Chemistry Letters</i> , 2019, 10, 7937-7941.	4.6	9
21	NMR Methods for Characterizing the Basic Side Chains of Proteins: Electrostatic Interactions, Hydrogen Bonds, and Conformational Dynamics. <i>Methods in Enzymology</i> , 2019, 615, 285-332.	1.0	13
22	Direct detection of lysine side chain $\text{NH}_3^+$ in protein-heparin complexes using NMR spectroscopy. <i>Analyst</i> , 2018, 143, 635-638.	3.5	10
23	Impact of two-bond $^{15}\text{N}$ - $^{15}\text{N}$ scalar couplings on $^{15}\text{N}$ transverse relaxation measurements for arginine side chains of proteins. <i>Journal of Biomolecular NMR</i> , 2018, 71, 45-51.	2.8	5
24	NMR-based investigations into target DNA search processes of proteins. <i>Methods</i> , 2018, 148, 57-66.	3.8	12
25	Lysines and Arginines play non-redundant roles in mediating chemokine-glycosaminoglycan interactions. <i>Scientific Reports</i> , 2018, 8, 12289.	3.3	18
26	Discrete-State Kinetics Model for NMR-Based Analysis of Protein Translocation on DNA at Equilibrium. <i>Journal of Physical Chemistry B</i> , 2017, 121, 9548-9556.	2.6	5
27	Internal Motions of Basic Side Chains of the Antennapedia Homeodomain in the Free and DNA-Bound States. <i>Biochemistry</i> , 2017, 56, 5866-5869.	2.5	19
28	Potential role of DNA methylation as a facilitator of target search processes for transcription factors through interplay with methyl-CpG-binding proteins. <i>Nucleic Acids Research</i> , 2017, 45, 7751-7759.	14.5	16
29	A Unique and Simple Approach to Improve Sensitivity in $^{15}\text{N}$ -NMR Relaxation Measurements for $\text{NH}_3^+$ Groups: Application to a Protein-DNA Complex. <i>Molecules</i> , 2017, 22, 1355.	3.8	5
30	Stereospecific Effects of Oxygen-Sulfur Substitution in DNA Phosphate on Ion Pair Dynamics and Protein-DNA Affinity. <i>ChemBioChem</i> , 2016, 17, 1636-1642.	2.6	15
31	Changes in conformational dynamics of basic side chains upon protein-DNA association. <i>Nucleic Acids Research</i> , 2016, 44, 6961-6970.	14.5	51
32	Regulation of transcription factors via natural decoys in genomic DNA. <i>Transcription</i> , 2016, 7, 115-120.	3.1	28
33	NMR Scalar Couplings across Intermolecular Hydrogen Bonds between Zinc-Finger Histidine Side Chains and DNA Phosphate Groups. <i>Journal of Physical Chemistry B</i> , 2016, 120, 10679-10685.	2.6	12
34	Thermodynamic Additivity for Impacts of Base-Pair Substitutions on Association of the Egr-1 Zinc-Finger Protein with DNA. <i>Biochemistry</i> , 2016, 55, 6467-6474.	2.5	9
35	Residence Times of Molecular Complexes in Solution from NMR Data of Intermolecular Hydrogen-Bond Scalar Coupling. <i>Journal of Physical Chemistry Letters</i> , 2016, 7, 820-824.	4.6	13
36	Physicochemical Properties of Ion Pairs of Biological Macromolecules. <i>Biomolecules</i> , 2015, 5, 2435-2463.	4.0	30

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37	Structural impact of complete CpG methylation within target DNA on specific complex formation of the inducible transcription factor Egr-1. <i>FEBS Letters</i> , 2015, 589, 1748-1753.	2.8	39
38	Temperature Dependence of Internal Motions of Protein Side-Chain NH <sub>3</sub> <sup>+</sup> Groups: Insight into Energy Barriers for Transient Breakage of Hydrogen Bonds. <i>Biochemistry</i> , 2015, 54, 538-545.	2.5	23
39	A chemical approach for site-specific identification of NMR signals from protein side-chain NH <sub>3</sub> <sup>+</sup> groups forming intermolecular ion pairs in protein-nucleic acid complexes. <i>Journal of Biomolecular NMR</i> , 2015, 62, 1-5.	2.8	15
40	Dynamic Equilibria of Short-Range Electrostatic Interactions at Molecular Interfaces of Protein-DNA Complexes. <i>Journal of Physical Chemistry Letters</i> , 2015, 6, 2733-2737.	4.6	39
41	Balancing between affinity and speed in target DNA search by zinc-finger proteins via modulation of dynamic conformational ensemble. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E5142-9.	7.1	90
42	Influence of Quasi-Specific Sites on Kinetics of Target DNA Search by a Sequence-Specific DNA-Binding Protein. <i>Biochemistry</i> , 2015, 54, 6684-6691.	2.5	22
43	Entropic Enhancement of Protein-DNA Affinity by Oxygen-to-Sulfur Substitution in DNA Phosphate. <i>Biophysical Journal</i> , 2015, 109, 1026-1037.	0.5	46
44	Positive and negative impacts of nonspecific sites during target location by a sequence-specific DNA-binding protein: origin of the optimal search at physiological ionic strength. <i>Nucleic Acids Research</i> , 2014, 42, 7039-7046.	14.5	65
45	Stopped-Flow Fluorescence Kinetic Study of Protein Sliding and Intersegment Transfer in the Target DNA Search Process. <i>Journal of Molecular Biology</i> , 2014, 426, 230-244.	4.2	49
46	Effective strategy to assign 1H-15N heteronuclear correlation NMR signals from lysine side-chain NH <sub>3</sub> <sup>+</sup> groups of proteins at low temperature. <i>Journal of Biomolecular NMR</i> , 2014, 60, 23-27.	2.8	19
47	Real-time Kinetics of High-mobility Group Box 1 (HMGB1) Oxidation in Extracellular Fluids Studied by in Situ Protein NMR Spectroscopy. <i>Journal of Biological Chemistry</i> , 2013, 288, 11621-11627.	3.4	70
48	Direct Observation of the Ion-Pair Dynamics at a Protein-DNA Interface by NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2013, 135, 3613-3619.	13.7	57
49	NMR Studies on the Dynamics of Hydrogen Bonds and Ion Pairs Involving Lysine Side Chains of Proteins. <i>Advances in Protein Chemistry and Structural Biology</i> , 2013, 93, 37-80.	2.3	29
50	Speed-stability paradox in DNA-scanning by zinc-finger proteins. <i>Transcription</i> , 2013, 4, 58-61.	3.1	22
51	Asymmetrical roles of zinc fingers in dynamic DNA-scanning process by the inducible transcription factor Egr-1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E1724-E1732.	7.1	90
52	Dynamics of Lysine Side-Chain Amino Groups in a Protein Studied by Heteronuclear <sup>1</sup> H- <sup>15</sup> N NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2011, 133, 909-919.	13.7	71
53	Signature of Mobile Hydrogen Bonding of Lysine Side Chains from Long-Range <sup>15</sup> N- <sup>13</sup> C Scalar <i>J</i> -Couplings and Computation. <i>Journal of the American Chemical Society</i> , 2011, 133, 9192-9195.	13.7	40
54	Structure-Independent Analysis of the Breadth of the Positional Distribution of Disordered Groups in Macromolecules from Order Parameters for Long, Variable-Length Vectors Using NMR Paramagnetic Relaxation Enhancement. <i>Journal of the American Chemical Society</i> , 2010, 132, 13346-13356.	13.7	39

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55	NMR Studies of Translocation of the Zif268 Protein between Its Target DNA Sites. <i>Biochemistry</i> , 2010, 49, 7998-8005.	2.5	31
56	Theory, Practice, and Applications of Paramagnetic Relaxation Enhancement for the Characterization of Transient Low-Population States of Biological Macromolecules and Their Complexes. <i>Chemical Reviews</i> , 2009, 109, 4108-4139.	47.7	692
57	Observing in-phase single-quantum <sup>15</sup> N multiplets for groups with two-dimensional heteronuclear correlation spectroscopy. <i>Journal of Magnetic Resonance</i> , 2008, 194, 313-316.	2.1	11
58	Redox properties of the A $\alpha$ domain of the HMGB1 protein. <i>FEBS Letters</i> , 2008, 582, 3973-3978.	2.8	37
59	Direct Evidence for Deprotonation of a Lysine Side Chain Buried in the Hydrophobic Core of a Protein. <i>Journal of the American Chemical Society</i> , 2008, 130, 6714-6715.	13.7	52
60	Investigations of Intermediates in Macromolecular Binding Process Using NMR-PRE Method. <i>Seibutsu Butsuri</i> , 2008, 48, 018-022.	0.1	1
61	Intramolecular domain-domain association/dissociation and phosphoryl transfer in the mannitol transporter of <i>Escherichia coli</i> are not coupled. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 3153-3158.	7.1	22
62	TROSY-Based <i>z</i> -Exchange Spectroscopy: Application to the Determination of the Activation Energy for Intermolecular Protein Translocation between Specific Sites on Different DNA Molecules. <i>Journal of the American Chemical Society</i> , 2007, 129, 13232-13237.	13.7	43
63	Heteronuclear NMR Spectroscopy for Lysine NH <sub>3</sub> Groups in Proteins: Unique Effect of Water Exchange on <sup>15</sup> N Transverse Relaxation. <i>Journal of the American Chemical Society</i> , 2007, 129, 2971-2980.	13.7	97
64	Practical aspects of <sup>1</sup> H transverse paramagnetic relaxation enhancement measurements on macromolecules. <i>Journal of Magnetic Resonance</i> , 2007, 184, 185-195.	2.1	239
65	Elucidating transient macromolecular interactions using paramagnetic relaxation enhancement. <i>Current Opinion in Structural Biology</i> , 2007, 17, 603-616.	5.7	201
66	KUJIRA, a package of integrated modules for systematic and interactive analysis of NMR data directed to high-throughput NMR structure studies. <i>Journal of Biomolecular NMR</i> , 2007, 39, 31-52.	2.8	153
67	Direct Observation of Enhanced Translocation of a Homeodomain between DNA Cognate Sites by NMR Exchange Spectroscopy. <i>Journal of the American Chemical Society</i> , 2006, 128, 404-405.	13.7	89
68	Detecting transient intermediates in macromolecular binding by paramagnetic NMR. <i>Nature</i> , 2006, 440, 1227-1230.	27.8	349
69	Visualization of transient encounter complexes in protein-protein association. <i>Nature</i> , 2006, 444, 383-386.	27.8	397
70	Sensitivity improvement for correlations involving arginine side-chain <sup>15</sup> N/ <sup>1</sup> H resonances in multi-dimensional NMR experiments using broadband <sup>15</sup> N 180° pulses. <i>Journal of Biomolecular NMR</i> , 2006, 36, 251-257.	2.8	14
71	NMR structural and kinetic characterization of a homeodomain diffusing and hopping on nonspecific DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 15062-15067.	7.1	172
72	Compensating increases in protein backbone flexibility occur when the Dead ringer AT-rich interaction domain (ARID) binds DNA: A nitrogen-15 relaxation study. <i>Protein Science</i> , 2005, 14, 1140-1150.	7.6	7

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73	Accurate Determination of Leucine and Valine Side-chain Conformations using U-[15N/13C/2H]/[1H-(methine/methyl)-Leu/Val] Isotope Labeling, NOE Pattern Recognition, and Methine C <sup>1</sup> â€“H <sup>3</sup> /C <sup>2</sup> â€“H <sup>2</sup> Residual Dipolar Couplings: Application to the 34-kDa Enzyme II AChitobiose. <i>Journal of Biomolecular NMR</i> , 2005, 33, 105-121.	2.8	12
74	Characterization of Nonspecific Proteinâ”DNA Interactions by 1H Paramagnetic Relaxation Enhancement. <i>Journal of the American Chemical Society</i> , 2004, 126, 12800-12808.	13.7	76
75	Ensemble Approach for NMR Structure Refinement against 1H Paramagnetic Relaxation Enhancement Data Arising from a Flexible Paramagnetic Group Attached to a Macromolecule. <i>Journal of the American Chemical Society</i> , 2004, 126, 5879-5896.	13.7	317
76	EDTA-Derivatized Deoxythymidine as a Tool for Rapid Determination of Protein Binding Polarity to DNA by Intermolecular Paramagnetic Relaxation Enhancement. <i>Journal of the American Chemical Society</i> , 2003, 125, 6634-6635.	13.7	72
77	Regulation of Directionality in Bacteriophage $\lambda$ Site-specific Recombination: Structure of the Xis Protein. <i>Journal of Molecular Biology</i> , 2002, 324, 791-805.	4.2	46
78	Solution structure determination of the two DNA-binding domains in the <i>Schizosaccharomyces pombe</i> Abp1 protein by a combination of dipolar coupling and diffusion anisotropy restraints. <i>Journal of Biomolecular NMR</i> , 2002, 22, 333-347.	2.8	17
79	The structure of the Dead ringer-DNA complex reveals how AT-rich interaction domains (ARIDs) recognize DNA. <i>EMBO Journal</i> , 2002, 21, 1197-1209.	7.8	59
80	An Efficient NMR Experiment for Analyzing Sugar-Puckering in Unlabeled DNA: Application to the 26-kDa Dead Ringerâ€“DNA Complex. <i>Journal of Magnetic Resonance</i> , 2001, 153, 262-266.	2.1	4
81	Improved NMR spectra of a protein-DNA complex through rational mutagenesis and the application of a sensitivity optimized isotope-filtered NOESY experiment. <i>Journal of Biomolecular NMR</i> , 2001, 19, 231-241.	2.8	60
82	Assignment of the 1H, 13C and 15N signals of Sortase. <i>Journal of Biomolecular NMR</i> , 2001, 19, 379-380.	2.8	13
83	The Mu repressor-DNA complex contains an immobilized 'wing' within the minor groove. <i>Nature Structural Biology</i> , 2001, 8, 84-90.	9.7	17
84	Letter to the Editor: 1H, 13C and 15N resonance assignments of the AT-rich interaction domain from the Dead Ringer protein. , 1999, 15, 85-86.		3
85	Solution structure of the Eps15 homology domain of a human POB1 (partner of RalBP1). <i>FEBS Letters</i> , 1999, 442, 138-142.	2.8	29
86	Gaussian Spectral-Density Function for Protein Internal Motions. <i>Journal of Magnetic Resonance Series B</i> , 1996, 111, 281-284.	1.6	3