

# Koh Takeuchi

## List of Publications by Year in descending order

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101  
papers

3,272  
citations

136950

32  
h-index

168389

53  
g-index

106  
all docs

106  
docs citations

106  
times ranked

4513  
citing authors

#	ARTICLE	IF	CITATIONS
1	3CL Protease Inhibitors with an Electrophilic Arylketone Moiety as Anti-SARS-CoV-2 Agents. <i>Journal of Medicinal Chemistry</i> , 2022, 65, 2926-2939.	6.4	75
2	Oligo( N -methylalanine) as a Peptide-Based Molecular Scaffold with a Minimal Structure and High Density of Functionalizable Sites. <i>Angewandte Chemie - International Edition</i> , 2022, , .	13.8	2
3	Role of the Orphan Transporter SLC35E1 in the Nuclear Egress of Herpes Simplex Virus 1. <i>Journal of Virology</i> , 2022, , e0030622.	3.4	1
4	The GTP responsiveness of PI5P4K <sup>2</sup> evolved from a compromised trade-off between activity and specificity. <i>Structure</i> , 2022, 30, 886-899.e4.	3.3	3
5	Conformational Plasticity of Cyclic Ras-Inhibitor Peptides Defines Cell Permeabilization Activity. <i>Angewandte Chemie</i> , 2021, 133, 6641-6646.	2.0	1
6	Conformational Plasticity of Cyclic Ras-Inhibitor Peptides Defines Cell Permeabilization Activity. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 6567-6572.	13.8	12
7	Flexibility and Cell Permeability of Cyclic Ras-Inhibitor Peptides Revealed by the Coupled Nos <sup>3</sup> Hoover Equation. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 1921-1930.	5.4	5
8	Nonthermal excitation effects mediated by sub-terahertz radiation on hydrogen exchange in ubiquitin. <i>Biophysical Journal</i> , 2021, 120, 2386-2393.	0.5	5
9	Divergent Mechanisms Activating RAS and Small GTPases Through Post-translational Modification. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 707439.	3.5	13
10	Function-Related Dynamics in Multi-Spanning Helical Membrane Proteins Revealed by Solution NMR. <i>Membranes</i> , 2021, 11, 604.	3.0	2
11	Role of NMR in High Ordered Structure Characterization of Monoclonal Antibodies. <i>International Journal of Molecular Sciences</i> , 2021, 22, 46.	4.1	10
12	Prediction of Passive Membrane Permeability by Semi-Empirical Method Considering Viscous and Inertial Resistances and Different Rates of Conformational Change and Diffusion. <i>Molecular Informatics</i> , 2020, 39, e1900071.	2.5	4
13	Targeting the cryptic sites: NMR-based strategy to improve protein druggability by controlling the conformational equilibrium. <i>Science Advances</i> , 2020, 6, .	10.3	15
14	Mutation-induced change in chignolin stability from $\beta$ -turn to $\beta$ -turn. <i>RSC Advances</i> , 2020, 10, 22797-22808.	3.6	9
15	The role of NMR in leveraging dynamics and entropy in drug design. <i>Journal of Biomolecular NMR</i> , 2020, 74, 479-498.	2.8	8
16	Structural Fingerprints of an Intact Monoclonal Antibody Acquired under Formulated Storage Conditions via <sup>15</sup> N Direct Detection Nuclear Magnetic Resonance. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 5360-5366.	6.4	8
17	Spotlight on the Ballet of Proteins: The Structural Dynamic Properties of Proteins Illuminated by Solution NMR. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1829.	4.1	7
18	Transcription Factor Binding in Embryonic Stem Cells Is Constrained by DNA Sequence Repeat Symmetry. <i>Biophysical Journal</i> , 2020, 118, 2015-2026.	0.5	9

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19	Emerging solution NMR methods to illuminate the structural and dynamic properties of proteins. <i>Current Opinion in Structural Biology</i> , 2019, 58, 294-304.	5.7	26
20	Structure determination using solution NMR: Is it worth the effort?. <i>Journal of Magnetic Resonance</i> , 2019, 306, 195-201.	2.1	18
21	A BRET-based assay reveals collagenâ€™s Hsp47 interaction dynamics in the endoplasmic reticulum and small-molecule inhibition of this interaction. <i>Journal of Biological Chemistry</i> , 2019, 294, 15962-15972.	3.4	8
22	Anti-Tumor Potential of IMP Dehydrogenase Inhibitors: A Century-Long Story. <i>Cancers</i> , 2019, 11, 1346.	3.7	72
23	Aromatic 19F-13C TROSY: a background-free approach to probe biomolecular structure, function, and dynamics. <i>Nature Methods</i> , 2019, 16, 333-340.	19.0	82
24	Screening for inhibitor of episomal DNA identified dicumarol as a hepatitis B virus inhibitor. <i>PLoS ONE</i> , 2019, 14, e0212233.	2.5	8
25	Conformational equilibrium defines the variable induction of the multidrug-binding transcriptional repressor QacR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 19963-19972.	7.1	14
26	<sup>15</sup> N detection harnesses the slow relaxation property of nitrogen: Delivering enhanced resolution for intrinsically disordered proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E1710-E1719.	7.1	40
27	Mixed pyruvate labeling enables backbone resonance assignment of large proteins using a single experiment. <i>Nature Communications</i> , 2018, 9, 356.	12.8	13
28	Application of C-Terminal 7-Azabicyclo[2.2.1]heptane to Stabilize $\beta^2$ -Strand-like Extended Conformation of a Neighboring $\alpha$ -Amino Acid. <i>Journal of Organic Chemistry</i> , 2018, 83, 13063-13079.	3.2	14
29	Competing protein-protein interactions regulate binding of Hsp27 to its client protein tau. <i>Nature Communications</i> , 2018, 9, 4563.	12.8	82
30	Phosphoinositide binding by the PH domain in ceramide transfer protein (CERT) is inhibited by hyperphosphorylation of an adjacent serine-repeat motif. <i>Journal of Biological Chemistry</i> , 2018, 293, 11206-11217.	3.4	21
31	Structure-based integrated approach for analysis of the GTP metabolism. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2018, 74, a208-a208.	0.1	0
32	Quantitative Structureâ€“activity Relationship (QSAR) Models for Docking Score Correction. <i>Molecular Informatics</i> , 2017, 36, 1600013.	2.5	14
33	The crystal structure of a new O <sup>6</sup> -methylase from <i>Sphingobium</i> sp. strain SYKâ€™6. <i>FEBS Journal</i> , 2017, 284, 1855-1867.	4.7	19
34	A small-molecule compound inhibits a collagen-specific molecular chaperone and could represent a potential remedy for fibrosis. <i>Journal of Biological Chemistry</i> , 2017, 292, 20076-20085.	3.4	45
35	Dynamic equilibrium on DNA defines transcriptional regulation of a multidrug binding transcriptional repressor, LmrR. <i>Scientific Reports</i> , 2017, 7, 267.	3.3	8
36	Forbidden Coherence Transfer of 19F Nuclei to Quantitatively Measure the Dynamics of a CF3-Containing Ligand in Receptor-Bound States. <i>Molecules</i> , 2017, 22, 1492.	3.8	5

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37	Nitrogen-detected TROSY yields comparable sensitivity to proton-detected TROSY for non-deuterated, large proteins under physiological salt conditions. <i>Journal of Biomolecular NMR</i> , 2016, 64, 143-151.	2.8	34
38	Perspective: revisiting the field dependence of TROSY sensitivity. <i>Journal of Biomolecular NMR</i> , 2016, 66, 221-225.	2.8	19
39	Improvement of Ligand Affinity and Thermodynamic Properties by NMR-Based Evaluation of Local Dynamics and Surface Complementarity in the Receptor-Bound State. <i>Angewandte Chemie</i> , 2016, 128, 14826-14829.	2.0	2
40	Improvement of Ligand Affinity and Thermodynamic Properties by NMR-Based Evaluation of Local Dynamics and Surface Complementarity in the Receptor-Bound State. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 14606-14609.	13.8	7
41	Structural reverse genetics study of the PI5P4K <sup>2</sup> nucleotide complexes reveals the presence of the GTP bioenergetic system in mammalian cells. <i>FEBS Journal</i> , 2016, 283, 3556-3562.	4.7	10
42	Use of Multiple Cryoprotectants to Improve Diffraction Quality from Protein Crystals. <i>Crystal Growth and Design</i> , 2016, 16, 1565-1571.	3.0	10
43	The Lipid Kinase PI5P4K <sup>2</sup> Is an Intracellular GTP Sensor for Metabolism and Tumorigenesis. <i>Molecular Cell</i> , 2016, 61, 187-198.	9.7	62
44	Nitrogen detected TROSY at high field yields high resolution and sensitivity for protein NMR. <i>Journal of Biomolecular NMR</i> , 2015, 63, 323-331.	2.8	40
45	NMR resonance assignments of the catalytic domain of human serine/threonine phosphatase calcineurin in unligated and PVIVIT-peptide-bound states. <i>Biomolecular NMR Assignments</i> , 2015, 9, 201-205.	0.8	5
46	Increased resolution of aromatic cross peaks using alternate <sup>13</sup> C labeling and TROSY. <i>Journal of Biomolecular NMR</i> , 2015, 62, 291-301.	2.8	26
47	Structure-Based Development of a Protein-Protein Interaction Inhibitor Targeting Tumor Necrosis Factor Receptor-Associated Factor 6. <i>Journal of Medicinal Chemistry</i> , 2015, 58, 5674-5683.	6.4	9
48	Development of a method for reconstruction of crowded NMR spectra from undersampled time-domain data. <i>Journal of Biomolecular NMR</i> , 2015, 62, 31-41.	2.8	3
49	Suppression of Problematic Compound Oligomerization by Cosolubilization of Nondetergent Sulfobetaines. <i>ChemMedChem</i> , 2015, 10, 736-741.	3.2	1
50	Cross-saturation and transferred cross-saturation experiments. <i>Quarterly Reviews of Biophysics</i> , 2014, 47, 143-187.	5.7	22
51	Degradation of Activated K-Ras Orthologue via K-Ras-specific Lysine Residues Is Required for Cytokinesis. <i>Journal of Biological Chemistry</i> , 2014, 289, 3950-3959.	3.4	8
52	Functional dynamics of cell surface membrane proteins. <i>Journal of Magnetic Resonance</i> , 2014, 241, 86-96.	2.1	11
53	The LxVP and PxlIT NFAT Motifs Bind Jointly to Overlapping Epitopes on Calcineurin's Catalytic Domain Distant to the Regulatory Domain. <i>Structure</i> , 2014, 22, 1016-1027.	3.3	15
54	Allosteric enhancement of MAP kinase p38 <sup>α</sup> 's activity and substrate selectivity by docking interactions. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 704-711.	8.2	44

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55	Structure-Based Approach To Improve a Small-Molecule Inhibitor by the Use of a Competitive Peptide Ligand. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 2597-2601.	13.8	20
56	Dynamic multidrug recognition by multidrug transcriptional repressor LmrR. <i>Scientific Reports</i> , 2014, 4, 6922.	3.3	40
57	Rapid Identification of Ligand-Binding Sites by Using an Assignment-Free NMR Approach. <i>Journal of Medicinal Chemistry</i> , 2013, 56, 9342-9350.	6.4	8
58	Perdeuteration and methyl-selective <sup>1</sup> H, <sup>13</sup> C-labeling by using a <i>Kluyveromyces lactis</i> expression system. <i>Journal of Biomolecular NMR</i> , 2013, 57, 297-304.	2.8	25
59	A Homogeneous, High-Throughput Assay for Phosphatidylinositol 5-Phosphate 4-Kinase with a Novel, Rapid Substrate Preparation. <i>PLoS ONE</i> , 2013, 8, e54127.	2.5	42
60	Solution NMR Study on Functional Mechanism of Membrane Proteins. <i>Seibutsu Butsuri</i> , 2013, 53, 236-241.	0.1	0
61	Structural Basis for the Golgi Association by the Pleckstrin Homology Domain of the Ceramide Trafficking Protein (CERT)*. <i>Journal of Biological Chemistry</i> , 2012, 287, 33706-33718.	3.4	51
62	Functional dynamics of proteins revealed by solution NMR. <i>Current Opinion in Structural Biology</i> , 2012, 22, 660-669.	5.7	32
63	Functional Equilibrium of the KcsA Structure Revealed by NMR*. <i>Journal of Biological Chemistry</i> , 2012, 287, 39634-39641.	3.4	50
64	Structure of the VP16 transactivator target in the Mediator. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 410-415.	8.2	75
65	Protein-ligand docking guided by ligand pharmacophore-mapping experiment by NMR. <i>Journal of Molecular Graphics and Modelling</i> , 2011, 31, 20-27.	2.4	12
66	HNCA-TOCSY-CANH experiments with alternate <sup>13</sup> C- <sup>12</sup> C labeling: a set of 3D experiment with unique supra-sequential information for mainchain resonance assignment. <i>Journal of Biomolecular NMR</i> , 2011, 49, 17-26.	2.8	10
67	Speeding up direct <sup>15</sup> N detection: hCaN 2D NMR experiment. <i>Journal of Biomolecular NMR</i> , 2011, 51, 497-504.	2.8	23
68	Ubiquitination of K-Ras Enhances Activation and Facilitates Binding to Select Downstream Effectors. <i>Science Signaling</i> , 2011, 4, ra13.	3.6	152
69	NMR Analyses of the <sup>3</sup> Cl <sup>-</sup> Binding and Conformational Rearrangements of the Cytoplasmic Pore of G Protein-activated Inwardly Rectifying Potassium Channel 1 (GIRK1). <i>Journal of Biological Chemistry</i> , 2011, 286, 2215-2223.	3.4	48
70	CACA-TOCSY with alternate <sup>13</sup> C- <sup>12</sup> C labeling: a <sup>13</sup> C direct detection experiment for mainchain resonance assignment, dihedral angle information, and amino acid type identification. <i>Journal of Biomolecular NMR</i> , 2010, 47, 55-63.	2.8	23
71	Nitrogen-detected CAN and CON experiments as alternative experiments for main chain NMR resonance assignments. <i>Journal of Biomolecular NMR</i> , 2010, 47, 271-282.	2.8	34
72	Structural basis underlying the dual gate properties of KcsA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 6216-6221.	7.1	113

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73	Distinctive CD3 Heterodimeric Ectodomain Topologies Maximize Antigen-Triggered Activation of $\hat{1}\pm\hat{1}^2$ T Cell Receptors. <i>Journal of Immunology</i> , 2010, 185, 2951-2959.	0.8	34
74	Autoinhibitory Interaction in the Multidomain Adaptor Protein Nck: Possible Roles in Improving Specificity and Functional Diversity. <i>Biochemistry</i> , 2010, 49, 5634-5641.	2.5	11
75	Poisson-Gap Sampling and Forward Maximum Entropy Reconstruction for Enhancing the Resolution and Sensitivity of Protein NMR Data. <i>Journal of the American Chemical Society</i> , 2010, 132, 2145-2147.	13.7	308
76	High-Resolution 3D CANCA NMR Experiments for Complete Mainchain Assignments Using $C\langle\sup\rangle\hat{1}\pm\langle\sup\rangle$ Direct Detection. <i>Journal of the American Chemical Society</i> , 2010, 132, 2945-2951.	13.7	25
77	The $\hat{1}\pm\hat{1}^2$ T Cell Receptor Is an Anisotropic Mechanosensor. <i>Journal of Biological Chemistry</i> , 2009, 284, 31028-31037.	3.4	350
78	Backbone resonance assignments for the cytoplasmic regions of G protein-activated inwardly rectifying potassium channel 1 (GIRK1). <i>Biomolecular NMR Assignments</i> , 2009, 3, 125-128.	0.8	5
79	Cross-saturation and transferred cross-saturation experiments. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2009, 54, 123-140.	7.5	44
80	A Biophysical Mechanosensor Model for T-Cell Receptor Signaling. <i>Biophysical Journal</i> , 2009, 96, 368a.	0.5	0
81	Structural and Functional Evidence that Nck Interaction with CD3 $\hat{1}\mu$ Regulates T-Cell Receptor Activity. <i>Journal of Molecular Biology</i> , 2008, 380, 704-716.	4.2	43
82	Alternate <sup>13</sup> C <sup>12</sup> C Labeling for Complete Mainchain Resonance Assignments using $C\hat{1}\pm$ Direct-Detection with Applicability Toward Fast Relaxing Protein Systems. <i>Journal of the American Chemical Society</i> , 2008, 130, 17210-17211.	13.7	42
83	Amino Acid Selective Cross-Saturation Method for Identification of Proximal Residue Pairs in a Protein $\hat{1}$ Protein Complex. <i>Journal of the American Chemical Society</i> , 2008, 130, 12168-12176.	13.7	14
84	Identification and Characterization of the Slowly Exchanging pH-dependent Conformational Rearrangement in KcsA. <i>Journal of Biological Chemistry</i> , 2007, 282, 15179-15186.	3.4	78
85	Structure of the Calcineurin-NFAT Complex: Defining a T Cell Activation Switch Using Solution NMR and Crystal Coordinates. <i>Structure</i> , 2007, 15, 587-597.	3.3	49
86	1-13C amino acid selective labeling in a 2H15N background for NMR studies of large proteins. <i>Journal of Biomolecular NMR</i> , 2007, 38, 89-98.	2.8	49
87	Analysis of Surgical Outcome in Complex Double-Outlet Right Ventricle With Heterotaxy Syndrome or Complete Atrioventricular Canal Defect. <i>Annals of Thoracic Surgery</i> , 2006, 82, 146-152.	1.3	41
88	Solution Structure of the First Src Homology 3 Domain of Human Nck2. <i>Journal of Biomolecular NMR</i> , 2006, 34, 203-208.	2.8	14
89	NMR studies of protein interactions. <i>Current Opinion in Structural Biology</i> , 2006, 16, 109-117.	5.7	106
90	Backbone Resonance Assignments for the Fv Fragment of Catalytic Antibody 6D9 Complexed with a Transition State Analogue. <i>Journal of Biomolecular NMR</i> , 2005, 33, 282-282.	2.8	2

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91	Bead-linked Proteoliposomes: A Reconstitution Method for NMR Analyses of Membrane Protein-Ligand Interactions. <i>Journal of the American Chemical Society</i> , 2005, 127, 12021-12027.	13.7	25
92	Direct Determination of a Membrane-Peptide Interface Using the Nuclear Magnetic Resonance Cross-Saturation Method. <i>Biophysical Journal</i> , 2005, 89, 4051-4055.	0.5	14
93	Channel-forming Membrane Permeabilization by an Antibacterial Protein, Sapecin. <i>Journal of Biological Chemistry</i> , 2004, 279, 4981-4987.	3.4	68
94	Molecular basis of the high-affinity activation of type 1 ryanodine receptors by imperatoxin A. <i>Biochemical Journal</i> , 2004, 377, 385-394.	3.7	37
95	Structural Basis of the KcsA K <sup>+</sup> Channel and Agitoxin2 Pore-Blocking Toxin Interaction by Using the Transferred Cross-Saturation Method. <i>Structure</i> , 2003, 11, 1381-1392.	3.3	45
96	Solution Structure of $\gamma$ -Grammotoxin SIA, A Gating Modifier of P/Q and N-type Ca <sup>2+</sup> Channel. <i>Journal of Molecular Biology</i> , 2002, 321, 517-526.	4.2	47
97	Identification and Characterization of an Antibacterial Peptide of the 26-kDa Protease of <i>Sarcophaga peregrina</i> with Antibacterial Activity. <i>Journal of Biochemistry</i> , 2001, 130, 313-318.	1.7	9
98	Impaired Glucose Transporter Activity in Pressure-Overload Hypertrophy Is an Early Indicator of Progression to Failure. <i>Circulation</i> , 1999, 100, .	1.6	7
99	Improved Protection of the Hypertrophied Left Ventricle by Histidine-Containing Cardioplegia. <i>Circulation</i> , 1995, 92, 395-399.	1.6	28
100	Chapter 2. Low- $\gamma$ ; Nuclei Detection Experiments for Biomolecular NMR. <i>RSC Biomolecular Sciences</i> , 0, , 25-52.	0.4	9
101	Oligo( N -methylalanine) as a Peptide-Based Molecular Scaffold with a Minimal Structure and High Density of Functionalizable Sites. <i>Angewandte Chemie</i> , 0, , .	2.0	0