

# Congbao Kang

## List of Publications by Year in descending order

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120  
papers

3,974  
citations

126907

33  
h-index

138484

58  
g-index

122  
all docs

122  
docs citations

122  
times ranked

4473  
citing authors

#	ARTICLE	IF	CITATIONS
1	FKBP Family Proteins: Immunophilins with Versatile Biological Functions. <i>NeuroSignals</i> , 2008, 16, 318-325.	0.9	278
2	Structure of KCNE1 and Implications for How It Modulates the KCNQ1 Potassium Channel. <i>Biochemistry</i> , 2008, 47, 7999-8006.	2.5	183
3	Structure of the NS2B-NS3 protease from Zika virus after self-cleavage. <i>Nature Communications</i> , 2016, 7, 13410.	12.8	169
4	Membrane Topology and Function of Dengue Virus NS2A Protein. <i>Journal of Virology</i> , 2013, 87, 4609-4622.	3.4	162
5	Crystal structure of unlinked NS2B-NS3 protease from Zika virus. <i>Science</i> , 2016, 354, 1597-1600.	12.6	156
6	Targeting the Central Pocket in Human Transcription Factor TEAD as a Potential Cancer Therapeutic Strategy. <i>Structure</i> , 2015, 23, 2076-2086.	3.3	146
7	Characterization of Dengue Virus NS4A and NS4B Protein Interaction. <i>Journal of Virology</i> , 2015, 89, 3455-3470.	3.4	116
8	Waste water produced from an oilfield and continuous treatment with an oil-degrading bacterium. <i>Process Biochemistry</i> , 2005, 40, 873-877.	3.7	96
9	NMR Analysis of a Novel Enzymatically Active Unlinked Dengue NS2B-NS3 Protease Complex. <i>Journal of Biological Chemistry</i> , 2013, 288, 12891-12900.	3.4	93
10	Progress in Developing Inhibitors of SARS-CoV-2 3C-Like Protease. <i>Microorganisms</i> , 2020, 8, 1250.	3.6	90
11	Mapping the Interactions between the NS4B and NS3 Proteins of Dengue Virus. <i>Journal of Virology</i> , 2015, 89, 3471-3483.	3.4	83
12	Structural Dynamics of Zika Virus NS2B-NS3 Protease Binding to Dipeptide Inhibitors. <i>Structure</i> , 2017, 25, 1242-1250.e3.	3.3	83
13	Zika Virus Protease: An Antiviral Drug Target. <i>Trends in Microbiology</i> , 2017, 25, 797-808.	7.7	80
14	Application of microbial enhanced oil recovery technique to Daqing Oilfield. <i>Biochemical Engineering Journal</i> , 2002, 11, 197-199.	3.6	79
15	Dimerization of Flavivirus NS4B Protein. <i>Journal of Virology</i> , 2014, 88, 3379-3391.	3.4	77
16	Discovery of Dengue Virus NS4B Inhibitors. <i>Journal of Virology</i> , 2015, 89, 8233-8244.	3.4	77
17	Solution NMR study of integral membrane proteins. <i>Current Opinion in Chemical Biology</i> , 2011, 15, 560-569.	6.1	71
18	Structural Insights into the Inhibition of Zika Virus NS2B-NS3 Protease by a Small-Molecule Inhibitor. <i>Structure</i> , 2018, 26, 555-564.e3.	3.3	70

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19	Dengue NS2A Protein Orchestrates Virus Assembly. <i>Cell Host and Microbe</i> , 2019, 26, 606-622.e8.	11.0	68
20	Membrane topology of NS2B of dengue virus revealed by NMR spectroscopy. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2015, 1848, 2244-2252.	2.6	63
21	NMR solution structure of the N-terminal domain of hERG and its interaction with the S4-S5 linker. <i>Biochemical and Biophysical Research Communications</i> , 2010, 403, 126-132.	2.1	62
22	Preparation, Functional Characterization, and NMR Studies of Human KCNE1, a Voltage-Gated Potassium Channel Accessory Subunit Associated with Deafness and Long QT Syndrome. <i>Biochemistry</i> , 2007, 46, 11459-11472.	2.5	61
23	PGE1 and PGA1 bind to Nurr1 and activate its transcriptional function. <i>Nature Chemical Biology</i> , 2020, 16, 876-886.	8.0	51
24	Molecular characterization of FK-506 binding protein 38 and its potential regulatory role on the anti-apoptotic protein Bcl-2. <i>Biochemical and Biophysical Research Communications</i> , 2005, 337, 30-38.	2.1	48
25	Determinants of Dengue Virus NS4A Protein Oligomerization. <i>Journal of Virology</i> , 2015, 89, 6171-6183.	3.4	48
26	The flexible loop of Bcl-2 is required for molecular interaction with immunosuppressant FK-506 binding protein 38 (FKBP38). <i>FEBS Letters</i> , 2005, 579, 1469-1476.	2.8	46
27	Structural basis for KCNE3 modulation of potassium recycling in epithelia. <i>Science Advances</i> , 2016, 2, e1501228.	10.3	45
28	The Dengue Virus Replication Complex: From RNA Replication to Protein-Protein Interactions to Evasion of Innate Immunity. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1062, 115-129.	1.6	45
29	NMR Solution Structure of Human Vaccinia-related Kinase 1 (VRK1) Reveals the C-terminal Tail Essential for Its Structural Stability and Autocatalytic Activity. <i>Journal of Biological Chemistry</i> , 2011, 286, 22131-22138.	3.4	40
30	Solution structure of the transmembrane domain of the insulin receptor in detergent micelles. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2014, 1838, 1313-1321.	2.6	37
31	Functional Delivery of a Membrane Protein into Oocyte Membranes Using Bicelles. <i>Biochemistry</i> , 2010, 49, 653-655.	2.5	36
32	Discovery of Covalent Inhibitors Targeting the Transcriptional Enhanced Associate Domain Central Pocket. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 11972-11989.	6.4	36
33	Structural characterization of the linked NS2B-NS3 protease of Zika virus. <i>FEBS Letters</i> , 2017, 591, 2338-2347.	2.8	35
34	Structural and ligand-binding analysis of the YAP-binding domain of transcription factor TEAD4. <i>Biochemical Journal</i> , 2018, 475, 2043-2055.	3.7	35
35	Secondary structure and membrane topology of dengue virus NS4B N-terminal 125 amino acids. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2015, 1848, 3150-3157.	2.6	34
36	Structural and Functional Analyses of an Allosteric EYA2 Phosphatase Inhibitor That Has On-Target Effects in Human Lung Cancer Cells. <i>Molecular Cancer Therapeutics</i> , 2019, 18, 1484-1496.	4.1	34

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37	Mechanisms of Action for Small Molecules Revealed by Structural Biology in Drug Discovery. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5262.	4.1	34
38	Exploring the binding of peptidic West Nile virus NS2B-NS3 protease inhibitors by NMR. <i>Antiviral Research</i> , 2013, 97, 137-144.	4.1	33
39	Targeting the Bacterial Epitranscriptome for Antibiotic Development: Discovery of Novel tRNA-(N <sup>1</sup> G37) Methyltransferase (TrmD) Inhibitors. <i>ACS Infectious Diseases</i> , 2019, 5, 326-335.	3.8	33
40	Applications of In-Cell NMR in Structural Biology and Drug Discovery. <i>International Journal of Molecular Sciences</i> , 2019, 20, 139.	4.1	33
41	Solution NMR Spectroscopy in Target-Based Drug Discovery. <i>Molecules</i> , 2017, 22, 1399.	3.8	32
42	Reconstitution of KCNE1 into Lipid Bilayers: Comparing the Structural, Dynamic, and Activity Differences in Micelle and Vesicle Environments. <i>Biochemistry</i> , 2011, 50, 10851-10859.	2.5	31
43	Expression, purification, and initial structural characterization of nonstructural protein 2B, an integral membrane protein of Dengue-2 virus, in detergent micelles. <i>Protein Expression and Purification</i> , 2011, 80, 169-175.	1.3	30
44	Drug Design For Flavivirus Proteases: What Are We Missing?. <i>Current Pharmaceutical Design</i> , 2014, 20, 3422-3427.	1.9	30
45	Secondary Structure and Membrane Topology of the Full-Length Dengue Virus NS4B in Micelles. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 12068-12072.	13.8	28
46	Biomimetic membrane platform containing hERG potassium channel and its application to drug screening. <i>Analyst</i> , 2013, 138, 2007.	3.5	27
47	Mechanistic basis for LQT1 caused by S3 mutations in the KCNQ1 subunit of <i>I<sub>Ks</sub></i> . <i>Journal of General Physiology</i> , 2010, 135, 433-448.	1.9	26
48	An NMR study of the N-terminal domain of wild-type hERG and a T65P trafficking deficient hERG mutant. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 2557-2565.	2.6	26
49	Structural Insight into the Transmembrane Domain and the Juxtamembrane Region of the Erythropoietin Receptor in Micelles. <i>Biophysical Journal</i> , 2014, 107, 2325-2336.	0.5	26
50	Identification of covalent active site inhibitors of dengue virus protease. <i>Drug Design, Development and Therapy</i> , 2015, 9, 6389.	4.3	25
51	The N-terminal domain of tumor suppressor p53 is involved in the molecular interaction with the anti-apoptotic protein Bcl-Xl. <i>Biochemical and Biophysical Research Communications</i> , 2006, 341, 938-944.	2.1	23
52	NMR structural study of the intracellular loop 3 of the serotonin 5-HT1A receptor and its interaction with calmodulin. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2011, 1808, 2224-2232.	2.6	22
53	Solution structure of a human minimembrane protein Ost4, a subunit of the oligosaccharyltransferase complex. <i>Biochemical and Biophysical Research Communications</i> , 2011, 409, 572-576.	2.1	22
54	<sup>19</sup> F-NMR in Target-based Drug Discovery. <i>Current Medicinal Chemistry</i> , 2019, 26, 4964-4983.	2.4	22

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55	Solution structure of the transmembrane domain of the mouse erythropoietin receptor in detergent micelles. <i>Scientific Reports</i> , 2015, 5, 13586.	3.3	21
56	Secondary structure and membrane topology of dengue virus NS4A protein in micelles. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2018, 1860, 442-450.	2.6	21
57	Expression, purification, and molecular characterization of <i>Plasmodium falciparum</i> FK506-binding protein 35 (PfkBP35). <i>Protein Expression and Purification</i> , 2007, 53, 179-185.	1.3	19
58	Solution NMR Study of the Transmembrane Domain of Single-Span Membrane Proteins: Opportunities and Strategies. <i>Current Protein and Peptide Science</i> , 2012, 13, 585-600.	1.4	19
59	Molecular Characterization of the Recombinant A-chain of a Type II Ribosome-Inactivating Protein (RIP) from <i>Viscum album coloratum</i> and Structural Basis on its Ribosome-Inactivating Activity and the Sugar-binding Properties of the B-chain. <i>BMB Reports</i> , 2006, 39, 560-570.	2.4	18
60	The solution structure of the S4â€‘S5 linker of the hERG potassium channel. <i>Journal of Peptide Science</i> , 2012, 18, 140-145.	1.4	17
61	Lyso-myristoyl phosphatidylcholine micelles sustain the activity of Dengue non-structural (NS) protein 3 protease domain fused with the full-length NS2B. <i>Protein Expression and Purification</i> , 2013, 92, 156-162.	1.3	17
62	Structural transition in Bcl-xL and its potential association with mitochondrial calcium ion transport. <i>Scientific Reports</i> , 2015, 5, 10609.	3.3	17
63	<sup>1</sup> H, <sup>13</sup> C and <sup>15</sup> N chemical shift assignments for the N-terminal domain of the voltage-gated potassium channel-hERG. <i>Biomolecular NMR Assignments</i> , 2010, 4, 211-213.	0.8	16
64	<i>Escherichia coli</i> Topoisomerase IV E Subunit and an Inhibitor Binding Mode Revealed by NMR Spectroscopy. <i>Journal of Biological Chemistry</i> , 2016, 291, 17743-17753.	3.4	15
65	Characterization of molecular interactions between Zika virus protease and peptides derived from the C-terminus of NS2B. <i>Biochemical and Biophysical Research Communications</i> , 2018, 503, 691-696.	2.1	15
66	Identification and structural characterization of small molecule fragments targeting Zika virus NS2B-NS3 protease. <i>Antiviral Research</i> , 2020, 175, 104707.	4.1	15
67	Perspectives on Fragment-based Drug Discovery: A Strategy Applicable to Diverse Targets. <i>Current Topics in Medicinal Chemistry</i> , 2021, 21, 1099-1112.	2.1	15
68	The impact of window functions on NMR-based paramagnetic relaxation enhancement measurements in membrane proteins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2010, 1798, 140-149.	2.6	14
69	Application of Fragmentâ€‘Based Drug Discovery against DNA Gyraseâ€‘. <i>ChemPlusChem</i> , 2015, 80, 1250-1254.2.8		14
70	Expression, purification of Zika virus membrane protein-NS2B in detergent micelles for NMR studies. <i>Protein Expression and Purification</i> , 2019, 154, 1-6.	1.3	13
71	Structure of the C-terminal Region of the Frizzled Receptor 1 in Detergent Micelles. <i>Molecules</i> , 2013, 18, 8579-8590.	3.8	12
72	NMR structural characterization of the Nâ€‘terminal active domain of the gyrase B subunit from <i>Pseudomonas aeruginosa</i> and its complex with an inhibitor. <i>FEBS Letters</i> , 2015, 589, 2683-2689.	2.8	12

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73	Elucidating the bactericidal mechanism of action of the linear antimicrobial tetrapeptide BRBR-NH <sub>2</sub> . <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2018, 1860, 1517-1527.	2.6	12
74	Structure of the transmembrane domain of human nicastrin-a component of $\beta$ -secretase. <i>Scientific Reports</i> , 2016, 6, 19522.	3.3	11
75	A Practical Perspective on the Roles of Solution NMR Spectroscopy in Drug Discovery. <i>Molecules</i> , 2020, 25, 2974.	3.8	11
76	Insights into Structures and Dynamics of Flavivirus Proteases from NMR Studies. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2527.	4.1	11
77	West Nile virus protease activity in detergent solutions and application for affinity tag removal. <i>Analytical Biochemistry</i> , 2013, 435, 44-46.	2.4	10
78	Functional role of the flexible N-terminal extension of FKBP38 in catalysis. <i>Scientific Reports</i> , 2013, 3, 2985.	3.3	10
79	Solution structure of the cyclic-nucleotide binding homology domain of a KCNH channel. <i>Journal of Structural Biology</i> , 2014, 186, 68-74.	2.8	10
80	Structure and Dynamics of Zika Virus Protease and Its Insights into Inhibitor Design. <i>Biomedicines</i> , 2021, 9, 1044.	3.2	10
81	Purification and structural characterization of the voltage-sensor domain of the hERG potassium channel. <i>Protein Expression and Purification</i> , 2012, 86, 98-104.	1.3	9
82	The Natively Disordered Loop of Bcl-2 Undergoes Phosphorylation-Dependent Conformational Change and Interacts with Pin1. <i>PLoS ONE</i> , 2012, 7, e52047.	2.5	9
83	Insight into the molecular interaction between the cyclic nucleotide-binding homology domain and the eag domain of the hERG channel. <i>FEBS Letters</i> , 2014, 588, 2782-2788.	2.8	9
84	Structure of the Cyclic Nucleotide-Binding Homology Domain of the hERG Channel and Its Insight into Type 2 Long QT Syndrome. <i>Scientific Reports</i> , 2016, 6, 23712.	3.3	9
85	Backbone assignment of the N-terminal 24-kDa fragment of Escherichia coli topoisomerase IV ParE subunit. <i>Biomolecular NMR Assignments</i> , 2016, 10, 135-138.	0.8	9
86	Targeting EYA2 tyrosine phosphatase activity in glioblastoma stem cells induces mitotic catastrophe. <i>Journal of Experimental Medicine</i> , 2021, 218, .	8.5	9
87	Structures and Dynamics of Dengue Virus Nonstructural Membrane Proteins. <i>Membranes</i> , 2022, 12, 231.	3.0	9
88	Expression and purification of the p75 neurotrophin receptor transmembrane domain using a ketosteroid isomerase tag. <i>Microbial Cell Factories</i> , 2012, 11, 45.	4.0	8
89	West Nile Virus (WNV) protease and membrane interactions revealed by NMR spectroscopy. <i>Biochemical and Biophysical Research Communications</i> , 2012, 423, 799-804.	2.1	7
90	<sup>1</sup> H, <sup>13</sup> C and <sup>15</sup> N chemical shift assignments for an intracellular proteinase inhibitor of <i>Bacillus subtilis</i> . <i>Biomolecular NMR Assignments</i> , 2013, 7, 129-132.	0.8	7

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91	Characterization of the interaction between Escherichia coli topoisomerase IV E subunit and an ATP competitive inhibitor. <i>Biochemical and Biophysical Research Communications</i> , 2015, 467, 961-966.	2.1	7
92	Biophysical Studies of Bacterial Topoisomerases Substantiate Their Binding Modes to an Inhibitor. <i>Biophysical Journal</i> , 2015, 109, 1969-1977.	0.5	6
93	Selection of suitable detergents for obtaining an active dengue protease in its natural form from E. coli. <i>Protein Expression and Purification</i> , 2016, 121, 141-148.	1.3	6
94	Secondary structure and topology of the transmembrane domain of Syndecan-2 in detergent micelles. <i>FEBS Letters</i> , 2019, 593, 554-561.	2.8	6
95	Secondary Structure and Membrane Topology of the Full-Length Dengue Virus NS4B in Micelles. <i>Angewandte Chemie</i> , 2016, 128, 12247-12251.	2.0	5
96	Breakthroughs in Medicinal Chemistry: New Targets and Mechanisms, New Drugs, New Hopes-7. <i>Molecules</i> , 2020, 25, 2968.	3.8	5
97	<sup>1</sup> H, <sup>13</sup> C and <sup>15</sup> N chemical shift assignments for the N-terminal PAS domain of the KCNH channel from Zebrafish. <i>Biomolecular NMR Assignments</i> , 2014, 8, 165-168.	0.8	4
98	Backbone resonance assignment for the N-terminal region of bacterial tRNA-(N1G37) methyltransferase. <i>Biomolecular NMR Assignments</i> , 2019, 13, 49-53.	0.8	4
99	Probing biological mechanisms with chemical tools. <i>Pharmacological Research</i> , 2020, 153, 104656.	7.1	4
100	Structure-activity relationship studies of allosteric inhibitors of EYA2 tyrosine phosphatase. <i>Protein Science</i> , 2022, 31, 422-431.	7.6	4
101	Secondary Structures of the Transmembrane Domain of SARS-CoV-2 Spike Protein in Detergent Micelles. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1040.	4.1	4
102	Structural insight into the transmembrane segments 3 and 4 of the hERG potassium channel. <i>Journal of Peptide Science</i> , 2014, 20, 935-944.	1.4	3
103	Structural analysis of the S4-S5 linker of the human KCNQ1 potassium channel. <i>Biochemical and Biophysical Research Communications</i> , 2015, 456, 410-414.	2.1	3
104	<sup>1</sup> H, <sup>13</sup> C and <sup>15</sup> N chemical shift assignments for the cyclic-nucleotide binding homology domain of a KCNH channel. <i>Biomolecular NMR Assignments</i> , 2015, 9, 55-58.	0.8	3
105	Backbone resonance assignments for the SET domain of human methyltransferase NSD3 in complex with its cofactor. <i>Biomolecular NMR Assignments</i> , 2017, 11, 225-229.	0.8	2
106	Erythropoietin Receptor Structural Domains. <i>Vitamins and Hormones</i> , 2017, 105, 1-17.	1.7	2
107	Secondary structures, dynamics, and DNA binding of the homeodomain of human SIX1. <i>Journal of Peptide Science</i> , 2022, 28, e3376.	1.4	2
108	<sup>1</sup> H, <sup>13</sup> C, and <sup>15</sup> N resonance assignments of FK506-binding domain of Plasmodium falciparum FKBP35. <i>Biomolecular NMR Assignments</i> , 2007, 1, 27-28.	0.8	1

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109	A Phenotypic Screen for Small-Molecule Inhibitors of Constitutively Active Mutant Thrombopoietin Receptor Implicated in Myeloproliferative Neoplasms. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2016, 19, 824-833.	1.1	1
110	$^1\text{H}$ , $^{15}\text{N}$ and $^{13}\text{C}$ resonance assignments of the Q61H mutant of human KRAS bound to GDP. <i>Biomolecular NMR Assignments</i> , 2021, , .	0.8	1
111	$^1\text{H}$ , $^{13}\text{C}$ and $^{15}\text{N}$ resonance assignments of the first BIR domain of cellular inhibitor of apoptosis protein 1. <i>Biomolecular NMR Assignments</i> , 2022, , 1.	0.8	1
112	Mechanistic insights into non-immunosuppressive immunophilin ligands as potential antimalarial therapeutics. <i>Malaria Journal</i> , 2010, 9, .	2.3	0
113	Structural Studies on the Conformation of Human KCNEL1 Membrane Protein via Electron Paramagnetic Resonance Spectroscopy. <i>Biophysical Journal</i> , 2011, 100, 144a.	0.5	0
114	The Structural, Dynamic, and Functional Changes in the KCNE1 Membrane Protein Between Detergent Micelles and Lipid Bilayers. <i>Biophysical Journal</i> , 2011, 100, 144a.	0.5	0
115	Probing the Structural and Dynamic Properties of KCNE1 using Site-Directed Spin Labeling EPR Spectroscopy. <i>Biophysical Journal</i> , 2012, 102, 406a.	0.5	0
116	EPR Spectroscopic Distance Measurements of the KCNE1 Membrane Protein in Micelles and Lipid Bilayers. <i>Biophysical Journal</i> , 2012, 102, 406a.	0.5	0
117	NMR Structural Study of the Domains of the KCNH Channels and its Insight into Channel Gating. <i>Biophysical Journal</i> , 2014, 106, 437a.	0.5	0
118	NMR Structural Characterization for Proteases of Dengue and West Nile Viruses and its Insight into Drug Discovery. <i>Biophysical Journal</i> , 2015, 108, 375a.	0.5	0
119	Characterization of the Molecular Interactions between ParE/Cyrb and an Inhibitor and its Insight into Developing Antibacterial Agents. <i>Biophysical Journal</i> , 2016, 110, 542a.	0.5	0
120	Backbone resonance assignment for the full length tRNA-(N1G37) methyltransferase of <i>Pseudomonas aeruginosa</i> . <i>Biomolecular NMR Assignments</i> , 2019, 13, 327-332.	0.8	0