

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 | Secondary structures, dynamics, and DNA binding of the homeodomain of human SIX1. <i>Journal of Peptide Science</i> , 2022, 28, e3376. | 1.4 | 2 |
| 2 | Structure-activity relationship studies of allosteric inhibitors of EYA2 tyrosine phosphatase. <i>Protein Science</i> , 2022, 31, 422-431. | 7.6 | 4 |
| 3 | 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 |
| 4 | ¹ H, ¹³ C and ¹⁵ 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 |
| 5 | Structures and Dynamics of Dengue Virus Nonstructural Membrane Proteins. <i>Membranes</i> , 2022, 12, 231. | 3.0 | 9 |
| 6 | Structure and Dynamics of Zika Virus Protease and Its Insights into Inhibitor Design. <i>Biomedicines</i> , 2021, 9, 1044. | 3.2 | 10 |
| 7 | 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 |
| 8 | Targeting EYA2 tyrosine phosphatase activity in glioblastoma stem cells induces mitotic catastrophe. <i>Journal of Experimental Medicine</i> , 2021, 218, . | 8.5 | 9 |
| 9 | ¹ H, ¹⁵ N and ¹³ C resonance assignments of the Q61H mutant of human KRAS bound to GDP. <i>Biomolecular NMR Assignments</i> , 2021, , . | 0.8 | 1 |
| 10 | 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 |
| 11 | 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 |
| 12 | Progress in Developing Inhibitors of SARS-CoV-2 3C-Like Protease. <i>Microorganisms</i> , 2020, 8, 1250. | 3.6 | 90 |
| 13 | A Practical Perspective on the Roles of Solution NMR Spectroscopy in Drug Discovery. <i>Molecules</i> , 2020, 25, 2974. | 3.8 | 11 |
| 14 | Breakthroughs in Medicinal Chemistry: New Targets and Mechanisms, New Drugs, New Hopes. <i>Molecules</i> , 2020, 25, 2968. | 3.8 | 5 |
| 15 | Identification and structural characterization of small molecule fragments targeting Zika virus NS2B-NS3 protease. <i>Antiviral Research</i> , 2020, 175, 104707. | 4.1 | 15 |
| 16 | Probing biological mechanisms with chemical tools. <i>Pharmacological Research</i> , 2020, 153, 104656. | 7.1 | 4 |
| 17 | Insights into Structures and Dynamics of Flavivirus Proteases from NMR Studies. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2527. | 4.1 | 11 |
| 18 | PGE1 and PGA1 bind to Nurr1 and activate its transcriptional function. <i>Nature Chemical Biology</i> , 2020, 16, 876-886. | 8.0 | 51 |

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|----|---|------|-----------|
| 19 | 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 |
| 20 | Dengue NS2A Protein Orchestrates Virus Assembly. <i>Cell Host and Microbe</i> , 2019, 26, 606-622.e8. | 11.0 | 68 |
| 21 | Targeting the Bacterial Epitranscriptome for Antibiotic Development: Discovery of Novel tRNA-(N ¹ G37) Methyltransferase (TrmD) Inhibitors. <i>ACS Infectious Diseases</i> , 2019, 5, 326-335. | 3.8 | 33 |
| 22 | 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 |
| 23 | 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 |
| 24 | Applications of In-Cell NMR in Structural Biology and Drug Discovery. <i>International Journal of Molecular Sciences</i> , 2019, 20, 139. | 4.1 | 33 |
| 25 | 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 |
| 26 | 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 |
| 27 | ¹⁹ F-NMR in Target-based Drug Discovery. <i>Current Medicinal Chemistry</i> , 2019, 26, 4964-4983. | 2.4 | 22 |
| 28 | 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 |
| 29 | 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 |
| 30 | Elucidating the bactericidal mechanism of action of the linear antimicrobial tetrapeptide BRBR-NH2. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2018, 1860, 1517-1527. | 2.6 | 12 |
| 31 | 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 |
| 32 | 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 |
| 33 | 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 |
| 34 | Structural characterization of the linked NS2B-NS3 protease of Zika virus. <i>FEBS Letters</i> , 2017, 591, 2338-2347. | 2.8 | 35 |
| 35 | 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 |
| 36 | Zika Virus Protease: An Antiviral Drug Target. <i>Trends in Microbiology</i> , 2017, 25, 797-808. | 7.7 | 80 |

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|----|---|------|-----------|
| 37 | Structural Dynamics of Zika Virus NS2B-NS3 Protease Binding to Dipeptide Inhibitors. <i>Structure</i> , 2017, 25, 1242-1250.e3. | 3.3 | 83 |
| 38 | Solution NMR Spectroscopy in Target-Based Drug Discovery. <i>Molecules</i> , 2017, 22, 1399. | 3.8 | 32 |
| 39 | Erythropoietin Receptor Structural Domains. <i>Vitamins and Hormones</i> , 2017, 105, 1-17. | 1.7 | 2 |
| 40 | Structure of the transmembrane domain of human nicastrin-a component of β 3-secretase. <i>Scientific Reports</i> , 2016, 6, 19522. | 3.3 | 11 |
| 41 | Crystal structure of unlinked NS2B-NS3 protease from Zika virus. <i>Science</i> , 2016, 354, 1597-1600. | 12.6 | 156 |
| 42 | Structural basis for KCNE3 modulation of potassium recycling in epithelia. <i>Science Advances</i> , 2016, 2, e1501228. | 10.3 | 45 |
| 43 | 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 |
| 44 | Characterization of the Molecular Interactions between ParE/GyrB and an Inhibitor and its Insight into Developing Antibacterial Agents. <i>Biophysical Journal</i> , 2016, 110, 542a. | 0.5 | 0 |
| 45 | Escherichia coli 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 |
| 46 | 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 |
| 47 | Structure of the NS2B-NS3 protease from Zika virus after self-cleavage. <i>Nature Communications</i> , 2016, 7, 13410. | 12.8 | 169 |
| 48 | 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 |
| 49 | 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 |
| 50 | 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 |
| 51 | 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 |
| 52 | Structural transition in Bcl-xL and its potential association with mitochondrial calcium ion transport. <i>Scientific Reports</i> , 2015, 5, 10609. | 3.3 | 17 |
| 53 | Solution structure of the transmembrane domain of the mouse erythropoietin receptor in detergent micelles. <i>Scientific Reports</i> , 2015, 5, 13586. | 3.3 | 21 |
| 54 | 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 |

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|----|--|-----|-----------|
| 55 | Application of Fragment-Based Drug Discovery against DNA Gyrase...B. ChemPlusChem, 2015, 80, 1250-1254.2.8 | | 14 |
| 56 | Identification of covalent active site inhibitors of dengue virus protease. Drug Design, Development and Therapy, 2015, 9, 6389. | 4.3 | 25 |
| 57 | Discovery of Dengue Virus NS4B Inhibitors. Journal of Virology, 2015, 89, 8233-8244. | 3.4 | 77 |
| 58 | Characterization of Dengue Virus NS4A and NS4B Protein Interaction. Journal of Virology, 2015, 89, 3455-3470. | 3.4 | 116 |
| 59 | Mapping the Interactions between the NS4B and NS3 Proteins of Dengue Virus. Journal of Virology, 2015, 89, 3471-3483. | 3.4 | 83 |
| 60 | Membrane topology of NS2B of dengue virus revealed by NMR spectroscopy. Biochimica Et Biophysica Acta - Biomembranes, 2015, 1848, 2244-2252. | 2.6 | 63 |
| 61 | Determinants of Dengue Virus NS4A Protein Oligomerization. Journal of Virology, 2015, 89, 6171-6183. | 3.4 | 48 |
| 62 | Secondary structure and membrane topology of dengue virus NS4B N-terminal 125 amino acids. Biochimica Et Biophysica Acta - Biomembranes, 2015, 1848, 3150-3157. | 2.6 | 34 |
| 63 | Targeting the Central Pocket in Human Transcription Factor TEAD as a Potential Cancer Therapeutic Strategy. Structure, 2015, 23, 2076-2086. | 3.3 | 146 |
| 64 | Characterization of the interaction between Escherichia coli topoisomerase IV E subunit and an ATP competitive inhibitor. Biochemical and Biophysical Research Communications, 2015, 467, 961-966. | 2.1 | 7 |
| 65 | Biophysical Studies of Bacterial Topoisomerases Substantiate Their Binding Modes to an Inhibitor. Biophysical Journal, 2015, 109, 1969-1977. | 0.5 | 6 |
| 66 | NMR structural characterization of the N-terminal active domain of the gyrase B subunit from <i>Pseudomonas aeruginosa</i> and its complex with an inhibitor. FEBS Letters, 2015, 589, 2683-2689. | 2.8 | 12 |
| 67 | Structural analysis of the S4-S5 linker of the human KCNQ1 potassium channel. Biochemical and Biophysical Research Communications, 2015, 456, 410-414. | 2.1 | 3 |
| 68 | ¹ H, ¹³ C and ¹⁵ N chemical shift assignments for the cyclic-nucleotide binding homology domain of a KCNH channel. Biomolecular NMR Assignments, 2015, 9, 55-58. | 0.8 | 3 |
| 69 | Structural insight into the transmembrane segments 3 and 4 of the hERG potassium channel. Journal of Peptide Science, 2014, 20, 935-944. | 1.4 | 3 |
| 70 | ¹ H, ¹³ C and ¹⁵ N chemical shift assignments for the N-terminal PAS domain of the KCNH channel from Zebrafish. Biomolecular NMR Assignments, 2014, 8, 165-168. | 0.8 | 4 |
| 71 | Solution structure of the transmembrane domain of the insulin receptor in detergent micelles. Biochimica Et Biophysica Acta - Biomembranes, 2014, 1838, 1313-1321. | 2.6 | 37 |
| 72 | Dimerization of Flavivirus NS4B Protein. Journal of Virology, 2014, 88, 3379-3391. | 3.4 | 77 |

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|----|---|-----|-----------|
| 73 | 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 |
| 74 | 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 |
| 75 | 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 |
| 76 | 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 |
| 77 | Drug Design For Flavivirus Proteases: What Are We Missing?. <i>Current Pharmaceutical Design</i> , 2014, 20, 3422-3427. | 1.9 | 30 |
| 78 | ¹ H, ¹³ C and ¹⁵ 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 |
| 79 | 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 |
| 80 | 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 |
| 81 | Biomimetic membrane platform containing hERG potassium channel and its application to drug screening. <i>Analyst</i> , The, 2013, 138, 2007. | 3.5 | 27 |
| 82 | Membrane Topology and Function of Dengue Virus NS2A Protein. <i>Journal of Virology</i> , 2013, 87, 4609-4622. | 3.4 | 162 |
| 83 | 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 |
| 84 | 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 |
| 85 | Functional role of the flexible N-terminal extension of FKBP38 in catalysis. <i>Scientific Reports</i> , 2013, 3, 2985. | 3.3 | 10 |
| 86 | Structure of the C-terminal Region of the Frizzled Receptor 1 in Detergent Micelles. <i>Molecules</i> , 2013, 18, 8579-8590. | 3.8 | 12 |
| 87 | 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 |
| 88 | 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 |
| 89 | 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 |
| 90 | 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 |

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|-----|---|-----|-----------|
| 91 | 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 |
| 92 | EPR Spectroscopic Distance Measurements of the KCNE1 Membrane Protein in Micelles and Lipid Bilayers. <i>Biophysical Journal</i> , 2012, 102, 406a. | 0.5 | 0 |
| 93 | 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 |
| 94 | The solution structure of the S4-S5 linker of the hERG potassium channel. <i>Journal of Peptide Science</i> , 2012, 18, 140-145. | 1.4 | 17 |
| 95 | 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 |
| 96 | Structural Studies on the Conformation of Human KCNE1 Membrane Protein via Electron Paramagnetic Resonance Spectroscopy. <i>Biophysical Journal</i> , 2011, 100, 144a. | 0.5 | 0 |
| 97 | 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 |
| 98 | 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 |
| 99 | 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 |
| 100 | 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 |
| 101 | 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 |
| 102 | Solution NMR study of integral membrane proteins. <i>Current Opinion in Chemical Biology</i> , 2011, 15, 560-569. | 6.1 | 71 |
| 103 | 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 |
| 104 | ¹ H, ¹³ C and ¹⁵ 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 |
| 105 | Mechanistic basis for LQT1 caused by S3 mutations in the KCNQ1 subunit of <i>I_{Ks}</i> . <i>Journal of General Physiology</i> , 2010, 135, 433-448. | 1.9 | 26 |
| 106 | Functional Delivery of a Membrane Protein into Oocyte Membranes Using Bicelles. <i>Biochemistry</i> , 2010, 49, 653-655. | 2.5 | 36 |
| 107 | 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 |
| 108 | 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 |

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|-----|---|-----|-----------|
| 109 | Mechanistic insights into non-immunosuppressive immunophilin ligands as potential antimalarial therapeutics. <i>Malaria Journal</i> , 2010, 9, . | 2.3 | 0 |
| 110 | Structure of KCNE1 and Implications for How It Modulates the KCNQ1 Potassium Channel. <i>Biochemistry</i> , 2008, 47, 7999-8006. | 2.5 | 183 |
| 111 | FKBP Family Proteins: Immunophilins with Versatile Biological Functions. <i>NeuroSignals</i> , 2008, 16, 318-325. | 0.9 | 278 |
| 112 | Expression, purification, and molecular characterization of <i>Plasmodium falciparum</i> FK506-binding protein 35 (PffFKBP35). <i>Protein Expression and Purification</i> , 2007, 53, 179-185. | 1.3 | 19 |
| 113 | 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 |
| 114 | ¹ H, ¹³ C, and ¹⁵ N resonance assignments of FK506-binding domain of <i>Plasmodium falciparum</i> FKBP35. <i>Biomolecular NMR Assignments</i> , 2007, 1, 27-28. | 0.8 | 1 |
| 115 | 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 |
| 116 | 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 |
| 117 | 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 |
| 118 | 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 |
| 119 | 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 |
| 120 | Application of microbial enhanced oil recovery technique to Daqing Oilfield. <i>Biochemical Engineering Journal</i> , 2002, 11, 197-199. | 3.6 | 79 |