# Wenjuan Wu

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/2056125/publications.pdf

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|---|---|---|---|
| 12 papers | 111 citations | 1478505 6 h-index | 1372567 10 g-index |
| 12 all docs | 12 docs citations | 12 times ranked | 177 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Studies on the bioactivities and molecular mechanism of antioxidant peptides by 3D-QSAR, in vitro evaluation and molecular dynamic simulations. Food and Function, 2020, 11, 3043-3052. | 4.6 | 29 |
| 2 | Studies on the Bioactivities of ACEâ€inhibitory Peptides with Phenylalanine Câ€terminus Using 3Dâ€QSAR, Molecular Docking and in vitro Evaluation. Molecular Informatics, 2017, 36, 1600157. | 2.5 | 18 |
| 3 | Investigating the binding mechanism of novel 6-aminonicotinate-based antagonists with P2Y12 by 3D-QSAR, docking and molecular dynamics simulations. Journal of Biomolecular Structure and Dynamics, 2017, 35, 2938-2965. | 3.5 | 14 |
| 4 | Identifying hQC Inhibitors of Alzheimerâ€™s Disease by Effective Customized Pharmacophore-Based Virtual Screening, Molecular Dynamic Simulation, and Binding Free Energy Analysis. Applied Biochemistry and Biotechnology, 2019, 187, 1173-1192. | 2.9 | 9 |
| 5 | Different Behaviors of Glutathione in Aqueous and DMSO Solutions: Molecular Dynamics Simulation and NMR Experimental Study. Journal of Solution Chemistry, 2011, 40, 1784-1795. | 1.2 | 8 |
| 6 | Studies on the Conformations and Hydrogen-Bonding Interactions of RGD Tri-peptide in Aqueous Solutions by Molecular Dynamics Simulations and 2D-NOESY Spectroscopy. Journal of Solution Chemistry, 2015, 44, 1281-1291. | 1.2 | 7 |
| 7 | Probing the binding mechanism of novel dual NF-ÎºB/AP-1 inhibitors by 3D-QSAR, docking and molecular dynamics simulations. RSC Advances, 2015, 5, 81523-81532. | 3.6 | 6 |
| 8 | Molecular Dynamics Simulations and NMR Experimental Study of Oxidized Glutathione in Aqueous Solution. Journal of Solution Chemistry, 2012, 41, 879-887. | 1.2 | 5 |
| 9 | Conformations of Oxidized Glutathione in Aqueous Urea Solution by All-Atom Molecular Dynamic Simulations and 2D-NOESY Spectrum. Journal of Solution Chemistry, 2013, 42, 2229-2239. | 1.2 | 5 |
| 10 | Computational analysis of binding between benzamide-based derivatives and Abl wt and T315I mutant kinases. RSC Advances, 2016, 6, 85355-85366. | 3.6 | 5 |
| 11 | Study of novel pyrazolo[3,4-d]pyrimidine derivatives as selective TgCDPK1 inhibitors: molecular docking, structure-based 3D-QSAR and molecular dynamics simulation. RSC Advances, 2016, 6, 100772-100782. | 3.6 | 4 |
| 12 | Conformational Features of ACE-Inhibitory Valine-Isoleucine-Proline Tripeptide in Aqueous Medium According to Molecular Dynamic Simulations and 2D-NMR Spectroscopy. Journal of Solution Chemistry, 2016, 45, 1213-1226. | 1.2 | 1 |