# Jianjun Tan

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8891443/publications.pdf

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| 43 | 889 | 687363 13 | 477307 29 |
|---|---|---|---|
| papers | citations | h-index | g-index |

| 46 | 46 | 46 | 1240 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | The Identification and Analysis of MicroRNAs Combined Biomarkers for Hepatocellular Carcinoma Diagnosis. Medicinal Chemistry, 2022, 18, 1073-1085. | 1.5 | 7 |
| 2 | Advances in Data Repositories for ncRNA-Protein Interaction Predictions Based on Machine Learning: A Mini-Review. Current Chinese Science, 2022, 2, 354-371. | 0.5 | 0 |
| 3 | LPI-CSFFR: Combining serial fusion with feature reuse for predicting LncRNA-protein interactions. Computational Biology and Chemistry, 2022, 99, 107718. | 2.3 | 6 |
| 4 | EDLMFC: an ensemble deep learning framework with multi-scale features combination for ncRNAâ€“protein interaction prediction. BMC Bioinformatics, 2021, 22, 133. | 2.6 | 18 |
| 5 | Quantitative Structure Activity/Pharmacokinetics Relationship Studies of HIV-1 Protease Inhibitors Using Three Modelling Methods. Medicinal Chemistry, 2021, 17, 396-406. | 1.5 | 4 |
| 6 | Recent Advances in Predicting ncRNA-Protein Interactions Based on Machine Learning. Current Chinese Science, 2021, 1, 513-522. | 0.5 | 1 |
| 7 | DM-RPIs: Predicting ncRNA-protein interactions using stacked ensembling strategy. Computational Biology and Chemistry, 2019, 83, 107088. | 2.3 | 17 |
| 8 | Computational identification and analysis of early diagnostic biomarkers for kidney cancer. Journal of Human Genetics, 2019, 64, 1015-1022. | 2.3 | 7 |
| 9 | A novel peptide shows excellent anti-HIV-1 potency as a gp41 fusion inhibitor. Bioorganic and Medicinal Chemistry Letters, 2018, 28, 910-914. | 2.2 | 2 |
| 10 | Combined topomer CoMFA and hologram QSAR studies of a series of pyrrole derivatives as potential HIV fusion inhibitors. Medicinal Chemistry Research, 2018, 27, 1770-1781. | 2.4 | 3 |
| 11 | An efficient perturbation method to predict the functionally key sites of glutamine binding protein. Computational Biology and Chemistry, 2017, 67, 62-68. | 2.3 | 3 |
| 12 | From machine learning to deep learning: progress in machine intelligence for rational drug discovery. Drug Discovery Today, 2017, 22, 1680-1685. | 6.4 | 468 |
| 13 | Identification of functionally key residues in maltose transporter with an elastic network model-based thermodynamic method. Molecular Physics, 2016, 114, 3407-3417. | 1.7 | 1 |
| 14 | Insights into the Functions of M-T Hook Structure in HIV Fusion Inhibitor Using Molecular Modeling. Computational Biology and Chemistry, 2016, 61, 202-209. | 2.3 | 2 |
| 15 | Structureâ€“activity relationship and binding mode studies for a series of diketo-acids as HIV integrase inhibitors by 3D-QSAR, molecular docking and molecular dynamics simulations. RSC Advances, 2016, 6, 27594-27606. | 3.6 | 8 |
| 16 | Design, synthesis and activity evaluation of novel peptide fusion inhibitors targeting HIV-1 gp41. Bioorganic and Medicinal Chemistry, 2016, 24, 201-206. | 3.0 | 7 |
| 17 | Allosteric transitions of ATPâ€binding cassette transporter MsbA studied by the adaptive anisotropic network model. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1643-1653. | 2.6 | 12 |
| 18 | Constructing a Bioinformatics Platform with Web and Mobile Services Based on NVIDIA Jetson TK1. International Journal of Grid and High Performance Computing, 2015, 7, 57-73. | 0.9 | 4 |

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|---|---|---|---|
| 19 | Constructing a Mobility and Acceleration Computing Platform with NVIDIA Jetson TK1. , 2015, , . | | 6 |
| 20 | Development of HIV-1 integrase inhibitors: recent molecular modeling perspectives. Drug Discovery Today, 2015, 20, 1337-1348. | 6.4 | 14 |
| 21 | Molecular Dynamics Studies of the Inhibitor C34 Binding to the Wild-Type and Mutant HIV-1 gp41: Inhibitory and Drug Resistant Mechanism. PLoS ONE, 2014, 9, e111923. | 2.5 | 4 |
| 22 | Allosteric transitions of the maltose transporter studied by an elastic network model. Biopolymers, 2014, 101, 758-768. | 2.4 | 8 |
| 23 | Cation-pi interactions at non-redundant protein-RNA interfaces. Biochemistry (Moscow), 2014, 79, 643-652. | 1.5 | 18 |
| 24 | Peptide HIV fusion inhibitors: modifications and conjugations. MedChemComm, 2014, 5, 1472-1482. | 3.4 | 5 |
| 25 | Pharmacophore and docking-based 3D-QSAR studies on HIV-1 integrase inhibitors. Chemical Research in Chinese Universities, 2014, 30, 297-305. | 2.6 | 2 |
| 26 | Reverse Virtual Screening on Persistent Organic Pollutants 4,4’-DDE and CB-153. Wuli Huaxue Xuebao/ Acta Physico - Chimica Sinica, 2013, 29, 2276-2285. | 4.9 | 2 |
| 27 | The Current Status and Challenges in the Development of Fusion Inhibitors as Therapeutics for HIV-1 Infection. Current Pharmaceutical Design, 2013, 19, 1810-1817. | 1.9 | 14 |
| 28 | 3D-QSAR studies of quinoline ring derivatives as HIV-1 integrase inhibitors. SAR and QSAR in Environmental Research, 2012, 23, 683-703. | 2.2 | 7 |
| 29 | Novel Nanotechnology Strategies for the Treatment and Prevention of HIV Infection. , 2012, , 467-489. | | 1 |
| 30 | Therapeutic strategies underpinning the development of novel techniques for the treatment of HIV infection. Drug Discovery Today, 2010, 15, 186-197. | 6.4 | 61 |
| 31 | Design, Synthesis and Anti-HIV Integrase Evaluation of N-(5-Chloro-8-Hydroxy-2-Styrylquinolin-7-yl)Benzenesulfonamide Derivatives. Molecules, 2010, 15, 1903-1917. | 3.8 | 20 |
| 32 | Development of Integrase Inhibitors of Quinolone Acid Derivatives for Treatment of AIDS: An Overview. Mini-Reviews in Medicinal Chemistry, 2010, 10, 1046-1057. | 2.4 | 28 |
| 33 | Computational Study of Binding Mode for N-substituted Pyrrole Derivatives to HIV-1 gp41*. Progress in Biochemistry and Biophysics, 2010, 37, 904-915. | 0.3 | 7 |
| 34 | Analysis of the Interactions between the N-Terminal Peptide of gp41 and T20 Using Molecular Dynamics and Free Energy Calculations. , 2009, , . | | 0 |
| 35 | Study on the Resistance and the Binding Mode of HIV-1 Integrase to NSC158393. , 2009, , . | | 0 |
| 36 | Study on the inhibitory mechanism and binding mode of the hydroxycoumarin compound NSC158393 to HIVâ€1 integrase by molecular modeling. Biopolymers, 2009, 91, 700-709. | 2.4 | 18 |

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|---|---|---|---|
| 37 | Molecular dynamics simulations of the bacterial periplasmic heme binding proteins ShuT and PhuT. Biophysical Chemistry, 2008, 138, 42-49. | 2.8 | 21 |
| 38 | An integrated GIS-based data model for multimodal urban public transportation analysis and management. , 2008, , . | | 1 |
| 39 | Estimation of soil moisture conditions with Landsat TM in Guangzhou. Proceedings of SPIE, 2008, , . | 0.8 | 0 |
| 40 | Prediction of the binding mode between BMS-378806 and HIV-1 gp120 by docking and molecular dynamics simulation. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2006, 1764, 766-772. | 2.3 | 39 |
| 41 | Investigating interactions between HIV-1 gp41 and inhibitors by molecular dynamics simulation and MMâ€“PBSA/GBSA calculations. Computational and Theoretical Chemistry, 2006, 766, 77-82. | 1.5 | 25 |
| 42 | Studies on binding free energies and the binding mode by docking and MM-PBSA in gp41-ligand complex. Molecular Simulation, 2005, 31, 1051-1056. | 2.0 | 7 |
| 43 | Molecular dynamics simulation on the complexes of N-terminal region of HIV-1 gp41 and its C-peptide inhibitors. Computational and Theoretical Chemistry, 2004, 682, 9-15. | 1.5 | 11 |