# Byungchan Kim

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/11024748/publications.pdf

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| 11 | 2,885 | 840776 11 | 1281871 11 |
|---|---|---|---|
| papers | citations | h-index | g-index |

| 11 | 11 | 11 | 3246 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Accurate Modeling of Scaffold Hopping Transformations in Drug Discovery. Journal of Chemical Theory and Computation, 2017, 13, 42-54. | 5.3 | 103 |
| 2 | Accurate and Reliable Prediction of Relative Ligand Binding Potency in Prospective Drug Discovery by Way of a Modern Free-Energy Calculation Protocol and Force Field. Journal of the American Chemical Society, 2015, 137, 2695-2703. | 13.7 | 931 |
| 3 | Docking and Free Energy Perturbation Studies of Ligand Binding in the Kappa Opioid Receptor. Journal of Physical Chemistry B, 2015, 119, 824-835. | 2.6 | 26 |
| 4 | Modeling Local Structural Rearrangements Using FEP/REST: Application to Relative Binding Affinity Predictions of CDK2 Inhibitors. Journal of Chemical Theory and Computation, 2013, 9, 1282-1293. | 5.3 | 179 |
| 5 | Thermodynamic analysis of water molecules at the surface of proteins and applications to binding site prediction and characterization. Proteins: Structure, Function and Bioinformatics, 2012, 80, 871-883. | 2.6 | 118 |
| 6 | Motifs for molecular recognition exploiting hydrophobic enclosure in proteinâ€“ligand binding. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 808-813. | 7.1 | 633 |
| 7 | Serial Replica Exchange. Journal of Physical Chemistry B, 2007, 111, 1416-1423. | 2.6 | 35 |
| 8 | Replica Exchange with Solute Tempering:Â Efficiency in Large Scale Systems. Journal of Physical Chemistry B, 2007, 111, 5405-5410. | 2.6 | 103 |
| 9 | Replica exchange with solute tempering: A method for sampling biological systems in explicit water. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 13749-13754. | 7.1 | 634 |
| 10 | Structure and Dynamics of the Solvation of Bovine Pancreatic Trypsin Inhibitor in Explicit Water:â€‰ A Comparative Study of the Effects of Solvent and Protein Polarizability. Journal of Physical Chemistry B, 2005, 109, 16529-16538. | 2.6 | 55 |
| 11 | Efficient Simulation Method for Polarizable Protein Force Fields:â€‰ Application to the Simulation of BPTI in Liquid Water. Journal of Chemical Theory and Computation, 2005, 1, 169-180. | 5.3 | 68 |