# Wookyung Yu

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2315804/publications.pdf

Version: 2024-02-01

| 18 | 317 | 1163117 | 888059 |
|---|---|---|---|
| papers | citations | 8 h-index | 17 g-index |

| 19 | 19 | 19 | 536 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Benchmarking all-atom simulations using hydrogen exchange. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15975-15980. | 7.1 | 67 |
| 2 | Functional Implications of an Intermeshing Cogwheel-like Interaction between TolC and MacA in the Action of Macrolide-specific Efflux Pump MacAB-TolC. Journal of Biological Chemistry, 2011, 286, 13541-13549. | 3.4 | 49 |
| 3 | PACSY, a relational database management system for protein structure and chemical shift analysis. Journal of Biomolecular NMR, 2012, 54, 169-179. | 2.8 | 33 |
| 4 | Perplexing cooperative folding and stability of a low-sequence complexity, polyproline 2 protein lacking a hydrophobic core. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 2241-2246. | 7.1 | 29 |
| 5 | Cooperative folding kinetics of BBL protein and peripheral subunit-binding domain homologues. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 2397-2402. | 7.1 | 26 |
| 6 | Exploring the Ligand Efficacy of Cannabinoid Receptor 1 (CB1) using Molecular Dynamics Simulations. Scientific Reports, 2018, 8, 13787. | 3.3 | 25 |
| 7 | Even with nonnative interactions, the updated folding transition states of the homologs Proteins G & L are extensive and similar. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 8302-8307. | 7.1 | 21 |
| 8 | De novo protein structure prediction using ultra-fast molecular dynamics simulation. PLoS ONE, 2018, 13, e0205819. | 2.5 | 21 |
| 9 | Conformational switch that induces GDP release from Gi. Journal of Structural Biology, 2021, 213, 107694. | 2.8 | 9 |
| 10 | Coevolution underlies GPCR-G protein selectivity and functionality. Scientific Reports, 2021, 11, 7858. | 3.3 | 7 |
| 11 | Cooperative folding near the downhill limit determined with amino acid resolution by hydrogen exchange. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 4747-4752. | 7.1 | 6 |
| 12 | Sibe: a computation tool to apply protein sequence statistics to predict folding and design in silico. BMC Bioinformatics, 2019, 20, 455. | 2.6 | 6 |
| 13 | Atomic insights into the effects of pathological mutants through the disruption of hydrophobic core in the prion protein. Scientific Reports, 2019, 9, 19144. | 3.3 | 6 |
| 14 | Uncovering symmetry-breaking vector and reliability order for assigning secondary structures of proteins from atomic NMR chemical shifts in amino acids. Journal of Biomolecular NMR, 2011, 51, 411-424. | 2.8 | 5 |
| 15 | Aggregation-Prone Structural Ensembles of Transthyretin Collected With Regression Analysis for NMR Chemical Shift. Frontiers in Molecular Biosciences, 2021, 8, 766830. | 3.5 | 2 |
| 16 | Understanding the role of the CB1 toggle switch in interaction networks using molecular dynamics simulation. Scientific Reports, 2021, 11, 22369. | 3.3 | 2 |
| 17 | Computational design of a thermolabile uracil-DNA glycosylase of Escherichia coli. Biophysical Journal, 2022, 121, 1276-1288. | 0.5 | 2 |
| 18 | Unveiling OASIS family as a key player in hypoxiaâ€“ischemia cases induced by cocaine using generative adversarial networks. Scientific Reports, 2022, 12, 6734. | 3.3 | 1 |