# Michele Seeber

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/9415487/publications.pdf

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| 22 | 1,229 | 643344 15 | 799663 21 |
|---|---|---|---|
| papers | citations | h-index | g-index |

| 22 | 22 | 22 | 1777 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | PSNtools for standalone and web-based structure network analyses of conformational ensembles. Computational and Structural Biotechnology Journal, 2022, 20, 640-649. | 1.9 | 17 |
| 2 | webPSN v2.0: a webserver to infer fingerprints of structural communication in biomacromolecules. Nucleic Acids Research, 2020, 48, W94-W103. | 6.5 | 56 |
| 3 | Small-Molecule Protein-Protein Interaction Inhibitor of Oncogenic Rho Signaling. Cell Chemical Biology, 2016, 23, 1135-1146. | 2.5 | 28 |
| 4 | Structure network analysis to gain insights into GPCR function. Biochemical Society Transactions, 2016, 44, 613-618. | 1.6 | 21 |
| 5 | WebPSN: a web server for high-throughput investigation of structural communication in biomacromolecules. Bioinformatics, 2015, 31, 779-781. | 1.8 | 49 |
| 6 | Quaternary Structure Predictions and Structural Communication Features of GPCR Dimers. Progress in Molecular Biology and Translational Science, 2013, 117, 105-142. | 0.9 | 14 |
| 7 | A Mixed Protein Structure Network and Elastic Network Model Approach to Predict the Structural Communication in Biomolecular Systems: The PDZ2 Domain from Tyrosine Phosphatase 1E As a Case Study. Journal of Chemical Theory and Computation, 2013, 9, 2504-2518. | 2.3 | 52 |
| 8 | Wordom: A userâ€friendly program for the analysis of molecular structures, trajectories, and free energy surfaces. Journal of Computational Chemistry, 2011, 32, 1183-1194. | 1.5 | 232 |
| 9 | Structural insights into retinitis pigmentosa from unfolding simulations of rhodopsin mutants. FASEB Journal, 2010, 24, 3196-3209. | 0.2 | 39 |
| 10 | Bulky Side Chains and Non-native Salt Bridges Slow down the Folding of a Cross-Linked Helical Peptide: A Combined Molecular Dynamics and Time-Resolved Infrared Spectroscopy Study. Journal of Physical Chemistry B, 2009, 113, 4435-4442. | 1.2 | 15 |
| 11 | Computational Screening of Rhodopsin Mutations Associated with Retinitis Pigmentosa. Journal of Chemical Theory and Computation, 2009, 5, 2472-2485. | 2.3 | 12 |
| 12 | Computational Modeling of Intramolecular and Intermolecular Communication in GPCRs. Current Protein and Peptide Science, 2009, 10, 173-185. | 0.7 | 16 |
| 13 | Mechanisms of Inter- and Intramolecular Communication in GPCRs and G Proteins. Journal of the American Chemical Society, 2008, 130, 4310-4325. | 6.6 | 37 |
| 14 | Wordom: a program for efficient analysis of molecular dynamics simulations. Bioinformatics, 2007, 23, 2625-2627. | 1.8 | 251 |
| 15 | Monomeric dark rhodopsin holds the molecular determinants for transducin recognition: Insights from computational analysis. FEBS Letters, 2007, 581, 944-948. | 1.3 | 21 |
| 16 | Sequential Unfolding of Individual Helices of Bacterioopsin Observed in Molecular Dynamics Simulations of Extraction from the Purple Membrane. Biophysical Journal, 2006, 91, 3276-3284. | 0.2 | 13 |
| 17 | Probing Fragment Complementation by Rigid-Body Docking:â€‰ in Silico Reconstitution of Calbindin D9k. Journal of Chemical Information and Modeling, 2005, 45, 1429-1438. | 2.5 | 15 |
| 18 | Replica exchange molecular dynamics simulations of amyloid peptide aggregation. Journal of Chemical Physics, 2004, 121, 10748-10756. | 1.2 | 192 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Synthesis, Screening, and Molecular Modeling of New Potent and Selective Antagonists at the Î±1dAdrenergic Receptor. Journal of Medicinal Chemistry, 2004, 47, 1900-1918. | 2.9 | 52 |
| 20 | Molecular Dynamics Simulations of the Ligand-Induced Chemical Information Transfer in the 5-HT1A Receptor.. ChemInform, 2003, 34, no. | 0.1 | 0 |
| 21 | Molecular Dynamics Simulations of the Ligand-Induced Chemical Information Transfer in the 5-HT1AReceptor. Journal of Chemical Information and Computer Sciences, 2003, 43, 1520-1531. | 2.8 | 29 |
| 22 | Mapping and Fitting the Peripheral Benzodiazepine Receptor Binding Site by Carboxamide Derivatives. Comparison of Different Approaches to Quantitative Ligandâ^'Receptor Interaction Modeling. Journal of Medicinal Chemistry, 2001, 44, 1134-1150. | 2.9 | 68 |