# Sebastian Salentin

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7497761/publications.pdf

Version: 2024-02-01

| | | 686830 | 996533 |
|---|---|---|---|
| 15 | 2,557 | 13 | 15 |
| papers | citations | h-index | g-index |

| | | | |
|---|---|---|---|
| 17 | 17 | 17 | 3475 |
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Structural binding site comparisons reveal Crizotinib as a novel LRRK2 inhibitor. Computational and Structural Biotechnology Journal, 2021, 19, 3674-3681. | 1.9 | 9 |
| 2 | PLIP 2021: expanding the scope of the proteinâ€“ligand interaction profiler to DNA and RNA. Nucleic Acids Research, 2021, 49, W530-W534. | 6.5 | 691 |
| 3 | Repositioned Drugs for Chagas Disease Unveiled via Structure-Based Drug Repositioning. International Journal of Molecular Sciences, 2020, 21, 8809. | 1.8 | 19 |
| 4 | The structural basis of the genetic code: amino acid recognition by aminoacyl-tRNA synthetases. Scientific Reports, 2020, 10, 12647. | 1.6 | 23 |
| 5 | Structure-based drug repositioning explains ibrutinib as VEGFR2 inhibitor. PLoS ONE, 2020, 15, e0233089. | 1.1 | 19 |
| 6 | Computational Drug Repositioning for Chagas Disease Using Protein-Ligand Interaction Profiling. International Journal of Molecular Sciences, 2020, 21, 4270. | 1.8 | 16 |
| 7 | Current and Future Roles of Artificial Intelligence in Medicinal Chemistry Synthesis. Journal of Medicinal Chemistry, 2020, 63, 8667-8682. | 2.9 | 118 |
| 8 | UniLectin3D, a database of carbohydrate binding proteins with curated information on 3D structures and interacting ligands. Nucleic Acids Research, 2019, 47, D1236-D1244. | 6.5 | 82 |
| 9 | Backbone Brackets and Arginine Tweezers delineate Class I and Class II aminoacyl tRNA synthetases. PLoS Computational Biology, 2018, 14, e1006101. | 1.5 | 17 |
| 10 | From malaria to cancer: Computational drug repositioning of amodiaquine using PLIP interaction patterns. Scientific Reports, 2017, 7, 11401. | 1.6 | 41 |
| 11 | MAGPIE: Simplifying access and execution of computational models in the life sciences. PLoS Computational Biology, 2017, 13, e1005898. | 1.5 | 6 |
| 12 | Discovery of Mycobacterium tuberculosis InhA Inhibitors by Binding Sites Comparison and Ligands Prediction. Journal of Medicinal Chemistry, 2016, 59, 11069-11078. | 2.9 | 26 |
| 13 | Computational Drug Repositioning by Target Hopping: A Use Case in Chagas Disease. Current Pharmaceutical Design, 2016, 22, 3124-3134. | 0.9 | 16 |
| 14 | PLIP: fully automated proteinâ€“ligand interaction profiler. Nucleic Acids Research, 2015, 43, W443-W447. | 6.5 | 1,381 |
| 15 | Polypharmacology rescored: Proteinâ€“ligand interaction profiles for remote binding site similarity assessment. Progress in Biophysics and Molecular Biology, 2014, 116, 174-186. | 1.4 | 92 |