

Andreas Martin Lisewski

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10929236/publications.pdf>

Version: 2024-02-01

17
papers

520
citations

933447

10
h-index

940533

16
g-index

17
all docs

17
docs citations

17
times ranked

708
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Supergenomic Network Compression and the Discovery of EXP1 as a Glutathione Transferase Inhibited by Artesunate. <i>Cell</i> , 2014, 158, 916-928. | 28.9 | 113 |
| 2 | Automated hypothesis generation based on mining scientific literature. , 2014, , . | | 82 |
| 3 | Prediction of enzyme function based on 3D templates of evolutionarily important amino acids. <i>BMC Bioinformatics</i> , 2008, 9, 17. | 2.6 | 70 |
| 4 | Graph sharpening plus graph integration: a synergy that improves protein functional classification. <i>Bioinformatics</i> , 2007, 23, 3217-3224. | 4.1 | 57 |
| 5 | Protein function prediction: towards integration of similarity metrics. <i>Current Opinion in Structural Biology</i> , 2011, 21, 180-188. | 5.7 | 42 |
| 6 | Recurrent use of evolutionary importance for functional annotation of proteins based on local structural similarity. <i>Protein Science</i> , 2006, 15, 1530-1536. | 7.6 | 30 |
| 7 | Rapid detection of similarity in protein structure and function through contact metric distances. <i>Nucleic Acids Research</i> , 2006, 34, e152-e152. | 14.5 | 30 |
| 8 | De-Orphaning the Structural Proteome through Reciprocal Comparison of Evolutionarily Important Structural Features. <i>PLoS ONE</i> , 2008, 3, e2136. | 2.5 | 21 |
| 9 | Graph sharpening. <i>Expert Systems With Applications</i> , 2010, 37, 7870-7879. | 7.6 | 18 |
| 10 | Accurate Protein Structure Annotation through Competitive Diffusion of Enzymatic Functions over a Network of Local Evolutionary Similarities. <i>PLoS ONE</i> , 2010, 5, e14286. | 2.5 | 16 |
| 11 | Untangling complex networks: Risk minimization in financial markets through accessible spin glass ground states. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2010, 389, 3250-3253. | 2.6 | 11 |
| 12 | Function prediction from networks of local evolutionary similarity in protein structure. <i>BMC Bioinformatics</i> , 2013, 14, S6. | 2.6 | 9 |
| 13 | The concept of strong and weak virtual reality. <i>Minds and Machines</i> , 2006, 16, 201-219. | 4.8 | 6 |
| 14 | Potential role of <i>Plasmodium falciparum</i> exported protein 1 in the chloroquine mode of action. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2018, 8, 31-35. | 3.4 | 6 |
| 15 | Random Amino Acid Mutations and Protein Misfolding Lead to Shannon Limit in Sequence-Structure Communication. <i>PLoS ONE</i> , 2008, 3, e3110. | 2.5 | 3 |
| 16 | Interim estimates in null models of COVID-19 vaccine effectiveness. <i>International Journal of Infectious Diseases</i> , 2021, 106, 169-170. | 3.3 | 3 |
| 17 | Effectiveness of England's initial vaccine roll out. <i>BMJ, The</i> , 2021, 373, n1201. | 6.0 | 3 |