Andreas Martin Lisewski

List of Publications by Year
in descending order

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