## Gordon H Lemmon

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6406004/publications.pdf Version: 2024-02-01

		686830	794141
20	2,511	13	19
papers	citations	h-index	g-index
22	22	22	6170
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	RosettaScripts: A Scripting Language Interface to the Rosetta Macromolecular Modeling Suite. PLoS ONE, 2011, 6, e20161.	1.1	506
2	Genomic Landscape of Ewing Sarcoma Defines an Aggressive Subtype with Co-Association of <i>STAG2</i> and <i>TP53</i> Mutations. Cancer Discovery, 2014, 4, 1342-1353.	7.7	418
3	Practically Useful: What the R <scp>osetta</scp> Protein Modeling Suite Can Do for You. Biochemistry, 2010, 49, 2987-2998.	1.2	360
4	The landscape of somatic mutations in epigenetic regulators across 1,000 paediatric cancer genomes. Nature Communications, 2014, 5, 3630.	5.8	342
5	Evolution of the H9N2 influenza genotype that facilitated the genesis of the novel H7N9 virus. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 548-553.	3.3	287
6	Small-molecule ligand docking into comparative models with Rosetta. Nature Protocols, 2013, 8, 1277-1298.	5.5	149
7	Rosetta Ligand Docking with Flexible XML Protocols. Methods in Molecular Biology, 2012, 819, 143-155.	0.4	135
8	De novo and recessive forms of congenital heart disease have distinct genetic and phenotypic landscapes. Nature Communications, 2019, 10, 4722.	5.8	58
9	Towards Ligand Docking Including Explicit Interface Water Molecules. PLoS ONE, 2013, 8, e67536.	1.1	56
10	Predicting the sensitivity and specificity of published real-time PCR assays. Annals of Clinical Microbiology and Antimicrobials, 2008, 7, 18.	1.7	46
11	Antigenic evolution of H9N2 chicken influenza viruses isolated in China during 2009–2013 and selection of a candidate vaccine strain with broad cross-reactivity. Veterinary Microbiology, 2016, 182, 1-7.	0.8	37
12	ABCB1 and GST polymorphisms associated with TP53 status in breast cancer. Pharmacogenetics and Genomics, 2007, 17, 127-136.	0.7	35
13	Computational design of protein-small molecule interfaces. Journal of Structural Biology, 2014, 185, 193-202.	1.3	24
14	An explainable artificial intelligence approach for predicting cardiovascular outcomes using electronic health records. , 2022, 1, e0000004.		13
15	Prediction of HIVâ€∃ Protease/Inhibitor Affinity using RosettaLigand. Chemical Biology and Drug Design, 2012, 79, 888-896.	1.5	12
16	Incidence of Germline Mutations in Cancer-Predisposition Genes in Children with Hematologic Malignancies: a Report from the Pediatric Cancer Genome Project. Blood, 2014, 124, 127-127.	0.6	9
17	Polyurethane foam response to fire in practical geometries. Polymer Degradation and Stability, 2004, 84, 183-197.	2.7	8
18	The history and geographic distribution of a KCNQ1 atrial fibrillation risk allele. Nature Communications, 2021, 12, 6442.	5.8	7

#	Article	IF	CITATIONS
19	A Poisson binomial-based statistical testing framework for comorbidity discovery across electronic health record datasets. Nature Computational Science, 2021, 1, 694-702.	3.8	6
20	Simultaneous prediction of binding free energy and specificity for PDZ domain–peptide interactions. Journal of Computer-Aided Molecular Design, 2013, 27, 1051-1065.	1.3	2