

Gordon H Lemmon

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6406004/publications.pdf>

Version: 2024-02-01

20
papers

2,511
citations

686830

13
h-index

794141

19
g-index

22
all docs

22
docs citations

22
times ranked

6170
citing authors

#	ARTICLE	IF	CITATIONS
1	An explainable artificial intelligence approach for predicting cardiovascular outcomes using electronic health records. , 2022, 1, e0000004.		13
2	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
3	The history and geographic distribution of a KCNQ1 atrial fibrillation risk allele. Nature Communications, 2021, 12, 6442.	5.8	7
4	De novo and recessive forms of congenital heart disease have distinct genetic and phenotypic landscapes. Nature Communications, 2019, 10, 4722.	5.8	58
5	Antigenic evolution of H9N2 chicken influenza viruses isolated in China during 2009â€“2013 and selection of a candidate vaccine strain with broad cross-reactivity. Veterinary Microbiology, 2016, 182, 1-7.	0.8	37
6	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
7	The landscape of somatic mutations in epigenetic regulators across 1,000 paediatric cancer genomes. Nature Communications, 2014, 5, 3630.	5.8	342
8	Computational design of protein-small molecule interfaces. Journal of Structural Biology, 2014, 185, 193-202.	1.3	24
9	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
10	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
11	Simultaneous prediction of binding free energy and specificity for PDZ domainâ€“peptide interactions. Journal of Computer-Aided Molecular Design, 2013, 27, 1051-1065.	1.3	2
12	Small-molecule ligand docking into comparative models with Rosetta. Nature Protocols, 2013, 8, 1277-1298.	5.5	149
13	Towards Ligand Docking Including Explicit Interface Water Molecules. PLoS ONE, 2013, 8, e67536.	1.1	56
14	Prediction of HIVâ€“1 Protease/Inhibitor Affinity using RosettaLigand. Chemical Biology and Drug Design, 2012, 79, 888-896.	1.5	12
15	Rosetta Ligand Docking with Flexible XML Protocols. Methods in Molecular Biology, 2012, 819, 143-155.	0.4	135
16	RosettaScripts: A Scripting Language Interface to the Rosetta Macromolecular Modeling Suite. PLoS ONE, 2011, 6, e20161.	1.1	506
17	Practically Useful: What the Rosetta Protein Modeling Suite Can Do for You. Biochemistry, 2010, 49, 2987-2998.	1.2	360
18	Predicting the sensitivity and specificity of published real-time PCR assays. Annals of Clinical Microbiology and Antimicrobials, 2008, 7, 18.	1.7	46

#	ARTICLE	IF	CITATIONS
19	ABCB1 and GST polymorphisms associated with TP53 status in breast cancer. <i>Pharmacogenetics and Genomics</i> , 2007, 17, 127-136.	0.7	35
20	Polyurethane foam response to fire in practical geometries. <i>Polymer Degradation and Stability</i> , 2004, 84, 183-197.	2.7	8