Darrell E Hurt

List of Publications by Year
in descending order

45 papers	3,337 citations

257450

24 h-index	41 g-index

276875

46 all docs	46 docs citations	46 times ranked	5906 citing authors

#	Article	IF	Citations
1	Noncoding RNA Gas5 Is a Growth Arrestâ€" and Starvation-Associated Repressor of the Glucocorticoid Receptor. Science Signaling, 2010, 3, ra8.	3.6	1,091
2	Targeting and Regulation of Reactive Oxygen Species Generation by Nox Family NADPH Oxidases. Antioxidants and Redox Signaling, 2009, 11, 2607-2619.	5.4	298
3	DBAASP v3: database of antimicrobial/cytotoxic activity and structure of peptides as a resource for development of new therapeutics. Nucleic Acids Research, 2021, 49, D288-D297.	14.5	233
4	DBAASP v.2: an enhanced database of structure and antimicrobial/cytotoxic activity of natural and synthetic peptides. Nucleic Acids Research, 2016, 44, D1104-D1112.	14.5	169
5	Structure of the Plasmodium falciparum Circumsporozoite Protein, a Leading Malaria Vaccine Candidate. Journal of Biological Chemistry, 2009, 284, 26951-26963.	3.4	132
6	A Novel Point Mutation in the KCNJ5 Gene Causing Primary Hyperaldosteronism and Early-Onset Autosomal Dominant Hypertension. Journal of Clinical Endocrinology and Metabolism, 2012, 97, E1532-E1539.	3.6	116
7	Nephele: a cloud platform for simplified, standardized and reproducible microbiome data analysis. Bioinformatics, 2018, 34, 1411-1413.	4.1	99
8	Structure ofPlasmodium falciparumdihydroorotate dehydrogenase with a bound inhibitor. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 312-323.	2.5	97
9	Glycosylation Focuses Sequence Variation in the Influenza A Virus H1 Hemagglutinin Globular Domain. PLoS Pathogens, 2010, 6, e1001211.	4.7	95
10	Unipro UGENE NGS pipelines and components for variant calling, RNA-seq and ChIP-seq data analyses. PeerJ, 2014, 2, e644.	2.0	95
11	The TB Portals: an Open-Access, Web-Based Platform for Global Drug-Resistant-Tuberculosis Data Sharing and Analysis. Journal of Clinical Microbiology, 2017, 55, 3267-3282.	3.9	89
12	Low-tech solutions for the COVID-19 supply chain crisis. Nature Reviews Materials, 2020, 5, 403-406.	48.7	89
13	The NIH 3D Print Exchange: A Public Resource for Bioscientific and Biomedical 3D Prints. 3D Printing and Additive Manufacturing, 2014, 1, 137-140.	2.9	62
14	Predictive Model of Linear Antimicrobial Peptides Active against Gram-Negative Bacteria. Journal of Chemical Information and Modeling, 2018, 58, 1141-1151.	5.4	57
15	A Novel Point Mutation in Helix 10 of the Human Glucocorticoid Receptor Causes Generalized Glucocorticoid Resistance by Disrupting the Structure of the Ligand-Binding Domain. Journal of Clinical Endocrinology and Metabolism, 2010, 95, 2281-2285.	3.6	56
16	A Novel Point Mutation of the Human Glucocorticoid Receptor Gene Causes Primary Generalized Glucocorticoid Resistance Through Impaired Interaction With the LXXLL Motif of the p160 Coactivators: Dissociation of the Transactivating and Transreppressive Activities. Journal of Clinical Endocrinology and Metabolism, 2014, 99, E902-E907.	3.6	49
17	De Novo Design and In Vitro Testing of Antimicrobial Peptides against Gram-Negative Bacteria. Pharmaceuticals, 2019, 12, 82.	3.8	42
18	Detecting drug-resistant tuberculosis in chest radiographs. International Journal of Computer Assisted Radiology and Surgery, 2018, 13, 1915-1925.	2.8	41

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19	Brequinar derivatives and species-specific drug design for dihydroorotate dehydrogenase. Bioorganic and Medicinal Chemistry Letters, 2006, 16, 1610-1615.	2.2	40
20	A Novel Point Mutation in the DNA-Binding Domain (DBD) of the Human Glucocorticoid Receptor Causes Primary Generalized Glucocorticoid Resistance by Disrupting the Hydrophobic Structure of its DBD. Journal of Clinical Endocrinology and Metabolism, 2013, 98, E790-E795.	3.6	34
21	Tyrosine sulfation in the second variable loop (V2) of HIV-1 gp120 stabilizes V2–V3 interaction and modulates neutralization sensitivity. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 3152-3157.	7.1	31
22	Comparison of Common Homology Modeling Algorithms: Application of User-Defined Alignments. Methods in Molecular Biology, 2011, 857, 399-414.	0.9	28
23	Analysis of the Conformation and Function of the Plasmodium falciparum Merozoite Proteins MTRAP and PTRAMP. Eukaryotic Cell, 2012, 11, 615-625.	3.4	28
24	Performance of Qure.ai automatic classifiers against a large annotated database of patients with diverse forms of tuberculosis. PLoS ONE, 2020, 15, e0224445.	2.5	23
25	Characterization of a protective Escherichia coli-expressed Plasmodium falciparum merozoite surface protein 3 indicates a non-linear, multi-domain structure. Molecular and Biochemical Parasitology, 2009, 164, 45-56.	1.1	19
26	"METAGENOTE: a simplified web platform for metadata annotation of genomic samples and streamlined submission to NCBI's sequence read archive" BMC Bioinformatics, 2020, 21, 378.	2.6	19
27	Structural Analysis on the Pathologic Mutant Glucocorticoid Receptor Ligand-Binding Domains. Molecular Endocrinology, 2016, 30, 173-188.	3.7	18
28	A retrospective genomic analysis of drug-resistant strains of M. tuberculosis in a high-burden setting, with an emphasis on comparative diagnostics and reactivation and reinfection status. BMC Infectious Diseases, 2020, 20, 17.	2.9	16
29	Metabolic Fate of Human Immunoactive Sterols in Mycobacterium tuberculosis. Journal of Molecular Biology, 2021, 433, 166763.	4.2	15
30	Differentiating between drug-sensitive and drug-resistant tuberculosis with machine learning for clinical and radiological features. Quantitative Imaging in Medicine and Surgery, 2022, 12, 675-687.	2.0	15
31	Determination of Molecular Structures of HIV Envelope Glycoproteins using Cryo-Electron Tomography and Automated Sub-tomogram Averaging. Journal of Visualized Experiments, 2011, , .	0.3	14
32	Toward quantitative X-ray CT phantoms of metastatic tumors using rapid prototyping technology. , 2011, , .		13
33	Tyrosine-sulfated V2 peptides inhibit HIV-1 infection via coreceptor mimicry. EBioMedicine, 2016, 10, 45-54.	6.1	13
34	TB DEPOT (Data Exploration Portal): A multi-domain tuberculosis data analysis resource. PLoS ONE, 2019, 14, e0217410.	2.5	13
35	Feasibility of virtual reality based training for optimising COVID-19 case handling in Uganda. BMC Medical Education, 2022, 22, 274.	2.4	10
36	Selectivity in the Use of $G_{i/o}$ Proteins Is Determined by the DRF Motif in CXCR6 and Is Cell-Type Specific. Molecular Pharmacology, 2015, 88, 894-910.	2.3	9

#	ARTICLE	IF	CITATIONS
37	Radiologist observations of computed tomography (CT) images predict treatment outcome in TB Portals, a real-world database of tuberculosis (TB) cases. PLoS ONE, 2021, 16, e0247906.	2.5	9
38	Comparative analysis of machine learning algorithms on the microbial strain-specific AMP prediction. Briefings in Bioinformatics, 2022, 23, .	6.5	8
39	Comparative analysis of genomic variability for drug-resistant strains of Mycobacterium tuberculosis: The special case of Belarus. Infection, Genetics and Evolution, 2020, 78, 104137.	2.3	6
40	The technology behind TB DEPOT: a novel public analytics platform integrating tuberculosis clinical, genomic, and radiological data for visual and statistical exploration. Journal of the American Medical Informatics Association: JAMIA, 2021, 28, 71-79.	4.4	5
41	Automated Drug-Resistant TB Screening: Importance of Demographic Features and Radiological Findings in Chest X-Ray. , 2021, , .		2
42	Evolutionary epidemiology ofNeisseria meningitidisstrains in Belarus compared to other European countries. Acta Microbiologica Et Immunologica Hungarica, 2013, 60, 397-410.	0.8	1
43	Patterns of genomic interrelatedness of publicly available samples in the TB portals database. Tuberculosis, 2022, 133, 102171.	1.9	1
44	Microarray Meta-Miner (MMM): An integrated method and a web tool to identify genes with similar expression profile. , 2010, , .		0
45	Biological Atomic Force Microscopic Imaging and Force Spectroscopy of Protein Constructs as Potential Anti-Malaria Vaccines. Biophysical Journal, 2011, 100, 164a.	0.5	0