Darrell E Hurt

List of Publications by Year
in descending order

45 papers	3,337 citations	257450 24 h-index	276875 41 g-index
46 all docs	46 docs citations	46 times ranked	5906 citing authors

#	Article	IF	Citations
1	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
2	Patterns of genomic interrelatedness of publicly available samples in the TB portals database. Tuberculosis, 2022, 133, 102171.	1.9	1
3	Feasibility of virtual reality based training for optimising COVID-19 case handling in Uganda. BMC Medical Education, 2022, 22, 274.	2.4	10
4	Comparative analysis of machine learning algorithms on the microbial strain-specific AMP prediction. Briefings in Bioinformatics, 2022, 23, .	6.5	8
5	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
6	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
7	Metabolic Fate of Human Immunoactive Sterols in Mycobacterium tuberculosis. Journal of Molecular Biology, 2021, 433, 166763.	4.2	15
8	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
9	Automated Drug-Resistant TB Screening: Importance of Demographic Features and Radiological Findings in Chest X-Ray. , 2021, , .		2
10	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
11	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
12	â€œMETAGENOTE: a simplified web platform for metadata annotation of genomic samples and streamlined submission to NCBIâ€™s sequence read archiveâ€. BMC Bioinformatics, 2020, 21, 378.	2.6	19
13	Low-tech solutions for the COVID-19 supply chain crisis. Nature Reviews Materials, 2020, 5, 403-406.	48.7	89
14	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
15	TB DEPOT (Data Exploration Portal): A multi-domain tuberculosis data analysis resource. PLoS ONE, 2019, 14, e0217410.	2.5	13
16	De Novo Design and In Vitro Testing of Antimicrobial Peptides against Gram-Negative Bacteria. Pharmaceuticals, 2019, 12, 82.	3.8	42
17	Nephele: a cloud platform for simplified, standardized and reproducible microbiome data analysis. Bioinformatics, 2018, 34, 1411-1413.	4.1	99
18	Predictive Model of Linear Antimicrobial Peptides Active against Gram-Negative Bacteria. Journal of Chemical Information and Modeling, 2018, 58, 1141-1151.	5.4	57

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19	Detecting drug-resistant tuberculosis in chest radiographs. International Journal of Computer Assisted Radiology and Surgery, 2018, 13, 1915-1925.	2.8	41
20	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
21	Tyrosine-sulfated V2 peptides inhibit HIV-1 infection via coreceptor mimicry. EBioMedicine, 2016, 10, 45-54.	6.1	13
22	Structural Analysis on the Pathologic Mutant Glucocorticoid Receptor Ligand-Binding Domains. Molecular Endocrinology, 2016, 30, 173-188.	3.7	18
23	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
24	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
25	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
26	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
27	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
28	Unipro UGENE NGS pipelines and components for variant calling, RNA-seq and ChIP-seq data analyses. PeerJ, 2014, 2, e644.	2.0	95
29	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
30	Evolutionary epidemiology ofNeisseria meningitidisstrains in Belarus compared to other European countries. Acta Microbiologica Et Immunologica Hungarica, 2013, 60, 397-410.	0.8	1
31	Analysis of the Conformation and Function of the Plasmodium falciparum Merozoite Proteins MTRAP and PTRAMP. Eukaryotic Cell, 2012, 11, 615-625.	3.4	28
32	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
33	Biological Atomic Force Microscopic Imaging and Force Spectroscopy of Protein Constructs as Potential Anti-Malaria Vaccines. Biophysical Journal, 2011, 100, 164a.	0.5	0
34	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
35	Comparison of Common Homology Modeling Algorithms: Application of User-Defined Alignments. Methods in Molecular Biology, 2011, 857, 399-414.	0.9	28
36	Toward quantitative X-ray CT phantoms of metastatic tumors using rapid prototyping technology. , 2011, , .		13

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37	Noncoding RNA Gas5 Is a Growth Arrestâ€" and Starvation-Associated Repressor of the Glucocorticoid Receptor. Science Signaling, 2010, 3, ra8.	3.6	1,091
38	Glycosylation Focuses Sequence Variation in the Influenza A Virus H1 Hemagglutinin Globular Domain. PLoS Pathogens, 2010, 6, e1001211.	4.7	95
39	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
40	Microarray Meta-Miner (MMM): An integrated method and a web tool to identify genes with similar expression profile. , 2010, , .		0
41	Structure of the Plasmodium falciparum Circumsporozoite Protein, a Leading Malaria Vaccine Candidate. Journal of Biological Chemistry, 2009, 284, 26951-26963.	3.4	132
42	Targeting and Regulation of Reactive Oxygen Species Generation by Nox Family NADPH Oxidases. Antioxidants and Redox Signaling, 2009, 11, 2607-2619.	5.4	298
43	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
44	Structure ofPlasmodium falciparumdihydroorotate dehydrogenase with a bound inhibitor. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 312-323.	2.5	97
45	Brequinar derivatives and species-specific drug design for dihydroorotate dehydrogenase. Bioorganic and Medicinal Chemistry Letters, 2006, 16, 1610-1615.	2.2	40