

Daniel H Haft

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

16,205
citations

304743

22
h-index

477307

29
g-index

31
all docs

31
docs citations

31
times ranked

23812
citing authors

#	ARTICLE	IF	CITATIONS
1	Reference sequence (RefSeq) database at NCBI: current status, taxonomic expansion, and functional annotation. <i>Nucleic Acids Research</i> , 2016, 44, D733-D745.	14.5	4,739
2	An updated evolutionary classification of CRISPR-Cas systems. <i>Nature Reviews Microbiology</i> , 2015, 13, 722-736.	28.6	2,081
3	Evolutionary classification of CRISPR-Cas systems: a burst of class 2 and derived variants. <i>Nature Reviews Microbiology</i> , 2020, 18, 67-83.	28.6	1,427
4	The InterPro protein families and domains database: 20 years on. <i>Nucleic Acids Research</i> , 2021, 49, D344-D354.	14.5	1,385
5	Genome Sequence of the Radioresistant Bacterium <i>Deinococcus radiodurans</i> R1. <i>Science</i> , 1999, 286, 1571-1577.	12.6	879
6	The TIGRFAMs database of protein families. <i>Nucleic Acids Research</i> , 2003, 31, 371-373.	14.5	821
7	Validating the AMRFinder Tool and Resistance Gene Database by Using Antimicrobial Resistance Genotype-Phenotype Correlations in a Collection of Isolates. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	760
8	RefSeq: an update on prokaryotic genome annotation and curation. <i>Nucleic Acids Research</i> , 2018, 46, D851-D860.	14.5	749
9	A bacterial genome in flux: the twelve linear and nine circular extrachromosomal DNAs in an infectious isolate of the Lyme disease spirochete <i>Borrelia burgdorferi</i> . <i>Molecular Microbiology</i> , 2000, 35, 490-516.	2.5	730
10	RefSeq: expanding the Prokaryotic Genome Annotation Pipeline reach with protein family model curation. <i>Nucleic Acids Research</i> , 2021, 49, D1020-D1028.	14.5	519
11	TIGRFAMs and Genome Properties in 2013. <i>Nucleic Acids Research</i> , 2012, 41, D387-D395.	14.5	484
12	TIGRFAMs: a protein family resource for the functional identification of proteins. <i>Nucleic Acids Research</i> , 2001, 29, 41-43.	14.5	445
13	AMRFinderPlus and the Reference Gene Catalog facilitate examination of the genomic links among antimicrobial resistance, stress response, and virulence. <i>Scientific Reports</i> , 2021, 11, 12728.	3.3	388
14	Biological Systems Discovery In Silico: Radical S-Adenosylmethionine Protein Families and Their Target Peptides for Posttranslational Modification. <i>Journal of Bacteriology</i> , 2011, 193, 2745-2755.	2.2	152
15	Methanobactin and MmoD work in concert to act as the "copper switch" in methanotrophs. <i>Environmental Microbiology</i> , 2013, 15, 3077-3086.	3.8	108
16	Proposal for assignment of allele numbers for mobile colistin resistance (mcr) genes. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 2625-2630.	3.0	101
17	Exopolysaccharide-associated protein sorting in environmental organisms: the PEP-CTERM/EpsH system. Application of a novel phylogenetic profiling heuristic. <i>BMC Biology</i> , 2006, 4, 29.	3.8	86
18	Genome Properties: a system for the investigation of prokaryotic genetic content for microbiology, genome annotation and comparative genomics. <i>Bioinformatics</i> , 2005, 21, 293-306.	4.1	72

#	ARTICLE	IF	CITATIONS
19	A Standard Numbering Scheme for Class C β -Lactamases. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	3.2	50
20	Permuting the PGF Signature Motif Blocks both Archaeosortase-Dependent C-Terminal Cleavage and Prenyl Lipid Attachment for the <i>Haloferax volcanii</i> S-Layer Glycoprotein. <i>Journal of Bacteriology</i> , 2016, 198, 808-815.	2.2	30
21	Using comparative genomics to drive new discoveries in microbiology. <i>Current Opinion in Microbiology</i> , 2015, 23, 189-196.	5.1	28
22	Folding the unfoldable: using AlphaFold to explore spurious proteins. <i>Bioinformatics Advances</i> , 2022, 2, .	2.4	28
23	Simultaneous non-contiguous deletions using large synthetic DNA and site-specific recombinases. <i>Nucleic Acids Research</i> , 2014, 42, e111-e111.	14.5	24
24	Consensus on β -Lactamase Nomenclature. <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, e0033322.	3.2	11
25	Comment on: Resistance gene naming and numbering: is it a new gene or not?. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 2677-2678.	3.0	10
26	A comprehensive software suite for protein family construction and functional site prediction. <i>PLoS ONE</i> , 2017, 12, e0171758.	2.5	9
27	Curation of the AMRFinderPlus databases: applications, functionality and impact. <i>Microbial Genomics</i> , 2022, 8, .	2.0	9
28	Creating a specialist protein resource network: a meeting report for the protein bioinformatics and community resources retreat: Figure 1.. Database: the <i>Journal of Biological Databases and Curation</i> , 2015, 2015, bav063.	3.0	8