

Nicole T Perna

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

24,180
citations

116194

36
h-index

169272

56
g-index

61
all docs

61
docs citations

61
times ranked

26422
citing authors

#	ARTICLE	IF	CITATIONS
1	Complete Genome Sequence of <i>Dickeya dianthicola</i> ME23, a Pathogen Causing Blackleg and Soft Rot Diseases of Potato. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	13
2	Identification of host-microbe interaction factors in the genomes of soft rot-associated pathogens <i>Dickeya dadantii</i> 3937 and <i>Pectobacterium carotovorum</i> WPP14 with supervised machine learning. <i>BMC Genomics</i> , 2014, 15, 508.	1.2	14
3	Evolution of extreme resistance to ionizing radiation via genetic adaptation of DNA repair. <i>ELife</i> , 2014, 3, e01322.	2.8	80
4	Inferring ancient metabolism using ancestral core metabolic models of enterobacteria. <i>BMC Systems Biology</i> , 2013, 7, 46.	3.0	11
5	Computing the Joint Distribution of Tree Shape and Tree Distance for Gene Tree Inference and Recombination Detection. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 1-1.	1.9	3
6	Transcriptome Changes Associated with Anaerobic Growth in <i>Yersinia intermedia</i> (ATCC29909). <i>PLoS ONE</i> , 2013, 8, e76567.	1.1	8
7	Insight into the Transmission Biology and Species-Specific Functional Capabilities of Tsetse (Diptera: Tj ETQq1 1 0.784314 rgBT /Ove	1.8	105
8	Using Comparative Genomics for Inquiry-Based Learning to Dissect Virulence of <i>Escherichia coli</i> O157:H7 and <i>Yersinia pestis</i> . <i>CBE Life Sciences Education</i> , 2012, 11, 81-93.	1.1	15
9	Evolution of the metabolic and regulatory networks associated with oxygen availability in two phytopathogenic enterobacteria. <i>BMC Genomics</i> , 2012, 13, 110.	1.2	39
10	Analysis of the <i>Lactobacillus casei</i> supragenome and its influence in species evolution and lifestyle adaptation. <i>BMC Genomics</i> , 2012, 13, 533.	1.2	144
11	The evolution of metabolic networks of <i>E. coli</i> . <i>BMC Systems Biology</i> , 2011, 5, 182.	3.0	60
12	The Comprehensive Phytopathogen Genomics Resource: a web-based resource for data-mining plant pathogen genomes. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar053-bar053.	1.4	26
13	Genome Sequence of the Plant-Pathogenic Bacterium <i>Dickeya dadantii</i> 3937. <i>Journal of Bacteriology</i> , 2011, 193, 2076-2077.	1.0	113
14	Genomics of <i>Escherichia</i> and <i>Shigella</i> . , 2011, , 119-139.		3
15	Annotation and overview of the <i>Pseudomonas savastanoi</i> pv. <i>savastanoi</i> NCPPB 3335 draft genome reveals the virulence gene complement of a tumour-inducing pathogen of woody hosts. <i>Environmental Microbiology</i> , 2010, 12, 1604-1620.	1.8	80
16	chipD: a web tool to design oligonucleotide probes for high-density tiling arrays. <i>Nucleic Acids Research</i> , 2010, 38, W321-W325.	6.5	23
17	progressiveMauve: Multiple Genome Alignment with Gene Gain, Loss and Rearrangement. <i>PLoS ONE</i> , 2010, 5, e11147.	1.1	3,652
18	Reordering contigs of draft genomes using the Mauve Aligner. <i>Bioinformatics</i> , 2009, 25, 2071-2073.	1.8	532

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19	Directed Evolution of Ionizing Radiation Resistance in <i>Escherichia coli</i> . Journal of Bacteriology, 2009, 191, 5240-5252.	1.0	131
20	Text-mining of PubMed abstracts by natural language processing to create a public knowledge base on molecular mechanisms of bacterial enteropathogens. BMC Bioinformatics, 2009, 10, 177.	1.2	16
21	Phylogeny and Virulence of Naturally Occurring Type III Secretion System-Deficient <i>Pectobacterium</i> Strains. Applied and Environmental Microbiology, 2009, 75, 4539-4549.	1.4	88
22	Directed evolution of ionizing radiation resistance in <i>Escherichia coli</i> . FASEB Journal, 2009, 23, 836.7.	0.2	0
23	Enteropathogen Resource Integration Center (ERIC): bioinformatics support for research on biodefense-relevant enterobacteria. Nucleic Acids Research, 2007, 36, D519-D523.	6.5	14
24	Analyzing Patterns of Microbial Evolution Using the Mauve Genome Alignment System. Methods in Molecular Biology, 2007, 396, 135-152.	0.4	51
25	Host Range and Molecular Phylogenies of the Soft Rot Enterobacterial Genera <i>Pectobacterium</i> and <i>Dickeya</i> . Phytopathology, 2007, 97, 1150-1163.	1.1	469
26	Construction and characterization of an expressed sequenced tag library for the mosquito vector <i>Armigeres subalbatus</i> . BMC Genomics, 2007, 8, 462.	1.2	12
27	A New Asset for Pathogen Informatics – the Enteropathogen Resource Integration Center (ERIC), an NIAID Bioinformatics Resource Center for Biodefense and Emerging/Re-emerging Infectious Disease. Advances in Experimental Medicine and Biology, 2007, 603, 28-42.	0.8	9
28	Genome-wide detection and analysis of homologous recombination among sequenced strains of <i>Escherichia coli</i> . Genome Biology, 2006, 7, R44.	13.9	63
29	<i>Escherichia coli</i> K-12: a cooperatively developed annotation snapshot–2005. Nucleic Acids Research, 2006, 34, 1-9.	6.5	606
30	Identification of potential virulence genes in <i>Erwinia chrysanthemi</i> 3937: transposon insertion into plant-upregulated genes. Journal of General Plant Pathology, 2006, 72, 360-368.	0.6	0
31	ASAP: a resource for annotating, curating, comparing, and disseminating genomic data. Nucleic Acids Research, 2006, 34, D41-D45.	6.5	56
32	Identifying Evolutionarily Conserved Segments Among Multiple Divergent and Rearranged Genomes. Lecture Notes in Computer Science, 2005, , 72-84.	1.0	1
33	Genomics of enterobacteriaceae. , 2005, , .		0
34	GRIL: genome rearrangement and inversion locator. Bioinformatics, 2004, 20, 122-124.	1.8	41
35	Description of the Transcriptomes of Immune Response-Activated Hemocytes from the Mosquito Vectors <i>Aedes aegypti</i> and <i>Armigeres subalbatus</i> . Infection and Immunity, 2004, 72, 4114-4126.	1.0	144
36	Insertions, Deletions, and Single-Nucleotide Polymorphisms at Rare Restriction Enzyme Sites Enhance Discriminatory Power of Polymorphic Amplified Typing Sequences, a Novel Strain Typing System for <i>Escherichia coli</i> O157:H7. Journal of Clinical Microbiology, 2004, 42, 2388-2397.	1.8	17

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37	Mauve: Multiple Alignment of Conserved Genomic Sequence With Rearrangements. <i>Genome Research</i> , 2004, 14, 1394-1403.	2.4	4,085
38	Genome-Wide Identification of Plant-Upregulated Genes of <i>Erwinia chrysanthemi</i> 3937 Using a GFP-Based IVET Leaf Array. <i>Molecular Plant-Microbe Interactions</i> , 2004, 17, 999-1008.	1.4	99
39	Acquisition of stcE, a C1 Esterase Inhibitor-Specific Metalloprotease, during the Evolution of <i>Escherichia coli</i> O157:H7. <i>Journal of Infectious Diseases</i> , 2003, 187, 1907-1914.	1.9	18
40	ASAP, a systematic annotation package for community analysis of genomes. <i>Nucleic Acids Research</i> , 2003, 31, 147-151.	6.5	152
41	Microarray Profiling of <i>Erwinia chrysanthemi</i> 3937 Genes That are Regulated During Plant Infection. <i>Molecular Plant-Microbe Interactions</i> , 2002, 15, 619-629.	1.4	70
42	Strains of <i>Escherichia coli</i> O157:H7 Differ Primarily by Insertions or Deletions, Not Single-Nucleotide Polymorphisms. <i>Journal of Bacteriology</i> , 2002, 184, 1873-1879.	1.0	97
43	Urease of Enterohemorrhagic <i>Escherichia coli</i> : Evidence for Regulation by Fur and a trans-Acting Factor. <i>Infection and Immunity</i> , 2002, 70, 1027-1031.	1.0	37
44	Genomic Variability of O Islands Encoding Tellurite Resistance in Enterohemorrhagic <i>Escherichia coli</i> O157:H7 Isolates. <i>Journal of Bacteriology</i> , 2002, 184, 4690-4698.	1.0	128
45	Identification and Characterization of <i>lpfABCC</i> DE, a Fimbrial Operon of Enterohemorrhagic <i>Escherichia coli</i> O157:H7. <i>Infection and Immunity</i> , 2002, 70, 5416-5427.	1.0	173
46	Polymorphic Amplified Typing Sequences Provide a Novel Approach to <i>Escherichia coli</i> O157:H7 Strain Typing. <i>Journal of Clinical Microbiology</i> , 2002, 40, 1152-1159.	1.8	18
47	Genome Sequence of <i>Yersinia pestis</i> KIM. <i>Journal of Bacteriology</i> , 2002, 184, 4601-4611.	1.0	534
48	A Whole-Genome Shotgun Optical Map of <i>Yersinia pestis</i> Strain KIM. <i>Applied and Environmental Microbiology</i> , 2002, 68, 6321-6331.	1.4	65
49	<i>hrp</i> Genes of <i>Erwinia chrysanthemi</i> 3937 Are Important Virulence Factors. <i>Molecular Plant-Microbe Interactions</i> , 2002, 15, 472-480.	1.4	114
50	The Genomes of <i>Escherichia coli</i> K-12 and Pathogenic <i>E. coli</i> . , 2002, , 3-53.		14
51	Characterization of Cah, a calcium-binding and heat-extractable autotransporter protein of enterohaemorrhagic <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 2002, 45, 951-966.	1.2	100
52	Genome sequence of enterohaemorrhagic <i>Escherichia coli</i> O157:H7. <i>Nature</i> , 2001, 409, 529-533.	13.7	1,895
53	erratum Genome sequence of enterohaemorrhagic <i>Escherichia coli</i> O157:H7. <i>Nature</i> , 2001, 410, 240-240.	13.7	19
54	Shotgun Optical Maps of the Whole <i>Escherichia coli</i> O157:H7 Genome. <i>Genome Research</i> , 2001, 11, 1584-1593.	2.4	78

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55	A Genomic Sample Sequence of the Entomopathogenic Bacterium <i>Photorhabdus luminescens</i> W14: Potential Implications for Virulence. <i>Applied and Environmental Microbiology</i> , 2000, 66, 3310-3329.	1.4	84
56	The complete DNA sequence and analysis of the large virulence plasmid of <i>Escherichia coli</i> O157:H7. <i>Nucleic Acids Research</i> , 1998, 26, 4196-4204.	6.5	326
57	Molecular Evolution of a Pathogenicity Island from Enterohemorrhagic <i>Escherichia coli</i> O157:H7. <i>Infection and Immunity</i> , 1998, 66, 3810-3817.	1.0	400
58	The Complete Genome Sequence of <i>Escherichia coli</i> K-12. <i>Science</i> , 1997, 277, 1453-1462.	6.0	7,145
59	Patterns of nucleotide composition at fourfold degenerate sites of animal mitochondrial genomes. <i>Journal of Molecular Evolution</i> , 1995, 41, 353-358.	0.8	1,185
60	Patterns of nucleotide composition at fourfold degenerate sites of animal mitochondrial genomes. <i>Journal of Molecular Evolution</i> , 1995, 41, 353-8.	0.8	693