

Todd D Taylor

List of Publications by Year in descending order

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Version: 2024-02-01

71
papers

28,836
citations

136885

32
h-index

133188

59
g-index

72
all docs

72
docs citations

72
times ranked

32799
citing authors

#	ARTICLE	IF	CITATIONS
1	Impact of dietary fructooligosaccharides (FOS) on murine gut microbiota and intestinal IgA secretion. <i>3 Biotech</i> , 2022, 12, 56.	1.1	2
2	Shotgun metagenomic sequencing revealed the prebiotic potential of a grain-based diet in mice. <i>Scientific Reports</i> , 2022, 12, 6748.	1.6	2
3	Gut microbiota alternation under the intestinal epithelium-specific knockout of mouse Piga gene. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
4	<i>Lactobacillus plantarum</i> USM8613 Aids in Wound Healing and Suppresses <i>Staphylococcus aureus</i> Infection at Wound Sites. <i>Probiotics and Antimicrobial Proteins</i> , 2020, 12, 125-137.	1.9	58
5	Gut microorganisms act together to exacerbate inflammation in spinal cords. <i>Nature</i> , 2020, 585, 102-106.	13.7	153
6	Association of colitis with gut-microbiota dysbiosis in clathrin adapter AP-1B knockout mice. <i>PLoS ONE</i> , 2020, 15, e0228358.	1.1	17
7	Association of colitis with gut-microbiota dysbiosis in clathrin adapter AP-1B knockout mice. , 2020, 15, e0228358.		0
8	Association of colitis with gut-microbiota dysbiosis in clathrin adapter AP-1B knockout mice. , 2020, 15, e0228358.		0
9	Association of colitis with gut-microbiota dysbiosis in clathrin adapter AP-1B knockout mice. , 2020, 15, e0228358.		0
10	Association of colitis with gut-microbiota dysbiosis in clathrin adapter AP-1B knockout mice. , 2020, 15, e0228358.		0
11	Association of colitis with gut-microbiota dysbiosis in clathrin adapter AP-1B knockout mice. , 2020, 15, e0228358.		0
12	Association of colitis with gut-microbiota dysbiosis in clathrin adapter AP-1B knockout mice. , 2020, 15, e0228358.		0
13	Extracellular transglycosylase and glyceraldehyde-3-phosphate dehydrogenase attributed to the anti-staphylococcal activity of <i>Lactobacillus plantarum</i> USM8613. <i>Journal of Biotechnology</i> , 2019, 300, 20-31.	1.9	9
14	A novel and wide substrate specific polyhydroxyalkanoate (PHA) synthase from unculturable bacteria found in mangrove soil. <i>Journal of Polymer Research</i> , 2018, 25, 1.	1.2	21
15	An integrative study on biologically recovered polyhydroxyalkanoates (PHAs) and simultaneous assessment of gut microbiome in yellow mealworm. <i>Journal of Biotechnology</i> , 2018, 265, 31-39.	1.9	43
16	<i>Lactobacillus fermentum</i> FTDC 8312 combats hypercholesterolemia via alteration of gut microbiota. <i>Journal of Biotechnology</i> , 2017, 262, 75-83.	1.9	52
17	Whole Exome Sequencing in Eight Thai Patients With Leber Congenital Amaurosis Reveals Mutations in the CTNNA1 and CYP4V2 Genes. , 2017, 58, 2413.		15
18	The rubber tree genome shows expansion of gene family associated with rubber biosynthesis. <i>Scientific Reports</i> , 2016, 6, 28594.	1.6	118

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19	Comparative metagenomic analysis of PAH degradation in soil by a mixed microbial consortium. <i>Journal of Hazardous Materials</i> , 2016, 318, 702-710.	6.5	94
20	Comparative genome analyses of novel <i>Mangrovimonas</i> -like strains isolated from estuarine mangrove sediments reveal xylan and arabinan utilization genes. <i>Marine Genomics</i> , 2016, 25, 115-121.	0.4	12
21	MetaTreeMap: An Alternative Visualization Method for Displaying Metagenomic Phylogenetic Trees. <i>PLoS ONE</i> , 2016, 11, e0158261.	1.1	4
22	A novel start codon mutation of the MERTK gene in a patient with retinitis pigmentosa. <i>Molecular Vision</i> , 2016, 22, 342-51.	1.1	13
23	Complete genome sequence of <i>Streptomyces</i> sp. strain CFMR 7, a natural rubber degrading actinomycete isolated from Penang, Malaysia. <i>Journal of Biotechnology</i> , 2015, 214, 47-48.	1.9	11
24	Whole genome amplification approach reveals novel polyhydroxyalkanoate synthases (PhaCs) from Japan Trench and Nankai Trough seawater. <i>BMC Microbiology</i> , 2014, 14, 318.	1.3	19
25	Genome Sequence of the Tsetse Fly (<i>Glossina morsitans</i>): Vector of African Trypanosomiasis. <i>Science</i> , 2014, 344, 380-386.	6.0	254
26	Whole Exome Sequencing in Thai Patients With Retinitis Pigmentosa Reveals Novel Mutations in Six Genes. , 2014, 55, 2259.		47
27	HMCJ (Japan). , 2014, , 1-5.		0
28	Comparative Analysis of DNA Word Abundances in Four Yeast Genomes Using a Novel Statistical Background Model. <i>PLoS ONE</i> , 2013, 8, e58038.	1.1	8
29	MetaBin. , 2013, , 1-7.		0
30	MetaBioME. , 2013, , 1-12.		0
31	Acetate-producing bifidobacteria protect the host from enteropathogenic infection via carbohydrate transporters. <i>Gut Microbes</i> , 2012, 3, 449-454.	4.3	174
32	Fast and Accurate Taxonomic Assignments of Metagenomic Sequences Using MetaBin. <i>PLoS ONE</i> , 2012, 7, e34030.	1.1	27
33	Characteristics of nucleosomes and linker DNA regions on the genome of the basidiomycete <i>Mixia osmundae</i> revealed by mono- and dinucleosome mapping. <i>Open Biology</i> , 2012, 2, 120043.	1.5	11
34	Functional assignment of metagenomic data: challenges and applications. <i>Briefings in Bioinformatics</i> , 2012, 13, 711-727.	3.2	150
35	Complete Genome Sequences of Rat and Mouse Segmented Filamentous Bacteria, a Potent Inducer of Th17 Cell Differentiation. <i>Cell Host and Microbe</i> , 2011, 10, 273-284.	5.1	125
36	Bifidobacteria can protect from enteropathogenic infection through production of acetate. <i>Nature</i> , 2011, 469, 543-547.	13.7	1,836

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37	Complete Genome Sequences of <i>Arcobacter butzleri</i> ED-1 and <i>Arcobacter</i> sp. Strain L, Both Isolated from a Microbial Fuel Cell. <i>Journal of Bacteriology</i> , 2011, 193, 6411-6412.	1.0	56
38	Genomes of Two Chronological Isolates (<i>Helicobacter pylori</i> 2017 and 2018) of the West African <i>Helicobacter pylori</i> Strain 908 Obtained from a Single Patient. <i>Journal of Bacteriology</i> , 2011, 193, 3385-3386.	1.0	29
39	Expression of Conjoined Genes: Another Mechanism for Gene Regulation in Eukaryotes. <i>PLoS ONE</i> , 2010, 5, e13284.	1.1	93
40	Genome of <i>Helicobacter pylori</i> Strain 908. <i>Journal of Bacteriology</i> , 2010, 192, 6488-6489.	1.0	25
41	Complete Genome Sequence of the Wild-Type Commensal <i>Escherichia coli</i> Strain SE15, Belonging to Phylogenetic Group B2. <i>Journal of Bacteriology</i> , 2010, 192, 1165-1166.	1.0	62
42	MetaBioME: a database to explore commercially useful enzymes in metagenomic datasets. <i>Nucleic Acids Research</i> , 2010, 38, D468-D472.	6.5	66
43	Complete Genome Sequence of the Probiotic <i>Lactobacillus rhamnosus</i> ATCC 53103. <i>Journal of Bacteriology</i> , 2009, 191, 7630-7631.	1.0	85
44	The Human Intestinal Microbiome: A New Frontier of Human Biology. <i>DNA Research</i> , 2009, 16, 1-12.	1.5	227
45	Genome of an Endosymbiont Coupling N ₂ Fixation to Cellulolysis Within Protist Cells in Termite Gut. <i>Science</i> , 2008, 322, 1108-1109.	6.0	217
46	Complete genome of the uncultured Termite Group 1 bacteria in a single host protist cell. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 5555-5560.	3.3	220
47	Complete Genome Sequence and Comparative Analysis of the Wild-type Commensal <i>Escherichia coli</i> Strain SE11 Isolated from a Healthy Adult. <i>DNA Research</i> , 2008, 15, 375-386.	1.5	88
48	Comparative Metagenomics Revealed Commonly Enriched Gene Sets in Human Gut Microbiomes. <i>DNA Research</i> , 2007, 14, 169-181.	1.5	760
49	Reply to "Has the chimpanzee Y chromosome been sequenced?". <i>Nature Genetics</i> , 2006, 38, 854-855.	9.4	2
50	Comparative analysis of chimpanzee and human Y chromosomes unveils complex evolutionary pathway. <i>Nature Genetics</i> , 2006, 38, 158-167.	9.4	110
51	Human chromosome 11 DNA sequence and analysis including novel gene identification. <i>Nature</i> , 2006, 440, 497-500.	13.7	74
52	A comprehensive analysis of allelic methylation status of CpG islands on human chromosome 11q: Comparison with chromosome 21q. <i>DNA Sequence</i> , 2006, 17, 300-306.	0.7	7
53	Identification of large ancient duplications associated with human gene deserts. <i>Nature Genetics</i> , 2005, 37, 1041-1043.	9.4	5
54	DNA sequence and analysis of human chromosome 18. <i>Nature</i> , 2005, 437, 551-555.	13.7	53

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55	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. <i>PLoS Biology</i> , 2004, 2, e162.	2.6	290
56	DNA sequence and comparative analysis of chimpanzee chromosome 22. <i>Nature</i> , 2004, 429, 382-388.	13.7	212
57	After 'completion': the changing face of human chromosomes 21 and 22. <i>Genome Biology</i> , 2004, 5, 111.	13.9	0
58	Human Versus Chimpanzee Chromosome-wide Sequence Comparison and Its Evolutionary Implication. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2003, 68, 455-460.	2.0	8
59	Construction and Analysis of a Human-Chimpanzee Comparative Clone Map. <i>Science</i> , 2002, 295, 131-134.	6.0	228
60	Identification of Two Novel Primate-Specific Genes in DSCR. <i>DNA Research</i> , 2002, 9, 89-97.	1.5	18
61	Comparative Genomic Sequence Analysis of the Human Chromosome 21 Down Syndrome Critical Region. <i>Genome Research</i> , 2002, 12, 1323-1332.	2.4	48
62	Architecture and anatomy of the genomic locus encoding the human leukemia-associated transcription factor RUNX1/AML1. <i>Gene</i> , 2001, 262, 23-33.	1.0	123
63	Molecular cloning and characterization of a gene expressed in mouse developing tongue, mDscr5 gene, a homolog of human DSCR5 (Down syndrome Critical Region gene 5). <i>Mammalian Genome</i> , 2001, 12, 347-351.	1.0	8
64	Part three in the book of genes. <i>Nature</i> , 2001, 414, 854-855.	13.7	7
65	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001, 409, 860-921.	13.7	21,074
66	The DNA sequence of human chromosome 21. <i>Nature</i> , 2000, 405, 311-319.	13.7	1,144
67	A Novel Gene, DSCR5, from the Distal Down Syndrome Critical Region on Chromosome 21q22.2. <i>DNA Research</i> , 2000, 7, 207-212.	1.5	4
68	Segregation analysis of Parkinson disease. , 1998, 80, 410-417.		19
69	Confirmation of Linkage of Clouston Syndrome (Hidrotic Ectodermal Dysplasia) to 13q11-q12.1 with Evidence for Multiple Independent Mutations. <i>Journal of Investigative Dermatology</i> , 1998, 111, 83-85.	0.3	29
70	Homozygosity mapping of Hallervordenâ€“Spatz syndrome to chromosome 20p12.3â€“p13. <i>Nature Genetics</i> , 1996, 14, 479-481.	9.4	158
71	Clouston Syndrome (Hidrotic Ectodermal Dysplasia) Is Not Linked to Keratin Gene Clusters on Chromosomes 12 and 17. <i>Journal of Investigative Dermatology</i> , 1996, 107, 11-14.	0.3	5