

# Tyson A Clark

## List of Publications by Year in descending order

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Version: 2024-02-01

72  
papers

11,950  
citations

34105

52  
h-index

79698

73  
g-index

77  
all docs

77  
docs citations

77  
times ranked

15418  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural and functional diversity among Type III restriction-modification systems that confer host DNA protection via methylation of the N4 atom of cytosine. PLoS ONE, 2021, 16, e0253267.	2.5	6
2	Universal Alternative Splicing of Noncoding Exons. Cell Systems, 2018, 6, 245-255.e5.	6.2	110
3	SMRT-Cappable-seq reveals complex operon variants in bacteria. Nature Communications, 2018, 9, 3676.	12.8	80
4	Detailed analysis of <i>HTT</i> repeat elements in human blood using targeted amplification-free long-read sequencing. Human Mutation, 2018, 39, 1262-1272.	2.5	62
5	Androgen Receptor Variant AR-V9 Is Coexpressed with AR-V7 in Prostate Cancer Metastases and Predicts Abiraterone Resistance. Clinical Cancer Research, 2017, 23, 4704-4715.	7.0	117
6	Complete Genome Sequence of Moraxella catarrhalis Strain CCRI-195ME, Isolated from the Middle Ear. Genome Announcements, 2017, 5, .	0.8	8
7	Methylomic and phenotypic analysis of the ModH5 phasevarion of Helicobacter pylori. Scientific Reports, 2017, 7, 16140.	3.3	35
8	Comparative Genomics Reveals the Diversity of Restriction-Modification Systems and DNA Methylation Sites in Listeria monocytogenes. Applied and Environmental Microbiology, 2017, 83, .	3.1	31
9	Methods for Genome-Wide Methylome Profiling of Campylobacter jejuni. Methods in Molecular Biology, 2017, 1512, 199-210.	0.9	1
10	Novel m4C modification in type I restriction-modification systems. Nucleic Acids Research, 2016, 44, gkw743.	14.5	23
11	Unveiling the complexity of the maize transcriptome by single-molecule long-read sequencing. Nature Communications, 2016, 7, 11708.	12.8	510
12	The Epigenomic Landscape of Prokaryotes. PLoS Genetics, 2016, 12, e1005854.	3.5	348
13	Genome-Wide Methylation Patterns in Salmonella enterica Subsp. enterica Serovars. PLoS ONE, 2015, 10, e0123639.	2.5	51
14	DNA Methylation Assessed by SMRT Sequencing Is Linked to Mutations in Neisseria meningitidis Isolates. PLoS ONE, 2015, 10, e0144612.	2.5	16
15	Genetic Stabilization of the Drug-Resistant PMEN1 Pneumococcus Lineage by Its Distinctive DpnIII Restriction-Modification System. MBio, 2015, 6, e00173.	4.1	31
16	Covalent Modification of Bacteriophage T4 DNA Inhibits CRISPR-Cas9. MBio, 2015, 6, e00648.	4.1	87
17	Defining the sequence requirements for the positioning of base J in DNA using SMRT sequencing. Nucleic Acids Research, 2015, 43, 2102-2115.	14.5	25
18	Specificity of the ModA11, ModA12 and ModD1 epigenetic regulator N6-adenine DNA methyltransferases of Neisseria meningitidis. Nucleic Acids Research, 2015, 43, 4150-4162.	14.5	58

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19	Complete Genome Sequence Analysis of <i>Bacillus subtilis</i> T30. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
20	Characterization of fusion genes and the significantly expressed fusion isoforms in breast cancer by hybrid sequencing. <i>Nucleic Acids Research</i> , 2015, 43, e116-e116.	14.5	104
21	A biphasic epigenetic switch controls immunoevasion, virulence and niche adaptation in non-typeable <i>Haemophilus influenzae</i> . <i>Nature Communications</i> , 2015, 6, 7828.	12.8	117
22	Identification of Restriction-Modification Systems of <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> CNCM I-2494 by SMRT Sequencing and Associated Methylome Analysis. <i>PLoS ONE</i> , 2014, 9, e94875.	2.5	25
23	A random six-phase switch regulates pneumococcal virulence via global epigenetic changes. <i>Nature Communications</i> , 2014, 5, 5055.	12.8	264
24	Simultaneous sequencing of oxidized methylcytosines produced by TET/JPB dioxygenases in <i>Coprinopsis cinerea</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E5149-58.	7.1	25
25	Genomic mapping of phosphorothioates reveals partial modification of short consensus sequences. <i>Nature Communications</i> , 2014, 5, 3951.	12.8	90
26	ModM DNA methyltransferase methylome analysis reveals a potential role for <i>Moraxella catarrhalis</i> phasevarions in otitis media. <i>FASEB Journal</i> , 2014, 28, 5197-5207.	0.5	73
27	Single-molecule sequencing to track plasmid diversity of hospital-associated carbapenemase-producing <i>Enterobacteriaceae</i> . <i>Science Translational Medicine</i> , 2014, 6, 254ra126.	12.4	307
28	Comparative genomics of enterohemorrhagic <i>Escherichia coli</i> O145:H28 demonstrates a common evolutionary lineage with <i>Escherichia coli</i> O157:H7. <i>BMC Genomics</i> , 2014, 15, 17.	2.8	84
29	Whole-Genome Assembly of <i>Klebsiella pneumoniae</i> Coproducing NDM-1 and OXA-232 Carbapenemases Using Single-Molecule, Real-Time Sequencing. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 5947-5953.	3.2	61
30	RNA motifs: prediction of multivalent RNA motifs that control alternative splicing. <i>Genome Biology</i> , 2014, 15, R20.	9.6	49
31	Complete Genome Sequences of Two <i>Escherichia coli</i> O145:H28 Outbreak Strains of Food Origin. <i>Genome Announcements</i> , 2014, 2, .	0.8	25
32	A comparative analysis of methylome profiles of <i>Campylobacter jejuni</i> sheep abortion isolate and gastroenteric strains using PacBio data. <i>Frontiers in Microbiology</i> , 2014, 5, 782.	3.5	24
33	Analysis of RNA base modification and structural rearrangement by single-molecule real-time detection of reverse transcription. <i>Journal of Nanobiotechnology</i> , 2013, 11, 8.	9.1	131
34	Enhanced 5-methylcytosine detection in single-molecule, real-time sequencing via Tet1 oxidation. <i>BMC Biology</i> , 2013, 11, 4.	3.8	125
35	Global methylation state at base-pair resolution of the <i>Caulobacter</i> genome throughout the cell cycle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E4658-67.	7.1	97
36	Modeling kinetic rate variation in third generation DNA sequencing data to detect putative modifications to DNA bases. <i>Genome Research</i> , 2013, 23, 129-141.	5.5	99

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37	Detecting DNA Modifications from SMRT Sequencing Data by Modeling Sequence Context Dependence of Polymerase Kinetic. PLoS Computational Biology, 2013, 9, e1002935.	3.2	67
38	Comprehensive Methylome Characterization of Mycoplasma genitalium and Mycoplasma pneumoniae at Single-Base Resolution. PLoS Genetics, 2013, 9, e1003191.	3.5	109
39	The methylomes of six bacteria. Nucleic Acids Research, 2012, 40, 11450-11462.	14.5	269
40	Characterization of DNA methyltransferase specificities using single-molecule, real-time DNA sequencing. Nucleic Acids Research, 2012, 40, e29-e29.	14.5	306
41	Genome-wide mapping of methylated adenine residues in pathogenic Escherichia coli using single-molecule real-time sequencing. Nature Biotechnology, 2012, 30, 1232-1239.	17.5	365
42	Sensitive and specific single-molecule sequencing of 5-hydroxymethylcytosine. Nature Methods, 2012, 9, 75-77.	19.0	219
43	Direct Detection and Sequencing of Damaged DNA Bases. Genome Integrity, 2011, 2, 10.	1.0	77
44	Human transcriptome array for high-throughput clinical studies. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 3707-3712.	7.1	122
45	Analysis of alternative splicing associated with aging and neurodegeneration in the human brain. Genome Research, 2011, 21, 1572-1582.	5.5	199
46	Aberrant alternative splicing and extracellular matrix gene expression in mouse models of myotonic dystrophy. Nature Structural and Molecular Biology, 2010, 17, 187-193.	8.2	301
47	Position-dependent alternative splicing activity revealed by global profiling of alternative splicing events regulated by PTB. Nature Structural and Molecular Biology, 2010, 17, 1114-1123.	8.2	218
48	Direct detection of DNA methylation during single-molecule, real-time sequencing. Nature Methods, 2010, 7, 461-465.	19.0	1,337
49	Exon-Level Microarray Analyses Identify Alternative Splicing Programs in Breast Cancer. Molecular Cancer Research, 2010, 8, 961-974.	3.4	121
50	Alternative splicing regulates mouse embryonic stem cell pluripotency and differentiation. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 10514-10519.	7.1	222
51	Affy exon tissues: exon levels in normal tissues in human, mouse and rat. Bioinformatics, 2009, 25, 2442-2443.	4.1	11
52	Identification of common genetic variants that account for transcript isoform variation between human populations. Human Genetics, 2009, 125, 81-93.	3.8	75
53	Alternative pre-mRNA splicing switches modulate gene expression in late erythropoiesis. Blood, 2009, 113, 3363-3370.	1.4	49
54	Evaluation of Genetic Variation Contributing to Differences in Gene Expression between Populations. American Journal of Human Genetics, 2008, 82, 631-640.	6.2	192

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55	HITS-CLIP yields genome-wide insights into brain alternative RNA processing. <i>Nature</i> , 2008, 456, 464-469.	27.8	1,245
56	Genetic Architecture of Transcript-Level Variation in Humans. <i>American Journal of Human Genetics</i> , 2008, 82, 1101-1113.	6.2	142
57	Evaluation of Genetic Variation Contributing to Differences in Gene Expression between Populations. <i>American Journal of Human Genetics</i> , 2008, 82, 1223.	6.2	2
58	A genome-wide approach to identify genetic variants that contribute to etoposide-induced cytotoxicity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 9758-9763.	7.1	195
59	Heritability of alternative splicing in the human genome. <i>Genome Research</i> , 2007, 17, 1210-1218.	5.5	101
60	A correlation with exon expression approach to identify cis-regulatory elements for tissue-specific alternative splicing. <i>Nucleic Acids Research</i> , 2007, 35, 4845-4857.	14.5	75
61	Ultraconserved elements are associated with homeostatic control of splicing regulators by alternative splicing and nonsense-mediated decay. <i>Genes and Development</i> , 2007, 21, 708-718.	5.9	470
62	Identification of Genetic Variants Contributing to Cisplatin-Induced Cytotoxicity by Use of a Genomewide Approach. <i>American Journal of Human Genetics</i> , 2007, 81, 427-437.	6.2	173
63	Discovery of tissue-specific exons using comprehensive human exon microarrays. <i>Genome Biology</i> , 2007, 8, R64.	9.6	255
64	Alternative splicing and differential gene expression in colon cancer detected by a whole genome exon array. <i>BMC Genomics</i> , 2006, 7, 325.	2.8	309
65	Unusual Intron Conservation near Tissue-Regulated Exons Found by Splicing Microarrays. <i>PLoS Computational Biology</i> , 2006, 2, e4.	3.2	175
66	Exploring functional relationships between components of the gene expression machinery. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 175-182.	8.2	89
67	Nova regulates brain-specific splicing to shape the synapse. <i>Nature Genetics</i> , 2005, 37, 844-852.	21.4	447
68	ANOSVA: a statistical method for detecting splice variation from expression data. <i>Bioinformatics</i> , 2005, 21, i107-i115.	4.1	50
69	Detection and measurement of alternative splicing using splicing-sensitive microarrays. <i>Methods</i> , 2005, 37, 345-359.	3.8	89
70	Gene structure-based splice variant deconvolution using a microarray platform. <i>Bioinformatics</i> , 2003, 19, i315-i322.	4.1	88
71	Genomewide Analysis of mRNA Processing in Yeast Using Splicing-Specific Microarrays. <i>Science</i> , 2002, 296, 907-910.	12.6	359
72	Removal of a Single $\beta$ -Tubulin Gene Intron Suppresses Cell Cycle Arrest Phenotypes of Splicing Factor Mutations in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 2002, 22, 801-815.	2.3	69