

# Tyson A Clark

## List of Publications by Year in descending order

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Version: 2024-02-01

72  
papers

11,950  
citations

39113

52  
h-index

90395

73  
g-index

77  
all docs

77  
docs citations

77  
times ranked

17248  
citing authors

#	ARTICLE	IF	CITATIONS
1	Direct detection of DNA methylation during single-molecule, real-time sequencing. <i>Nature Methods</i> , 2010, 7, 461-465.	9.0	1,337
2	HITS-CLIP yields genome-wide insights into brain alternative RNA processing. <i>Nature</i> , 2008, 456, 464-469.	13.7	1,245
3	Unveiling the complexity of the maize transcriptome by single-molecule long-read sequencing. <i>Nature Communications</i> , 2016, 7, 11708.	5.8	510
4	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.	2.7	470
5	Nova regulates brain-specific splicing to shape the synapse. <i>Nature Genetics</i> , 2005, 37, 844-852.	9.4	447
6	Genome-wide mapping of methylated adenine residues in pathogenic <i>Escherichia coli</i> using single-molecule real-time sequencing. <i>Nature Biotechnology</i> , 2012, 30, 1232-1239.	9.4	365
7	Genomewide Analysis of mRNA Processing in Yeast Using Splicing-Specific Microarrays. <i>Science</i> , 2002, 296, 907-910.	6.0	359
8	The Epigenomic Landscape of Prokaryotes. <i>PLoS Genetics</i> , 2016, 12, e1005854.	1.5	348
9	Alternative splicing and differential gene expression in colon cancer detected by a whole genome exon array. <i>BMC Genomics</i> , 2006, 7, 325.	1.2	309
10	Single-molecule sequencing to track plasmid diversity of hospital-associated carbapenemase-producing Enterobacteriaceae. <i>Science Translational Medicine</i> , 2014, 6, 254ra126.	5.8	307
11	Characterization of DNA methyltransferase specificities using single-molecule, real-time DNA sequencing. <i>Nucleic Acids Research</i> , 2012, 40, e29-e29.	6.5	306
12	Aberrant alternative splicing and extracellular matrix gene expression in mouse models of myotonic dystrophy. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 187-193.	3.6	301
13	The methylomes of six bacteria. <i>Nucleic Acids Research</i> , 2012, 40, 11450-11462.	6.5	269
14	A random six-phase switch regulates pneumococcal virulence via global epigenetic changes. <i>Nature Communications</i> , 2014, 5, 5055.	5.8	264
15	Discovery of tissue-specific exons using comprehensive human exon microarrays. <i>Genome Biology</i> , 2007, 8, R64.	13.9	255
16	Alternative splicing regulates mouse embryonic stem cell pluripotency and differentiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 10514-10519.	3.3	222
17	Sensitive and specific single-molecule sequencing of 5-hydroxymethylcytosine. <i>Nature Methods</i> , 2012, 9, 75-77.	9.0	219
18	Position-dependent alternative splicing activity revealed by global profiling of alternative splicing events regulated by PTB. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1114-1123.	3.6	218

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19	Analysis of alternative splicing associated with aging and neurodegeneration in the human brain. <i>Genome Research</i> , 2011, 21, 1572-1582.	2.4	199
20	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.	3.3	195
21	Evaluation of Genetic Variation Contributing to Differences in Gene Expression between Populations. <i>American Journal of Human Genetics</i> , 2008, 82, 631-640.	2.6	192
22	Unusual Intron Conservation near Tissue-Regulated Exons Found by Splicing Microarrays. <i>PLoS Computational Biology</i> , 2006, 2, e4.	1.5	175
23	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.	2.6	173
24	Genetic Architecture of Transcript-Level Variation in Humans. <i>American Journal of Human Genetics</i> , 2008, 82, 1101-1113.	2.6	142
25	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.	4.2	131
26	Enhanced 5-methylcytosine detection in single-molecule, real-time sequencing via Tet1 oxidation. <i>BMC Biology</i> , 2013, 11, 4.	1.7	125
27	Human transcriptome array for high-throughput clinical studies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 3707-3712.	3.3	122
28	Exon-Level Microarray Analyses Identify Alternative Splicing Programs in Breast Cancer. <i>Molecular Cancer Research</i> , 2010, 8, 961-974.	1.5	121
29	A biphasic epigenetic switch controls immunoevasion, virulence and niche adaptation in non-typeable <i>Haemophilus influenzae</i> . <i>Nature Communications</i> , 2015, 6, 7828.	5.8	117
30	Androgen Receptor Variant AR-V9 Is Coexpressed with AR-V7 in Prostate Cancer Metastases and Predicts Abiraterone Resistance. <i>Clinical Cancer Research</i> , 2017, 23, 4704-4715.	3.2	117
31	Universal Alternative Splicing of Noncoding Exons. <i>Cell Systems</i> , 2018, 6, 245-255.e5.	2.9	110
32	Comprehensive Methylome Characterization of <i>Mycoplasma genitalium</i> and <i>Mycoplasma pneumoniae</i> at Single-Base Resolution. <i>PLoS Genetics</i> , 2013, 9, e1003191.	1.5	109
33	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.	6.5	104
34	Heritability of alternative splicing in the human genome. <i>Genome Research</i> , 2007, 17, 1210-1218.	2.4	101
35	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.	2.4	99
36	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.	3.3	97

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37	Genomic mapping of phosphorothioates reveals partial modification of short consensus sequences. <i>Nature Communications</i> , 2014, 5, 3951.	5.8	90
38	Exploring functional relationships between components of the gene expression machinery. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 175-182.	3.6	89
39	Detection and measurement of alternative splicing using splicing-sensitive microarrays. <i>Methods</i> , 2005, 37, 345-359.	1.9	89
40	Gene structure-based splice variant deconvolution using a microarray platform. <i>Bioinformatics</i> , 2003, 19, i315-i322.	1.8	88
41	Covalent Modification of Bacteriophage T4 DNA Inhibits CRISPR-Cas9. <i>MBio</i> , 2015, 6, e00648.	1.8	87
42	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.	1.2	84
43	SMRT-Cappable-seq reveals complex operon variants in bacteria. <i>Nature Communications</i> , 2018, 9, 3676.	5.8	80
44	Direct Detection and Sequencing of Damaged DNA Bases. <i>Genome Integrity</i> , 2011, 2, 10.	1.0	77
45	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.	6.5	75
46	Identification of common genetic variants that account for transcript isoform variation between human populations. <i>Human Genetics</i> , 2009, 125, 81-93.	1.8	75
47	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.	0.2	73
48	Removal of a Single $\alpha$ -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.	1.1	69
49	Detecting DNA Modifications from SMRT Sequencing Data by Modeling Sequence Context Dependence of Polymerase Kinetic. <i>PLoS Computational Biology</i> , 2013, 9, e1002935.	1.5	67
50	Detailed analysis of <i>HTT</i> repeat elements in human blood using targeted amplification-free long-read sequencing. <i>Human Mutation</i> , 2018, 39, 1262-1272.	1.1	62
51	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.	1.4	61
52	Specificity of the ModA11, ModA12 and ModD1 epigenetic regulator N6-adenine DNA methyltransferases of <i>Neisseria meningitidis</i> . <i>Nucleic Acids Research</i> , 2015, 43, 4150-4162.	6.5	58
53	Genome-Wide Methylation Patterns in <i>Salmonella enterica</i> Subsp. <i>enterica</i> Serovars. <i>PLoS ONE</i> , 2015, 10, e0123639.	1.1	51
54	ANOSVA: a statistical method for detecting splice variation from expression data. <i>Bioinformatics</i> , 2005, 21, i107-i115.	1.8	50

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55	Alternative pre-mRNA splicing switches modulate gene expression in late erythropoiesis. <i>Blood</i> , 2009, 113, 3363-3370.	0.6	49
56	RNA motifs: prediction of multivalent RNA motifs that control alternative splicing. <i>Genome Biology</i> , 2014, 15, R20.	13.9	49
57	Methylomic and phenotypic analysis of the ModH5 phasevarion of <i>Helicobacter pylori</i> . <i>Scientific Reports</i> , 2017, 7, 16140.	1.6	35
58	Genetic Stabilization of the Drug-Resistant PMEN1 <i>Pneumococcus</i> Lineage by Its Distinctive DpnIII Restriction-Modification System. <i>MBio</i> , 2015, 6, e00173.	1.8	31
59	Comparative Genomics Reveals the Diversity of Restriction-Modification Systems and DNA Methylation Sites in <i>Listeria monocytogenes</i> . <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	31
60	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.	1.1	25
61	Simultaneous sequencing of oxidized methylcytosines produced by TET/JP 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.	3.3	25
62	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
63	Defining the sequence requirements for the positioning of base J in DNA using SMRT sequencing. <i>Nucleic Acids Research</i> , 2015, 43, 2102-2115.	6.5	25
64	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.	1.5	24
65	Novel m4C modification in type I restriction-modification systems. <i>Nucleic Acids Research</i> , 2016, 44, gkw743.	6.5	23
66	DNA Methylation Assessed by SMRT Sequencing Is Linked to Mutations in <i>Neisseria meningitidis</i> Isolates. <i>PLoS ONE</i> , 2015, 10, e0144612.	1.1	16
67	Affy exon tissues: exon levels in normal tissues in human, mouse and rat. <i>Bioinformatics</i> , 2009, 25, 2442-2443.	1.8	11
68	Complete Genome Sequence of <i>Moraxella catarrhalis</i> Strain CCRI-195ME, Isolated from the Middle Ear. <i>Genome Announcements</i> , 2017, 5, .	0.8	8
69	Structural and functional diversity among Type III restriction-modification systems that confer host DNA protection via methylation of the N4 atom of cytosine. <i>PLoS ONE</i> , 2021, 16, e0253267.	1.1	6
70	Complete Genome Sequence Analysis of <i>Bacillus subtilis</i> T30. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
71	Evaluation of Genetic Variation Contributing to Differences in Gene Expression between Populations. <i>American Journal of Human Genetics</i> , 2008, 82, 1223.	2.6	2
72	Methods for Genome-Wide Methylome Profiling of <i>Campylobacter jejuni</i> . <i>Methods in Molecular Biology</i> , 2017, 1512, 199-210.	0.4	1