## Aaron M Tarone

List of Publications by Year in descending order

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85541 109321 6,276 77 35 71 h-index citations g-index papers 80 80 80 7180 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Genome-wide association study of 107 phenotypes in Arabidopsis thaliana inbred lines. Nature, 2010, 465, 627-631.	27.8	1,651
2	Natural variation in genome architecture among 205 <i>Drosophila melanogaster</i> Genetic Reference Panel lines. Genome Research, 2014, 24, 1193-1208.	5 <b>.</b> 5	565
3	Population-Based Resequencing of Experimentally Evolved Populations Reveals the Genetic Basis of Body Size Variation in Drosophila melanogaster. PLoS Genetics, 2011, 7, e1001336.	3.5	265
4	The potential use of bacterial community succession in forensics as described by high throughput metagenomic sequencing. International Journal of Legal Medicine, 2014, 128, 193-205.	2.2	254
5	Genome Sequence of the Tsetse Fly ( <i>Glossina morsitans</i> ): Vector of African Trypanosomiasis. Science, 2014, 344, 380-386.	12.6	254
6	A Roadmap for Bridging Basic and Applied Research in Forensic Entomology. Annual Review of Entomology, 2011, 56, 401-421.	11.8	248
7	A rapidly evolving MYB-related protein causes species isolation in Drosophila. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 5302-5307.	7.1	243
8	Antitoxin MqsA helps mediate the bacterial general stress response. Nature Chemical Biology, 2011, 7, 359-366.	8.0	201
9	Microbial Community Functional Change during Vertebrate Carrion Decomposition. PLoS ONE, 2013, 8, e79035.	2.5	147
10	Human Thanatomicrobiome Succession and Time Since Death. Scientific Reports, 2016, 6, 29598.	3.3	136
11	Genome-wide survey of Arabidopsis natural variation in downy mildew resistance using combined association and linkage mapping. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 10302-10307.	7.1	120
12	A Survey of Bacterial Diversity From Successive Life Stages of Black Soldier Fly (Diptera:) Tj ETQq0 0 0 rgBT/Ove	rlock 10 Tf	f 50 302 Td (S
13	<i>Proteus mirabilis</i> interkingdom swarming signals attract blow flies. ISME Journal, 2012, 6, 1356-1366.	9.8	101
14	Pigs vs people: the use of pigs as analogues for humans in forensic entomology and taphonomy research. International Journal of Legal Medicine, 2020, 134, 793-810.	2.2	100
15	Population and Temperature Effects on <i>Lucilia sericata</i> (Diptera: Calliphoridae) Body Size and Minimum Development Time. Journal of Medical Entomology, 2011, 48, 1062-1068.	1.8	99
16	A metagenomic assessment of the bacteria associated with Lucilia sericata and Lucilia cuprina (Diptera:) Tj ETQq	0 0 0 rgBT	Overlock 10
17	Basic research in evolution and ecology enhances forensics. Trends in Ecology and Evolution, 2011, 26, 53-55.	8.7	87
18	Gene Expression During Blow Fly Development: Improving the Precision of Age Estimates in Forensic Entomology* <sup>,â€</sup> . Journal of Forensic Sciences, 2011, 56, S112-22.	1.6	87

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19	Delayed insect access alters carrion decomposition and necrophagous insect community assembly. Ecosphere, 2014, 5, 1-21.	2.2	86
20	Functional Divergence Caused by Ancient Positive Selection of a Drosophila Hybrid Incompatibility Locus. PLoS Biology, 2004, 2, e142.	5.6	85
21	Interkingdom responses of flies to bacteria mediated by fly physiology and bacterial quorum sensing. Animal Behaviour, 2012, 84, 1449-1456.	1.9	83
22	Bacteria Mediate Oviposition by the Black Soldier Fly, Hermetia illucens (L.), (Diptera: Stratiomyidae). Scientific Reports, 2013, 3, 2563.	3.3	83
23	Generalized Additive Models and <i>Lucilia sericata</i> Growth: Assessing Confidence Intervals and Error Rates in Forensic Entomology*. Journal of Forensic Sciences, 2008, 53, 942-948.	1.6	74
24	Components of Developmental Plasticity in a Michigan Population of <i>Lucilia sericata</i> (Diptera:) Tj ETQq0 0	0 rgBT /Ov	verlock 10 Tf 5
25	A Review of Bacterial Interactions With Blow Flies (Diptera: Calliphoridae) of Medical, Veterinary, and Forensic Importance. Annals of the Entomological Society of America, 2017, 110, 19-36.	2.5	71
26	Intrapopulation Genome Size Variation in D. melanogaster Reflects Life History Variation and Plasticity. PLoS Genetics, 2014, 10, e1004522.	3.5	64
27	Aging Blow Fly Eggs Using Gene Expression: A Feasibility Study. Journal of Forensic Sciences, 2007, 52, 1350-1354.	1.6	59
28	Developmental variation among Cochliomyia macellaria Fabricius (Diptera: Calliphoridae) populations from three ecoregions of Texas, USA. International Journal of Legal Medicine, 2014, 128, 709-717.	2.2	55
29	Temporal and Spatial Impact of Human Cadaver Decomposition on Soil Bacterial and Arthropod Community Structure and Function. Frontiers in Microbiology, 2017, 8, 2616.	3.5	55
30	A <i>de novo</i> transcriptome assembly of <i>Lucilia sericata</i> (Diptera: Calliphoridae) with predicted alternative splices, single nucleotide polymorphisms and transcript expression estimates. Insect Molecular Biology, 2012, 21, 205-221.	2.0	52
31	Responses of Lucilia sericata (Diptera: Calliphoridae) to compounds from microbial decomposition of larval resources. Animal Behaviour, 2016, 115, 217-225.	1.9	46
32	Components of Developmental Plasticity in a Michigan Population of <i>Lucilia sericata</i> (Diptera:) Tj ETQq0 (	0 0 rgBT /C	Overlock 10 Tf
33	Mapping Genetically Compensatory Pathways from Synthetic Lethal Interactions in Yeast. PLoS ONE, 2008, 3, e1922.	2.5	41
34	Protecting the environment through insect farming as a means to produce protein for use as livestock, poultry, and aquaculture feed. Journal of Insects As Food and Feed, 2015, 1, 307-309.	3.9	39
35	Is PMI the Hypothesis or the Null Hypothesis?. Journal of Medical Entomology, 2017, 54, 1109-1115.	1.8	38
36	Genetic variation for expression of the sex determination pathway genes in Drosophila melanogaster. Genetical Research, 2005, 86, 31-40.	0.9	36

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37	The role of ants in vertebrate carrion decomposition. Food Webs, 2019, 18, e00109.	1.2	36
38	Genome Sizes of Forensically Relevant Diptera. Journal of Medical Entomology, 2012, 49, 192-197.	1.8	33
39	Machine learning performance in a microbial molecular autopsy context: A cross-sectional postmortem human population study. PLoS ONE, 2019, 14, e0213829.	2.5	32
40	Genetic variation in the Yolk protein expression network of Drosophila melanogaster: sex-biased negative correlations with longevity. Heredity, 2012, 109, 226-234.	2.6	28
41	The Role of Spatial Aggregation in Forensic Entomology: Table 1 Journal of Medical Entomology, 2014, 51, 1-9.	1.8	25
42	Sex Determination Mechanisms in the Calliphoridae (Blow Flies). Sexual Development, 2014, 8, 29-37.	2.0	25
43	Increasing Precision in Development-Based Postmortem Interval Estimates: What's Sex Got to Do With It?. Journal of Medical Entomology, 2013, 50, 425-431.	1.8	23
44	Functional characterization of calliphorid cell death genes and cellularization gene promoters for controlling gene expression and cell viability in early embryos. Insect Molecular Biology, 2015, 24, 58-70.	2.0	19
45	Suppressing tawny crazy ant (Nylanderia fulva) by RNAi technology. Insect Science, 2020, 27, 113-121.	3.0	19
46	The genome of the stable fly, Stomoxys calcitrans, reveals potential mechanisms underlying reproduction, host interactions, and novel targets for pest control. BMC Biology, 2021, 19, 41.	3.8	19
47	Interkingdom Cues by Bacteria Associated with Conspecific and Heterospecific Eggs of <i>Cochliomyia macellaria </i> and <i>Chrysomya rufifacies </i> (Diptera: Calliphoridae) Potentially Govern Succession on Carrion. Annals of the Entomological Society of America, 2017, 110, 73-82.	2.5	14
48	Structural and Genetic Investigation of the Egg and First-Instar Larva of an Egg-Laying Population of <i>Blaesoxipha plinthopyga</i> (Diptera: Sarcophagidae), a Species of Forensic Importance. Journal of Medical Entomology, 2014, 51, 1283-1295.	1.8	11
49	The upper thermal tolerance of the secondary screwworm, Cochliomyia macellaria Fabricius (Diptera:) Tj ETQq1	1 0,78431 2.5	4 rgBT /Oven
50	<scp>RNA</scp> meets toxicology: efficacy indicators from the experimental design of <scp>RNAi</scp> studies for insect pest management. Pest Management Science, 2022, 78, 3215-3225.	3.4	10
51	Field Documentation of Unusual Post-Mortem Arthropod Activity on Human Remains. Journal of Medical Entomology, 2015, 52, 105-108.	1.8	9
52	Impacts of dietary amino acid composition and microbial presence on preference and performance of immature <i>Lucilia sericata</i> (Diptera: Calliphoridae). Ecological Entomology, 2018, 43, 612-620.	2.2	9
53	Field Validation of a Development Data Set for Cochliomyia macellaria (Diptera: Calliphoridae): Estimating Insect Age Based on Development Stage. Journal of Medical Entomology, 2020, 57, 39-49.	1.8	9
54	Forensic Entomology: Evaluating Uncertainty Associated With Postmortem Interval (PMI) Estimates With Ecological Models. Journal of Medical Entomology, 2016, 53, 1117-1130.	1.8	7

#	Article	IF	Citations
55	A scalable and memory-efficient algorithm for de novo transcriptome assembly of non-model organisms. BMC Genomics, 2017, 18, 387.	2.8	7
56	The upper thermal tolerance for a Texas population of the hairy maggot blow flyChrysomya rufifaciesMacquart (Diptera: Calliphoridae). Ecological Entomology, 2020, 45, 1146-1157.	2.2	7
57	Wing buzzing as a potential antipredator defense against an invasive predator. Food Webs, 2021, 27, e00192.	1.2	7
58	The genomes of a monogenic fly: views of primitive sex chromosomes. Scientific Reports, 2020, 10, 15728.	3.3	6
59	Effect of Phenotype Selection on Genome Size Variation in Two Species of Diptera. Genes, 2020, 11, 218.	2.4	6
60	Reply: A Correspondence From a Maturing Discipline. Journal of Medical Entomology, 2014, 51, 490-492.	1.8	5
61	A memory-efficient algorithm to obtain splicing graphs and de novoexpression estimates from de Bruijn graphs of RNA-Seq data. BMC Genomics, 2014, 15, S6.	2.8	5
62	Introduction to Carrion Ecology, Evolution, and Their Applications. , 2015, , 3-12.		5
63	Genome Sequence of a <i>Proteus mirabilis</i> Strain Isolated from the Salivary Glands of Larval <i>Lucilia sericata</i> Genome Announcements, 2016, 4, .	0.8	5
64	Gene expression correlates of facultative predation in the blow fly Chrysomya rufifacies (Diptera:) Tj ETQq0 0 0	rgBT_{Ove	rlock 10 Tf 50
65	An Evaluation of Differentially Spliced Genes as Markers of Sex for Forensic Entomology,,. Journal of Forensic Sciences, 2020, 65, 1579-1587.	1.6	5
66	Heuristic pairwise alignment of de Bruijn graphs to facilitate simultaneous transcript discovery in related organisms from RNA-Seq data. BMC Genomics, 2015, 16, S5.	2.8	4
67	Genome Sequence of a Providencia stuartii Strain Isolated from <i>Lucilia sericata</i> Salivary Glands. Genome Announcements, 2017, 5, .	0.8	3
68	Evaluation of Development Datasets for <i>Hermetia illucens</i> (L.) (Diptera: Stratiomyidae) for Estimating the Time of Placement of Human and Swine Remains in Texas, USA. Journal of Medical Entomology, 2021, 58, 1654-1662.	1.8	3
69	Facultative Viviparity in a Flesh Fly (Diptera: Sarcophagidae): Forensic Implications of High Variability in Rates of Oviparity in Blaesoxipha plinthopyga (Diptera: Sarcophagidae). Journal of Medical Entomology, 2020, 57, 697-704.	1.8	2
70	The discrepancy between fire ant recruitment to and performance on rodent carrion. Scientific Reports, 2022, 12, 71.	3.3	2
71	Cloning and Functional Characterization of a Double-Stranded RNA-Degrading Nuclease in the Tawny Crazy Ant (Nylanderia fulva). Frontiers in Physiology, 2022, 13, 833652.	2.8	2
72	Sexual Dimorphism in Growth Rate and Gene Expression Throughout Immature Development in Wild Type Chrysomya rufifacies (Diptera: Calliphoridae) Macquart. Frontiers in Ecology and Evolution, 2021, 9, .	2.2	1

#	Article	IF	CITATIONS
73	A Fly in the Ointment: How to Predict Environmentally Driven Phenology of an Organism That Partially Regulates Its Microclimate. Frontiers in Ecology and Evolution, 2022, 10, .	2.2	1
74	A memory-efficient algorithm to obtain splicing graphs and de novo expression estimates from de bruijn graphs of RNA-seq data. , $2013$ , , .		0
75	A divide-and-conquer algorithm for large-scale de novo transcriptome assembly through combining small assemblies from existing algorithms. BMC Genomics, 2017, 18, 895.	2.8	O
76	Identifying similar transcripts in a related organism from de Bruijn graphs of RNA-Seq data, with applications to the study of salt and waterlogging tolerance in Melilotus. BMC Genomics, 2019, 20, 425.	2.8	0
77	Developmental Plasticity of the Flesh Fly Blaesoxipha plinthopyga (Diptera: Sarcophagidae) on Different Substrates. Journal of Medical Entomology, 2020, 57, 1686-1693.	1.8	0