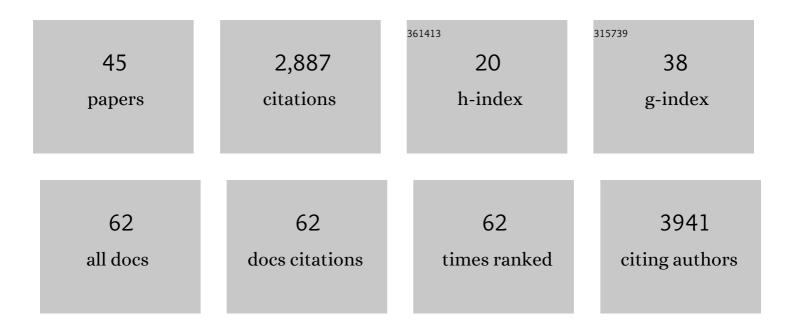
## Seth A Ament

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/690716/publications.pdf Version: 2024-02-01



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#	Article	IF	CITATIONS
1	Rare variants implicate NMDA receptor signaling and cerebellar gene networks in risk for bipolar disorder. Molecular Psychiatry, 2022, 27, 3842-3856.	7.9	5
2	Early and Late Transcriptional Changes in Blood, Neural, and Colon Tissues in Rat Models of Stress-Induced and Comorbid Pain Hypersensitivity Reveal Regulatory Roles in Neurological Disease. Frontiers in Pain Research, 2022, 3, .	2.0	1
3	Genetic versus stress and mood determinants of sleep in the Amish. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2021, 186, 113-121.	1.7	2
4	Multiple dimensions of stress vs. genetic effects on depression. Translational Psychiatry, 2021, 11, 254.	4.8	4
5	Single-Nucleus RNA-Seq Reveals Dysregulation of Striatal Cell Identity Due to Huntington's Disease Mutations. Journal of Neuroscience, 2021, 41, 5534-5552.	3.6	30
6	gEAR: Gene Expression Analysis Resource portal for community-driven, multi-omic data exploration. Nature Methods, 2021, 18, 843-844.	19.0	100
7	41. A RARE VARIANT IN D-AMINO ACID OXIDASE IMPLICATES NMDA RECEPTOR SIGNALING AND CEREBELLAR GENE NETWORKS IN RISK FOR BIPOLAR DISORDER. European Neuropsychopharmacology, 2021, 51, e63.	0.7	1
8	A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. Nature, 2021, 598, 103-110.	27.8	166
9	Single-cell epigenomics reveals mechanisms of human cortical development. Nature, 2021, 598, 205-213.	27.8	154
10	Comparative cellular analysis of motor cortex in human, marmoset and mouse. Nature, 2021, 598, 111-119.	27.8	361
11	A multimodal cell census and atlas of the mammalian primary motor cortex. Nature, 2021, 598, 86-102.	27.8	316
12	NeMO-AD, a new neuroscience multi-omic visualization and analysis platform for Alzheimer's disease research Alzheimer's and Dementia, 2021, 17 Suppl 3, e055686.	0.8	0
13	Biological insights from multi-omic analysis of 31 genomic risk loci for adult hearing difficulty. PLoS Genetics, 2020, 16, e1009025.	3.5	42
14	Atlas of Transcription Factor Binding Sites from ENCODE DNase Hypersensitivity Data across 27 Tissue Types. Cell Reports, 2020, 32, 108029.	6.4	28
15	Repeated sampling facilitates within- and between-subject modeling of the human sperm transcriptome to identify dynamic and stress-responsive sncRNAs. Scientific Reports, 2020, 10, 17498.	3.3	16
16	NeMO analyticsâ€AD: The neuroscience multiâ€omic visualization and analysis platform, now extended to support Alzheimer's disease. Alzheimer's and Dementia, 2020, 16, e046097.	0.8	0
17	Reproductive tract extracellular vesicles are sufficient to transmit intergenerational stress and program neurodevelopment. Nature Communications, 2020, 11, 1499.	12.8	125
18	Biological insights from multi-omic analysis of 31 genomic risk loci for adult hearing difficulty. , 2020, 16, e1009025.		0

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#	Article	IF	CITATIONS
19	Biological insights from multi-omic analysis of 31 genomic risk loci for adult hearing difficulty. , 2020, 16, e1009025.		0
20	Biological insights from multi-omic analysis of 31 genomic risk loci for adult hearing difficulty. , 2020, 16, e1009025.		0
21	Biological insights from multi-omic analysis of 31 genomic risk loci for adult hearing difficulty. , 2020, 16, e1009025.		0
22	Rediscovering the value of families for psychiatric genetics research. Molecular Psychiatry, 2019, 24, 523-535.	7.9	43
23	VARIANTS IN THE PROMOTER OF TRKB ARE ASSOCIATED WITH A GOOD RESPONSE TO LITHIUM IN BIPOLAR DISORDER. European Neuropsychopharmacology, 2019, 29, S965.	0.7	0
24	Whole Genome Sequencing Identifies CRISPLD2 as a Lung Function Gene in Children With Asthma. Chest, 2019, 156, 1068-1079.	0.8	5
25	Clinical and genetic validity of quantitative bipolarity. Translational Psychiatry, 2019, 9, 228.	4.8	4
26	Genome-Scale Transcriptional Regulatory Network Models of Psychiatric and Neurodegenerative Disorders. Cell Systems, 2019, 8, 122-135.e7.	6.2	45
27	Efficient region-based test strategy uncovers genetic risk factors for functional outcome in bipolar disorder. European Neuropsychopharmacology, 2019, 29, 156-170.	0.7	7
28	Transcriptional regulatory networks underlying gene expression changes in Huntington's disease. Molecular Systems Biology, 2018, 14, e7435.	7.2	55
29	Motivational, proteostatic and transcriptional deficits precede synapse loss, gliosis and neurodegeneration in the B6.HttQ111/+ model of Huntington's disease. Scientific Reports, 2017, 7, 41570.	3.3	16
30	High resolution time-course mapping of early transcriptomic, molecular and cellular phenotypes in Huntington's disease CAG knock-in mice across multiple genetic backgrounds. Human Molecular Genetics, 2017, 26, 913-922.	2.9	37
31	Lipid Metabolism, Abdominal Adiposity, and Cerebral Health in the Amish. Obesity, 2017, 25, 1876-1880.	3.0	8
32	Peripheral huntingtin silencing does not ameliorate central signs of disease in the B6.HttQ111/+ mouse model of Huntington's disease. PLoS ONE, 2017, 12, e0175968.	2.5	13
33	B18â€Transcriptome profiling of B6.HttQ111/+ hepatocytes in response to chemical perturbagens. Journal of Neurology, Neurosurgery and Psychiatry, 2016, 87, A15.2-A15.	1.9	0
34	Identification of copy number variants in whole-genome data using Reference Coverage Profiles. Frontiers in Genetics, 2015, 6, 45.	2.3	18
35	Rare variants in neuronal excitability genes influence risk for bipolar disorder. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3576-3581.	7.1	152
36	Diet and endocrine effects on behavioral maturation-related gene expression in the <i>pars intercerebralis</i> of the honey bee brain. Journal of Experimental Biology, 2015, 218, 4005-14.	1.7	17

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37	Cell type-specific genes show striking and distinct patterns of spatial expression in the mouse brain. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 3095-3100.	7.1	61
38	The Transcription Factor Ultraspiracle Influences Honey Bee Social Behavior and Behavior-Related Gene Expression. PLoS Genetics, 2012, 8, e1002596.	3.5	74
39	New meta-analysis tools reveal common transcriptional regulatory basis for multiple determinants of behavior. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1801-10.	7.1	52
40	Mechanisms of stable lipid loss in a social insect. Journal of Experimental Biology, 2011, 214, 3808-3821.	1.7	88
41	Behavior-specific changes in transcriptional modules lead to distinct and predictable neurogenomic states. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 18020-18025.	7.1	156
42	Nutritional regulation of division of labor in honey bees: toward a systems biology perspective. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2010, 2, 566-576.	6.6	100
43	Quantitative peptidomics reveal brain peptide signatures of behavior. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 2383-2388.	7.1	125
44	Insulin signaling is involved in the regulation of worker division of labor in honey bee colonies. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 4226-4231.	7.1	289
45	Polarization Reflecting Iridophores in the Arms of the Squid Loligo pealeii. Biological Bulletin, 2001, 201, 267-268.	1.8	16