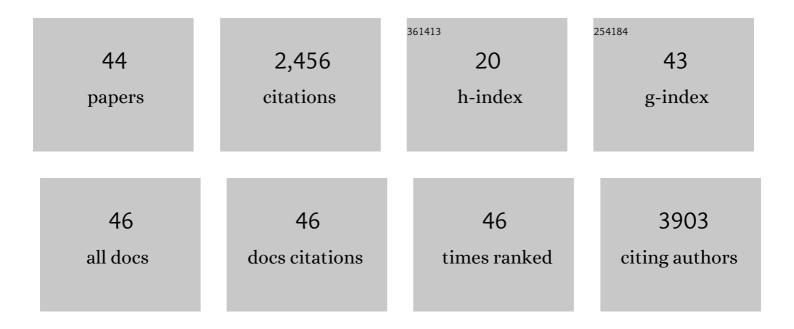
Robert E Settlage

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	A large nucleolar U3 ribonucleoprotein required for 18S ribosomal RNA biogenesis. Nature, 2002, 417, 967-970.	27.8	618
2	Androgen Receptor Phosphorylation. Journal of Biological Chemistry, 2002, 277, 29304-29314.	3.4	299
3	A Myosin I Isoform in the Nucleus. Science, 2000, 290, 337-341.	12.6	220
4	Host adaptive immunity alters gut microbiota. ISME Journal, 2015, 9, 770-781.	9.8	198
5	Biochemical Identification of a Mutated Human Melanoma Antigen Recognized by CD4+ T Cells. Journal of Experimental Medicine, 1999, 189, 757-766.	8.5	171
6	Alterations of a Cellular Cholesterol Metabolism Network Are a Molecular Feature of Obesity-Related Type 2 Diabetes and Cardiovascular Disease. Diabetes, 2015, 64, 3464-3474.	0.6	82
7	Immunodominance Among EBV-Derived Epitopes Restricted by HLA-B27 Does Not Correlate with Epitope Abundance in EBV-Transformed B-Lymphoblastoid Cell Lines. Journal of Immunology, 2000, 164, 6120-6129.	0.8	73
8	A Receptor for Activated C Kinase Is Part of Messenger Ribonucleoprotein Complexes Associated with PolyA-mRNAs in Neurons. Journal of Neuroscience, 2002, 22, 8827-8837.	3.6	66
9	A novel μ-ESI source for coupling capillary electrophoresis and mass spectrometry: Sequence determination of tumor peptides at the attomole level. Journal of Separation Science, 1998, 10, 281-285.	1.0	59
10	High Resolution Discovery Proteomics Reveals Candidate Disease Progression Markers of Alzheimer's Disease in Human Cerebrospinal Fluid. PLoS ONE, 2015, 10, e0135365.	2.5	57
11	Identification of the Surfactant Protein A Receptor 210 as the Unconventional Myosin 18A. Journal of Biological Chemistry, 2005, 280, 34447-34457.	3.4	49
12	Quantitative Analysis of Histone Deacetylase-1 Selective Histone Modifications by Differential Mass Spectrometry. Journal of Proteome Research, 2008, 7, 5177-5186.	3.7	45
13	Application of an End-to-End Biomarker Discovery Platform to Identify Target Engagement Markers in Cerebrospinal Fluid by High Resolution Differential Mass Spectrometry. Journal of Proteome Research, 2010, 9, 1392-1401.	3.7	45
14	Specific labeling of synaptic schwann cells reveals unique cellular and molecular features. ELife, 2020, 9, .	6.0	45
15	Proteomic Characterization of Messenger Ribonucleoprotein Complexes Bound to Nontranslated or Translated Poly(A) mRNAs in the Rat Cerebral Cortex. Journal of Biological Chemistry, 2005, 280, 6496-6503.	3.4	39
16	Discovery of Novel Antimicrobial Peptides from <i>Varanus komodoensis</i> (Komodo Dragon) by Large-Scale Analyses and De-Novo-Assisted Sequencing Using Electron-Transfer Dissociation Mass Spectrometry. Journal of Proteome Research, 2017, 16, 1470-1482.	3.7	39
17	Response of the Hepatic Transcriptome to Aflatoxin B1 in Domestic Turkey (Meleagris gallopavo). PLoS ONE, 2014, 9, e100930.	2.5	28
18	RNA-Seq Analysis of Developing Pecan (<i>Carya illinoinensis</i>) Embryos Reveals Parallel Expression Patterns among Allergen and Lipid Metabolism Genes. Journal of Agricultural and Food Chemistry, 2017, 65, 1443-1455.	5.2	27

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19	Modulation of the spleen transcriptome in domestic turkey (Meleagris gallopavo) in response to aflatoxin B1 and probiotics. Immunogenetics, 2015, 67, 163-178.	2.4	24
20	<i>Fusobacterium</i> Genomics Using MinION and Illumina Sequencing Enables Genome Completion and Correction. MSphere, 2018, 3, .	2.9	23
21	Characterizing the Genetic Basis for Nicotine Induced Cancer Development: A Transcriptome Sequencing Study. PLoS ONE, 2013, 8, e67252.	2.5	22
22	Genomic Signatures of Speciation in Sympatric and Allopatric Hawaiian Picture-Winged <i>Drosophila</i> . Genome Biology and Evolution, 2016, 8, 1482-1488.	2.5	21
23	Identification of peptidase substrates in human plasma by FTMS based differential mass spectrometry. International Journal of Mass Spectrometry, 2007, 259, 174-183.	1.5	20
24	The ABRF Proteomics Research Group Studies: Educational exercises for qualitative and quantitative proteomic analyses. Proteomics, 2011, 11, 1371-1381.	2.2	18
25	Cutting Edge: Plasmacytoid Dendritic Cells in Late-Stage Lupus Mice Defective in Producing IFN-α. Journal of Immunology, 2015, 195, 4578-4582.	0.8	18
26	Gene Expression Profiling of Human Vaginal Cells In Vitro Discriminates Compounds with Pro-Inflammatory and Mucosa-Altering Properties: Novel Biomarkers for Preclinical Testing of HIV Microbicide Candidates. PLoS ONE, 2015, 10, e0128557.	2.5	17
27	The Beginning of the End: A Chromosomal Assembly of the New World Malaria Mosquito Ends with a Novel Telomere. G3: Genes, Genomes, Genetics, 2020, 10, 3811-3819.	1.8	17
28	The microRNA miRâ€133b functions to slow Duchenne muscular dystrophy pathogenesis. Journal of Physiology, 2021, 599, 171-192.	2.9	15
29	Revised Genome Sequence of Brucella suis 1330. Journal of Bacteriology, 2011, 193, 6410-6410.	2.2	13
30	The Endoribonuclease RNase E Coordinates Expression of mRNAs and Small Regulatory RNAs and Is Critical for the Virulence of Brucella abortus. Journal of Bacteriology, 2020, 202, .	2.2	12
31	Differential Mass Spectrometry of Rat Plasma Reveals Proteins That Are Responsive to 17Î2-Estradiol and a Selective Estrogen Receptor Modulator PPT. Journal of Proteome Research, 2008, 7, 4373-4383.	3.7	11
32	Hypothalamic differences in expression of genes involved in monoamine synthesis and signaling pathways after insulin injection in chickens from lines selected for high and low body weight. Neurogenetics, 2015, 16, 133-144.	1.4	11
33	Complete Genome Sequence of Brucella suis VBI22, Isolated from Bovine Milk. Journal of Bacteriology, 2012, 194, 910-910.	2.2	10
34	Targeted capture enrichment and sequencing identifies extensive nucleotide variation in the turkey MHC-B. Immunogenetics, 2016, 68, 219-229.	2.4	6
35	Roles of the proteasome and inhibitor of DNA binding 1 protein in myoblast differentiation. FASEB Journal, 2019, 33, 7403-7416.	0.5	6
36	Improved variation calling via an iterative backbone remapping and local assembly method for bacterial genomes. Genomics, 2012, 100, 271-276.	2.9	5

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#	Article	IF	CITATIONS
37	Estimating transient populations of unmarked individuals at a migratory stopover site using generalized Nâ€mixture models. Journal of Applied Ecology, 2018, 55, 2917-2932.	4.0	5

Major histocompatibility complex genes and locus organization in the Komodo dragon (Varanus) Tj ETQq000 rgBT_2/Qverlock 10 Tf 50 7

39	Next-generation sequencing strategies for characterizing the turkey genome. Poultry Science, 2014, 93, 479-484.	3.4	4
40	Open OnDemand: State of the platform, project, and the future. Concurrency Computation Practice and Experience, 2021, 33, e6114.	2.2	4
41	Open OnDemand: HPC for Everyone. Lecture Notes in Computer Science, 2019, , 504-513.	1.3	3
42	A database of global coastal conditions. Scientific Data, 2021, 8, 304.	5.3	2
43	Open OnDemand as a Platformfor Virtual Learning in Higher Education. Lecture Notes in Networks and Systems, 2022, , 323-331.	0.7	1
44	Portals for Interactive Steering of HPC Workflows. Communications in Computer and Information Science, 2020, , 179-189.	0.5	0