

# Jay R Hesselberth

## List of Publications by Year in descending order

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Version: 2024-02-01

65  
papers

3,848  
citations

147801

31  
h-index

144013

57  
g-index

86  
all docs

86  
docs citations

86  
times ranked

6820  
citing authors

#	ARTICLE	IF	CITATIONS
1	Global mapping of protein-DNA interactions in vivo by digital genomic footprinting. <i>Nature Methods</i> , 2009, 6, 283-289.	19.0	533
2	Venetoclax with azacitidine disrupts energy metabolism and targets leukemia stem cells in patients with acute myeloid leukemia. <i>Nature Medicine</i> , 2018, 24, 1859-1866.	30.7	496
3	A protein interaction network of the malaria parasite <i>Plasmodium falciparum</i> . <i>Nature</i> , 2005, 438, 103-107.	27.8	480
4	Automated selection of aptamers against protein targets translated in vitro: from gene to aptamer. <i>Nucleic Acids Research</i> , 2002, 30, 108e-108.	14.5	155
5	The <i>RtcB</i> RNA ligase is an essential component of the metazoan unfolded protein response. <i>EMBO Reports</i> , 2014, 15, 1278-1285.	4.5	139
6	Single-cell RNA sequencing identifies TGF- $\beta$ 2 as a key regenerative cue following LPS-induced lung injury. <i>JCI Insight</i> , 2019, 4, .	5.0	111
7	Ribose-seq: global mapping of ribonucleotides embedded in genomic DNA. <i>Nature Methods</i> , 2015, 12, 251-257.	19.0	101
8	In Vitro Selection of RNA Molecules That Inhibit the Activity of Ricin A-chain. <i>Journal of Biological Chemistry</i> , 2000, 275, 4937-4942.	3.4	91
9	In vitro selection of nucleic acids for diagnostic applications. <i>Reviews in Molecular Biotechnology</i> , 2000, 74, 15-25.	2.8	90
10	High resolution mapping of modified DNA nucleobases using excision repair enzymes. <i>Genome Research</i> , 2014, 24, 1534-1542.	5.5	81
11	TCR signal strength controls thymic differentiation of iNKT cell subsets. <i>Nature Communications</i> , 2018, 9, 2650.	12.8	79
12	Simultaneous detection of diverse analytes with an aptazyme ligase array. <i>Analytical Biochemistry</i> , 2003, 312, 106-112.	2.4	73
13	clustifyr: an R package for automated single-cell RNA sequencing cluster classification. <i>F1000Research</i> , 2020, 9, 223.	1.6	71
14	Genome-Wide Analysis of miRNA-mRNA Interactions in Marrow Stromal Cells. <i>Stem Cells</i> , 2014, 32, 662-673.	3.2	67
15	HITS-CLIP reveals key regulators of nuclear receptor signaling in breast cancer. <i>Breast Cancer Research and Treatment</i> , 2014, 146, 85-97.	2.5	66
16	Binding specificity of Toll-like receptor cytoplasmic domains. <i>European Journal of Immunology</i> , 2006, 36, 742-753.	2.9	63
17	Lives that introns lead after splicing. <i>Wiley Interdisciplinary Reviews RNA</i> , 2013, 4, 677-691.	6.4	63
18	Mitochondrial energy failure in HSD10 disease is due to defective mtDNA transcript processing. <i>Mitochondrion</i> , 2015, 21, 1-10.	3.4	55

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19	Neoplastic and immune single-cell transcriptomics define subgroup-specific intra-tumoral heterogeneity of childhood medulloblastoma. <i>Neuro-Oncology</i> , 2022, 24, 273-286.	1.2	52
20	valr: Reproducible genome interval analysis in R. <i>F1000Research</i> , 2017, 6, 1025.	1.6	50
21	Capture and sequence analysis of RNAs with terminal 2'3'-cyclic phosphates. <i>Rna</i> , 2010, 16, 621-631.	3.5	49
22	RNase L Targets Distinct Sites in Influenza A Virus RNAs. <i>Journal of Virology</i> , 2015, 89, 2764-2776.	3.4	49
23	Chronic Liver Disease in Humans Causes Expansion and Differentiation of Liver Lymphatic Endothelial Cells. <i>Frontiers in Immunology</i> , 2019, 10, 1036.	4.8	47
24	Single-Cell RNA Sequencing of Childhood Ependymoma Reveals Neoplastic Cell Subpopulations That Impact Molecular Classification and Etiology. <i>Cell Reports</i> , 2020, 32, 108023.	6.4	47
25	Ribonuclease L and metal-ion-independent endoribonuclease cleavage sites in host and viral RNAs. <i>Nucleic Acids Research</i> , 2014, 42, 5202-5216.	14.5	46
26	A dynamic Bayesian network for identifying protein-binding footprints from single molecule-based sequencing data. <i>Bioinformatics</i> , 2010, 26, i334-i342.	4.1	43
27	Computational selection of nucleic acid biosensors via a slip structure model. <i>Biosensors and Bioelectronics</i> , 2007, 22, 1939-1947.	10.1	40
28	Global analysis of RNA cleavage by 5'-hydroxyl RNA sequencing. <i>Nucleic Acids Research</i> , 2015, 43, e108-e108.	14.5	39
29	Diverse fates of uracilated HIV-1 DNA during infection of myeloid lineage cells. <i>ELife</i> , 2016, 5, .	6.0	37
30	Genome-wide identification of spliced introns using a tiling microarray. <i>Genome Research</i> , 2007, 17, 503-509.	5.5	36
31	Improvements to the HITS-CLIP protocol eliminate widespread mispriming artifacts. <i>BMC Genomics</i> , 2016, 17, 338.	2.8	36
32	Optimization and optimality of a short ribozyme ligase that joins non-Watson-Crick base pairings. <i>Rna</i> , 2001, 7, 513-523.	3.5	35
33	A homolog of lariat-debranching enzyme modulates turnover of branched RNA. <i>Rna</i> , 2014, 20, 1337-1348.	3.5	34
34	Dynamic temperature-sensitive A-to-I RNA editing in the brain of a heterothermic mammal during hibernation. <i>Rna</i> , 2018, 24, 1481-1495.	3.5	31
35	Enhanced stability and polyadenylation of select mRNAs support rapid thermogenesis in the brown fat of a hibernator. <i>ELife</i> , 2015, 4, .	6.0	29
36	High-throughput profiling of amino acids in strains of the <i>Saccharomyces cerevisiae</i> deletion collection. <i>Genome Research</i> , 2010, 20, 1288-1296.	5.5	28

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37	Physiologic RNA targets and refined sequence specificity of coronavirus EndoU. <i>Rna</i> , 2020, 26, 1976-1999.	3.5	24
38	Comprehensive in vivo RNA-binding site analyses reveal a role of Prp8 in spliceosomal assembly. <i>Nucleic Acids Research</i> , 2013, 41, 3805-3818.	14.5	22
39	Multiple decay events target HAC1 mRNA during splicing to regulate the unfolded protein response. <i>ELife</i> , 2019, 8, .	6.0	21
40	clustifyr: an R package for automated single-cell RNA sequencing cluster classification. <i>F1000Research</i> , 2020, 9, 223.	1.6	21
41	Alternative Polyadenylation of <i>PRELID1</i> Regulates Mitochondrial ROS Signaling and Cancer Outcomes. <i>Molecular Cancer Research</i> , 2017, 15, 1741-1751.	3.4	19
42	Genetic bypass of essential RNA repair enzymes in budding yeast. <i>Rna</i> , 2018, 24, 313-323.	3.5	19
43	Molecular tracking devices quantify antigen distribution and archiving in the murine lymph node. <i>ELife</i> , 2021, 10, .	6.0	18
44	MARCO lymphatic endothelial cells sequester arthritogenic alphaviruses to limit viremia and viral dissemination. <i>EMBO Journal</i> , 2021, 40, e108966.	7.8	18
45	Coordination between <i>Drosophila</i> Arc1 and a specific population of brain neurons regulates organismal fat. <i>Developmental Biology</i> , 2015, 405, 280-290.	2.0	17
46	Recovery and analysis of transcriptome subsets from pooled single-cell RNA-seq libraries. <i>Nucleic Acids Research</i> , 2019, 47, e20-e20.	14.5	16
47	Switching nucleic acids for antibodies. <i>Nature Biotechnology</i> , 2001, 19, 313-314.	17.5	14
48	Redistribution of EC-SOD resolves bleomycin-induced inflammation via increased apoptosis of recruited alveolar macrophages. <i>FASEB Journal</i> , 2019, 33, 13465-13475.	0.5	14
49	Dynamic RNA Regulation in the Brain Underlies Physiological Plasticity in a Hibernating Mammal. <i>Frontiers in Physiology</i> , 2020, 11, 624677.	2.8	10
50	Haploinsufficiency, Dominant Negative, and Gain-of-Function Mechanisms in Epilepsy: Matching Therapeutic Approach to the Pathophysiology. <i>Neurotherapeutics</i> , 2021, 18, 1500-1514.	4.4	9
51	Enhancing Hematopoiesis from Murine Embryonic Stem Cells through MLL1-Induced Activation of a Rac/Rho/Integrin Signaling Axis. <i>Stem Cell Reports</i> , 2020, 14, 285-299.	4.8	8
52	Cell-level metadata are indispensable for documenting single-cell sequencing datasets. <i>PLoS Biology</i> , 2021, 19, e3001077.	5.6	7
53	A (ribo) switch in the paradigms of genetic regulation. <i>Nature Structural Biology</i> , 2002, 9, 891-893.	9.7	6
54	Localization of Cdc7 Protein Kinase During DNA Replication in <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3757-3774.	1.8	6

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55	Simultaneous measurement of biochemical phenotypes and gene expression in single cells. <i>Nucleic Acids Research</i> , 2020, 48, e59-e59.	14.5	6
56	Combinatorial methods: aptamers and aptazymes. , 1999, 3858, 126.		5
57	High-Resolution Mapping of Modified DNA Nucleobases Using Excision Repair Enzymes. <i>Methods in Molecular Biology</i> , 2018, 1672, 63-76.	0.9	5
58	O Cdc7 kinase where art thou?. <i>Current Genetics</i> , 2018, 64, 677-680.	1.7	1
59	High Throughput Sequencing Following Cross-Linked Immune Precipitation (HITS-CLIP) of Argonaute (AGO) Identifies Mir-9 As a Regulator of MMP2 in the Marrow Microenvironment (ME). <i>Blood</i> , 2011, 118, 2392-2392.	1.4	1
60	Nucleosome patterning evolution: steady aim despite moving targets. <i>Molecular Systems Biology</i> , 2010, 6, 376.	7.2	0
61	EPEN-21. SINGLE CELL RNASEQ IDENTIFIES A PUTATIVE CANCER STEM CELL POPULATION IN POSTERIOR FOSSA EPN. <i>Neuro-Oncology</i> , 2018, 20, i77-i77.	1.2	0
62	High Throughput Sequencing Following Cross-Linked Immune Precipitation (HITS-CLIP) of Argonaute (AGO) Identifies Mir-193a as a Regulator of Jagged1 In Marrow Stromal Cells.. <i>Blood</i> , 2010, 116, 3847-3847.	1.4	0
63	Ribose-seq: ribonucleotides in DNA to Illumina library. <i>Protocol Exchange</i> , 0, , .	0.3	0
64	MBRS-46. CHARTING NEOPLASTIC AND IMMUNE CELL HETEROGENEITY IN HUMAN AND GEM MODELS OF MEDULLOBLASTOMA USING scRNAseq. <i>Neuro-Oncology</i> , 2020, 22, iii406-iii406.	1.2	0
65	EPEN-31. SINGLE-CELL RNAseq OF CHILDHOOD EPENDYMOMA REVEALS DISTINCT NEOPLASTIC CELL SUBPOPULATIONS THAT IMPACT ETIOLOGY, MOLECULAR CLASSIFICATION AND OUTCOME. <i>Neuro-Oncology</i> , 2020, 22, iii314-iii314.	1.2	0