## Tyra G Wolfsberg

## List of Publications by Year in Descending Order

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Version: 2024-04-27

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

72	11,299	34	78
papers	citations	h-index	g-index
78	12,654 ext. citations	11	6.04
ext. papers		avg, IF	L-index

#	Paper	IF	Citations
72	AniProtDB: A Collection of Consistently Generated Metazoan Proteomes for Comparative Genomics Studies. <i>Molecular Biology and Evolution</i> , <b>2021</b> , 38, 4628-4633	8.3	1
71	Perceptions of uncertainties about carrier results identified by exome sequencing in a randomized controlled trial. <i>Translational Behavioral Medicine</i> , <b>2020</b> , 10, 441-450	3.2	1
70	De novo assembly of the goldfish () genome and the evolution of genes after whole-genome duplication. <i>Science Advances</i> , <b>2019</b> , 5, eaav0547	14.3	66
69	Multiple non-catalytic ADAMs are novel integrin & ligands. <i>Molecular and Cellular Biochemistry</i> , <b>2018</b> , 442, 29-38	4.2	7
68	Mapping Complex Traits in a Diversity Outbred F1 Mouse Population Identifies Germline Modifiers of Metastasis in Human Prostate Cancer. <i>Cell Systems</i> , <b>2017</b> , 4, 31-45.e6	10.6	31
67	CRISPRz: a database of zebrafish validated sgRNAs. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, D822-6	20.1	32
66	A 2.5-year snapshot of Mendelian discovery. <i>Molecular Genetics &amp; amp; Genomic Medicine</i> , <b>2016</b> , 4, 392-4	2.3	7
65	MLV integration site selection is driven by strong enhancers and active promoters. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, 4257-69	20.1	74
64	A customized Web portal for the genome of the ctenophore Mnemiopsis leidyi. <i>BMC Genomics</i> , <b>2014</b> , 15, 316	4.5	15
63	Mutational analysis of the tyrosine kinome in serous and clear cell endometrial cancer uncovers rare somatic mutations in TNK2 and DDR1. <i>BMC Cancer</i> , <b>2014</b> , 14, 884	4.8	12
62	trieFinder: an efficient program for annotating Digital Gene Expression (DGE) tags. <i>BMC Bioinformatics</i> , <b>2014</b> , 15, 329	3.6	2
61	The genome of the ctenophore Mnemiopsis leidyi and its implications for cell type evolution. <i>Science</i> , <b>2013</b> , 342, 1242592	33.3	466
60	Clinical genomic database. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 9851-5	11.5	75
59	A large-scale zebrafish gene knockout resource for the genome-wide study of gene function. <i>Genome Research</i> , <b>2013</b> , 23, 727-35	9.7	84
58	A multicenter study of glucocerebrosidase mutations in dementia with Lewy bodies. <i>JAMA Neurology</i> , <b>2013</b> , 70, 727-35	17.2	285
57	The Zebrafish Insertion Collection (ZInC): a web based, searchable collection of zebrafish mutations generated by DNA insertion. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D861-4	20.1	25
56	High-efficiency transduction of rhesus hematopoietic repopulating cells by a modified HIV1-based lentiviral vector. <i>Molecular Therapy</i> , <b>2012</b> , 20, 1882-92	11.7	30

## (2008-2012)

55	The stat3/socs3a pathway is a key regulator of hair cell regeneration in zebrafish. [corrected]. <i>Journal of Neuroscience</i> , <b>2012</b> , 32, 10662-73	6.6	72
54	Using the NCBI Map Viewer to browse genomic sequence data. <i>Current Protocols in Human Genetics</i> , <b>2011</b> , Chapter 18, Unit18.5	3.2	13
53	Predisposition to cancer caused by genetic and functional defects of mammalian Atad5. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1002245	6	55
52	High Transgene Expression Rates After Extended Follow up Among Rhesus Macaque Recipients of Autologous Hematopoietic Stem Cells Transduced with a Modified HIV1-Based Lentiviral Vector. <i>Blood</i> , <b>2011</b> , 118, 3118-3118	2.2	
51	Feline leukemia virus integrase and capsid packaging functions do not change the insertion profile of standard Moloney retroviral vectors. <i>Gene Therapy</i> , <b>2010</b> , 17, 799-804	4	5
50	A curated online resource for SOX10 and pigment cell molecular genetic pathways. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2010</b> , 2010, baq025	5	6
49	Using the NCBI map viewer to browse genomic sequence data. <i>Current Protocols in Bioinformatics</i> , <b>2010</b> , Chapter 1, Unit 1.5.1-25	24.2	15
48	No evidence for clonal selection due to lentiviral integration sites in human induced pluripotent stem cells. <i>Stem Cells</i> , <b>2010</b> , 28, 687-94	5.8	32
47	Development and evaluation of new mask protocols for gene expression profiling in humans and chimpanzees. <i>BMC Bioinformatics</i> , <b>2009</b> , 10, 77	3.6	8
46	Matriptase-deficient mice exhibit ichthyotic skin with a selective shift in skin microbiota. <i>Journal of Investigative Dermatology</i> , <b>2009</b> , 129, 2435-42	4.3	49
45	Identifying putative promoter regions of Hermansky-Pudlak syndrome genes by means of phylogenetic footprinting. <i>Annals of Human Genetics</i> , <b>2009</b> , 73, 422-8	2.2	2
44	Multicenter analysis of glucocerebrosidase mutations in Parkinson's disease. <i>New England Journal of Medicine</i> , <b>2009</b> , 361, 1651-61	59.2	1351
43	Gpnmb is a melanoblast-expressed, MITF-dependent gene. <i>Pigment Cell and Melanoma Research</i> , <b>2009</b> , 22, 99-110	4.5	42
42	Sustained high-level polyclonal hematopoietic marking and transgene expression 4 years after autologous transplantation of rhesus macaques with SIV lentiviral vector-transduced CD34+ cells. <i>Blood</i> , <b>2009</b> , 113, 5434-43	2.2	43
41	Analysis of Viral Integration Sites in Human Induced Pluripotent Stem Cells <i>Blood</i> , <b>2009</b> , 114, 1485-148	<b>35</b> .2	1
40	DNA methylation profiles in diffuse large B-cell lymphoma and their relationship to gene expression status. <i>Leukemia</i> , <b>2008</b> , 22, 1035-43	10.7	78
39	A diversity profile of the human skin microbiota. <i>Genome Research</i> , <b>2008</b> , 18, 1043-50	9.7	665
38	Identification of neural crest and glial enhancers at the mouse Sox10 locus through transgenesis in zebrafish. <i>PLoS Genetics</i> , <b>2008</b> , 4, e1000174	6	89

37	Reduced genotoxicity of avian sarcoma leukosis virus vectors in rhesus long-term repopulating cells compared to standard murine retrovirus vectors. <i>Molecular Therapy</i> , <b>2008</b> , 16, 1617-23	11.7	34
36	Informatic and genomic analysis of melanocyte cDNA libraries as a resource for the study of melanocyte development and function. <i>Pigment Cell &amp; Melanoma Research</i> , <b>2007</b> , 20, 201-9		3
35	The ENCODEdb portal: simplified access to ENCODE Consortium data. <i>Genome Research</i> , <b>2007</b> , 17, 954-	<b>9</b> 9.7	13
34	Using the NCBI Map Viewer to browse genomic sequence data. <i>Current Protocols in Bioinformatics</i> , <b>2007</b> , Chapter 1, Unit 1.5	24.2	7
33	Distinctive Integration Profile of Avian Sarcoma Leukosis Virus Vectors in Rhesus Long-Term Repopulating Cells <i>Blood</i> , <b>2007</b> , 110, 198-198	2.2	0
32	DNase-chip: a high-resolution method to identify DNase I hypersensitive sites using tiled microarrays. <i>Nature Methods</i> , <b>2006</b> , 3, 503-9	21.6	188
31	Genome-wide mapping of DNase hypersensitive sites using massively parallel signature sequencing (MPSS). <i>Genome Research</i> , <b>2006</b> , 16, 123-31	9.7	363
30	A 200 kb Survey of Chromatin in the ANK-1 Locus Demonstrates an Erythroid-Specific Chromatin Hub That Activates the Erythrocyte Ankyrin (ANK-1E) Promoter <i>Blood</i> , <b>2006</b> , 108, 536-536	2.2	
29	Introduction to the ADAM Family <b>2005</b> , 1-28		4
28	Global regulation by the yeast Spt10 protein is mediated through chromatin structure and the histone upstream activating sequence elements. <i>Molecular and Cellular Biology</i> , <b>2005</b> , 25, 9127-37	4.8	50
27	Identifying gene regulatory elements by genome-wide recovery of DNase hypersensitive sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2004</b> , 101, 992-7	11.5	150
26	Short interfering RNAs can induce unexpected and divergent changes in the levels of untargeted proteins in mammalian cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2004</b> , 101, 1892-7	11.5	488
25	Distinct genomic integration of MLV and SIV vectors in primate hematopoietic stem and progenitor cells. <i>PLoS Biology</i> , <b>2004</b> , 2, e423	9.7	213
24	GeneLink: a database to facilitate genetic studies of complex traits. <i>BMC Genomics</i> , <b>2004</b> , 5, 81	4.5	7
23	The ENCODE (ENCyclopedia Of DNA Elements) Project. Science, 2004, 306, 636-40	33.3	1692
22	Analysis of Retroviral Vector Insertion Sites after T-Cell Directed Gene Therapy <i>Blood</i> , <b>2004</b> , 104, 289-2	2 <u>89</u>	9
21	ADAM metalloproteinases <b>2004</b> , 709-714		1
20	Guide to the draft human genome. <i>Nature</i> , <b>2001</b> , 409, 824-6	50.4	39

19	Organelle genome resource at NCBI. <i>Trends in Biochemical Sciences</i> , <b>2001</b> , 26, 199-203	10.3	23
18	Web alert. Oncogenes and cell proliferation. <i>Current Opinion in Genetics and Development</i> , <b>2001</b> , 11, 9-7	104.9	
17	Chromosomes and expression mechanisms. Web alert. <i>Current Opinion in Genetics and Development</i> , <b>2001</b> , 11, 119	4.9	
16	Identification of motifs in protein sequences. <i>Current Protocols in Cell Biology</i> , <b>2001</b> , Appendix 1, Appendix 1C	2.3	
15	Sequence similarity searching using the BLAST family of programs. <i>Current Protocols in Molecular Biology</i> , <b>2001</b> , Chapter 19, Unit 19.3	2.9	6
14	Sequence similarity searching using the BLAST family of programs. <i>Current Protocols in Protein Science</i> , <b>2001</b> , Chapter 2, Unit2.5	3.1	4
13	Sequence Similarity Searching Using the BLAST Family of Programs. <i>Current Protocols in Human Genetics</i> , <b>2000</b> , 27, 6.8.1	3.2	
12	Web alert. Pattern formation and developmental mechanisms. <i>Current Opinion in Genetics and Development</i> , <b>2000</b> , 10, 345-6	4.9	
11	Genomes and evolution. Web alert. Current Opinion in Genetics and Development, 1999, 9, 619	4.9	
10	Candidate Regulatory Sequence Elements for Cell Cycle-Dependent Transcription in Saccharomyces cerevisiae. <i>Genome Research</i> , <b>1999</b> , 9, 775-792	9.7	36
9	A genome-wide transcriptional analysis of the mitotic cell cycle. <i>Molecular Cell</i> , <b>1998</b> , 2, 65-73	17.6	1659
8	A comparison of expressed sequence tags (ESTs) to human genomic sequences. <i>Nucleic Acids Research</i> , <b>1997</b> , 25, 1626-32	20.1	105
7	ADAM 13: a novel ADAM expressed in somitic mesoderm and neural crest cells during Xenopus laevis development. <i>Developmental Biology</i> , <b>1997</b> , 182, 314-30	3.1	99
6	Virus-cell and cell-cell fusion. Annual Review of Cell and Developmental Biology, 1996, 12, 627-61	12.6	500
5	ADAMs in fertilization and development. <i>Developmental Biology</i> , <b>1996</b> , 180, 389-401	3.1	229
4	ADAM, a novel family of membrane proteins containing A Disintegrin And Metalloprotease domain: multipotential functions in cell-cell and cell-matrix interactions. <i>Journal of Cell Biology</i> , <b>1995</b> , 131, 275-	8 <sup>7.3</sup>	442
3	ADAM, a widely distributed and developmentally regulated gene family encoding membrane proteins with a disintegrin and metalloprotease domain. <i>Developmental Biology</i> , <b>1995</b> , 169, 378-83	3.1	365
2	The precursor region of a protein active in sperm-egg fusion contains a metalloprotease and a disintegrin domain: structural, functional, and evolutionary implications. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1993</b> , 90, 10783-7	11.5	159

A potential fusion peptide and an integrin ligand domain in a protein active in sperm-egg fusion. Nature, **1992**, 356, 248-52

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