

Albertha Jm Walhout

List of Publications by Citations

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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.

95
papers

8,022
citations

45
h-index

89
g-index

111
ext. papers

9,592
ext. citations

14.3
avg, IF

5.92
L-index

#	Paper	IF	Citations
95	Evidence for dynamically organized modularity in the yeast protein-protein interaction network. <i>Nature</i> , 2004 , 430, 88-93	50.4	1381
94	GATEWAY recombinational cloning: application to the cloning of large numbers of open reading frames or ORFeomes. <i>Methods in Enzymology</i> , 2000 , 328, 575-92	1.7	496
93	Integrating OmicInformation: a bridge between genomics and systems biology. <i>Trends in Genetics</i> , 2003 , 19, 551-60	8.5	363
92	Widespread macromolecular interaction perturbations in human genetic disorders. <i>Cell</i> , 2015 , 161, 647-660	9.7	343
91	Gene regulatory networks and the role of robustness and stochasticity in the control of gene expression. <i>Genome Research</i> , 2011 , 21, 645-57	9.7	209
90	High-throughput yeast two-hybrid assays for large-scale protein interaction mapping. <i>Methods</i> , 2001 , 24, 297-306	4.6	208
89	Chromatin immunoprecipitation (ChIP) coupled to detection by quantitative real-time PCR to study transcription factor binding to DNA in <i>Caenorhabditis elegans</i> . <i>Nature Protocols</i> , 2008 , 3, 698-709	18.8	205
88	A multiparameter network reveals extensive divergence between <i>C. elegans</i> bHLH transcription factors. <i>Cell</i> , 2009 , 138, 314-27	56.2	196
87	A gene-centered <i>C. elegans</i> protein-DNA interaction network. <i>Cell</i> , 2006 , 125, 1193-205	56.2	194
86	The interplay between transcription factors and microRNAs in genome-scale regulatory networks. <i>BioEssays</i> , 2009 , 31, 435-45	4.1	181
85	A <i>C. elegans</i> genome-scale microRNA network contains composite feedback motifs with high flux capacity. <i>Genes and Development</i> , 2008 , 22, 2535-49	12.6	178
84	Diet-induced developmental acceleration independent of TOR and insulin in <i>C. elegans</i> . <i>Cell</i> , 2013 , 153, 240-52	56.2	170
83	Genome-scale spatiotemporal analysis of <i>Caenorhabditis elegans</i> microRNA promoter activity. <i>Genome Research</i> , 2008 , 18, 2005-15	9.7	162
82	A gateway-compatible yeast one-hybrid system. <i>Genome Research</i> , 2004 , 14, 2093-101	9.7	162
81	Integrating interactome, phenome, and transcriptome mapping data for the <i>C. elegans</i> germline. <i>Current Biology</i> , 2002 , 12, 1952-8	6.3	157
80	A protein-protein interaction map of the <i>Caenorhabditis elegans</i> 26S proteasome. <i>EMBO Reports</i> , 2001 , 2, 821-8	6.5	156
79	A compendium of <i>Caenorhabditis elegans</i> regulatory transcription factors: a resource for mapping transcription regulatory networks. <i>Genome Biology</i> , 2005 , 6, R110	18.3	142

78	Using networks to measure similarity between genes: association index selection. <i>Nature Methods</i> , 2013 , 10, 1169-76	21.6	141
77	A first version of the Caenorhabditis elegans Promoterome. <i>Genome Research</i> , 2004 , 14, 2169-75	9.7	133
76	A stele-enriched gene regulatory network in the Arabidopsis root. <i>Molecular Systems Biology</i> , 2011 , 7, 459	12.2	127
75	Unraveling transcription regulatory networks by protein-DNA and protein-protein interaction mapping. <i>Genome Research</i> , 2006 , 16, 1445-54	9.7	121
74	Bacterial Metabolism Affects the C. elegans Response to Cancer Chemotherapeutics. <i>Cell</i> , 2017 , 169, 431-441.e8	56.2	120
73	Protein interaction maps for model organisms. <i>Nature Reviews Molecular Cell Biology</i> , 2001 , 2, 55-62	48.7	118
72	Interspecies systems biology uncovers metabolites affecting C. elegans gene expression and life history traits. <i>Cell</i> , 2014 , 156, 759-70	56.2	111
71	C. elegans 14-3-3 proteins regulate life span and interact with SIR-2.1 and DAF-16/FOXO. <i>Mechanisms of Ageing and Development</i> , 2006 , 127, 741-7	5.6	107
70	Insight into transcription factor gene duplication from Caenorhabditis elegans Promoterome-driven expression patterns. <i>BMC Genomics</i> , 2007 , 8, 27	4.5	103
69	Enhanced Y1H assays for Arabidopsis. <i>Nature Methods</i> , 2011 , 8, 1053-5	21.6	92
68	C. elegans tubby regulates life span and fat storage by two independent mechanisms. <i>Cell Metabolism</i> , 2005 , 2, 35-42	24.6	91
67	Enhanced yeast one-hybrid assays for high-throughput gene-centered regulatory network mapping. <i>Nature Methods</i> , 2011 , 8, 1059-64	21.6	82
66	Integration of metabolic and gene regulatory networks modulates the C. elegans dietary response. <i>Cell</i> , 2013 , 153, 253-66	56.2	81
65	Human gene-centered transcription factor networks for enhancers and disease variants. <i>Cell</i> , 2015 , 161, 661-673	56.2	80
64	Transcription factor modularity in a gene-centered C. elegans core neuronal protein-DNA interaction network. <i>Genome Research</i> , 2007 , 17, 1061-71	9.7	80
63	c-Myc/Max heterodimers bind cooperatively to the E-box sequences located in the first intron of the rat ornithine decarboxylase (ODC) gene. <i>Nucleic Acids Research</i> , 1997 , 25, 1493-501	20.1	69
62	Functional modularity of nuclear hormone receptors in a Caenorhabditis elegans metabolic gene regulatory network. <i>Molecular Systems Biology</i> , 2010 , 6, 367	12.2	65
61	Complex expression dynamics and robustness in C. elegans insulin networks. <i>Genome Research</i> , 2013 , 23, 954-65	9.7	64

60	Matrix and Steiner-triple-system smart pooling assays for high-performance transcription regulatory network mapping. <i>Nature Methods</i> , 2007 , 4, 659-64	21.6	59
59	A Caenorhabditis elegans Genome-Scale Metabolic Network Model. <i>Cell Systems</i> , 2016 , 2, 297-311	10.6	55
58	Extensive rewiring and complex evolutionary dynamics in a C. elegans multiparameter transcription factor network. <i>Molecular Cell</i> , 2013 , 51, 116-27	17.6	55
57	Using a structural and logics systems approach to infer bHLH-DNA binding specificity determinants. <i>Nucleic Acids Research</i> , 2011 , 39, 4553-63	20.1	54
56	Metabolic network rewiring of propionate flux compensates vitamin B12 deficiency in C. elegans. <i>ELife</i> , 2016 , 5,	8.9	51
55	Worms, bacteria, and micronutrients: an elegant model of our diet. <i>Trends in Genetics</i> , 2014 , 30, 496-503	8.5	50
54	A genetic strategy to eliminate self-activator baits prior to high-throughput yeast two-hybrid screens. <i>Genome Research</i> , 1999 , 9, 1128-34	9.7	48
53	Mapping and analysis of Caenorhabditis elegans transcription factor sequence specificities. <i>ELife</i> , 2015 , 4,	8.9	48
52	RNA Interference in Caenorhabditis elegans. <i>Current Protocols in Molecular Biology</i> , 2015 , 109, 26.3.1-26.3.30	3.0	46
51	What does biologically meaningful mean? A perspective on gene regulatory network validation. <i>Genome Biology</i> , 2011 , 12, 109	18.3	45
50	C. elegans and its bacterial diet as a model for systems-level understanding of host-microbiota interactions. <i>Current Opinion in Biotechnology</i> , 2017 , 46, 74-80	11.4	41
49	Yeast one-hybrid assays for gene-centered human gene regulatory network mapping. <i>Nature Methods</i> , 2011 , 8, 1050-2	21.6	41
48	Transcription Factor Activity Mapping of a Tissue-Specific Gene Regulatory Network. <i>Cell Systems</i> , 2015 , 1, 152-162	10.6	40
47	The FLYWCH transcription factors FLH-1, FLH-2, and FLH-3 repress embryonic expression of microRNA genes in C. elegans. <i>Genes and Development</i> , 2008 , 22, 2520-34	12.6	40
46	Metabolic network modeling with model organisms. <i>Current Opinion in Chemical Biology</i> , 2017 , 36, 32-39	9.7	39
45	Chromosome-biased binding and gene regulation by the Caenorhabditis elegans DRM complex. <i>PLoS Genetics</i> , 2011 , 7, e1002074	6	39
44	A gene-centered C. elegans protein-DNA interaction network provides a framework for functional predictions. <i>Molecular Systems Biology</i> , 2016 , 12, 884	12.2	39
43	WormPaths: metabolic pathway annotation and visualization 2020 ,		36

42	Gene-centered regulatory networks. <i>Briefings in Functional Genomics</i> , 2010 , 9, 4-12	4.9	35
41	WormCat: An Online Tool for Annotation and Visualization of Genome-Scale Data. <i>Genetics</i> , 2020 , 214, 279-294	4	33
40	Gateway Recombinational Cloning. <i>Cold Spring Harbor Protocols</i> , 2018 , 2018,	1.2	31
39	The C. elegans Snail homolog CES-1 can activate gene expression in vivo and share targets with bHLH transcription factors. <i>Nucleic Acids Research</i> , 2009 , 37, 3689-98	20.1	30
38	EDGEdb: a transcription factor-DNA interaction database for the analysis of C. elegans differential gene expression. <i>BMC Genomics</i> , 2007 , 8, 21	4.5	29
37	Understanding Metabolic Regulation at a Systems Level: Metabolite Sensing, Mathematical Predictions, and Model Organisms. <i>Annual Review of Genetics</i> , 2015 , 49, 553-75	14.5	26
36	The Oxidative Stress Response in Requires the GATA Transcription Factor ELT-3 and SKN-1/Nrf2. <i>Genetics</i> , 2017 , 206, 1909-1922	4	23
35	A compendium of Caenorhabditis elegans RNA binding proteins predicts extensive regulation at multiple levels. <i>G3: Genes, Genomes, Genetics</i> , 2013 , 3, 297-304	3.2	22
34	Food, pathogen, signal: The multifaceted nature of a bacterial diet. <i>Worm</i> , 2013 , 2, e26454		20
33	Caenorhabditis elegans metabolic gene regulatory networks govern the cellular economy. <i>Trends in Endocrinology and Metabolism</i> , 2014 , 25, 502-8	8.8	17
32	A model of elegance. <i>American Journal of Human Genetics</i> , 1998 , 63, 955-61	11	17
31	A Persistence Detector for Metabolic Network Rewiring in an Animal. <i>Cell Reports</i> , 2019 , 26, 460-468.e4	10.6	17
30	Transcription factor functionality and transcription regulatory networks. <i>Molecular BioSystems</i> , 2008 , 4, 309-14		16
29	A green fluorescent protein-based reverse two-hybrid system: application to the characterization of large numbers of potential protein-protein interactions. <i>Methods in Enzymology</i> , 2000 , 328, 74-88	1.7	16
28	A Delicate Balance between Bacterial Iron and Reactive Oxygen Species Supports Optimal C. elegans Development. <i>Cell Host and Microbe</i> , 2019 , 26, 400-411.e3	23.4	15
27	Gene-centered regulatory network mapping. <i>Methods in Cell Biology</i> , 2011 , 106, 271-88	1.8	15
26	lin-8, which antagonizes Caenorhabditis elegans Ras-mediated vulval induction, encodes a novel nuclear protein that interacts with the LIN-35 Rb protein. <i>Genetics</i> , 2005 , 171, 1017-31	4	15
25	Transcription factor binding to Caenorhabditis elegans first introns reveals lack of redundancy with gene promoters. <i>Nucleic Acids Research</i> , 2014 , 42, 153-62	20.1	14

24	E1A functions as a coactivator of retinoic acid-dependent retinoic acid receptor-beta 2 promoter activation. <i>Molecular Endocrinology</i> , 1993 , 7, 604-615		12
23	C. elegans MRP-5 Exports Vitamin B12 from Mother to Offspring to Support Embryonic Development. <i>Cell Reports</i> , 2018 , 22, 3126-3133	10.6	10
22	Gene-Centered Yeast One-Hybrid Assays. <i>Cold Spring Harbor Protocols</i> , 2016 , 2016,	1.2	10
21	Generating Bait Strains for Yeast One-Hybrid Assays. <i>Cold Spring Harbor Protocols</i> , 2016 , 2016,	1.2	9
20	A regulatory cascade of three transcription factors in a single specific neuron, DVC, in <i>Caenorhabditis elegans</i> . <i>Gene</i> , 2012 , 494, 73-84	3.8	8
19	Integrated version of reverse two-hybrid system for the postproteomic era. <i>Methods in Enzymology</i> , 2002 , 350, 525-45	1.7	8
18	Modeling tissue-relevant <i>Caenorhabditis elegans</i> metabolism at network, pathway, reaction, and metabolite levels. <i>Molecular Systems Biology</i> , 2020 , 16, e9649	12.2	8
17	methionine/S-adenosylmethionine cycle activity is sensed and adjusted by a nuclear hormone receptor. <i>ELife</i> , 2020 , 9,	8.9	7
16	Multiple transcription factors directly regulate Hox gene lin-39 expression in ventral hypodermal cells of the <i>C. elegans</i> embryo and larva, including the hypodermal fate regulators LIN-26 and ELT-6. <i>BMC Developmental Biology</i> , 2014 , 14, 17	3.1	5
15	Many transcription factors contribute to <i>C. elegans</i> growth and fat storage. <i>Genes To Cells</i> , 2017 , 22, 770-784	2.3	5
14	Evolved bacterial resistance against fluoropyrimidines can lower chemotherapy impact in the host. <i>ELife</i> , 2020 , 9,	8.9	4
13	Generating Yeast One-Hybrid DNA-Bait Strains. <i>Cold Spring Harbor Protocols</i> , 2018 , 2018,	1.2	4
12	PRIMA: a gene-centered, RNA-to-protein method for mapping RNA-protein interactions. <i>Translation</i> , 2017 , 5, e1295130		2
11	Transcriptional regulation of metabolic flux: A <i>Caenorhabditis elegans</i> perspective. <i>Current Opinion in Systems Biology</i> , 2019 , 15, 12-18	3.2	2
10	If two deletions don't stop growth, try three. <i>Science</i> , 2018 , 360, 269-270	33.3	2
9	Genetic adaptation to diet preserves longevity. <i>Cell Metabolism</i> , 2014 , 19, 177-8	24.6	2
8	WormCat: an online tool for annotation and visualization of <i>Caenorhabditis elegans</i> genome-scale data		2
7	<i>C. elegans</i> and its bacterial diet: An interspecies model to explore the effects of microbiota on drug response. <i>Drug Discovery Today: Disease Models</i> , 2018 , 28, 21-26	1.3	2

6	Gateway-Compatible Yeast One-Hybrid and Two-Hybrid Assays. <i>Cold Spring Harbor Protocols</i> , 2018 , 2018,	1.2	2
5	Worms, bugs and drugs: <i>Caenorhabditis elegans</i> as a model for host-microbe-drug interactions. <i>Current Opinion in Systems Biology</i> , 2017 , 6, 46-50	3.2	0
4	Compartmentalization of metabolism between cell types in multicellular organisms: a computational perspective.. <i>Current Opinion in Systems Biology</i> , 2022 , 29, 100407-100407	3.2	0
3	Genomics in 2011: challenges and opportunities. <i>Genome Biology</i> , 2011 , 12, 137	18.3	
2	Marian Walhout: transcriptional mapmaker. Interviewed by Ben Short. <i>Journal of Cell Biology</i> , 2009 , 186, 4-5	7.3	
1	gene-centered regulatory networks. <i>FASEB Journal</i> , 2010 , 24, 314.1	0.9	