

# Albertha Jm Walhout

## List of Publications by Year in descending order

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96  
papers

10,533  
citations

41323

49  
h-index

42364

92  
g-index

111  
all docs

111  
docs citations

111  
times ranked

12510  
citing authors

#	ARTICLE	IF	CITATIONS
1	Evidence for dynamically organized modularity in the yeast protein-protein interaction network. <i>Nature</i> , 2004, 430, 88-93.	13.7	1,683
2	[34] GATEWAY recombinational cloning: Application to the cloning of large numbers of open reading frames or ORFs. <i>Methods in Enzymology</i> , 2000, 328, 575-587.	0.4	570
3	Widespread Macromolecular Interaction Perturbations in Human Genetic Disorders. <i>Cell</i> , 2015, 161, 647-660.	13.5	482
4	Integrating omic information: a bridge between genomics and systems biology. <i>Trends in Genetics</i> , 2003, 19, 551-560.	2.9	407
5	Gene regulatory networks and the role of robustness and stochasticity in the control of gene expression. <i>Genome Research</i> , 2011, 21, 645-657.	2.4	277
6	Diet-Induced Developmental Acceleration Independent of TOR and Insulin in <i>C. elegans</i> . <i>Cell</i> , 2013, 153, 240-252.	13.5	260
7	High-Throughput Yeast Two-Hybrid Assays for Large-Scale Protein Interaction Mapping. <i>Methods</i> , 2001, 24, 297-306.	1.9	258
8	A Multiparameter Network Reveals Extensive Divergence between <i>C. elegans</i> bHLH Transcription Factors. <i>Cell</i> , 2009, 138, 314-327.	13.5	242
9	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.	5.5	237
10	The interplay between transcription factors and microRNAs in genome-scale regulatory networks. <i>BioEssays</i> , 2009, 31, 435-445.	1.2	226
11	A Gene-Centered <i>C. elegans</i> Protein-DNA Interaction Network. <i>Cell</i> , 2006, 125, 1193-1205.	13.5	224
12	Bacterial Metabolism Affects the <i>C. elegans</i> Response to Cancer Chemotherapeutics. <i>Cell</i> , 2017, 169, 431-441.e8.	13.5	215
13	Using networks to measure similarity between genes: association index selection. <i>Nature Methods</i> , 2013, 10, 1169-1176.	9.0	209
14	Interspecies Systems Biology Uncovers Metabolites Affecting <i>C. elegans</i> Gene Expression and Life History Traits. <i>Cell</i> , 2014, 156, 759-770.	13.5	209
15	A <i>C. elegans</i> genome-scale microRNA network contains composite feedback motifs with high flux capacity. <i>Genes and Development</i> , 2008, 22, 2535-2549.	2.7	207
16	Genome-scale spatiotemporal analysis of <i>Caenorhabditis elegans</i> microRNA promoter activity. <i>Genome Research</i> , 2008, 18, 2005-2015.	2.4	190
17	A Gateway-Compatible Yeast One-Hybrid System. <i>Genome Research</i> , 2004, 14, 2093-2101.	2.4	189
18	A compendium of <i>Caenorhabditis elegans</i> regulatory transcription factors: a resource for mapping transcription regulatory networks. <i>Genome Biology</i> , 2005, 6, R110.	13.9	175

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19	A protein-protein interaction map of the <i>Caenorhabditis elegans</i> 26S proteasome. <i>EMBO Reports</i> , 2001, 2, 821-828.	2.0	173
20	Integrating Interactome, Phenome, and Transcriptome Mapping Data for the <i>C. elegans</i> Germline. <i>Current Biology</i> , 2002, 12, 1952-1958.	1.8	170
21	A First Version of the <i>Caenorhabditis elegans</i> Promoterome. <i>Genome Research</i> , 2004, 14, 2169-2175.	2.4	155
22	A stem-enriched gene regulatory network in the <i>Arabidopsis</i> root. <i>Molecular Systems Biology</i> , 2011, 7, 459.	3.2	145
23	Protein interaction maps for model organisms. <i>Nature Reviews Molecular Cell Biology</i> , 2001, 2, 55-63.	16.1	139
24	Unraveling transcription regulatory networks by protein-DNA and protein-protein interaction mapping. <i>Genome Research</i> , 2006, 16, 1445-1454.	2.4	136
25	Integration of Metabolic and Gene Regulatory Networks Modulates the <i>C. elegans</i> Dietary Response. <i>Cell</i> , 2013, 153, 253-266.	13.5	136
26	WormCat: An Online Tool for Annotation and Visualization of <i>Caenorhabditis elegans</i> Genome-Scale Data. <i>Genetics</i> , 2020, 214, 279-294.	1.2	125
27	Insight into transcription factor gene duplication from <i>Caenorhabditis elegans</i> Promoterome-driven expression patterns. <i>BMC Genomics</i> , 2007, 8, 27.	1.2	120
28	<i>C. elegans</i> 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, 741-747.	2.2	117
29	Enhanced yeast one-hybrid assays for high-throughput gene-centered regulatory network mapping. <i>Nature Methods</i> , 2011, 8, 1059-1064.	9.0	117
30	Enhanced Y1H assays for <i>Arabidopsis</i> . <i>Nature Methods</i> , 2011, 8, 1053-1055.	9.0	115
31	Human Gene-Centered Transcription Factor Networks for Enhancers and Disease Variants. <i>Cell</i> , 2015, 161, 661-673.	13.5	111
32	<i>C. elegans</i> tubby regulates life span and fat storage by two independent mechanisms. <i>Cell Metabolism</i> , 2005, 2, 35-42.	7.2	110
33	A <i>Caenorhabditis elegans</i> Genome-Scale Metabolic Network Model. <i>Cell Systems</i> , 2016, 2, 297-311.	2.9	96
34	Metabolic network rewiring of propionate flux compensates vitamin B12 deficiency in <i>C. elegans</i> . <i>ELife</i> , 2016, 5, .	2.8	96
35	RNA Interference in <i>Caenorhabditis elegans</i> . <i>Current Protocols in Molecular Biology</i> , 2015, 109, 26.3.1-26.3.30.	2.9	94
36	Functional modularity of nuclear hormone receptors in a <i>Caenorhabditis elegans</i> metabolic gene regulatory network. <i>Molecular Systems Biology</i> , 2010, 6, 367.	3.2	93

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37	Transcription factor modularity in a gene-centered <i>C. elegans</i> core neuronal protein-DNA interaction network. <i>Genome Research</i> , 2007, 17, 1061-1071.	2.4	87
38	Complex expression dynamics and robustness in <i>C. elegans</i> insulin networks. <i>Genome Research</i> , 2013, 23, 954-965.	2.4	87
39	Mapping and analysis of <i>Caenorhabditis elegans</i> transcription factor sequence specificities. <i>ELife</i> , 2015, 4, .	2.8	85
40	Extensive Rewiring and Complex Evolutionary Dynamics in a <i>C. elegans</i> Multiparameter Transcription Factor Network. <i>Molecular Cell</i> , 2013, 51, 116-127.	4.5	83
41	<i>C. elegans</i> 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.	3.3	82
42	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, 1493-1501.	6.5	77
43	Using a structural and logics systems approach to infer bHLH DNA binding specificity determinants. <i>Nucleic Acids Research</i> , 2011, 39, 4553-4563.	6.5	73
44	Worms, bacteria, and micronutrients: an elegant model of our diet. <i>Trends in Genetics</i> , 2014, 30, 496-503.	2.9	72
45	A gene-centered <i>C. elegans</i> protein-DNA interaction network provides a framework for functional predictions. <i>Molecular Systems Biology</i> , 2016, 12, 884.	3.2	71
46	Gateway Recombinational Cloning. <i>Cold Spring Harbor Protocols</i> , 2018, 2018, pdb.top094912.	0.2	65
47	Transcription Factor Activity Mapping of a Tissue-Specific In Vivo Gene Regulatory Network. <i>Cell Systems</i> , 2015, 1, 152-162.	2.9	64
48	Matrix and Steiner-triple-system smart pooling assays for high-performance transcription regulatory network mapping. <i>Nature Methods</i> , 2007, 4, 659-664.	9.0	62
49	Metabolic network modeling with model organisms. <i>Current Opinion in Chemical Biology</i> , 2017, 36, 32-39.	2.8	55
50	What does biologically meaningful mean? A perspective on gene regulatory network validation. <i>Genome Biology</i> , 2011, 12, 109.	13.9	54
51	Understanding Metabolic Regulation at a Systems Level: Metabolite Sensing, Mathematical Predictions, and Model Organisms. <i>Annual Review of Genetics</i> , 2015, 49, 553-575.	3.2	52
52	A Genetic Strategy to Eliminate Self-Activator Baits Prior to High-Throughput Yeast Two-Hybrid Screens. <i>Genome Research</i> , 1999, 9, 1128-1134.	2.4	51
53	The FLYWCH transcription factors FLH-1, FLH-2, and FLH-3 repress embryonic expression of microRNA genes in <i>C. elegans</i> . <i>Genes and Development</i> , 2008, 22, 2520-2534.	2.7	50
54	Chromosome-Biased Binding and Gene Regulation by the <i>Caenorhabditis elegans</i> DRM Complex. <i>PLoS Genetics</i> , 2011, 7, e1002074.	1.5	50

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55	A Persistence Detector for Metabolic Network Rewiring in an Animal. <i>Cell Reports</i> , 2019, 26, 460-468.e4.	2.9	50
56	Yeast one-hybrid assays for gene-centered human gene regulatory network mapping. <i>Nature Methods</i> , 2011, 8, 1050-1052.	9.0	48
57	<i>Caenorhabditis elegans</i> methionine/S-adenosylmethionine cycle activity is sensed and adjusted by a nuclear hormone receptor. <i>ELife</i> , 2020, 9, .	2.8	44
58	A Delicate Balance between Bacterial Iron and Reactive Oxygen Species Supports Optimal <i>C.Âelegans</i> Development. <i>Cell Host and Microbe</i> , 2019, 26, 400-411.e3.	5.1	43
59	Gene-centered regulatory networks. <i>Briefings in Functional Genomics</i> , 2010, 9, 4-12.	1.3	40
60	<i>Caenorhabditis elegans</i> metabolic gene regulatory networks govern the cellular economy. <i>Trends in Endocrinology and Metabolism</i> , 2014, 25, 502-508.	3.1	39
61	The Oxidative Stress Response in <i>Caenorhabditis elegans</i> Requires the GATA Transcription Factor ELT-3 and SKN-1/Nrf2. <i>Genetics</i> , 2017, 206, 1909-1922.	1.2	37
62	The <i>C. elegans</i> Snail homolog CES-1 can activate gene expression in vivo and share targets with bHLH transcription factors. <i>Nucleic Acids Research</i> , 2009, 37, 3689-3698.	6.5	36
63	Modeling tissueâ€relevant <i>Caenorhabditis elegans</i> metabolism at network, pathway, reaction, and metabolite levels. <i>Molecular Systems Biology</i> , 2020, 16, e9649.	3.2	32
64	A Compendium of <i>Caenorhabditis elegans</i> RNA Binding Proteins Predicts Extensive Regulation at Multiple Levels. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 297-304.	0.8	31
65	EDGEDb: a transcription factor-DNA Interaction database for the analysis of <i>C. elegans</i> differential gene expression. <i>BMC Genomics</i> , 2007, 8, 21.	1.2	30
66	Food, pathogen, signal. <i>Worm</i> , 2013, 2, e26454.	1.0	28
67	Transcription factor binding to <i>Caenorhabditis elegans</i> first introns reveals lack of redundancy with gene promoters. <i>Nucleic Acids Research</i> , 2014, 42, 153-162.	6.5	27
68	A Model of Elegance. <i>American Journal of Human Genetics</i> , 1998, 63, 955-961.	2.6	22
69	<i>C.Âelegans</i> MRP-5 Exports Vitamin B12 from Mother to Offspring to Support Embryonic Development. <i>Cell Reports</i> , 2018, 22, 3126-3133.	2.9	21
70	Transcription factor functionality and transcription regulatory networks. <i>Molecular BioSystems</i> , 2008, 4, 309.	2.9	20
71	[6] 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-IN1.	0.4	19
72	Gene-Centered Regulatory Network Mapping. <i>Methods in Cell Biology</i> , 2011, 106, 271-288.	0.5	19

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73	Evolved bacterial resistance against fluoropyrimidines can lower chemotherapy impact in the <i>Caenorhabditis elegans</i> host. <i>ELife</i> , 2020, 9, .	2.8	19
74	<i>lin-8</i> , Which Antagonizes <i>Caenorhabditis elegans</i> Ras-Mediated Vulval Induction, Encodes a Novel Nuclear Protein That Interacts With the LIN-35 Rb Protein. <i>Genetics</i> , 2005, 171, 1017-1031.	1.2	18
75	E1A functions as a coactivator of retinoic acid-dependent retinoic acid receptor-beta 2 promoter activation. <i>Molecular Endocrinology</i> , 1993, 7, 604-615.	3.7	13
76	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.	1.0	12
77	Gene-Centered Yeast One-Hybrid Assays. <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.top077669.	0.2	12
78	Generating Bait Strains for Yeast One-Hybrid Assays. <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.prot088948.	0.2	11
79	Integrated version of reverse two-hybrid system for the postproteomic era. <i>Methods in Enzymology</i> , 2002, 350, 525-545.	0.4	10
80	Many transcription factors contribute to <i>C.Âelegans</i> growth and fat storage. <i>Genes To Cells</i> , 2017, 22, 770-784.	0.5	9
81	Transcriptional regulation of metabolic flux: A <i>Caenorhabditis elegans</i> perspective. <i>Current Opinion in Systems Biology</i> , 2019, 15, 12-18.	1.3	9
82	A metabolic regulatory network for the <i>Caenorhabditis elegans</i> intestine. <i>IScience</i> , 2022, 25, 104688.	1.9	8
83	Multiple transcription factors directly regulate Hox gene <i>lin-39</i> 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.	2.1	5
84	<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.	1.2	5
85	Generating Yeast One-Hybrid DNA-Bait Strains. <i>Cold Spring Harbor Protocols</i> , 2018, 2018, pdb.prot094961.	0.2	5
86	Gateway-Compatible Yeast One-Hybrid and Two-Hybrid Assays. <i>Cold Spring Harbor Protocols</i> , 2018, 2018, pdb.top094953.	0.2	4
87	Genetic Adaptation to Diet Preserves Longevity. <i>Cell Metabolism</i> , 2014, 19, 177-178.	7.2	3
88	PRIMA: a gene-centered, RNA-to-protein method for mapping RNA-protein interactions. <i>Translation</i> , 2017, 5, e1295130.	2.9	2
89	If two deletions don't stop growth, try three. <i>Science</i> , 2018, 360, 269-270.	6.0	2
90	Compartmentalization of metabolism between cell types in multicellular organisms: A computational perspective. <i>Current Opinion in Systems Biology</i> , 2021, 29, 100407.	1.3	2

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91	Getting an edge on human disease. <i>Molecular Systems Biology</i> , 2009, 5, 322.	3.2	1
92	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.	1.3	1
93	Marian Walhout: Transcriptional mapmaker. <i>Journal of Cell Biology</i> , 2009, 186, 4-5.	2.3	0
94	As we come to the end of 2011, several members of the <i>Genome Biology</i> Editorial Board give their views on the state of play in genomics. <i>Genome Biology</i> , 2011, 12, 137.	13.9	0
95	Identifying Interactors from an Activation Domain Prey Library. <i>Cold Spring Harbor Protocols</i> , 2018, 2018, pdb.prot094987.	0.2	0
96	gene-centered regulatory networks. <i>FASEB Journal</i> , 2010, 24, 314.1.	0.2	0