

Marc Halfon

List of Publications by Year in descending order

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53
papers

2,905
citations

186265

28
h-index

175258

52
g-index

57
all docs

57
docs citations

57
times ranked

3698
citing authors

#	ARTICLE	IF	CITATIONS
1	Common Themes and Future Challenges in Understanding Gene Regulatory Network Evolution. <i>Cells</i> , 2022, 11, 510.	4.1	5
2	REDfly: An Integrated Knowledgebase for Insect Regulatory Genomics. <i>Insects</i> , 2022, 13, 618.	2.2	9
3	PeakMatcher facilitates updated <i>Aedes aegypti</i> embryonic cis-regulatory element map. <i>Hereditas</i> , 2021, 158, 7.	1.4	2
4	Identification of new <i>Anopheles gambiae</i> transcriptional enhancers using a cross-species prediction approach. <i>Insect Molecular Biology</i> , 2021, 30, 410-419.	2.0	8
5	Annotating the Insect Regulatory Genome. <i>Insects</i> , 2021, 12, 591.	2.2	4
6	Silencers, Enhancers, and the Multifunctional Regulatory Genome. <i>Trends in Genetics</i> , 2020, 36, 149-151.	6.7	24
7	Behavior-related gene regulatory networks: A new level of organization in the brain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 23270-23279.	7.1	52
8	How to study enhancers in non-traditional insect models. <i>Journal of Experimental Biology</i> , 2020, 223, .	1.7	5
9	Distinct roles and requirements for <i>Ras</i> pathway signaling in visceral versus somatic muscle founder specification. <i>Development (Cambridge)</i> , 2019, 146, .	2.5	3
10	Computational enhancer prediction: evaluation and improvements. <i>BMC Bioinformatics</i> , 2019, 20, 174.	2.6	12
11	CRM Discovery Beyond Model Insects. <i>Methods in Molecular Biology</i> , 2019, 1858, 117-139.	0.9	6
12	REDfly: the transcriptional regulatory element database for <i>Drosophila</i> . <i>Nucleic Acids Research</i> , 2019, 47, D828-D834.	14.5	59
13	Studying Transcriptional Enhancers: The Founder Fallacy, Validation Creep, and Other Biases. <i>Trends in Genetics</i> , 2019, 35, 93-103.	6.7	55
14	Enhancer identification and activity evaluation in the red flour beetle, <i>Tribolium castaneum</i> . <i>Development (Cambridge)</i> , 2018, 145, .	2.5	39
15	Perspectives on Gene Regulatory Network Evolution. <i>Trends in Genetics</i> , 2017, 33, 436-447.	6.7	66
16	Redeployment of a conserved gene regulatory network during <i>Aedes aegypti</i> development. <i>Developmental Biology</i> , 2016, 416, 402-413.	2.0	19
17	Identifying transcriptional cis-regulatory modules in animal genomes. <i>Wiley Interdisciplinary Reviews: Developmental Biology</i> , 2015, 4, 59-84.	5.9	54
18	Insect Regulatory Genomics. <i>True Bugs (Heteroptera) of the Neotropics</i> , 2015, , 119-155.	1.2	1

#	ARTICLE	IF	CITATIONS
19	Evidence for Deep Regulatory Similarities in Early Developmental Programs across Highly Diverged Insects. <i>Genome Biology and Evolution</i> , 2014, 6, 2301-2320.	2.5	37
20	REGULATION OF GENE EXPRESSION IN THE GENOMIC CONTEXT. <i>Computational and Structural Biotechnology Journal</i> , 2014, 9, e201401001.	4.1	40
21	Whole-Genome Analysis of Muscle Founder Cells Implicates the Chromatin Regulator Sin3A in Muscle Identity. <i>Cell Reports</i> , 2014, 8, 858-870.	6.4	23
22	Combinatorial Peptide Ligand Library Treatment Followed by a Dual-Enzyme, Dual-Activation Approach on a Nanoflow Liquid Chromatography/Orbitrap/Electron Transfer Dissociation System for Comprehensive Analysis of Swine Plasma Proteome. <i>Analytical Chemistry</i> , 2011, 83, 4802-4813.	6.5	49
23	Erroneous attribution of relevant transcription factor binding sites despite successful prediction of cis-regulatory modules. <i>BMC Genomics</i> , 2011, 12, 578.	2.8	13
24	REDfly v3.0: toward a comprehensive database of transcriptional regulatory elements in <i>Drosophila</i> . <i>Nucleic Acids Research</i> , 2011, 39, D118-D123.	14.5	152
25	Improved accuracy of supervised CRM discovery with interpolated Markov models and cross-species comparison. <i>Nucleic Acids Research</i> , 2011, 39, 9463-9472.	14.5	37
26	A wholly defined Agilent microarray spike-in dataset. <i>Bioinformatics</i> , 2011, 27, 1284-1289.	4.1	7
27	Preferred analysis methods for Affymetrix GeneChips. II. An expanded, balanced, wholly-defined spike-in dataset. <i>BMC Bioinformatics</i> , 2010, 11, 285.	2.6	31
28	Genome-wide search identifies <i>Ccnd2</i> as a direct transcriptional target of <i>Elf5</i> in mouse mammary gland. <i>BMC Molecular Biology</i> , 2010, 11, 68.	3.0	16
29	Identification of Receptor-Tyrosine-Kinase-Signaling Target Genes Reveals Receptor-Specific Activities and Pathway Branchpoints During <i>Drosophila</i> Development. <i>Genetics</i> , 2009, 181, 1335-1345.	2.9	8
30	Complex organizational structure of the genome revealed by genome-wide analysis of single and alternative promoters in <i>Drosophila melanogaster</i> . <i>BMC Genomics</i> , 2009, 10, 9.	2.8	17
31	Motif-Blind, Genome-Wide Discovery of cis-Regulatory Modules in <i>Drosophila</i> and Mouse. <i>Developmental Cell</i> , 2009, 17, 568-579.	7.0	60
32	Computational discovery of cis-regulatory modules in <i>Drosophila</i> without prior knowledge of motifs. <i>Genome Biology</i> , 2008, 9, R22.	9.6	45
33	A Combinatorial Code for Pattern Formation in <i>Drosophila</i> Oogenesis. <i>Developmental Cell</i> , 2008, 15, 725-737.	7.0	65
34	Vector-Dependent Gene Expression Driven by Insulated P-Element Reporter Vectors. <i>Fly</i> , 2007, 1, 55-56.	1.7	12
35	ORegAnno: an open-access community-driven resource for regulatory annotation. <i>Nucleic Acids Research</i> , 2007, 36, D107-D113.	14.5	227
36	New Tools, Resources for Gene Regulatory Analysis in <i>Drosophila</i> . <i>Fly</i> , 2007, 1, 123-124.	1.7	0

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37	REDfly 2.0: an integrated database of cis-regulatory modules and transcription factor binding sites in <i>Drosophila</i> . <i>Nucleic Acids Research</i> , 2007, 36, D594-D598.	14.5	86
38	Large-scale analysis of transcriptional cis-regulatory modules reveals both common features and distinct subclasses. <i>Genome Biology</i> , 2007, 8, R101.	9.6	64
39	(Re)modeling the transcriptional enhancer. <i>Nature Genetics</i> , 2006, 38, 1102-1103.	21.4	17
40	An Integrated Strategy for Analyzing the Unique Developmental Programs of Different Myoblast Subtypes. <i>PLoS Genetics</i> , 2006, 2, e16.	3.5	80
41	REDfly: a Regulatory Element Database for <i>Drosophila</i> . <i>Bioinformatics</i> , 2006, 22, 381-383.	4.1	76
42	Preferred analysis methods for Affymetrix GeneChips revealed by a wholly defined control dataset. <i>Genome Biology</i> , 2005, 6, R16.	9.6	318
43	Prediction of similarly acting cis-regulatory modules by subsequence profiling and comparative genomics in <i>Drosophila melanogaster</i> and <i>D.pseudoobscura</i> . <i>Bioinformatics</i> , 2004, 20, 2738-2750.	4.1	59
44	Reciprocal Regulatory Interactions between the Notch and Ras Signaling Pathways in the <i>Drosophila</i> Embryonic Mesoderm. <i>Developmental Biology</i> , 2002, 244, 226-242.	2.0	130
45	Exploring genetic regulatory networks in metazoan development: methods and models. <i>Physiological Genomics</i> , 2002, 10, 131-143.	2.3	29
46	New fluorescent protein reporters for use with the <i>Drosophila</i> gal4 expression system and for vital detection of balancer chromosomes. <i>Genesis</i> , 2002, 34, 135-138.	1.6	111
47	Ras Pathway Specificity Is Determined by the Integration of Multiple Signal-Activated and Tissue-Restricted Transcription Factors. <i>Cell</i> , 2000, 103, 63-74.	28.9	308
48	The Toll Pathway Is Required in the Epidermis for Muscle Development in the <i>Drosophila</i> Embryo. <i>Developmental Biology</i> , 1998, 199, 164-174.	2.0	41
49	Targeted gene expression without a tissue-specific promoter: Creating mosaic embryos using laser-induced single-cell heat shock. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 6255-6260.	7.1	61
50	The <i>Drosophila</i> Toll Gene Functions Zygotically and Is Necessary for Proper Motoneuron and Muscle Development. <i>Developmental Biology</i> , 1995, 169, 151-167.	2.0	96
51	Cellular mechanisms governing synaptic development in <i>Drosophila melanogaster</i> . <i>Journal of Neurobiology</i> , 1993, 24, 757-787.	3.6	139
52	Elements controlling follicular expression of the <i>s36</i> chorion gene during <i>Drosophila</i> oogenesis.. <i>Molecular and Cellular Biology</i> , 1993, 13, 5898-5906.	2.3	15
53	Elements Controlling Follicular Expression of the <i>s36</i> Chorion Gene during <i>Drosophila</i> Oogenesis. <i>Molecular and Cellular Biology</i> , 1993, 13, 5898-5906.	2.3	9