

Soojin V Yi

List of Publications by Year in descending order

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89
papers

5,743
citations

87723
38
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85405
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97
docs citations

97
times ranked

7402
citing authors

#	ARTICLE	IF	CITATIONS
1	Dnmt1a is essential for gene body methylation and the regulation of the zygotic genome in a wasp. <i>PLoS Genetics</i> , 2022, 18, e1010181.	1.5	13
2	Myxosporea (Myxozoa, Cnidaria) Lack DNA Cytosine Methylation. <i>Molecular Biology and Evolution</i> , 2021, 38, 393-404.	3.5	12
3	Koala methylomes reveal divergent and conserved DNA methylation signatures of X chromosome regulation. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20202244.	1.2	4
4	Enhancer Pleiotropy, Gene Expression, and the Architecture of Human Enhancer-Gene Interactions. <i>Molecular Biology and Evolution</i> , 2021, 38, 3898-3909.	3.5	17
5	On the origin and evolution of SARS-CoV-2. <i>Experimental and Molecular Medicine</i> , 2021, 53, 537-547.	3.2	177
6	Evolution of DNA methylation in the human brain. <i>Nature Communications</i> , 2021, 12, 2021.	5.8	53
7	The impact of epigenetic information on genome evolution. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2021, 376, 20200114.	1.8	17
8	Genome-wide variation in DNA methylation linked to developmental stage and chromosomal suppression of recombination in white-throated sparrows. <i>Molecular Ecology</i> , 2021, 30, 3453-3467.	2.0	12
9	Inside the supergene of the bird with four sexes. <i>Hormones and Behavior</i> , 2020, 126, 104850.	1.0	11
10	A supergene-linked estrogen receptor drives alternative phenotypes in a polymorphic songbird. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 21673-21680.	3.3	31
11	Distinct epigenomic and transcriptomic modifications associated with Wolbachia-mediated asexuality. <i>PLoS Pathogens</i> , 2020, 16, e1008397.	2.1	18
12	Lineage and Parent-of-Origin Effects in DNA Methylation of Honey Bees (<i>Apis mellifera</i>) Revealed by Reciprocal Crosses and Whole-Genome Bisulfite Sequencing. <i>Genome Biology and Evolution</i> , 2020, 12, 1482-1492.	1.1	16
13	Cell type-specific epigenetic links to schizophrenia risk in the brain. <i>Genome Biology</i> , 2019, 20, 135.	3.8	76
14	Accelerated evolution of oligodendrocytes in the human brain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 24334-24342.	3.3	43
15	Regional epigenetic differentiation of the Z Chromosome between sexes in a female heterogametic system. <i>Genome Research</i> , 2019, 29, 1673-1684.	2.4	19
16	Correlation Patterns Between DNA Methylation and Gene Expression in The Cancer Genome Atlas. <i>Cancer Informatics</i> , 2019, 18, 117693511982877.	0.9	120
17	Diversity of Human CpG Islands. , 2019, , 265-280.		1
18	Detecting differential DNA methylation from sequencing of bisulfite converted DNA of diverse species. <i>Briefings in Bioinformatics</i> , 2019, 20, 33-46.	3.2	17

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19	Rapid regulatory evolution of a nonrecombining autosome linked to divergent behavioral phenotypes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 2794-2799.	3.3	28
20	Functional conservation of sequence determinants at rapidly evolving regulatory regions across mammals. <i>PLoS Computational Biology</i> , 2018, 14, e1006451.	1.5	8
21	Genomic Landscape of Methylation Islands in Hymenopteran Insects. <i>Genome Biology and Evolution</i> , 2018, 10, 2766-2776.	1.1	19
22	Comparative genomics of the miniature wasp and pest control agent <i>Trichogramma pretiosum</i> . <i>BMC Biology</i> , 2018, 16, 54.	1.7	57
23	Selection on the regulation of sympathetic nervous activity in humans and chimpanzees. <i>PLoS Genetics</i> , 2018, 14, e1007311.	1.5	6
24	Development of novel EST-SSR markers for ploidy identification based on de novo transcriptome assembly for <i>Misgurnus anguillicaudatus</i> . <i>PLoS ONE</i> , 2018, 13, e0195829.	1.1	23
25	Insights into Epigenome Evolution from Animal and Plant Methylomes. <i>Genome Biology and Evolution</i> , 2017, 9, 3189-3201.	1.1	35
26	Comparison of age and growth performance of diploid and tetraploid loach <i>Misgurnus anguillicaudatus</i> in the Yangtze River basin, China. <i>Environmental Biology of Fishes</i> , 2017, 100, 815-828.	0.4	10
27	Body-hypomethylated human genes harbor extensive intragenic transcriptional activity and are prone to cancer-associated dysregulation. <i>Nucleic Acids Research</i> , 2017, 45, gkx020.	6.5	34
28	Diversity of Human CpG Islands. , 2017, , 1-16.		0
29	The multivariate association between genomewide <sc>DNA</sc> methylation and climate across the range of <i>Arabidopsis thaliana</i>. <i>Molecular Ecology</i> , 2016, 25, 1823-1837.	2.0	60
30	Evaluation of Possible Proximate Mechanisms Underlying the Kinship Theory of Intragenomic Conflict in Social Insects. <i>Integrative and Comparative Biology</i> , 2016, 56, 1206-1214.	0.9	7
31	Evolutionary Transition of Promoter and Gene Body DNA Methylation across Invertebrateâ€“Vertebrate Boundary. <i>Molecular Biology and Evolution</i> , 2016, 33, 1019-1028.	3.5	98
32	Comparative Methylome Analyses Identify Epigenetic Regulatory Loci of Human Brain Evolution. <i>Molecular Biology and Evolution</i> , 2016, 33, 2947-2959.	3.5	49
33	What Signatures Dominantly Associate with Gene Age?. <i>Genome Biology and Evolution</i> , 2016, 8, 3083-3089.	1.1	39
34	Effects of DNA Methylation and Chromatin State on Rates of Molecular Evolution in Insects. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 357-363.	0.8	37
35	Whole-genome bisulfite sequencing maps from multiple human tissues reveal novel CpG islands associated with tissue-specific regulation. <i>Human Molecular Genetics</i> , 2016, 25, 69-82.	1.4	44
36	Parallel Epigenomic and Transcriptomic Responses to Viral Infection in Honey Bees (<i>Apis mellifera</i>). <i>PLoS Pathogens</i> , 2015, 11, e1004713.	2.1	145

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37	The tempo and mode of New World monkey evolution and biogeography in the context of phylogenomic analysis. <i>Molecular Phylogenetics and Evolution</i> , 2015, 82, 386-399.	1.2	66
38	Impacts of Chromatin States and Long-Range Genomic Segments on Aging and DNA Methylation. <i>PLoS ONE</i> , 2015, 10, e0128517.	1.1	27
39	Fundamental diversity of human CpG islands at multiple biological levels. <i>Epigenetics</i> , 2014, 9, 483-491.	1.3	28
40	Specific Modifications of Histone Tails, but Not DNA Methylation, Mirror the Temporal Variation of Mammalian Recombination Hotspots. <i>Genome Biology and Evolution</i> , 2014, 6, 2918-2929.	1.1	18
41	Epigenetic inheritance and genome regulation: is DNA methylation linked to ploidy in haplodiploid insects?. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20140411.	1.2	36
42	Epigenetics and Evolution. <i>Integrative and Comparative Biology</i> , 2014, 54, 31-42.	0.9	61
43	Bis-class: a new classification tool of methylation status using bayes classifier and local methylation information. <i>BMC Genomics</i> , 2014, 15, 608.	1.2	12
44	DNA methylation and evolution of duplicate genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5932-5937.	3.3	88
45	An explanatory evo-devo model for the developmental hourglass. <i>F1000Research</i> , 2014, 3, 156.	0.8	7
46	DNA methylation and transcriptional noise. <i>Epigenetics and Chromatin</i> , 2013, 6, 9.	1.8	115
47	The evolution of lineage-specific clusters of single nucleotide substitutions in the human genome. <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 276-285.	1.2	3
48	Morris Goodman's hominoid rate slowdown: The importance of being neutral. <i>Molecular Phylogenetics and Evolution</i> , 2013, 66, 569-574.	1.2	15
49	Patterning and Regulatory Associations of DNA Methylation Are Mirrored by Histone Modifications in Insects. <i>Genome Biology and Evolution</i> , 2013, 5, 591-598.	1.1	91
50	The Function of Intragenic DNA Methylation: Insights from Insect Epigenomes. <i>Integrative and Comparative Biology</i> , 2013, 53, 319-328.	0.9	96
51	The draft genome of a socially polymorphic halictid bee, <i>Lasioglossum albipes</i> . <i>Genome Biology</i> , 2013, 14, R142.	13.9	72
52	The Evolution of Invertebrate Gene Body Methylation. <i>Molecular Biology and Evolution</i> , 2012, 29, 1907-1916.	3.5	214
53	What are the determinants of gene expression levels and breadths in the human genome?. <i>Human Molecular Genetics</i> , 2012, 21, 46-56.	1.4	38
54	Birds do it, bees do it, worms and ciliates do it too: DNA methylation from unexpected corners of the tree of life. <i>Genome Biology</i> , 2012, 13, 174.	13.9	34

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55	Divergent Whole-Genome Methylation Maps of Human and Chimpanzee Brains Reveal Epigenetic Basis of Human Regulatory Evolution. <i>American Journal of Human Genetics</i> , 2012, 91, 455-465.	2.6	147
56	LINEAGE-SPECIFIC VARIATION IN SLOW- AND FAST-X EVOLUTION IN PRIMATES. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 1751-1761.	1.1	18
57	On the presence and role of human gene-body DNA methylation. <i>Oncotarget</i> , 2012, 3, 462-474.	0.8	409
58	Path lengths in protein-protein interaction networks and biological complexity. <i>Proteomics</i> , 2011, 11, 1857-1867.	1.3	30
59	Functional Relevance of CpG Island Length for Regulation of Gene Expression. <i>Genetics</i> , 2011, 187, 1077-1083.	1.2	53
60	Comparative Analyses of DNA Methylation and Sequence Evolution Using <i>Nasonia</i> Genomes. <i>Molecular Biology and Evolution</i> , 2011, 28, 3345-3354.	3.5	95
61	DNA Methylation and Genome Evolution in Honeybee: Gene Length, Expression, Functional Enrichment Covary with the Evolutionary Signature of DNA Methylation. <i>Genome Biology and Evolution</i> , 2010, 2, 770-780.	1.1	45
62	Sociality Is Linked to Rates of Protein Evolution in a Highly Social Insect. <i>Molecular Biology and Evolution</i> , 2010, 27, 497-500.	3.5	50
63	Functional Conservation of DNA Methylation in the Pea Aphid and the Honeybee. <i>Genome Biology and Evolution</i> , 2010, 2, 719-728.	1.1	109
64	Functional and Evolutionary Insights from the Genomes of Three Parasitoid <i>Nasonia</i> Species. <i>Science</i> , 2010, 327, 343-348.	6.0	808
65	Computational approaches for understanding the evolution of DNA methylation in animals. <i>Epigenetics</i> , 2009, 4, 551-556.	1.3	55
66	DNA methylation is widespread and associated with differential gene expression in castes of the honeybee, <i>Apis mellifera</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 11206-11211.	3.3	303
67	Evolutionary rate variation in Old World monkeys. <i>Biology Letters</i> , 2009, 5, 405-408.	1.0	34
68	Primate phylogenomics: developing numerous nuclear non-coding, non-repetitive markers for ecological and phylogenetic applications and analysis of evolutionary rate variation. <i>BMC Genomics</i> , 2009, 10, 247.	1.2	27
69	Doubts about complex speciation between humans and chimpanzees. <i>Trends in Ecology and Evolution</i> , 2009, 24, 533-540.	4.2	48
70	DNA Methylation and Structural and Functional Bimodality of Vertebrate Promoters. <i>Molecular Biology and Evolution</i> , 2008, 25, 1602-1608.	3.5	90
71	Mutations of Different Molecular Origins Exhibit Contrasting Patterns of Regional Substitution Rate Variation. <i>PLoS Computational Biology</i> , 2008, 4, e1000015.	1.5	77
72	Mammalian Nonsynonymous Sites Are Not Overdispersed: Comparative Genomic Analysis of Index of Dispersion of Mammalian Proteins. <i>Molecular Biology and Evolution</i> , 2008, 25, 634-642.	3.5	6

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73	Predicted Functional RNAs within Coding Regions Constrain Evolutionary Rates of Yeast Proteins. PLoS ONE, 2008, 3, e1559.	1.1	15
74	Understanding relationship between sequence and functional evolution in yeast proteins. Genetica, 2007, 131, 151-156.	0.5	79
75	Understanding Neutral Genomic Molecular Clocks. Evolutionary Biology, 2007, 34, 144-151.	0.5	6
76	Variable molecular clocks in hominoids. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 1370-1375.	3.3	94
77	Non-adaptive evolution of genome complexity. BioEssays, 2006, 28, 979-982.	1.2	21
78	Heterogeneous Genomic Molecular Clocks in Primates. PLoS Genetics, 2006, 2, e163.	1.5	89
79	Correlated Asymmetry of Sequence and Functional Divergence Between Duplicate Proteins of Saccharomyces cerevisiae. Molecular Biology and Evolution, 2006, 23, 1068-1075.	3.5	68
80	Genome size is negatively correlated with effective population size in ray-finned fish. Trends in Genetics, 2005, 21, 643-646.	2.9	66
81	Molecular Evolution of Recombination Hotspots and Highly Recombining Pseudoautosomal Regions in Hominoids. Molecular Biology and Evolution, 2005, 22, 1223-1230.	3.5	15
82	Recombination Has Little Effect on the Rate of Sequence Divergence in Pseudoautosomal Boundary 1 Among Humans and Great Apes. Genome Research, 2003, 14, 37-43.	2.4	27
83	Unusual pattern of single nucleotide polymorphism at the exuperantia2 locus of Drosophila pseudoobscura. Genetical Research, 2003, 82, 101-106.	0.3	2
84	A Survey of Chromosomal and Nucleotide Sequence Variation in <i>Drosophila miranda</i> . Genetics, 2003, 164, 1369-1381.	1.2	29
85	Slow Molecular Clocks in Old World Monkeys, Apes, and Humans. Molecular Biology and Evolution, 2002, 19, 2191-2198.	3.5	129
86	Functional Promiscuity of Squirrel Monkey Growth Hormone Receptor Toward both Primate and Nonprimate Growth Hormones. Molecular Biology and Evolution, 2002, 19, 1083-1092.	3.5	27
87	Male-driven evolution. Current Opinion in Genetics and Development, 2002, 12, 650-656.	1.5	206
88	Contrasting Patterns of Molecular Evolution of the Genes on the New and Old Sex Chromosomes of <i>Drosophila miranda</i> . Molecular Biology and Evolution, 2000, 17, 703-717.	3.5	51
89	A Selective Sweep Associated With a Recent Gene Transposition in <i>Drosophila miranda</i> . Genetics, 2000, 156, 1753-1763.	1.2	30