

Soojin V Yi

List of Publications by Year in descending order

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89
papers

5,743
citations

87723

38
h-index

85405

71
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97
all docs

97
docs citations

97
times ranked

7402
citing authors

#	ARTICLE	IF	CITATIONS
1	Functional and Evolutionary Insights from the Genomes of Three Parasitoid <i>Nasonia</i> Species. <i>Science</i> , 2010, 327, 343-348.	6.0	808
2	On the presence and role of human gene-body DNA methylation. <i>Oncotarget</i> , 2012, 3, 462-474.	0.8	409
3	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
4	The Evolution of Invertebrate Gene Body Methylation. <i>Molecular Biology and Evolution</i> , 2012, 29, 1907-1916.	3.5	214
5	Male-driven evolution. <i>Current Opinion in Genetics and Development</i> , 2002, 12, 650-656.	1.5	206
6	On the origin and evolution of SARS-CoV-2. <i>Experimental and Molecular Medicine</i> , 2021, 53, 537-547.	3.2	177
7	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
8	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
9	Slow Molecular Clocks in Old World Monkeys, Apes, and Humans. <i>Molecular Biology and Evolution</i> , 2002, 19, 2191-2198.	3.5	129
10	Correlation Patterns Between DNA Methylation and Gene Expression in The Cancer Genome Atlas. <i>Cancer Informatics</i> , 2019, 18, 117693511982877.	0.9	120
11	DNA methylation and transcriptional noise. <i>Epigenetics and Chromatin</i> , 2013, 6, 9.	1.8	115
12	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
13	Evolutionary Transition of Promoter and Gene Body DNA Methylation across Invertebrate-Vertebrate Boundary. <i>Molecular Biology and Evolution</i> , 2016, 33, 1019-1028.	3.5	98
14	The Function of Intragenic DNA Methylation: Insights from Insect Epigenomes. <i>Integrative and Comparative Biology</i> , 2013, 53, 319-328.	0.9	96
15	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
16	Variable molecular clocks in hominoids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 1370-1375.	3.3	94
17	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
18	DNA Methylation and Structural and Functional Bimodality of Vertebrate Promoters. <i>Molecular Biology and Evolution</i> , 2008, 25, 1602-1608.	3.5	90

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19	Heterogeneous Genomic Molecular Clocks in Primates. <i>PLoS Genetics</i> , 2006, 2, e163.	1.5	89
20	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
21	Understanding relationship between sequence and functional evolution in yeast proteins. <i>Genetica</i> , 2007, 131, 151-156.	0.5	79
22	Mutations of Different Molecular Origins Exhibit Contrasting Patterns of Regional Substitution Rate Variation. <i>PLoS Computational Biology</i> , 2008, 4, e1000015.	1.5	77
23	Cell type-specific epigenetic links to schizophrenia risk in the brain. <i>Genome Biology</i> , 2019, 20, 135.	3.8	76
24	The draft genome of a socially polymorphic halictid bee, <i>Lasioglossum albipes</i> . <i>Genome Biology</i> , 2013, 14, R142.	13.9	72
25	Correlated Asymmetry of Sequence and Functional Divergence Between Duplicate Proteins of <i>Saccharomyces cerevisiae</i> . <i>Molecular Biology and Evolution</i> , 2006, 23, 1068-1075.	3.5	68
26	Genome size is negatively correlated with effective population size in ray-finned fish. <i>Trends in Genetics</i> , 2005, 21, 643-646.	2.9	66
27	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
28	Epigenetics and Evolution. <i>Integrative and Comparative Biology</i> , 2014, 54, 31-42.	0.9	61
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	Comparative genomics of the miniature wasp and pest control agent <i>Trichogramma pretiosum</i> . <i>BMC Biology</i> , 2018, 16, 54.	1.7	57
31	Computational approaches for understanding the evolution of DNA methylation in animals. <i>Epigenetics</i> , 2009, 4, 551-556.	1.3	55
32	Functional Relevance of CpG Island Length for Regulation of Gene Expression. <i>Genetics</i> , 2011, 187, 1077-1083.	1.2	53
33	Evolution of DNA methylation in the human brain. <i>Nature Communications</i> , 2021, 12, 2021.	5.8	53
34	Contrasting Patterns of Molecular Evolution of the Genes on the New and Old Sex Chromosomes of <i>Drosophila miranda</i> . <i>Molecular Biology and Evolution</i> , 2000, 17, 703-717.	3.5	51
35	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
36	Comparative Methylome Analyses Identify Epigenetic Regulatory Loci of Human Brain Evolution. <i>Molecular Biology and Evolution</i> , 2016, 33, 2947-2959.	3.5	49

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37	Doubts about complex speciation between humans and chimpanzees. <i>Trends in Ecology and Evolution</i> , 2009, 24, 533-540.	4.2	48
38	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
39	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
40	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
41	What Signatures Dominantly Associate with Gene Age?. <i>Genome Biology and Evolution</i> , 2016, 8, 3083-3089.	1.1	39
42	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
43	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
44	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
45	Insights into Epigenome Evolution from Animal and Plant Methylomes. <i>Genome Biology and Evolution</i> , 2017, 9, 3189-3201.	1.1	35
46	Evolutionary rate variation in Old World monkeys. <i>Biology Letters</i> , 2009, 5, 405-408.	1.0	34
47	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
48	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
49	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
50	Path lengths in protein-protein interaction networks and biological complexity. <i>Proteomics</i> , 2011, 11, 1857-1867.	1.3	30
51	A Selective Sweep Associated With a Recent Gene Transposition in <i>Drosophila miranda</i> . <i>Genetics</i> , 2000, 156, 1753-1763.	1.2	30
52	A Survey of Chromosomal and Nucleotide Sequence Variation in <i>Drosophila miranda</i> . <i>Genetics</i> , 2003, 164, 1369-1381.	1.2	29
53	Fundamental diversity of human CpG islands at multiple biological levels. <i>Epigenetics</i> , 2014, 9, 483-491.	1.3	28
54	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

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55	Functional Promiscuity of Squirrel Monkey Growth Hormone Receptor Toward both Primate and Nonprimate Growth Hormones. <i>Molecular Biology and Evolution</i> , 2002, 19, 1083-1092.	3.5	27
56	Recombination Has Little Effect on the Rate of Sequence Divergence in Pseudoautosomal Boundary 1 Among Humans and Great Apes. <i>Genome Research</i> , 2003, 14, 37-43.	2.4	27
57	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
58	Impacts of Chromatin States and Long-Range Genomic Segments on Aging and DNA Methylation. <i>PLoS ONE</i> , 2015, 10, e0128517.	1.1	27
59	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
60	Non-adaptive evolution of genome complexity. <i>BioEssays</i> , 2006, 28, 979-982.	1.2	21
61	Genomic Landscape of Methylation Islands in Hymenopteran Insects. <i>Genome Biology and Evolution</i> , 2018, 10, 2766-2776.	1.1	19
62	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
63	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
64	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
65	Distinct epigenomic and transcriptomic modifications associated with <i>Wolbachia</i> -mediated asexuality. <i>PLoS Pathogens</i> , 2020, 16, e1008397.	2.1	18
66	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
67	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
68	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
69	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
70	Molecular Evolution of Recombination Hotspots and Highly Recombining Pseudoautosomal Regions in Hominoids. <i>Molecular Biology and Evolution</i> , 2005, 22, 1223-1230.	3.5	15
71	Morris Goodman's hominoid rate slowdown: The importance of being neutral. <i>Molecular Phylogenetics and Evolution</i> , 2013, 66, 569-574.	1.2	15
72	Predicted Functional RNAs within Coding Regions Constrain Evolutionary Rates of Yeast Proteins. <i>PLoS ONE</i> , 2008, 3, e1559.	1.1	15

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73	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
74	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
75	Myxosporea (Myxozoa, Cnidaria) Lack DNA Cytosine Methylation. <i>Molecular Biology and Evolution</i> , 2021, 38, 393-404.	3.5	12
76	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
77	Inside the supergene of the bird with four sexes. <i>Hormones and Behavior</i> , 2020, 126, 104850.	1.0	11
78	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
79	Functional conservation of sequence determinants at rapidly evolving regulatory regions across mammals. <i>PLoS Computational Biology</i> , 2018, 14, e1006451.	1.5	8
80	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
81	An explanatory evo-devo model for the developmental hourglass. <i>F1000Research</i> , 2014, 3, 156.	0.8	7
82	Understanding Neutral Genomic Molecular Clocks. <i>Evolutionary Biology</i> , 2007, 34, 144-151.	0.5	6
83	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
84	Selection on the regulation of sympathetic nervous activity in humans and chimpanzees. <i>PLoS Genetics</i> , 2018, 14, e1007311.	1.5	6
85	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
86	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
87	Unusual pattern of single nucleotide polymorphism at the <i>exuperantia2</i> locus of <i>Drosophila pseudoobscura</i> . <i>Genetical Research</i> , 2003, 82, 101-106.	0.3	2
88	Diversity of Human CpG Islands. , 2019, , 265-280.		1
89	Diversity of Human CpG Islands. , 2017, , 1-16.		0