

# Yoonsoo Hahn

## List of Publications by Year in descending order

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98  
papers

3,170  
citations

172457

29  
h-index

175258

52  
g-index

102  
all docs

102  
docs citations

102  
times ranked

4686  
citing authors

#	ARTICLE	IF	CITATIONS
1	Meiosis-specific cohesin complexes display essential and distinct roles in mitotic embryonic stem cell chromosomes. <i>Genome Biology</i> , 2022, 23, 70.	8.8	8
2	Analysis of proteolytic processing sites in potyvirus polyproteins revealed differential amino acid preferences of Nla-Pro protease in each of seven cleavage sites. <i>PLoS ONE</i> , 2021, 16, e0245853.	2.5	11
3	A novel tepovirus, Agave virus T, identified by the analysis of the transcriptome data of blue agave ( <i>Agave tequilana</i> ). <i>Acta Virologica</i> , 2021, 65, 68-71.	0.8	5
4	Identification of genome sequences of novel partitiviruses in the quinoa ( <i>Chenopodium quinoa</i> ) transcriptome datasets. <i>Journal of General Plant Pathology</i> , 2021, 87, 236-241.	1.0	3
5	Diet-Related Alterations of Gut Bile Salt Hydrolases Determined Using a Metagenomic Analysis of the Human Microbiome. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3652.	4.1	15
6	Rapid protein sequence evolution via compensatory frameshift is widespread in RNA virus genomes. <i>BMC Bioinformatics</i> , 2021, 22, 251.	2.6	6
7	Response to Veitia et al. <i>EMBO Journal</i> , 2021, 40, e108671.	7.8	0
8	Two novel closteroviruses, fig virus A and fig virus B, identified by the analysis of the high-throughput RNA-sequencing data of fig ( <i>Ficus carica</i> ) latex. <i>Acta Virologica</i> , 2021, 65, 42-48.	0.8	10
9	Metagenomic analysis of the human microbiome reveals the association between the abundance of gut bile salt hydrolases and host health. <i>Gut Microbes</i> , 2020, 11, 1300-1313.	9.8	59
10	An alternative miRISC targets a cancer-associated coding sequence mutation in FOXL2. <i>EMBO Journal</i> , 2020, 39, e104719.	7.8	18
11	Divergent rRNAs as regulators of gene expression at the ribosome level. <i>Nature Microbiology</i> , 2019, 4, 515-526.	13.3	52
12	Genomic and metatranscriptomic analyses of carbon remineralization in an Antarctic polynya. <i>Microbiome</i> , 2019, 7, 29.	11.1	13
13	The coordinated action of RNase III and RNase G controls enolase expression in response to oxygen availability in <i>Escherichia coli</i> . <i>Scientific Reports</i> , 2019, 9, 17257.	3.3	8
14	Identification of a novel plant RNA virus species of the genus Amalgavirus in the family Amalgaviridae from chia ( <i>Salvia hispanica</i> ). <i>Genes and Genomics</i> , 2019, 41, 507-514.	1.4	10
15	Functional relevance of synonymous alleles reflected in allele rareness in the population. <i>Genomics</i> , 2018, 110, 347-354.	2.9	4
16	Identification of novel RNA viruses in alfalfa ( <i>Medicago sativa</i> ): an Alphapartitivirus, a Deltapartitivirus, and a Marafivirus. <i>Gene</i> , 2018, 638, 7-12.	2.2	37
17	Loss of conserved ubiquitylation sites in conserved proteins during human evolution. <i>International Journal of Molecular Medicine</i> , 2018, 42, 2203-2212.	4.0	1
18	Deacetylase activity-independent transcriptional activation by HDAC2 during TPA-induced HL-60 cell differentiation. <i>PLoS ONE</i> , 2018, 13, e0202935.	2.5	4

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19	Identification of Two Novel Amalgaviruses in the Common Eelgrass ( <i>Zostera marina</i> ) and in Silico Analysis of the Amalgavirus +1 Programmed Ribosomal Frameshifting Sites. <i>Plant Pathology Journal</i> , 2018, 34, 150-156.	1.7	21
20	The effects of increasing the number of taxa on inferences of molecular convergence. <i>Genome Biology and Evolution</i> , 2017, 9, evw306.	2.5	20
21	Genome sequence of a distinct watermelon mosaic virus identified from ginseng ( <i>Panax ginseng</i> ) transcriptome. <i>Acta Virologica</i> , 2017, 61, 479-482.	0.8	5
22	Cellular Dynamics of Rad51 and Rad54 in Response to Postreplicative Stress and DNA Damage in HeLa Cells. <i>Molecules and Cells</i> , 2017, 40, 143-150.	2.6	16
23	Genome Sequence of Spinach Cryptic Virus 1, a New Member of the Genus Alphapartivirus (Family) Tj ETQq1 1 0.784314 rgBT /Overl...	2.1	6
24	Genome Sequences of Spinach Deltapartivirus 1, Spinach Amalgavirus 1, and Spinach Latent Virus Identified in Spinach Transcriptome. <i>Journal of Microbiology and Biotechnology</i> , 2017, 27, 1324-1330.	2.1	15
25	MOXD2, a Gene Possibly Associated with Olfaction, Is Frequently Inactivated in Birds. <i>PLoS ONE</i> , 2016, 11, e0152431.	2.5	2
26	Functional analysis of recombinant human and <i>Yarrowia lipolytica</i> O-GlcNAc transferases expressed in <i>Saccharomyces cerevisiae</i> . <i>Journal of Microbiology</i> , 2016, 54, 667-674.	2.8	4
27	Gene Tree Discordance Can Generate Patterns of Diminishing Convergence over Time. <i>Molecular Biology and Evolution</i> , 2016, 33, 3299-3307.	8.9	58
28	Normalization of human RNA-seq experiments using chimpanzee RNA as a spike-in standard. <i>Scientific Reports</i> , 2016, 6, 31923.	3.3	0
29	Genome-wide transcriptional responses of <i>Alteromonas naphthalenivorans</i> SN2 to contaminated seawater and marine tidal flat sediment. <i>Scientific Reports</i> , 2016, 6, 21796.	3.3	18
30	SiNG-PCRseq: Accurate inter-sequence quantification achieved by spiking-in a neighbor genome for competitive PCR amplicon sequencing. <i>Scientific Reports</i> , 2015, 5, 11879.	3.3	5
31	Reference Materials for Calibration of Analytical Biases in Quantification of DNA Methylation. <i>PLoS ONE</i> , 2015, 10, e0137006.	2.5	6
32	H3K9 methyltransferase G9a negatively regulates UHRF1 transcription during leukemia cell differentiation. <i>Nucleic Acids Research</i> , 2015, 43, 3509-3523.	14.5	35
33	Loss of ancestral N-glycosylation sites in conserved proteins during human evolution. <i>International Journal of Molecular Medicine</i> , 2015, 36, 1685-1692.	4.0	5
34	The acquisition of novel N-glycosylation sites in conserved proteins during human evolution. <i>BMC Bioinformatics</i> , 2015, 16, 29.	2.6	13
35	Regulation of <i>Escherichia coli</i> RNase III activity. <i>Journal of Microbiology</i> , 2015, 53, 487-494.	2.8	14
36	Heat Shock RNA 1, Known as a Eukaryotic Temperature-Sensing Noncoding RNA, Is of Bacterial Origin. <i>Journal of Microbiology and Biotechnology</i> , 2015, 25, 1234-1240.	2.1	15

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37	Loss of gene function and evolution of human phenotypes. <i>BMB Reports</i> , 2015, 48, 373-379.	2.4	9
38	Retroduplication and loss of parental genes is a mechanism for the generation of intronless genes in <i>Ciona intestinalis</i> and <i>Ciona savignyi</i> . <i>Development Genes and Evolution</i> , 2014, 224, 255-260.	0.9	5
39	H3K9 histone methyltransferase G9a-mediated transcriptional activation of <i>p21</i> . <i>FEBS Letters</i> , 2014, 588, 685-691.	2.8	26
40	Frequent Loss and Alteration of the <i>MOXD2</i> Gene in Catarrhines and Whales: A Possible Connection with the Evolution of Olfaction. <i>PLoS ONE</i> , 2014, 9, e104085.	2.5	7
41	Plant RNA Virus Sequences Identified in Kimchi by Microbial Metatranscriptome Analysis. <i>Journal of Microbiology and Biotechnology</i> , 2014, 24, 979-986.	2.1	5
42	The $\beta$ -barrel tip region of <i>Escherichia coli</i> TolC homologs of <i>Vibrio vulnificus</i> interacts with the MacA protein to form the functional macrolide-specific efflux pump MacAB-TolC. <i>Journal of Microbiology</i> , 2013, 51, 154-159.	2.8	19
43	The RNA Polymerase II C-terminal Domain-interacting Domain of Yeast Nrd1 Contributes to the Choice of Termination Pathway and Couples to RNA Processing by the Nuclear Exosome. <i>Journal of Biological Chemistry</i> , 2013, 288, 36676-36690.	3.4	21
44	Metatranscriptomic analysis of lactic acid bacterial gene expression during kimchi fermentation. <i>International Journal of Food Microbiology</i> , 2013, 163, 171-179.	4.7	133
45	Evidence for the dissemination of cryptic non-coding RNAs transcribed from intronic and intergenic segments by retroposition. <i>Bioinformatics</i> , 2013, 29, 1593-1599.	4.1	1
46	Negative Regulation of JAK2 by H3K9 Methyltransferase G9a in Leukemia. <i>Molecular and Cellular Biology</i> , 2012, 32, 3681-3694.	2.3	33
47	KDM3B Is the H3K9 Demethylase Involved in Transcriptional Activation of <i>lmo2</i> in Leukemia. <i>Molecular and Cellular Biology</i> , 2012, 32, 2917-2933.	2.3	99
48	Inactivation of the <i>MSLNL</i> gene encoding mesothelin-like protein during African great ape evolution. <i>Gene</i> , 2012, 496, 17-21.	2.2	3
49	Human-specific protein isoforms produced by novel splice sites in the human genome after the human-chimpanzee divergence. <i>BMC Bioinformatics</i> , 2012, 13, 299.	2.6	6
50	Gains of ubiquitylation sites in highly conserved proteins in the human lineage. <i>BMC Bioinformatics</i> , 2012, 13, 306.	2.6	13
51	Identification of a Hyperactive Variant of the SecM Motif Involved in Ribosomal Arrest. <i>Current Microbiology</i> , 2012, 64, 17-23.	2.2	1
52	Comparative Genomics Reveals Adaptation by <i>Alteromonas</i> sp. SN2 to Marine Tidal-Flat Conditions: Cold Tolerance and Aromatic Hydrocarbon Metabolism. <i>PLoS ONE</i> , 2012, 7, e35784.	2.5	132
53	Exon deletion in the <i>MSLN</i> gene encoding MPF/mesothelin precursor protein during Laurasiatherian mammal evolution. <i>International Journal of Molecular Medicine</i> , 2011, 27, 289-93.	4.0	1
54	Identification of human-specific transcript variants induced by DNA insertions in the human genome. <i>Bioinformatics</i> , 2011, 27, 14-21.	4.1	31

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55	Metagenomic Analysis of Kimchi, a Traditional Korean Fermented Food. <i>Applied and Environmental Microbiology</i> , 2011, 77, 2264-2274.	3.1	416
56	Identification of novel phosphorylation modification sites in human proteins that originated after the human-chimpanzee divergence. <i>Bioinformatics</i> , 2011, 27, 2494-2501.	4.1	17
57	Eisenstasin, new antistasin family inhibitor from the earthworm. <i>Biologia (Poland)</i> , 2010, 65, 284-288.	1.5	5
58	<i>Escherichia coli</i> ribonuclease III activity is downregulated by osmotic stress: consequences for the degradation of <i>bdm</i> mRNA in biofilm formation. <i>Molecular Microbiology</i> , 2010, 75, 413-425.	2.5	71
59	Transcriptional regulation of 1-cys peroxiredoxin by the proto-oncogene protein DEK. <i>Molecular Medicine Reports</i> , 2010, 3, 877-81.	2.4	9
60	Evidence for bacterial origin of heat shock RNA-1. <i>Rna</i> , 2010, 16, 274-279.	3.5	14
61	Identification of sequence features that predict competition potency of siRNAs. <i>Biochemical and Biophysical Research Communications</i> , 2010, 398, 92-97.	2.1	6
62	Human-specific antisense transcripts induced by the insertion of transposable element. <i>International Journal of Molecular Medicine</i> , 2010, 26, 151-7.	4.0	14
63	Anoctamin and transmembrane channel-like proteins are evolutionarily related. <i>International Journal of Molecular Medicine</i> , 2009, 24, 51-5.	4.0	42
64	Molecular Evolution of TEPP Protein Genes in Metazoans. <i>Biochemical Genetics</i> , 2009, 47, 651-664.	1.7	2
65	A 2.7-kb Deletion in the Human NLRP10 Gene Exon 2 Occurred After the Human-Chimpanzee Divergence. <i>Biochemical Genetics</i> , 2009, 47, 665-670.	1.7	4
66	Antiobesity effect of baicalin involves the modulations of proadipogenic and antiadipogenic regulators of the adipogenesis pathway. <i>Phytotherapy Research</i> , 2009, 23, 1615-1623.	5.8	47
67	Mesothelin, Stereocilin, and Otoancorin are predicted to have superhelical structures with ARM-type repeats. <i>BMC Structural Biology</i> , 2009, 9, 1.	2.3	64
68	Non-AUG translational initiation of a short CAPC transcript generating protein isoform. <i>Biochemical and Biophysical Research Communications</i> , 2009, 380, 508-513.	2.1	6
69	Topology of NGEF, a Prostate-Specific Cell:Cell Junction Protein Widely Expressed in Many Cancers of Different Grade Level. <i>Cancer Research</i> , 2008, 68, 6306-6312.	0.9	64
70	PATE Gene Clusters Code for Multiple, Secreted TFP/Ly-6/uPAR Proteins That Are Expressed in Reproductive and Neuron-rich Tissues and Possess Neuromodulatory Activity. <i>Journal of Biological Chemistry</i> , 2008, 283, 16928-16939.	3.4	54
71	<i>LRRC3B</i> , Encoding a Leucine-Rich Repeat-Containing Protein, Is a Putative Tumor Suppressor Gene in Gastric Cancer. <i>Cancer Research</i> , 2008, 68, 7147-7155.	0.9	49
72	A model for obesity and gigantism due to disruption of the <i>Ankrd26</i> gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 270-275.	7.1	79

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73	Selective POTE Paralogs on Chromosome 2 are Expressed in Human Embryonic Stem Cells. <i>Stem Cells and Development</i> , 2008, 17, 325-332.	2.1	19
74	Inactivation of MOXD2 and S100A15A by Exon Deletion during Human Evolution. <i>Molecular Biology and Evolution</i> , 2007, 24, 2203-2212.	8.9	23
75	Accurate quantitation of allele-specific expression patterns by analysis of DNA melting. <i>Genome Research</i> , 2007, 17, 1093-1100.	5.5	17
76	NGEP, a Prostate-Specific Plasma Membrane Protein that Promotes the Association of LNCaP Cells. <i>Cancer Research</i> , 2007, 67, 1594-1601.	0.9	48
77	Duplication and extensive remodeling shaped POTE family genes encoding proteins containing ankyrin repeat and coiled coil domains. <i>Gene</i> , 2006, 366, 238-245.	2.2	42
78	Human-specific nonsense mutations identified by genome sequence comparisons. <i>Human Genetics</i> , 2006, 119, 169-178.	3.8	32
79	Evolution and expression of chimeric POTE-actin genes in the human genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 17885-17890.	7.1	42
80	POTE Paralogs Are Induced and Differentially Expressed in Many Cancers. <i>Cancer Research</i> , 2006, 66, 52-56.	0.9	59
81	Structure and expression of the zebrafish mest gene, an ortholog of mammalian imprinted gene PEG1/MEST. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2005, 1731, 125-132.	2.4	10
82	Transcriptome analysis of human gastric cancer. <i>Mammalian Genome</i> , 2005, 16, 942-954.	2.2	23
83	Identification of nine human-specific frameshift mutations by comparative analysis of the human and the chimpanzee genome sequences. <i>Bioinformatics</i> , 2005, 21, i186-i194.	4.1	53
84	NGEP, a gene encoding a membrane protein detected only in prostate cancer and normal prostate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 3059-3064.	7.1	74
85	Finding fusion genes resulting from chromosome rearrangement by analyzing the expressed sequence databases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 13257-13261.	7.1	52
86	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. <i>PLoS Biology</i> , 2004, 2, e162.	5.6	290
87	Rapid grouping of monoclonal antibodies based on their topographical epitopes by a label-free competitive immunoassay. <i>Journal of Immunological Methods</i> , 2004, 292, 141-155.	1.4	24
88	Gene cataloging and expression profiling in human gastric cancer cells by expressed sequence tags. <i>Genomics</i> , 2004, 83, 1024-1045.	2.9	29
89	Discovery of genes for ginsenoside biosynthesis by analysis of ginseng expressed sequence tags. <i>Plant Cell Reports</i> , 2003, 22, 224-230.	5.6	109
90	TEPP, a new gene specifically expressed in testis, prostate, and placenta and well conserved in chordates. <i>Biochemical and Biophysical Research Communications</i> , 2003, 312, 1209-1215.	2.1	11

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91	Characterization of JDP genes, an evolutionarily conserved J domain-only protein family, from human and moths. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2000, 1491, 355-363.	2.4	13
92	<i>Mit1</i> and <i>Lb9</i> and <i>Copg2</i> , new members of mouse imprinted genes closely linked to <i>Peg1</i> and <i>Mest</i> . <i>FEBS Letters</i> , 2000, 472, 230-234.	2.8	51
93	Duplication of genes encoding non-clathrin coat protein $\beta$ -COP in vertebrate, insect and plant evolution. <i>FEBS Letters</i> , 2000, 482, 31-36.	2.8	10
94	Identification of the genes encoding enzymes involved in the early biosynthetic pathway of pteridines in <i>Synechocystis</i> PCC 6803. <i>FEMS Microbiology Letters</i> , 1999, 176, 169-176.	1.8	26
95	Cloning of mouse sepiapterin reductase gene and characterization of its promoter region. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1999, 1445, 165-171.	2.4	10
96	Structural analysis of phylogenetically conserved J domain protein gene. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1999, 1447, 325-333.	2.4	11
97	Genomic structure and expression of murine poly(A) binding protein II gene. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1998, 1395, 40-46.	2.4	8
98	Structure and Expression of the Tenecin 3 Gene in <i>Tenebrio molitor</i> . <i>Biochemical and Biophysical Research Communications</i> , 1996, 218, 6-11.	2.1	50