Vivian G Cheung

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Genetic analysis of genome-wide variation in human gene expression. Nature, 2004, 430, 743-747.	13.7	1,146
2	Making and reading microarrays. Nature Genetics, 1999, 21, 15-19.	9.4	606
3	Mapping determinants of human gene expression by regional and genome-wide association. Nature, 2005, 437, 1365-1369.	13.7	550
4	Widespread RNA and DNA Sequence Differences in the Human Transcriptome. Science, 2011, 333, 53-58.	6.0	414
5	Genetics of human gene expression: mapping DNA variants that influence gene expression. Nature Reviews Genetics, 2009, 10, 595-604.	7.7	210
6	Identification of active transcriptional regulatory elements from GRO-seq data. Nature Methods, 2015, 12, 433-438.	9.0	198
7	Senataxin Mutation Reveals How R-Loops Promote Transcription by Blocking DNA Methylation at Gene Promoters. Molecular Cell, 2018, 69, 426-437.e7.	4.5	147
8	Genetic Analysis of Variation in Human Meiotic Recombination. PLoS Genetics, 2009, 5, e1000648.	1.5	142
9	Polymorphic Cis- and Trans-Regulation of Human Gene Expression. PLoS Biology, 2010, 8, e1000480.	2.6	142
10	Human proteins that interact with RNA/DNA hybrids. Genome Research, 2018, 28, 1405-1414.	2.4	130
11	Saving the Endangered Physician-Scientist — A Plan for Accelerating Medical Breakthroughs. New England Journal of Medicine, 2019, 381, 399-402.	13.9	104
12	Polymorphic Variation in Human Meiotic Recombination. American Journal of Human Genetics, 2007, 80, 526-530.	2.6	74
13	Divergence of a conserved elongation factor and transcription regulation in budding and fission yeast. Genome Research, 2016, 26, 799-811.	2.4	73
14	Monozygotic Twins Reveal Germline Contribution to Allelic Expression Differences. American Journal of Human Genetics, 2008, 82, 1357-1360.	2.6	55
15	RNA-DNA Differences Are Generated in Human Cells within Seconds after RNA Exits Polymerase II. Cell Reports, 2014, 6, 906-915.	2.9	52
16	A call for direct sequencing of full-length RNAs to identify all modifications. Nature Genetics, 2021, 53, 1113-1116.	9.4	33
17	RNA abasic sites in yeast and human cells. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 20689-20695.	3.3	27
18	cis Elements that Mediate RNA Polymerase II Pausing Regulate Human Gene Expression. American Journal of Human Genetics, 2019, 105, 677-688.	2.6	26

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19	Clinical and Molecular Aspects of Senataxin Mutations in Amyotrophic Lateral Sclerosis 4. Annals of Neurology, 2020, 87, 547-555.	2.8	26
20	Genetic Control of Hotspots. Science, 2010, 327, 791-792.	6.0	24
21	Heterozygous carriers of Nijmegen Breakage Syndrome have a distinct gene expression phenotype. Genome Research, 2006, 16, 973-979.	2.4	17
22	R-Loop Analysis by Dot-Blot. Journal of Visualized Experiments, 2021, , .	0.2	17
23	RNA–DNA sequence differences in <i>Saccharomyces cerevisiae</i> . Genome Research, 2016, 26, 1544-1554.	2.4	16
24	An Examination of the Relationship between Hotspots and Recombination Associated with Chromosome 21 Nondisjunction. PLoS ONE, 2014, 9, e99560.	1.1	15
25	Genetic variation in insulinâ€induced kinase signaling. Molecular Systems Biology, 2015, 11, 820.	3.2	14
26	Translating science to medicine: The case for physician-scientists. Science Translational Medicine, 2022, 14, eabg7852.	5.8	11
27	Genome-Wide Association Study of Meiotic Recombination Phenotypes. G3: Genes, Genomes, Genetics, 2016, 6, 3995-4007.	0.8	9
28	Prejudice. JAMA - Journal of the American Medical Association, 2020, 324, 2261.	3.8	4
29	Abasic Sites in RNA of Yeast and Human. SSRN Electronic Journal, 2018, , .	0.4	1
30	SRSF1 Is a Mediator of Radiation-Induced Alternative Splicing in B-Lymphocytes. Blood, 2016, 128, 1341-1341.	0.6	1
31	Bridging genetics and genomics in neurology. Neurologic Clinics, 2002, 20, 867-877.	0.8	0