Vivian G Cheung

List of Publications by Year
in descending order

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31 papers	4,285 citations	394286 19 h-index	454834 30 g-index
33 all docs	33 docs citations	33 times ranked	5988 citing authors

#	Article	IF	Citations
1	Translating science to medicine: The case for physician-scientists. Science Translational Medicine, 2022, 14, eabg7852.	5.8	11
2	A call for direct sequencing of full-length RNAs to identify all modifications. Nature Genetics, 2021, 53, 1113-1116.	9.4	33
3	R-Loop Analysis by Dot-Blot. Journal of Visualized Experiments, 2021, , .	0.2	17
4	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
5	Clinical and Molecular Aspects of Senataxin Mutations in Amyotrophic Lateral Sclerosis 4. Annals of Neurology, 2020, 87, 547-555.	2.8	26
6	Prejudice. JAMA - Journal of the American Medical Association, 2020, 324, 2261.	3.8	4
7	Saving the Endangered Physician-Scientist â€" A Plan for Accelerating Medical Breakthroughs. New England Journal of Medicine, 2019, 381, 399-402.	13.9	104
8	cis Elements that Mediate RNA Polymerase II Pausing Regulate Human Gene Expression. American Journal of Human Genetics, 2019, 105, 677-688.	2.6	26
9	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
10	Abasic Sites in RNA of Yeast and Human. SSRN Electronic Journal, 2018, , .	0.4	1
11	Human proteins that interact with RNA/DNA hybrids. Genome Research, 2018, 28, 1405-1414.	2.4	130
12	Genome-Wide Association Study of Meiotic Recombination Phenotypes. G3: Genes, Genomes, Genetics, 2016, 6, 3995-4007.	0.8	9
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	RNAâ€“DNA sequence differences in Saccharomyces cerevisiae. Genome Research, 2016, 26, 1544-1554.	2.4	16
15	SRSF1 Is a Mediator of Radiation-Induced Alternative Splicing in B-Lymphocytes. Blood, 2016, 128, 1341-1341.	0.6	1
16	Genetic variation in insulinâ€induced kinase signaling. Molecular Systems Biology, 2015, 11, 820.	3.2	14
17	Identification of active transcriptional regulatory elements from GRO-seq data. Nature Methods, 2015, 12, 433-438.	9.0	198
18	RNA-DNA Differences Are Generated in Human Cells within Seconds after RNA Exits Polymerase II. Cell Reports, 2014, 6, 906-915.	2.9	52

#	Article	IF	Citations
19	An Examination of the Relationship between Hotspots and Recombination Associated with Chromosome 21 Nondisjunction. PLoS ONE, 2014, 9, e99560.	1.1	15
20	Widespread RNA and DNA Sequence Differences in the Human Transcriptome. Science, 2011, 333, 53-58.	6.0	414
21	Polymorphic Cis- and Trans-Regulation of Human Gene Expression. PLoS Biology, 2010, 8, e1000480.	2.6	142
22	Genetic Control of Hotspots. Science, 2010, 327, 791-792.	6.0	24
23	Genetic Analysis of Variation in Human Meiotic Recombination. PLoS Genetics, 2009, 5, e1000648.	1.5	142
24	Genetics of human gene expression: mapping DNA variants that influence gene expression. Nature Reviews Genetics, 2009, 10, 595-604.	7.7	210
25	Monozygotic Twins Reveal Germline Contribution to Allelic Expression Differences. American Journal of Human Genetics, 2008, 82, 1357-1360.	2.6	55
26	Polymorphic Variation in Human Meiotic Recombination. American Journal of Human Genetics, 2007, 80, 526-530.	2.6	74
27	Heterozygous carriers of Nijmegen Breakage Syndrome have a distinct gene expression phenotype. Genome Research, 2006, 16, 973-979.	2.4	17
28	Mapping determinants of human gene expression by regional and genome-wide association. Nature, 2005, 437, 1365-1369.	13.7	550
29	Genetic analysis of genome-wide variation in human gene expression. Nature, 2004, 430, 743-747.	13.7	1,146
30	Bridging genetics and genomics in neurology. Neurologic Clinics, 2002, 20, 867-877.	0.8	0
31	Making and reading microarrays. Nature Genetics, 1999, 21, 15-19.	9.4	606