

# A Kong

## List of Publications by Year in descending order

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Version: 2024-02-01

16  
papers

2,973  
citations

686830

13  
h-index

940134

16  
g-index

16  
all docs

16  
docs citations

16  
times ranked

3558  
citing authors

#	ARTICLE	IF	CITATIONS
1	CDKN2A mutations and melanoma risk in the Icelandic population. <i>Journal of Medical Genetics</i> , 2008, 45, 284-289.	1.5	30
2	The role of linkage studies for common diseases. <i>Current Opinion in Genetics and Development</i> , 2001, 11, 264-267.	1.5	26
3	A genome-wide scan for preeclampsia in the Netherlands. <i>European Journal of Human Genetics</i> , 2001, 9, 758-764.	1.4	140
4	Allelic Frequencies and Patterns of Single-nucleotide Polymorphisms in Candidate Genes for Asthma and Atopy in Iceland. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2001, 164, 2036-2044.	2.5	85
5	Allegro, a new computer program for multipoint linkage analysis. <i>Nature Genetics</i> , 2000, 25, 12-13.	9.4	737
6	Familial Aggregation of Parkinson's Disease in Iceland. <i>New England Journal of Medicine</i> , 2000, 343, 1765-1770.	13.9	271
7	On a Randomization Procedure. <i>American Journal of Human Genetics</i> , 2000, 67, 1352-1355.	2.6	4
8	A Genome-Wide Scan Reveals a Maternal Susceptibility Locus for Pre-Eclampsia on Chromosome 2p13. <i>Human Molecular Genetics</i> , 1999, 8, 1799-1805.	1.4	196
9	Loci on chromosomes 2 (NIDDM1) and 15 interact to increase susceptibility to diabetes in Mexican Americans. <i>Nature Genetics</i> , 1999, 21, 213-215.	9.4	374
10	Allele-Sharing Models: LOD Scores and Accurate Linkage Tests. <i>American Journal of Human Genetics</i> , 1997, 61, 1179-1188.	2.6	931
11	Graphical templates for model registration. <i>IEEE Transactions on Pattern Analysis and Machine Intelligence</i> , 1996, 18, 225-236.	9.7	104
12	Asymptotic theory for gene mapping.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994, 91, 9705-9709.	3.3	22
13	Sequential imputation and multipoint linkage analysis. <i>Genetic Epidemiology</i> , 1993, 10, 483-488.	0.6	18
14	Linkage analysis with adjustment for covariates: A method combining peeling with Gibbs sampling. <i>Cytogenetic and Genome Research</i> , 1992, 59, 208-210.	0.6	6
15	Importance sampling. I. Computing multimodel p values in linkage analysis. <i>American Journal of Human Genetics</i> , 1992, 51, 1413-29.	2.6	13
16	Efficient methods for computing linkage likelihoods of recessive diseases in inbred pedigrees. <i>Genetic Epidemiology</i> , 1991, 8, 81-103.	0.6	16