

Kees Albers

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9151609/publications.pdf>

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13
papers

17,235
citations

840776

11
h-index

1125743

13
g-index

13
all docs

13
docs citations

13
times ranked

35943
citing authors

#	ARTICLE	IF	CITATIONS
1	New insights into the genetic basis of TAR (thrombocytopenia-absent radii) syndrome. <i>Current Opinion in Genetics and Development</i> , 2013, 23, 316-323.	3.3	74
2	SMIM1 underlies the Vel blood group and influences red blood cell traits. <i>Nature Genetics</i> , 2013, 45, 542-545.	21.4	96
3	The origin, evolution, and functional impact of short insertion-deletion variants identified in 179 human genomes. <i>Genome Research</i> , 2013, 23, 749-761.	5.5	206
4	Maps of open chromatin highlight cell type-restricted patterns of regulatory sequence variation at hematological trait loci. <i>Genome Research</i> , 2013, 23, 1130-1141.	5.5	34
5	Seventy-five genetic loci influencing the human red blood cell. <i>Nature</i> , 2012, 492, 369-375.	27.8	320
6	An integrated map of genetic variation from 1,092 human genomes. <i>Nature</i> , 2012, 491, 56-65.	27.8	7,199
7	Compound inheritance of a low-frequency regulatory SNP and a rare null mutation in exon-junction complex subunit RBM8A causes TAR syndrome. <i>Nature Genetics</i> , 2012, 44, 435-439.	21.4	355
8	A Systematic Survey of Loss-of-Function Variants in Human Protein-Coding Genes. <i>Science</i> , 2012, 335, 823-828.	12.6	1,095
9	Dindel: Accurate indel calls from short-read data. <i>Genome Research</i> , 2011, 21, 961-973.	5.5	383
10	Exome sequencing identifies NBEAL2 as the causative gene for gray platelet syndrome. <i>Nature Genetics</i> , 2011, 43, 735-737.	21.4	245
11	A map of human genome variation from population-scale sequencing. <i>Nature</i> , 2010, 467, 1061-1073.	27.8	7,209
12	Multipoint Approximations of Identity-by-Descent Probabilities for Accurate Linkage Analysis of Distantly Related Individuals. <i>American Journal of Human Genetics</i> , 2008, 82, 607-622.	6.2	9
13	Haplotype Inference in General Pedigrees Using the Cluster Variation Method. <i>Genetics</i> , 2007, 177, 1101-1116.	2.9	10