

Kees Albers

List of Publications by Year in descending order

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

Version: 2024-02-01

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 | A map of human genome variation from population-scale sequencing. <i>Nature</i> , 2010, 467, 1061-1073. | 27.8 | 7,209 |
| 2 | An integrated map of genetic variation from 1,092 human genomes. <i>Nature</i> , 2012, 491, 56-65. | 27.8 | 7,199 |
| 3 | A Systematic Survey of Loss-of-Function Variants in Human Protein-Coding Genes. <i>Science</i> , 2012, 335, 823-828. | 12.6 | 1,095 |
| 4 | Dindel: Accurate indel calls from short-read data. <i>Genome Research</i> , 2011, 21, 961-973. | 5.5 | 383 |
| 5 | 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 |
| 6 | Seventy-five genetic loci influencing the human red blood cell. <i>Nature</i> , 2012, 492, 369-375. | 27.8 | 320 |
| 7 | Exome sequencing identifies NBEAL2 as the causative gene for gray platelet syndrome. <i>Nature Genetics</i> , 2011, 43, 735-737. | 21.4 | 245 |
| 8 | 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 |
| 9 | SMIM1 underlies the Vel blood group and influences red blood cell traits. <i>Nature Genetics</i> , 2013, 45, 542-545. | 21.4 | 96 |
| 10 | 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 |
| 11 | 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 |
| 12 | Haplotype Inference in General Pedigrees Using the Cluster Variation Method. <i>Genetics</i> , 2007, 177, 1101-1116. | 2.9 | 10 |
| 13 | 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 |