# Alexander T Dilthey

List of Publications by Year
in descending order



| 46 | 10,486 | 159358 30 | 253896 43 |
|---|---|---|---|
| papers | citations | h-index | g-index |

| 65 | 65 | 65 | 18993 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. Nature, 2011, 476, 214-219. | 13.7 | 2,400 |
| 2 | Nanopore sequencing and assembly of a human genome with ultra-long reads. Nature Biotechnology, 2018, 36, 338-345. | 9.4 | 1,443 |
| 3 | Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. Nature Genetics, 2013, 45, 1353-1360. | 9.4 | 1,213 |
| 4 | A genome-wide association study identifies new psoriasis susceptibility loci and an interaction between HLA-C and ERAP1. Nature Genetics, 2010, 42, 985-990. | 9.4 | 918 |
| 5 | Interaction between ERAP1 and HLA-B27 in ankylosing spondylitis implicates peptide handling in the mechanism for HLA-B27 in disease susceptibility. Nature Genetics, 2011, 43, 761-767. | 9.4 | 778 |
| 6 | Genetics of gene expression in primary immune cells identifies cell typeâ€“specific master regulators and roles of HLA alleles. Nature Genetics, 2012, 44, 502-510. | 9.4 | 445 |
| 7 | <scp>SARS</scp> â€CoVâ€2 targets neurons of 3D human brain organoids. EMBO Journal, 2020, 39, e106230. | 3.5 | 401 |
| 8 | De novo assembly of haplotype-resolved genomes with trio binning. Nature Biotechnology, 2018, 36, 1174-1182. | 9.4 | 352 |
| 9 | Class II HLA interactions modulate genetic risk for multiple sclerosis. Nature Genetics, 2015, 47, 1107-1113. | 9.4 | 312 |
| 10 | Improved genome inference in the MHC using a population reference graph. Nature Genetics, 2015, 47, 682-688. | 9.4 | 197 |
| 11 | Multi-Population Classical HLA Type Imputation. PLoS Computational Biology, 2013, 9, e1002877. | 1.5 | 157 |
| 12 | HLA*IMPâ€”an integrated framework for imputing classical HLA alleles from SNP genotypes. Bioinformatics, 2011, 27, 968-972. | 1.8 | 151 |
| 13 | DNA methylation as a mediator of HLA-DRB1*15:01 and a protective variant in multiple sclerosis. Nature Communications, 2018, 9, 2397. | 5.8 | 147 |
| 14 | Molecular mimicry between Anoctamin 2 and Epstein-Barr virus nuclear antigen 1 associates with multiple sclerosis risk. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 16955-16960. | 3.3 | 120 |
| 15 | A fast adaptive algorithm for computing whole-genome homology maps. Bioinformatics, 2018, 34, i748-i756. | 1.8 | 110 |
| 16 | Strain-level metagenomic assignment and compositional estimation for long reads with MetaMaps. Nature Communications, 2019, 10, 3066. | 5.8 | 98 |
| 17 | Pangenome-based genome inference allows efficient and accurate genotyping across a wide spectrum of variant classes. Nature Genetics, 2022, 54, 518-525. | 9.4 | 92 |
| 18 | HLA*LAâ€”HLA typing from linearly projected graph alignments. Bioinformatics, 2019, 35, 4394-4396. | 1.8 | 88 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | High-Accuracy HLA Type Inference from Whole-Genome Sequencing Data Using Population Reference Graphs. PLoS Computational Biology, 2016, 12, e1005151. | 1.5 | 87 |
| 20 | Emergence of the E484K mutation in SARS-COV-2-infected immunocompromised patients treated with bamlanivimab in Germany. Lancet Regional Health - Europe, The, 2021, 8, 100164. | 3.0 | 83 |
| 21 | Imputation of KIR Types from SNP Variation Data. American Journal of Human Genetics, 2015, 97, 593-607. | 2.6 | 73 |
| 22 | Emu: species-level microbial community profiling of full-length 16S rRNA Oxford Nanopore sequencing data. Nature Methods, 2022, 19, 845-853. | 9.0 | 69 |
| 23 | Psoriasis Patients Are Enriched for Genetic Variants That Protect against HIV-1 Disease. PLoS Genetics, 2012, 8, e1002514. | 1.5 | 66 |
| 24 | Variation in human chromosome 21 ribosomal RNA genes characterized by TAR cloning and long-read sequencing. Nucleic Acids Research, 2018, 46, 6712-6725. | 6.5 | 61 |
| 25 | Bayesian analysis of genetic association across tree-structured routine healthcare data in the UK Biobank. Nature Genetics, 2017, 49, 1311-1318. | 9.4 | 56 |
| 26 | A diploid assembly-based benchmark for variants in the major histocompatibility complex. Nature Communications, 2020, 11, 4794. | 5.8 | 56 |
| 27 | Genetic structure of SARS-CoV-2 reflects clonal superspreading and multiple independent introduction events, North-Rhine Westphalia, Germany, February and March 2020. Eurosurveillance, 2020, 25, . | 3.9 | 45 |
| 28 | Genetic fine mapping of systemic lupus erythematosus MHC associations in Europeans and African Americans. Human Molecular Genetics, 2018, 27, 3813-3824. | 1.4 | 43 |
| 29 | A Fast Approximate Algorithm for Mapping Long Reads to Large Reference Databases. Journal of Computational Biology, 2018, 25, 766-779. | 0.8 | 41 |
| 30 | Multiple Hodgkin lymphomaâ€“associated loci within the HLA region at chromosome 6p21.3. Blood, 2011, 118, 670-674. | 0.6 | 37 |
| 31 | Development and validation of a universal blood donor genotyping platform: a multinational prospective study. Blood Advances, 2020, 4, 3495-3506. | 2.5 | 31 |
| 32 | MHC variation and risk of childhood B-cell precursor acute lymphoblastic leukemia. Blood, 2011, 117, 1633-1640. | 0.6 | 24 |
| 33 | Distinct genetic architectures and environmental factors associate with host response to the Î²2-herpesvirus infections. Nature Communications, 2020, 11, 3849. | 5.8 | 24 |
| 34 | State-of-the-art genome inference in the human MHC. International Journal of Biochemistry and Cell Biology, 2021, 131, 105882. | 1.2 | 22 |
| 35 | Characterization of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Infection Clusters Based on Integrated Genomic Surveillance, Outbreak Analysis and Contact Tracing in an Urban Setting. Clinical Infectious Diseases, 2022, 74, 1039-1046. | 2.9 | 21 |
| 36 | Accelerating Sequence Alignment to Graphs. , 2019, , . | | 16 |

| # | Article | IF | Citations |
|---|---|---|---|
| 37 | Haploflow: strain-resolved de novo assembly of viral genomes. Genome Biology, 2021, 22, 212. | 3.8 | 16 |
| 38 | Horizontally transferred genes cluster spatially and metabolically. Biology Direct, 2015, 10, 72. | 1.9 | 12 |
| 39 | Characterisation of the changing genomic landscape of metastatic melanoma using cell free DNA. Npj Genomic Medicine, 2017, 2, 25. | 1.7 | 12 |
| 40 | NovoGraph: Genome graph construction from multiple long-read de novo assemblies. F1000Research, 2018, 7, 1391. | 0.8 | 8 |
| 41 | European families reveal MHC class I and II associations with autoimmune-mediated congenital heart block. Annals of the Rheumatic Diseases, 2018, 77, 1381-1382. | 0.5 | 6 |
| 42 | Ultraplexing: increasing the efficiency of long-read sequencing for hybrid assembly with k-mer-based multiplexing. Genome Biology, 2020, 21, 68. | 3.8 | 6 |
| 43 | NovoGraph: Human genome graph construction from multiple long-read de novo assemblies. F1000Research, 2018, 7, 1391. | 0.8 | 5 |
| 44 | pmrCAB Recombination Events among Colistin-Susceptible and -Resistant Acinetobacter baumannii Clinical Isolates Belonging to International Clone 7. MSphere, 2021, 6, e0074621. | 1.3 | 3 |
| 45 | RNA transcription and degradation of Alu retrotransposons depends on sequence features and evolutionary history. G3: Genes, Genomes, Genetics, 2022, 12, . | 0.8 | 1 |
| 46 | Modifying splice site usage with ModCon: Maintaining the genetic code while changing the underlying mRNP code. Computational and Structural Biotechnology Journal, 2021, 19, 3069-3076. | 1.9 | 0 |