Alexander T Dilthey

List of Publications by Year
in descending order

46 papers	10,486 citations	159525 30 h-index	254106 43 g-index
65 all docs	65 docs citations	65 times ranked	18993 citing authors

#	Article	IF	Citations
1	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
2	RNA transcription and degradation of Alu retrotransposons depends on sequence features and evolutionary history. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	1
3	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
4	Emu: species-level microbial community profiling of full-length 16S rRNA Oxford Nanopore sequencing data. Nature Methods, 2022, 19, 845-853.	9.0	69
5	State-of-the-art genome inference in the human MHC. International Journal of Biochemistry and Cell Biology, 2021, 131, 105882.	1.2	22
6	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
7	Haploflow: strain-resolved de novo assembly of viral genomes. Genome Biology, 2021, 22, 212.	3.8	16
8	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
9	pmrCAB Recombination Events among Colistin-Susceptible and -Resistant Acinetobacter baumannii Clinical Isolates Belonging to International Clone 7. MSphere, 2021, 6, e0074621.	1.3	3
10	Development and validation of a universal blood donor genotyping platform: a multinational prospective study. Blood Advances, 2020, 4, 3495-3506.	2.5	31
11	Distinct genetic architectures and environmental factors associate with host response to the Î32-herpesvirus infections. Nature Communications, 2020, 11, 3849.	5.8	24
12	A diploid assembly-based benchmark for variants in the major histocompatibility complex. Nature Communications, 2020, 11, 4794.	5.8	56
13	Ultraplexing: increasing the efficiency of long-read sequencing for hybrid assembly with k-mer-based multiplexing. Genome Biology, 2020, 21, 68.	3.8	6
14	<scp>SARS</scp> â€CoVâ€2 targets neurons of 3D human brain organoids. EMBO Journal, 2020, 39, e106230.	3.5	401
15	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
16	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
17	Strain-level metagenomic assignment and compositional estimation for long reads with MetaMaps. Nature Communications, 2019, 10, 3066.	5.8	98
18	HLA*LAâ€”HLA typing from linearly projected graph alignments. Bioinformatics, 2019, 35, 4394-4396.	1.8	88

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19	Accelerating Sequence Alignment to Graphs. , 2019, , .		16
20	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
21	Nanopore sequencing and assembly of a human genome with ultra-long reads. Nature Biotechnology, 2018, 36, 338-345.	9.4	1,443
22	A Fast Approximate Algorithm for Mapping Long Reads to Large Reference Databases. Journal of Computational Biology, 2018, 25, 766-779.	0.8	41
23	A fast adaptive algorithm for computing whole-genome homology maps. Bioinformatics, 2018, 34, i748-i756.	1.8	110
24	De novo assembly of haplotype-resolved genomes with trio binning. Nature Biotechnology, 2018, 36, 1174-1182.	9.4	352
25	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
26	Genetic fine mapping of systemic lupus erythematosus MHC associations in Europeans and African Americans. Human Molecular Genetics, 2018, 27, 3813-3824.	1.4	43
27	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
28	NovoGraph: Human genome graph construction from multiple long-read de novo assemblies. F1000Research, 2018, 7, 1391.	0.8	5
29	NovoGraph: Genome graph construction from multiple long-read de novo assemblies. F1000Research, 2018, 7, 1391.	0.8	8
30	Characterisation of the changing genomic landscape of metastatic melanoma using cell free DNA. Npj Genomic Medicine, 2017, 2, 25.	1.7	12
31	Bayesian analysis of genetic association across tree-structured routine healthcare data in the UK Biobank. Nature Genetics, 2017, 49, 1311-1318.	9.4	56
32	High-Accuracy HLA Type Inference from Whole-Genome Sequencing Data Using Population Reference Graphs. PLoS Computational Biology, 2016, 12, e1005151.	1.5	87
33	Horizontally transferred genes cluster spatially and metabolically. Biology Direct, 2015, 10, 72.	1.9	12
34	Improved genome inference in the MHC using a population reference graph. Nature Genetics, 2015, 47, 682-688.	9.4	197
35	Imputation of KIR Types from SNP Variation Data. American Journal of Human Genetics, 2015, 97, 593-607.	2.6	73
36	Class II HLA interactions modulate genetic risk for multiple sclerosis. Nature Genetics, 2015, 47, 1107-1113.	9.4	312

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37	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. Nature Genetics, 2013, 45, 1353-1360.	9.4	1,213
38	Multi-Population Classical HLA Type Imputation. PLoS Computational Biology, 2013, 9, e1002877.	1.5	157
39	Psoriasis Patients Are Enriched for Genetic Variants That Protect against HIV-1 Disease. PLoS Genetics, 2012, 8, e1002514.	1.5	66
40	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
41	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. Nature, 2011, 476, 214-219.	13.7	2,400
42	MHC variation and risk of childhood B-cell precursor acute lymphoblastic leukemia. Blood, 2011, 117, 1633-1640.	0.6	24
43	Multiple Hodgkin lymphomaâ€“associated loci within the HLA region at chromosome 6p21.3. Blood, 2011, 118, 670-674.	0.6	37
44	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
45	HLA*IMPâ€”an integrated framework for imputing classical HLA alleles from SNP genotypes. Bioinformatics, 2011, 27, 968-972.	1.8	151
46	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