Andreas W Schreiber

List of Publications by Year
in descending order

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83 papers	4,350 citations	236925 25 h-index	110387 64 g-index
86 all docs	86 docs citations	86 times ranked	7377 citing authors

#	Article	IF	Citations
1	The RNA Binding Protein Quaking Regulates Formation of circRNAs. Cell, 2015, 160, 1125-1134.	28.9	1,698
2	Cell-Specific Vacuolar Calcium Storage Mediated by CAX1 Regulates Apoplastic Calcium Concentration, Gas Exchange, and Plant Productivity in Arabidopsis Â Â. Plant Cell, 2011, 23, 240-257.	6.6	222
3	Mutations in the mammalian target of rapamycin pathway regulators NPRL2 and NPRL3 cause focal epilepsy. Annals of Neurology, 2016, 79, 120-131.	5.3	190
4	Novel germ line DDX41 mutations define families with a lower age of MDS/AML onset and lymphoid malignancies. Blood, 2016, 127, 1017-1023.	1.4	179
5	Integrative genomic analysis reveals cancer-associated mutations at diagnosis of CML in patients with high-risk disease. Blood, 2018, 132, 948-961.	1.4	152
6	An atlas of gene expression from seed to seed through barley development. Functional and Integrative Genomics, 2006, 6, 202-211.	3.5	138
7	A framework for gene expression analysis. Bioinformatics, 2007, 23, 191-197.	4.1	128
8	Discovery of barley miRNAs through deep sequencing of short reads. BMC Genomics, 2011, 12, 129.	2.8	118
9	Structure functions in the bag model. Physical Review D, 1991, 44, 2653-2662.	4.7	115
10	Deep-inelastic scattering from off-shell nucleons. Physical Review D, 1994, 49, 1183-1198.	4.7	103
11	RUNX1-mutated families show phenotype heterogeneity and a somatic mutation profile unique to germline predisposed AML. Blood Advances, 2020, 4, 1131-1144.	5.2	102
12	ARMC5Mutations Are Common in Familial Bilateral Macronodular Adrenal Hyperplasia. Journal of Clinical Endocrinology and Metabolism, 2014, 99, E1784-E1792.	3.6	96
13	A comparative analysis of algorithms for somatic SNV detection in cancer. Bioinformatics, 2013, 29, 2223-2230.	4.1	86
14	miRâ€200/375 control epithelial plasticityâ€associated alternative splicing by repressing the <scp>RNA</scp> â€binding protein Quaking. EMBO Journal, 2018, 37, .	7.8	82
15	Comparative transcriptomics in the Triticeae. BMC Genomics, 2009, 10, 285.	2.8	62
16	Transcriptome-scale homoeolog-specific transcript assemblies of bread wheat. BMC Genomics, 2012, 13, 492.	2.8	51
17	The mutational burden of therapy-related myeloid neoplasms is similar to primary myelodysplastic syndrome but has a distinctive distribution. Leukemia, 2019, 33, 2842-2853.	7.2	43
18	Pion cloud of the nucleon and its effect on deep-inelastic structure. Physical Review D, 1992, 45, 3069-3078.	4.7	41

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19	BAM-matcher: a tool for rapid NGS sample matching. Bioinformatics, 2016, 32, 2699-2701.	4.1	33
20	A tale of two siblings: two cases of AML arising from a single pre-leukemic DNMT3A mutant clone. Leukemia, 2015, 29, 2101-2104.	7.2	32
21	RUNX1 mutations in blast-phase chronic myeloid leukemia associate with distinct phenotypes, transcriptional profiles, and drug responses. Leukemia, 2021, 35, 1087-1099.	7.2	32
22	Targeted gene panels identify a high frequency of pathogenic germline variants in patients diagnosed with a hematological malignancy and at least one other independent cancer. Leukemia, 2021, 35, 3245-3256.	7.2	32
23	Ectrodactyly and Lethal Pulmonary Acinar Dysplasia Associated with HomozygousFGFR2Mutations Identified by Exome Sequencing. Human Mutation, 2016, 37, 955-963.	2.5	30
24	QCD evolution of the spin structure functions of the neutron and proton. Physical Review D, 1990, 42, 2226-2236.	4.7	29
25	Clusters of genes encoding fructan biosynthesizing enzymes in wheat and barley. Plant Molecular Biology, 2012, 80, 299-314.	3.9	29
26	The RUNX1 database (RUNX1db): establishment of an expert curated RUNX1 registry and genomics database as a public resource for familial platelet disorder with myeloid malignancy. Haematologica, 2021, 106, 3004-3007.	3.5	29
27	Worldline path integral for the massive Dirac propagator: A four-dimensional approach. Physical Review A, 1999, 59, 1762-1776.	2.5	28
28	Polaron variational methods in the particle representation of field theory. I. General formalism. Physical Review D, 1996, 53, 3337-3353.	4.7	27
29	Aberrant RAG-mediated recombination contributes to multiple structural rearrangements in lymphoid blast crisis of chronic myeloid leukemia. Leukemia, 2020, 34, 2051-2063.	7.2	27
30	Self-reverting mutations partially correct the blood phenotype in a Diamond Blackfan anemia patient. Haematologica, 2017, 102, e506-e509.	3.5	26
31	Maize maintains growth in response to decreased nitrate supply through a highly dynamic and developmental stageâ€specific transcriptional response. Plant Biotechnology Journal, 2016, 14, 342-353.	8.3	25
32	Nutlin-3a Efficacy in Sarcoma Predicted by Transcriptomic and Epigenetic Profiling. Cancer Research, 2014, 74, 921-931.	0.9	24
33	De novo UBE2A mutations are recurrently acquired during chronic myeloid leukemia progression and interfere with myeloid differentiation pathways. Haematologica, 2019, 104, 1789-1797.	3.5	21
34	Dimensionally regularized study of nonperturbative quenched QED. Physical Review D, 1998, 58, .	4.7	19
35	Sequencing error correction without a reference genome. BMC Bioinformatics, 2013, 14, 367.	2.6	19
36	ASXL1 and BIM germ line variants predict response and identify CML patients with the greatest risk of imatinib failure. Blood Advances, 2017, 1, 1369-1381.	5.2	17

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37	Identification and targeted management of a neurodegenerative disorder caused by biallelic mutations in SLC5A6. Npj Genomic Medicine, 2019, 4, 28.	3.8	16
38	A novel single-cell based method for breast cancer prognosis. PLoS Computational Biology, 2020, 16, e1008133.	3.2	16
39	Polaron variational methods in the particle representation of field theory. II. Numerical results for the propagator. Physical Review D, 1996, 53, 3354-3365.	4.7	15
40	Regularization-independent studies of nonperturbative field theory. Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics, 2001, 499, 261-269.	4.1	14
41	The Genomic Landscape of Sporadic Prolactinomas. Endocrine Pathology, 2019, 30, 318-328.	9.0	14
42	A novel germline SAMD9L mutation in a family with ataxia-pancytopenia syndrome and pediatric acute lymphoblastic leukemia. Haematologica, 2019, 104, e318-e321.	3.5	14
43	Clonal hematopoiesis in patients with ANKRD26 or ETV6 germline mutations. Blood Advances, 2022, 6, 4357-4359.	5.2	14
44	On the best quadratic approximation in Feynman's path integral treatment of the polaron. Physics Letters, Section A: General, Atomic and Solid State Physics, 2001, 284, 63-71.	2.1	13
45	First-order variational calculation of form factor in a scalar nucleon-meson theory. Nuclear Physics A, 1996, 601, 397-424.	1.5	12
46	Paternal mosaicism for a novel <scp>PBX1</scp> mutation associated with recurrent perinatal death: Phenotypic expansion of the <scp>PBX1</scp>â€related syndrome. American Journal of Medical Genetics, Part A, 2020, 182, 1273-1277.	1.2	12
47	Combining transcriptional datasets using the generalized singular value decomposition. BMC Bioinformatics, 2008, 9, 335.	2.6	11
48	T cell receptor assessment in autoimmune disease requires access to the most adjacent immunologically active organ. Journal of Autoimmunity, 2017, 81, 24-33.	6.5	10
49	Integration of cell adhesion reactionsâ€"a balance of forces?. Journal of Theoretical Biology, 2006, 238, 608-615.	1.7	9
50	Allanâ€"Herndonâ€"Dudley syndrome with unusual profound sensorineural hearing loss. American Journal of Medical Genetics, Part A, 2015, 167, 1872-1876.	1.2	9
51	Aberrant Splicing of SDHC in Families With Unexplained Succinate Dehydrogenase-Deficient Paragangliomas. Journal of the Endocrine Society, 2020, 4, bvaa071.	0.2	9
52	Delayed diagnosis leading to accelerated-phase chronic eosinophilic leukemia due to a cytogenetically cryptic, imatinib-responsive TNIP1â€"PDFGRB fusion gene. Leukemia, 2016, 30, 1402-1405.	7.2	8
53	Pseudodiastrophic dysplasia expands the known phenotypic spectrum of defects in proteoglycan biosynthesis. Journal of Medical Genetics, 2020, 57, 454-460.	3.2	8
54	A putative role for the aryl hydrocarbon receptor (AHR) gene in a patient with cyclical Cushingâ€™s disease. BMC Endocrine Disorders, 2020, 20, 18.	2.2	6

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55	Variational field theoretic approach to relativistic meson-nucleon scattering. Nuclear Physics A, 1998, 628, 427-457.	1.5	5
56	Compound heterozygous variants in LAMC3 in association with posterior periventricular nodular heterotopia. BMC Medical Genomics, 2021, 14, 64.	1.5	5
57	Childhood acute myeloid leukemia shows a high level of germline predisposition. Blood, 2021, 138, 2293-2298.	1.4	5
58	ARMC5 is not implicated in familial hyperaldosteronism type II (FH-II). Journal of Human Hypertension, 2017, 31, 857-859.	2.2	4
59	Mutated Cancer-Related Genes Detected at Diagnosis of CML and a Novel Class of Variant Associated with the Philadelphia Translocation Are Both Independent Predictors of Inferior Outcomes. Blood, 2020, 136, 46-47.	1.4	4
60	High Incidence of Mutated Cancer-Associated Genes at Diagnosis in CML Patients with Early Transformation to Blast Crisis. Blood, 2015, 126, 600-600.	1.4	4
61	Improved Parton Distributions from the Quark Model. Australian Journal of Physics, 1991, 44, 363.	0.6	3
62	Detection of BCR-ABL1 Compound and Polyclonal Mutants in Chronic Myeloid Leukemia Patients Using a Novel Next Generation Sequencing Approach That Minimises PCR and Sequencing Errors. Blood, 2014, 124, 399-399.	1.4	3
63	Two monogenic disorders masquerading as one: severe congenital neutropenia with monocytosis and non-syndromic sensorineural hearing loss. BMC Medical Genetics, 2020, 21, 35.	2.1	3
64	Comment on â€œUnique Translation between Hamiltonian Operators and Functional Integralsâ€• Physical Review Letters, 2002, 88, 078901.	7.8	2
65	Regulator-free Schwinger-Dyson equation studies of the non-perturbative field theory. Nuclear Physics, Section B, Proceedings Supplements, 2002, 109, 173-177.	0.4	2
66	Australian Familial Haematological Cancer Study - Findings from 15 Years of Aggregated Clinical, Genomic and Transcriptomic Data. Blood, 2019, 134, 1439-1439.	1.4	2
67	Rare and Common Germline Variants Contribute to Occurrence of Myelodysplastic Syndrome. Blood, 2015, 126, 1644-1644.	1.4	2
68	Germline Genetic Variation of ASXL1 and BIM Predicts Response to Imatinib and Identifies a Subset of High Sokal Risk Patients with the Greatest Risk of Treatment Failure and Disease Progression. Blood, 2015, 126, 475-475.	1.4	2
69	Expanded Phenotypic and Genetic Heterogeneity in the Clinical Spectrum of FPD-AML: Lymphoid Malignancies and Skin Disorders Are Common Features in Carriers of Germline RUNX1 Mutations. Blood, 2016, 128, 1212-1212.	1.4	2
70	Novel Fusion Genes at CML Diagnosis Reveal a Complex Pattern of Genomic Rearrangements and Sequence Inversions Associated with the Philadelphia Chromosome in Patients with Early Blast Crisis. Blood, 2016, 128, 1219-1219.	1.4	2
71	RNA-Based Targeted Gene Sequencing Improves the Diagnostic Yield of Mutant Detection in Chronic Myeloid Leukemia. Journal of Molecular Diagnostics, 2022, 24, 803-822.	2.8	2
72	Familial clustering of haematological malignancies: harbingers of wider germline cancer susceptibility. Pathology, 2017, 49, S32-S33.	0.6	1

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73	An Integrative Genomic Approach to Examine Mutations and Biological Pathways Associated with Hematological Malignancy Development in DDX41 Mutated Families. Blood, 2019, 134, 2686-2686.	1.4	1
74	RNA Splicing Defects in Cancer-Linked Genes Indicate Mutation or Focal Gene Deletion and Are Associated with TKI Resistance in CML. Blood, 2019, 134, 662-662.	1.4	1
75	Cover Image, Volume 37, Issue 9. Human Mutation, 2016, 37, i-i.	2.5	0
76	Clonal Diversity of Recurrently Mutated Genes in Myelodysplastic Syndromes. Blood, 2014, 124, 4634-4634.	1.4	0
77	The Frequency of Genetic Mutations in T-MN Is High and Comparable to Primary MDS but the Spectrum Is Different. Blood, 2016, 128, 3157-3157.	1.4	0
78	Genetic Predisposition to Therapy-Related Myeloid Neoplasm By Rare, Deleterious Germline Variants in DNA Repair Pathway and Myeloid Driver Genes. Blood, 2018, 132, 1802-1802.	1.4	0
79	High Recombination Activating Gene (RAG) Expression and RAG Mediated Recombination Is Associated with Oncogenic Rearrangement Observed with Tyrosine Kinase Inhibitor Resistant CML. Blood, 2018, 132, 3001-3001.	1.4	0
80	OR34-6 A Novel Mechanism of SDH-Deficient Tumorigenesis and Implications for Genetic Testing in Patients with Pheochromocytoma-Paraganglioma. Journal of the Endocrine Society, 2019, 3, .	0.2	0
81	An RNA-Based Next Generation Sequencing (NGS) Strategy Detects More Cancer Gene Mutations Than a DNA-Based Approach for the Prediction and Assessment of Resistance in CML. Blood, 2019, 134, 2918-2918.	1.4	0
82	Familial Clustering of Hematological Malignancies: Harbingers of Wider Germline Cancer Susceptibility. Blood, 2019, 134, 3794-3794.	1.4	0
83	Therapy-Related Myeloid Neoplasm Has a Distinct Pro-Inflammatory Bone Marrow Microenvironment and Delayed DNA Damage Repair. Blood, 2020, 136, 37-38.	1.4	0