Michael Baudis

List of Publications by Year
in descending order

84 papers	4,312 citations	147566 31 h-index	123241 61 g-index
103 all docs	103 docs citations	103 times ranked	7686 citing authors

#	Article	IF	Citations
1	Integrated Molecular Meta-Analysis of 1,000 Pediatric High-Grade and Diffuse Intrinsic Pontine Glioma. Cancer Cell, 2017, 32, 520-537.e5.	7.7	716
2	Analysis of genomic alterations in benign, atypical, and anaplastic meningiomas: Toward a genetic model of meningioma progression. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 14719-14724.	3.3	372
3	Translocations involving 8q24 in Burkitt lymphoma and other malignant lymphomas: a historical review of cytogenetics in the light of todays knowledge. Leukemia, 2009, 23, 225-234.	3.3	192
4	Progenetix.net: an online repository for molecular cytogenetic aberration data. Bioinformatics, 2001, 17, 1228-1229.	1.8	168
5	Unequivocal Delineation of Clinicogenetic Subgroups and Development of a New Model for Improved Outcome Prediction in Neuroblastoma. Journal of Clinical Oncology, 2005, 23, 2280-2299.	0.8	160
6	Gain of chromosome arm 9p is characteristic of primary mediastinal b-cell lymphoma (MBL): Comprehensive molecular cytogenetic analysis and presentation of a novel MBL cell line. Genes Chromosomes and Cancer, 2001, 30, 393-401.	1.5	138
7	t(11;14)-positive mantle cell lymphomas exhibit complex karyotypes and share similarities with B-cell chronic lymphocytic leukemia. , 2000, 27, 285-294.		137
8	Genomic imbalances in 5918 malignant epithelial tumors: an explorative meta-analysis of chromosomal CGH data. BMC Cancer, 2007, 7, 226.	1.1	131
9	Randomized Study to Evaluate the Use of High-Dose Therapy as Part of Primary Treatment for â€œAggressiveâ€•Lymphoma. Journal of Clinical Oncology, 2002, 20, 4413-4419.	0.8	126
10	Quantifying cancer progression with conjunctive Bayesian networks. Bioinformatics, 2009, 25, 2809-2815.	1.8	104
11	A harmonized meta-knowledgebase of clinical interpretations of somatic genomic variants in cancer. Nature Genetics, 2020, 52, 448-457.	9.4	104
12	Chromothripsis-like patterns are recurring but heterogeneously distributed features in a survey of 22,347 cancer genome screens. BMC Genomics, 2014, 15, 82.	1.2	100
13	GA4GH: International policies and standards for data sharing across genomic research and healthcare. Cell Genomics, 2021, 1, 100029.	3.0	94
14	Combined single nucleotide polymorphism-based genomic mapping and global gene expression profiling identifies novel chromosomal imbalances, mechanisms and candidate genes important in the pathogenesis of T-cell prolymphocytic leukemia with inv(14)(q11q32). Leukemia, 2007, 21, 2153-2163.	3.3	93
15	Federated discovery and sharing of genomic data using Beacons. Nature Biotechnology, 2019, 37, 220-224.	9.4	75
16	Microarray comparative genomic hybridization detection of chromosomal imbalances in uterine cervix carcinoma. BMC Cancer, 2005, 5, 77.	1.1	74
17	Leveraging European infrastructures to access 1 million human genomes by 2022. Nature Reviews Genetics, 2019, 20, 693-701.	7.7	69
18	The Ubiquitin Ligase TRIP12 Limits PARP1 Trapping and Constrains PARP Inhibitor Efficiency. Cell Reports, 2020, 32, 107985.	2.9	68

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19	SIL1 mutations and clinical spectrum in patients with Marinesco-SjÃ¶gren syndrome. Brain, 2013, 136, 3634-3644.	3.7	65
20	Recurrent loss of heterozygosity in 1p36 associated with TNFRSF14 mutations in IRF4 translocation negative pediatric follicular lymphomas. Haematologica, 2013, 98, 1237-1241.	1.7	65
21	The SIB Swiss Institute of Bioinformaticsâ€™ resources: focus on curated databases. Nucleic Acids Research, 2016, 44, D27-D37.	6.5	64
22	Comprehensive Characterization of Genomic Aberrations in Gangliogliomas by CGH, Arrayâ€based CGH and Interphase FISH. Brain Pathology, 2008, 18, 326-337.	2.1	58
23	Distance-based clustering of CGH data. Bioinformatics, 2006, 22, 1971-1978.	1.8	55
24	Silver-Russell patients showing a broad range of ICR1 and ICR2 hypomethylation in different tissues. Clinical Genetics, 2011, 80, 83-88.	1.0	54
25	Chromosome imbalances in papillary renal cell carcinoma and first cytogenetic data of familial cases analyzed by comparative genomic hybridization. Cytogenetic and Genome Research, 1996, 75, 17-21.	0.6	44
26	Submicroscopic chromosomal imbalances in idiopathic Silver-Russell syndrome (SRS): the SRS phenotype overlaps with the 12q14 microdeletion syndrome. Journal of Medical Genetics, 2010, 47, 356-360.	1.5	44
27	Progenetix: 12 years of oncogenomic data curation. Nucleic Acids Research, 2014, 42, D1055-D1062.	6.5	44
28	MUC1 oncogene amplification correlates with protein overexpression in invasive breast carcinoma cells. Cancer Genetics and Cytogenetics, 2010, 201, 102-110.	1.0	43
29	PKC signaling prevents irradiation-induced apoptosis of primary human fibroblasts. Cell Death and Disease, 2013, 4, e498-e498.	2.7	40
30	Molecular Karyotyping as a Relevant Diagnostic Tool in Children with Growth Retardation with Silver-Russell Features. Journal of Pediatrics, 2012, 161, 933-942.e1.	0.9	39
31	The GA4GH Phenopacket schema defines a computable representation of clinical data. Nature Biotechnology, 2022, 40, 817-820.	9.4	38
32	Genomic Instability of Osteosarcoma Cell Lines in Culture: Impact on the Prediction of Metastasis Relevant Genes. PLoS ONE, 2015, 10, e0125611.	1.1	35
33	arrayMap: A Reference Resource for Genomic Copy Number Imbalances in Human Malignancies. PLoS ONE, 2012, 7, e36944.	1.1	34
34	Chromosomal changes characterize head and neck cancer with poor prognosis. Journal of Molecular Medicine, 2008, 86, 1353-1365.	1.7	33
35	Registered access: authorizing data access. European Journal of Human Genetics, 2018, 26, 1721-1731.	1.4	33
36	High resolution copy number analysis of IRF4 translocationâ€positive diffuse large Bâ€cell and follicular lymphomas. Genes Chromosomes and Cancer, 2013, 52, 150-155.	1.5	30

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37	arrayMap 2014: an updated cancer genome resource. Nucleic Acids Research, 2015, 43, D825-D830.	6.5	29
38	segment_liftover : a Python tool to convert segments between genome assemblies. F1000Research, 2018, 7, 319.	0.8	29
39	Online database and bioinformatics toolbox to support data mining in cancer cytogenetics. BioTechniques, 2006, 40, 269-272.	0.8	25
40	Integrative genome-wide expression profiling identifies three distinct molecular subgroups of renal cell carcinoma with different patient outcome. BMC Cancer, 2012, 12, 310.	1.1	25
41	Chromosome 11p15 duplication in Silverâ€Russell syndrome due to a maternally inherited translocation t(11;15). American Journal of Medical Genetics, Part A, 2010, 152A, 1484-1487.	0.7	24
42	Increased expression of cellular retinol-binding protein 1 in laryngeal squamous cell carcinoma. Journal of Cancer Research and Clinical Oncology, 2010, 136, 931-938.	1.2	22
43	International federation of genomic medicine databases using GA4GH standards. Cell Genomics, 2021, 1, 100032.	3.0	22
44	Recurrent loss, but lack of mutations, of the SMARCB1 tumor suppressor gene in T-cell prolymphocytic leukemia with TCL1Aâ€“TCRAD juxtaposition. Cancer Genetics and Cytogenetics, 2009, 192, 44-47.	1.0	21
45	2p21 Deletions in hypotoniaâ€“cystinuria syndrome. European Journal of Medical Genetics, 2012, 55, 561-563.	0.7	19
46	Improved multiplex ligationâ€dependent probe amplification analysis identifies a deleterious PMS2 allele generated by recombination with crossover between PMS2 and PMS2CL. Genes Chromosomes and Cancer, 2012, 51, 819-831.	1.5	19
47	Allele-specific loss of heterozygosity in multiple colorectal adenomas: toward an integrated molecular cytogenetic map II. Cancer Genetics and Cytogenetics, 2006, 167, 1-14.	1.0	18
48	The GA4GH Variation Representation Specification: A computational framework for variation representation and federated identification. Cell Genomics, 2021, 1, 100027.	3.0	18
49	Recurrent loss of the Y chromosome and homozygous deletions within the pseudoautosomal region 1: association with male predominance in mantle cell lymphoma. Haematologica, 2008, 93, 949-950.	1.7	17
50	Identification of a 21q22 duplication in a Silverâ€“Russell syndrome patient further narrows down the Down syndrome critical region. American Journal of Medical Genetics, Part A, 2010, 152A, 356-359.	0.7	17
51	Identification of genetic imbalances in malignant lymphoma using comparative genomic hybridization. Stem Cells, 1995, 13, 83-87.	1.4	16
52	ABCB1 over-expression and drug-efflux in acute lymphoblastic leukemia cell lines with t(17;19) and E2A-HLF expression. Pediatric Blood and Cancer, 2006, 47, 757-764.	0.8	16
53	segment_liftover : a Python tool to convert segments between genome assemblies. F1000Research, 2018, 7, 319.	0.8	16
54	PKCÎ± and HMGB1 antagonistically control hydrogen peroxide-induced poly-ADP-ribose formation. Nucleic Acids Research, 2016, 44, 7630-7645.	6.5	15

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55	DNA copy number alterations in central primitive neuroectodermal tumors and tumors of the pineal region: an international individual patient data meta-analysis. Journal of Neuro-Oncology, 2012, 109, 415-423.	1.4	13
56	The Progenetix oncogenomic resource in 2021. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	1.4	13
57	Genetic losses in breast cancer: toward an integrated molecular cytogenetic map. Cancer Genetics and Cytogenetics, 2005, 160, 141-151.	1.0	12
58	KrÃ¼ppel-Like Factor 10 participates in cervical cancer immunoediting through transcriptional regulation of Pregnancy-Specific Beta-1 Glycoproteins. Scientific Reports, 2018, 8, 9445.	1.6	11
59	DNA copy number imbalances in primary cutaneous lymphomas. Journal of the European Academy of Dermatology and Venereology, 2019, 33, 1062-1075.	1.3	11
60	Inferring progression models for CGH data. Bioinformatics, 2009, 25, 2208-2215.	1.8	10
61	Beacon v2 and Beacon networks: A â€œlingua francaâ€•for federated data discovery in biomedical genomics, and beyond. Human Mutation, 2022, , .	1.1	10
62	A 10.7 Mb interstitial deletion of 13q21 without phenotypic effect defines a further nonâ€pathogenic euchromatic variant. American Journal of Medical Genetics, Part A, 2008, 146A, 2417-2420.	0.7	9
63	Losses at chromosome 4q are associated with poor survival in operable ductal pancreatic adenocarcinoma. Pancreatology, 2012, 12, 16-22.	0.5	9
64	DNA Copy Number Changes in Diffuse Large B Cell Lymphomas. Frontiers in Oncology, 2020, 10, 584095.	1.3	9
65	CDCOCA: A statistical method to define complexity dependence of co-occuring chromosomal aberrations. BMC Medical Genomics, 2011, 4, 21.	0.7	7
66	Oncology Informatics: Status Quo and Outlook. Oncology, 2020, 98, 329-331.	0.9	7
67	Enabling population assignment from cancer genomes with SNP2pop. Scientific Reports, 2020, 10, 4846.	1.6	7
68	Minimum error calibration and normalization for genomic copy number analysis. Genomics, 2020, 112, 3331-3341.	1.3	6
69	Signatures of Discriminative Copy Number Aberrations in 31 Cancer Subtypes. Frontiers in Genetics, 2021, 12, 654887.	1.1	6
70	Mountains and Chasms: Surveying the Oncogenomic Publication Landscape. Oncology, 2020, 98, 332-343.	0.9	5
71	The ELIXIR Human Copy Number Variations Community: building bioinformatics infrastructure for research. F1000Research, 2020, 9, 1229.	0.8	5
72	Specific Genomic Regions Are Differentially Affected by Copy Number Alterations across Distinct Cancer Types, in Aggregated Cytogenetic Data. PLoS ONE, 2012, 7, e43689.	1.1	5

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73	CNARA: reliability assessment for genomic copy number profiles. BMC Genomics, 2016, 17, 799.	1.2	4
74	Geographic assessment of cancer genome profiling studies. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	3
75	Pathways and Crossroads to Colorectal Cancer. , 2011, , 369-394.		3
76	CDCOCA: a statistical method to define complexity dependent co-occurring chromosomal aberrations. Genome Biology, 2010, 11, P23.	13.9	2
77	Comparative Genomic Hybridization for the Analysis of Leukemias and Lymphomas. , 2001, 55, 43-64.		1
78	HIGH GRADE GLIOMAS AND DIPG. Neuro-Oncology, 2014, 16, i40-i59.	0.6	1
79	HG-11 * INTEGRATIVE MOLECULAR META-ANALYSIS OF 700 PEDIATRIC HIGH GRADE GLIOMA AND DIPG DEFINES WIDESPREAD INTER- AND INTRA-TUMORAL HETEROGENEITY. Neuro-Oncology, 2015, 17, iii12-iii13.	0.6	1
80	Biopsying parapsoriasis: quo vadis? Are morphological stains enough or are ancillary tests needed?. Romanian Journal of Morphology and Embryology, 2014, 55, 1085-92.	0.4	1
81	P25: Computational Aspects ofÂLarge Scale Cytogenetic Data Mining. European Journal of Medical Genetics, 2005, 48, 473-474.	0.7	0
82	Supernumerary Asymmetric Dic(15;15) With Secondary Mosaic Formation in One of Two Developmentally Retarded Twins. International Journal of Human Genetics, 2011, 11, 75-82.	0.1	0
83	HG-95INTEGRATED MOLECULAR META-ANALYSIS OF 1000 PAEDIATRIC HIGH GRADE GLIOMA AND DIPG. Neuro-Oncology, 2016, 18, iii70.3-iii70.	0.6	0
84	Translocations Involving 8q24 in Burkitt Lymphoma and Other Malignant Lymphomas: A Historical Review of Cytogenetics in the Light of Todays Knowledge. Blood, 2008, 112, 2814-2814.	0.6	0