Michael Baudis

List of Publications by Citations

86 papers	3,273 citations	29 h-index	56 g-index
102 ext. papers	3,996 ext. citations	7.3 avg, IF	4.91 L-index

#	Paper	IF	Citations
86	Integrated Molecular Meta-Analysis of 1,000 Pediatric High-Grade and Diffuse Intrinsic Pontine Glioma. *Cancer Cell*, **2017**, 32, 520-537.e5	24.3	423
85	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, 14719-24	11.5	324
84	Translocations involving 8q24 in Burkitt lymphoma and other malignant lymphomas: a historical review of cytogenetics in the light of todays knowledge. *Leukemia*, **2009**, 23, 225-34	10.7	165
83	Progenetix.net: an online repository for molecular cytogenetic aberration data. *Bioinformatics*, **2001**, 17, 1228-9	7.2	155
82	Unequivocal delineation of clinicogenetic subgroups and development of a new model for improved outcome prediction in neuroblastoma. *Journal of Clinical Oncology*, **2005**, 23, 2280-99	2.2	145
81	Randomized study to evaluate the use of high-dose therapy as part of primary treatment for "aggressive" lymphoma. *Journal of Clinical Oncology*, **2002**, 20, 4413-9	2.2	118
80	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	5	117
79	t(11;14)-positive mantle cell lymphomas exhibit complex karyotypes and share similarities with B-cell chronic lymphocytic leukemia **2000**, 27, 285-294		112
78	Genomic imbalances in 5918 malignant epithelial tumors: an explorative meta-analysis of chromosomal CGH data. *BMC Cancer*, **2007**, 7, 226	4.8	109
77	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, 2153-63	10.7	80
76	Chromothripsis-like patterns are recurring but heterogeneously distributed features in a survey of 22,347 cancer genome screens. *BMC Genomics*, **2014**, 15, 82	4.5	78
75	HIGH GRADE GLIOMAS AND DIPG. *Neuro-Oncology*, **2014**, 16, i40-i59	1	78
74	HG-95INTEGRATED MOLECULAR META-ANALYSIS OF 1000 PAEDIATRIC HIGH GRADE GLIOMA AND DIPG. *Neuro-Oncology*, **2016**, 18, iii70.3-iii70	1	78
73	Quantifying cancer progression with conjunctive Bayesian networks. *Bioinformatics*, **2009**, 25, 2809-15	7.2	76
72	Microarray comparative genomic hybridization detection of chromosomal imbalances in uterine cervix carcinoma. *BMC Cancer*, **2005**, 5, 77	4.8	63
71	A harmonized meta-knowledgebase of clinical interpretations of somatic genomic variants in cancer. *Nature Genetics*, **2020**, 52, 448-457	36.3	58
70	SIL1 mutations and clinical spectrum in patients with Marinesco-Sjogren syndrome. *Brain*, **2013**, 136, 3634-44	11.2	58

69	Comprehensive characterization of genomic aberrations in gangliogliomas by CGH, array-based CGH and interphase FISH. *Brain Pathology*, **2008**, 18, 326-37	6	53
68	Silver-Russell patients showing a broad range of ICR1 and ICR2 hypomethylation in different tissues. *Clinical Genetics*, **2011**, 80, 83-8	4	51
67	Distance-based clustering of CGH data. *Bioinformatics*, **2006**, 22, 1971-8	7.2	47
66	Recurrent loss of heterozygosity in 1p36 associated with TNFRSF14 mutations in IRF4 translocation negative pediatric follicular lymphomas. *Haematologica*, **2013**, 98, 1237-41	6.6	43
65	Federated discovery and sharing of genomic data using Beacons. *Nature Biotechnology*, **2019**, 37, 220-224	44.5	42
64	The SIB Swiss Institute of Bioinformatics' resources: focus on curated databases. *Nucleic Acids Research*, **2016**, 44, D27-37	20.1	41
63	Submicroscopic chromosomal imbalances in idiopathic Silver-Russell syndrome (SRS): the SRS phenotype overlaps with the 12q14 microdeletion syndrome. *Journal of Medical Genetics*, **2010**, 47, 356-60	5.8	38
62	MUC1 oncogene amplification correlates with protein overexpression in invasive breast carcinoma cells. *Cancer Genetics and Cytogenetics*, **2010**, 201, 102-10		37
61	Leveraging European infrastructures to access 1 million human genomes by 2022. *Nature Reviews Genetics*, **2019**, 20, 693-701	30.1	36
60	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	1.9	36
59	PKC signaling prevents irradiation-induced apoptosis of primary human fibroblasts. *Cell Death and Disease*, **2013**, 4, e498	9.8	33
58	Molecular karyotyping as a relevant diagnostic tool in children with growth retardation with Silver-Russell features. *Journal of Pediatrics*, **2012**, 161, 933-42	3.6	32
57	Progenetix: 12 years of oncogenomic data curation. *Nucleic Acids Research*, **2014**, 42, D1055-62	20.1	28
56	Chromosomal changes characterize head and neck cancer with poor prognosis. *Journal of Molecular Medicine*, **2008**, 86, 1353-65	5.5	27
55	arrayMap: a reference resource for genomic copy number imbalances in human malignancies. *PLoS ONE*, **2012**, 7, e36944	3.7	27
54	Integrative genome-wide expression profiling identifies three distinct molecular subgroups of renal cell carcinoma with different patient outcome. *BMC Cancer*, **2012**, 12, 310	4.8	23
53	Online database and bioinformatics toolbox to support data mining in cancer cytogenetics. *BioTechniques*, **2006**, 40, 269-70, 272	2.5	22
52	The Ubiquitin Ligase TRIP12 Limits PARP1 Trapping and Constrains PARP Inhibitor Efficiency. *Cell Reports*, **2020**, 32, 107985	10.6	22

51	Genomic instability of osteosarcoma cell lines in culture: impact on the prediction of metastasis relevant genes. *PLoS ONE*, **2015**, 10, e0125611	3.7	21
50	GA4GH: International policies and standards for data sharing across genomic research and healthcare.. *Cell Genomics*, **2021**, 1, 100029-100029		20
49	High resolution copy number analysis of IRF4 translocation-positive diffuse large B-cell and follicular lymphomas. *Genes Chromosomes and Cancer*, **2013**, 52, 150-5	5	19
48	Recurrent loss, but lack of mutations, of the SMARCB1 tumor suppressor gene in T-cell prolymphocytic leukemia with TCL1A-TCRAD juxtaposition. *Cancer Genetics and Cytogenetics*, **2009**, 192, 44-7		19
47	Increased expression of cellular retinol-binding protein 1 in laryngeal squamous cell carcinoma. *Journal of Cancer Research and Clinical Oncology*, **2010**, 136, 931-8	4.9	18
46	Registered access: authorizing data access. *European Journal of Human Genetics*, **2018**, 26, 1721-1731	5.3	17
45	Allele-specific loss of heterozygosity in multiple colorectal adenomas: toward an integrated molecular cytogenetic map II. *Cancer Genetics and Cytogenetics*, **2006**, 167, 1-14		17
44	Improved multiplex ligation-dependent probe amplification analysis identifies a deleterious PMS2 allele generated by recombination with crossover between PMS2 and PMS2CL. *Genes Chromosomes and Cancer*, **2012**, 51, 819-31	5	16
43	arrayMap 2014: an updated cancer genome resource. *Nucleic Acids Research*, **2015**, 43, D825-30	20.1	15
42	Identification of genetic imbalances in malignant lymphoma using comparative genomic hybridization. *Stem Cells*, **1995**, 13 Suppl 3, 83-7	5.8	14
41	2p21 Deletions in hypotonia-cystinuria syndrome. *European Journal of Medical Genetics*, **2012**, 55, 561-3	2.6	13
40	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, 949-50	6.6	13
39	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, 757-64	3	13
38	segment_liftover : a Python tool to convert segments between genome assemblies. *F1000Research* , **2018**, 7, 319	3.6	13
37	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, 415-23	4.8	12
36	Identification of a 21q22 duplication in a Silver-Russell syndrome patient further narrows down the Down syndrome critical region. *American Journal of Medical Genetics, Part A*, **2010**, 152A, 356-9	2.5	12
35	Genetic losses in breast cancer: toward an integrated molecular cytogenetic map. *Cancer Genetics and Cytogenetics*, **2005**, 160, 141-51		12
34	segment_liftover : a Python tool to convert segments between genome assemblies. *F1000Research* , **2018**, 7, 319	3.6	12

33	PKCδ and HMGB1 antagonistically control hydrogen peroxide-induced poly-ADP-ribose formation. *Nucleic Acids Research*, **2016**, 44, 7630-45	20.1	12
32	Chromosome 11p15 duplication in Silver-Russell syndrome due to a maternally inherited translocation t(11;15). *American Journal of Medical Genetics, Part A*, **2010**, 152A, 1484-7	2.5	11
31	Inferring progression models for CGH data. *Bioinformatics*, **2009**, 25, 2208-15	7.2	9
30	A 10.7 Mb interstitial deletion of 13q21 without phenotypic effect defines a further non-pathogenic euchromatic variant. *American Journal of Medical Genetics, Part A*, **2008**, 146A, 2417-20	2.5	8
29	Losses at chromosome 4q are associated with poor survival in operable ductal pancreatic adenocarcinoma. *Pancreatology*, **2012**, 12, 16-22	3.8	7
28	International federation of genomic medicine databases using GA4GH standards.. *Cell Genomics*, **2021**, 1, 100032-100032		7
27	CDCOCA: a statistical method to define complexity dependence of co-occuring chromosomal aberrations. *BMC Medical Genomics*, **2011**, 4, 21	3.7	6
26	Oncology Informatics: Status Quo and Outlook. *Oncology*, **2020**, 98, 329-331	3.6	5
25	Krüppel-Like Factor 10 participates in cervical cancer immunoediting through transcriptional regulation of Pregnancy-Specific Beta-1 Glycoproteins. *Scientific Reports*, **2018**, 8, 9445	4.9	5
24	A harmonized meta-knowledgebase of clinical interpretations of cancer genomic variants		5
23	The ELIXIR Human Copy Number Variations Community: building bioinformatics infrastructure for research. *F1000Research*, **2020**, 9,	3.6	4
22	The GA4GH Variation Representation Specification: A computational framework for variation representation and federated identification.. *Cell Genomics*, **2021**, 1, 100027-100027		4
21	DNA Copy Number Changes in Diffuse Large B Cell Lymphomas. *Frontiers in Oncology*, **2020**, 10, 584095	5.3	4
20	DNA copy number imbalances in primary cutaneous lymphomas. *Journal of the European Academy of Dermatology and Venereology*, **2019**, 33, 1062-1075	4.6	3
19	Enabling population assignment from cancer genomes with SNP2pop. *Scientific Reports*, **2020**, 10, 4846	4.9	3
18	Specific genomic regions are differentially affected by copy number alterations across distinct cancer types, in aggregated cytogenetic data. *PLoS ONE*, **2012**, 7, e43689	3.7	3
17	Mountains and Chasms: Surveying the Oncogenomic Publication Landscape. *Oncology*, **2020**, 98, 332-343	3.6	3
16	The GA4GH Variation Representation Specification (VRS): a Computational Framework for the Precise Representation and Federated Identification of Molecular Variation		3

15	Pathways and Crossroads to Colorectal Cancer **2011**, 369-394		3
14	CNARA: reliability assessment for genomic copy number profiles. *BMC Genomics*, **2016**, 17, 799	4.5	2
13	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	1	1
12	Geographic assessment of cancer genome profiling studies. *Database: the Journal of Biological Databases and Curation*, **2020**, 2020,	5	1
11	Minimum error calibration and normalization for genomic copy number analysis. *Genomics*, **2020**, 112, 3331-3341	4.3	1
10	CDCOCA: a statistical method to define complexity dependent co-occurring chromosomal aberrations **2010**, 11, P23		1
9	Comparative genomic hybridization for the analysis of leukemias and lymphomas. *Methods in Molecular Medicine*, **2001**, 55, 43-64		1
8	Signatures of Discriminative Copy Number Aberrations in 31 Cancer Subtypes. *Frontiers in Genetics*, **2021**, 12, 654887	4.5	1
7	The Progenetix oncogenomic resource in 2021. *Database: the Journal of Biological Databases and Curation*, **2021**, 2021,	5	1
6	Biopsying parapsoriasis: quo vadis? Are morphological stains enough or are ancillary tests needed?. *Romanian Journal of Morphology and Embryology*, **2014**, 55, 1085-92	0.6	1
5	Beacon v2 and Beacon Networks: a "lingua franca" for federated data discovery in biomedical genomics, and beyond.. *Human Mutation*, **2022**,	4.7	1
4	Array-basierter Nachweis chromosomaler Aberrationen bei malignen Neoplasien. *Medizinische Genetik*, **2012**, 24, 114-122	0.5	
3	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	1	
2	Genomisches Profiling mittels SCOMP bei duktalen Adenokarzinomen des Pankreas. *Langenbecks Archiv Fu r Chirurgie Supplement*, **2006**, 27-28		
1	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	2.2	