

Stefan Wiemann

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

204
papers

11,321
citations

53
h-index

102
g-index

216
ext. papers

12,881
ext. citations

8.8
avg, IF

5.64
L-index

#	Paper	IF	Citations
204	A Dual HiBiT-GFP-LC3 Lentiviral Reporter for Autophagy Flux Assessment.. <i>Methods in Molecular Biology</i> , 2022 , 2445, 75-98	1.4	1
203	The genomic and transcriptional landscape of primary central nervous system lymphoma.. <i>Nature Communications</i> , 2022 , 13, 2558	17.4	4
202	Disentangling ERBB Signaling in Breast Cancer Subtypes: A Model-Based Analysis. <i>Cancers</i> , 2022 , 14, 2379	6.6	0
201	Coordinated regulation of WNT/ β -catenin, c-Met, and integrin signalling pathways by miR-193b controls triple negative breast cancer metastatic traits. <i>BMC Cancer</i> , 2021 , 21, 1296	4.8	0
200	Stromal NRG1 in luminal breast cancer defines pro-fibrotic and migratory cancer-associated fibroblasts. <i>Oncogene</i> , 2021 , 40, 2651-2666	9.2	7
199	Gene Expression in Solitary Fibrous Tumors (SFTs) Correlates with Anatomic Localization and NAB2-STAT6 Gene Fusion Variants. <i>American Journal of Pathology</i> , 2021 , 191, 602-617	5.8	9
198	Host-Dependent Phenotypic Resistance to EGFR Tyrosine Kinase Inhibitors. <i>Cancer Research</i> , 2021 , 81, 3862-3875	10.1	1
197	Integrating proteomics into precision oncology. <i>International Journal of Cancer</i> , 2021 , 148, 1438-1451	7.5	5
196	Abrogating GPT2 in triple-negative breast cancer inhibits tumor growth and promotes autophagy. <i>International Journal of Cancer</i> , 2021 , 148, 1993-2009	7.5	3
195	IFN γ secreted by breast cancer cells undergoing chemotherapy reprograms stromal fibroblasts to support tumour growth after treatment. <i>Molecular Oncology</i> , 2021 , 15, 1308-1329	7.9	4
194	Lipomatous Solitary Fibrous Tumors Harbor Rare NAB2-STAT6 Fusion Variants and Show Up-Regulation of the Gene PPAR γ , Encoding for a Regulator of Adipocyte Differentiation. <i>American Journal of Pathology</i> , 2021 , 191, 1314-1324	5.8	3
193	Cancer-Associated Fibroblasts: Implications for Cancer Therapy. <i>Cancers</i> , 2021 , 13,	6.6	6
192	WNT11/ROR2 signaling is associated with tumor invasion and poor survival in breast cancer.. <i>Journal of Experimental and Clinical Cancer Research</i> , 2021 , 40, 395	12.8	3
191	TNFR2+ TILs are significantly associated with improved survival in triple-negative breast cancer patients. <i>Cancer Immunology, Immunotherapy</i> , 2020 , 69, 1315-1326	7.4	5
190	Time-Resolved Profiling Reveals ATF3 as a Novel Mediator of Endocrine Resistance in Breast Cancer. <i>Cancers</i> , 2020 , 12,	6.6	3
189	Candidate methylation sites associated with endocrine therapy resistance in ER+/HER2- breast cancer. <i>BMC Cancer</i> , 2020 , 20, 676	4.8	3
188	Nuclear NR4A2 (Nurr1) Immunostaining is a Novel Marker for Acinic Cell Carcinoma of the Salivary Glands Lacking the Classic NR4A3 (NOR-1) Upregulation. <i>American Journal of Surgical Pathology</i> , 2020 , 44, 1290-1292	6.7	7

187	Molecular Analysis of a Patient With Neurofibromatosis 2 (NF2) and Peritoneal Malignant Mesothelioma. <i>American Journal of Surgical Pathology</i> , 2020 , 44, 1290-1292	6.7	1
186	Enhancer hijacking activates oncogenic transcription factor NR4A3 in acinic cell carcinomas of the salivary glands. <i>Nature Communications</i> , 2019 , 10, 368	17.4	89
185	Notch-Mediated Tumor-Stroma-Inflammation Networks Promote Invasive Properties and CXCL8 Expression in Triple-Negative Breast Cancer. <i>Frontiers in Immunology</i> , 2019 , 10, 804	8.4	37
184	Tumor-Stroma-Inflammation Networks Promote Pro-metastatic Chemokines and Aggressiveness Characteristics in Triple-Negative Breast Cancer. <i>Frontiers in Immunology</i> , 2019 , 10, 757	8.4	63
183	Reconstruction of Different Modes of WNT Dependent Protein Networks from Time Series Protein Quantification. <i>Studies in Health Technology and Informatics</i> , 2019 , 267, 175-180	0.5	1
182	Nuclear NR4A3 Immunostaining Is a Specific and Sensitive Novel Marker for Acinic Cell Carcinoma of the Salivary Glands. <i>American Journal of Surgical Pathology</i> , 2019 , 43, 1264-1272	6.7	47
181	Assembly of a parts list of the human mitotic cell cycle machinery. <i>Journal of Molecular Cell Biology</i> , 2019 , 11, 703-718	6.3	31
180	Functional Proteomics of Breast Cancer Metabolism Identifies GLUL as Responder during Hypoxic Adaptation. <i>Journal of Proteome Research</i> , 2019 , 18, 1352-1362	5.6	5
179	Cutis laxa, exocrine pancreatic insufficiency and altered cellular metabolomics as additional symptoms in a new patient with ATP6AP1-CDG. <i>Molecular Genetics and Metabolism</i> , 2018 , 123, 364-374	3.7	15
178	Reactivation of cAMP Pathway by PDE4D Inhibition Represents a Novel Druggable Axis for Overcoming Tamoxifen Resistance in ER-positive Breast Cancer. <i>Clinical Cancer Research</i> , 2018 , 24, 1987-2001	12.9	19
177	Targeting PLK1 overcomes T-DM1 resistance via CDK1-dependent phosphorylation and inactivation of Bcl-2/xL in HER2-positive breast cancer. <i>Oncogene</i> , 2018 , 37, 2251-2269	9.2	30
176	TGF β regulates HGF-induced cell migration and hepatocyte growth factor receptor MET expression via C-ets-1 and miR-128-3p in basal-like breast cancer. <i>Molecular Oncology</i> , 2018 , 12, 1447-1463	7.9	18
175	Identification and Prioritization of Causal Variants of Human Genetic Disorders from Exome or Whole Genome Sequencing Data 2018 , 2, 1-1		3
174	Identification of SLC20A1 and SLC15A4 among other genes as potential risk factors for combined pituitary hormone deficiency. <i>Genetics in Medicine</i> , 2018 , 20, 728-736	8.1	10
173	PI3K: A master regulator of brain metastasis-promoting macrophages/microglia. <i>Glia</i> , 2018 , 66, 2438-2455	5.5	34
172	Long-peptide vaccination with driver gene mutations in p53 and Kras induces cancer mutation-specific effector as well as regulatory T cell responses. <i>Onc Immunology</i> , 2018 , 7, e1500671	7.2	18
171	Long noncoding RNA HOTAIR is upregulated in an aggressive subgroup of gastrointestinal stromal tumors (GIST) and mediates the establishment of gene-specific DNA methylation patterns. <i>Genes Chromosomes and Cancer</i> , 2018 , 57, 584-597	5	10
170	Coordinated Pulses of mRNA and of Protein Translation or Degradation Produce EGF-Induced Protein Bursts. <i>Cell Reports</i> , 2017 , 18, 3129-3142	10.6	11

169	Integrated genome and transcriptome sequencing identifies a noncoding mutation in the genome replication factor as the cause of microcephaly-micromelia syndrome. <i>Genome Research</i> , 2017 , 27, 1323-1335	9.7	27
168	Epigenetic mechanisms underlie the crosstalk between growth factors and a steroid hormone. <i>Nucleic Acids Research</i> , 2017 , 45, 12681-12699	20.1	15
167	Proteomic profiling of breast cancer metabolism identifies SHMT2 and ASCT2 as prognostic factors. <i>Breast Cancer Research</i> , 2017 , 19, 112	8.3	50
166	The expression of hematopoietic progenitor cell antigen CD34 is regulated by DNA methylation in a site-dependent manner in gastrointestinal stromal tumours. <i>International Journal of Cancer</i> , 2017 , 141, 2296-2304	7.5	6
165	MicroRNA-519a-3p mediates apoptosis resistance in breast cancer cells and their escape from recognition by natural killer cells. <i>Cell Death and Disease</i> , 2017 , 8, e2973	9.8	53
164	Recurrent Somatic PDGFRB Mutations in Sporadic Infantile/Solitary Adult Myofibromas But Not in Angioleiomyomas and Myopericytomas. <i>American Journal of Surgical Pathology</i> , 2017 , 41, 195-203	6.7	60
163	Liquid-phase electron microscopy of molecular drug response in breast cancer cells reveals irresponsive cell subpopulations related to lack of HER2 homodimers. <i>Molecular Biology of the Cell</i> , 2017 ,	3.5	17
162	Single Molecule and Single Cell Analysis of HER2 Receptors in Breast Cancer Cells Using Liquid Phase Scanning Transmission Electron Microscopy. <i>Microscopy and Microanalysis</i> , 2017 , 23, 1106-1107	0.5	
161	A novel homozygous ARL13B variant in patients with Joubert syndrome impairs its guanine nucleotide-exchange factor activity. <i>European Journal of Human Genetics</i> , 2017 , 25, 1324-1334	5.3	4
160	Impact of clinical exomes in neurodevelopmental and neurometabolic disorders. <i>Molecular Genetics and Metabolism</i> , 2017 , 121, 297-307	3.7	30
159	Co-Inflammatory Roles of TGF β in the Presence of TNF α Drive a Pro-inflammatory Fate in Mesenchymal Stem Cells. <i>Frontiers in Immunology</i> , 2017 , 8, 479	8.4	20
158	miRNA-1246 induces pro-inflammatory responses in mesenchymal stem/stromal cells by regulating PKA and PP2A. <i>Oncotarget</i> , 2017 , 8, 43897-43914	3.3	48
157	Findings made in gene panel to whole genome sequencing: data, knowledge, ethics - and consequences?. <i>Expert Review of Molecular Diagnostics</i> , 2016 , 16, 1259-1270	3.8	11
156	Homozygous missense mutation in the LMAN2L gene segregates with intellectual disability in a large consanguineous Pakistani family. <i>Journal of Medical Genetics</i> , 2016 , 53, 138-44	5.8	10
155	The ORFeome Collaboration: a genome-scale human ORF-clone resource. <i>Nature Methods</i> , 2016 , 13, 191-2	21.6	80
154	Chemokine axes in breast cancer: factors of the tumor microenvironment reshape the CCR7-driven metastatic spread of luminal-A breast tumors. <i>Journal of Leukocyte Biology</i> , 2016 , 99, 1009-25	6.5	21
153	Role of Heterogeneity in Cancer Cells Examined through Quantitative Analysis of Single HER2 Protein Distribution and Activation Status. <i>Microscopy and Microanalysis</i> , 2016 , 22, 26-27	0.5	
152	The highly expressed 5'omiR of hsa-miR-140-3p contributes to the tumor-suppressive effects of miR-140 by reducing breast cancer proliferation and migration. <i>BMC Genomics</i> , 2016 , 17, 566	4.5	61

151	Paediatric and adult soft tissue sarcomas with NTRK1 gene fusions: a subset of spindle cell sarcomas unified by a prominent myopericytic/haemangiopericytic pattern. <i>Journal of Pathology</i> , 2016 , 238, 700-10	9.4	73
150	Environment-induced epigenetic reprogramming in genomic regulatory elements in smoking mothers and their children. <i>Molecular Systems Biology</i> , 2016 , 12, 861	12.2	71
149	LIMT is a novel metastasis inhibiting lncRNA suppressed by EGF and downregulated in aggressive breast cancer. <i>EMBO Molecular Medicine</i> , 2016 , 8, 1052-64	12	66
148	Synaptojanin 2 is a druggable mediator of metastasis and the gene is overexpressed and amplified in breast cancer. <i>Science Signaling</i> , 2015 , 8, ra7	8.8	40
147	Advances in CRISPR-Cas9 genome engineering: lessons learned from RNA interference. <i>Nucleic Acids Research</i> , 2015 , 43, 3407-19	20.1	104
146	MicroRNA-206 functions as a pleiotropic modulator of cell proliferation, invasion and lymphangiogenesis in pancreatic adenocarcinoma by targeting ANXA2 and KRAS genes. <i>Oncogene</i> , 2015 , 34, 4867-78	9.2	104
145	Navigator-3, a modulator of cell migration, may act as a suppressor of breast cancer progression. <i>EMBO Molecular Medicine</i> , 2015 , 7, 299-314	12	22
144	So rare we need to hunt for them: reframing the ethical debate on incidental findings. <i>Genome Medicine</i> , 2015 , 7, 83	14.4	16
143	EGF induces microRNAs that target suppressors of cell migration: miR-15b targets MTSS1 in breast cancer. <i>Science Signaling</i> , 2015 , 8, ra29	8.8	50
142	MicroRNA-30c-2-3p negatively regulates NF- κ B signaling and cell cycle progression through downregulation of TRADD and CCNE1 in breast cancer. <i>Molecular Oncology</i> , 2015 , 9, 1106-19	7.9	61
141	Recurrent mutations within the amino-terminal region of E-catenin are probable key molecular driver events in sinonasal hemangiopericytoma. <i>American Journal of Pathology</i> , 2015 , 185, 563-71	5.8	35
140	Combined DNA methylation and gene expression profiling in gastrointestinal stromal tumors reveals hypomethylation of SPP1 as an independent prognostic factor. <i>International Journal of Cancer</i> , 2015 , 136, 1013-23	7.5	21
139	Protein signatures of oxidative stress response in a patient specific cell line model for autism. <i>Molecular Autism</i> , 2014 , 5, 10	6.5	20
138	MicroRNA-519a is a novel oncomir conferring tamoxifen resistance by targeting a network of tumour-suppressor genes in ER+ breast cancer. <i>Journal of Pathology</i> , 2014 , 233, 368-79	9.4	89
137	Diurnal suppression of EGFR signalling by glucocorticoids and implications for tumour progression and treatment. <i>Nature Communications</i> , 2014 , 5, 5073	17.4	42
136	Metabolic transformations in breast cancer subtypes. <i>Cancer & Metabolism</i> , 2014 , 2,	5.4	3
135	Profiling metabolic changes in breast cancer with targeted proteomics. <i>Cancer & Metabolism</i> , 2014 , 2,	5.4	1
134	Enhancer hijacking activates GFI1 family oncogenes in medulloblastoma. <i>Nature</i> , 2014 , 511, 428-34	50.4	377

133	Solitary fibrous tumors/hemangiopericytomas with different variants of the NAB2-STAT6 gene fusion are characterized by specific histomorphology and distinct clinicopathological features. <i>American Journal of Pathology</i> , 2014 , 184, 1209-1218	5.8	155
132	Aberrant DNA hypermethylation of SDHC: a novel mechanism of tumor development in Carney triad. <i>Endocrine-Related Cancer</i> , 2014 , 21, 567-77	5.7	130
131	Reverse phase protein array based tumor profiling identifies a biomarker signature for risk classification of hormone receptor-positive breast cancer. <i>Translational Proteomics</i> , 2014 , 2, 52-59		16
130	Differential response to Exoaldehydes in tamoxifen resistant MCF-7 breast cancer cells. <i>PLoS ONE</i> , 2014 , 9, e101473	3.7	21
129	Phenotypical and molecular distinctness of sinonasal haemangiopericytoma compared to solitary fibrous tumour of the sinonasal tract. <i>Histopathology</i> , 2014 , 65, 667-73	7.3	29
128	microRNAs [kleine Moleküle ganz groß] <i>Biologie in Unserer Zeit</i> , 2014 , 44, 258-266	0.1	
127	Combinatorial targeting of FGF and ErbB receptors blocks growth and metastatic spread of breast cancer models. <i>Breast Cancer Research</i> , 2013 , 15, R8	8.3	56
126	Re-expression of microRNA-375 reverses both tamoxifen resistance and accompanying EMT-like properties in breast cancer. <i>Oncogene</i> , 2013 , 32, 1173-82	9.2	216
125	Epigenetic upregulation of lncRNAs at 13q14.3 in leukemia is linked to the In Cis downregulation of a gene cluster that targets NF-kB. <i>PLoS Genetics</i> , 2013 , 9, e1003373	6	108
124	MicroRNA-31 sensitizes human breast cells to apoptosis by direct targeting of protein kinase C epsilon (PKCepsilon). <i>Journal of Biological Chemistry</i> , 2013 , 288, 8750-8761	5.4	112
123	qCMA: a desktop application for quantitative collective cell migration analysis. <i>Journal of Biomolecular Screening</i> , 2013 , 18, 356-60		6
122	Genetically coupled receptor-ligand pair NKp80-AICL enables autonomous control of human NK cell responses. <i>Blood</i> , 2013 , 122, 2380-9	2.2	27
121	Epidermal growth-factor-induced transcript isoform variation drives mammary cell migration. <i>PLoS ONE</i> , 2013 , 8, e80566	3.7	15
120	MicroRNA-520/373 family functions as a tumor suppressor in estrogen receptor negative breast cancer by targeting NF- κ B and TGF- β signaling pathways. <i>Oncogene</i> , 2012 , 31, 4150-63	9.2	223
119	Dissecting the genomic complexity underlying medulloblastoma. <i>Nature</i> , 2012 , 488, 100-5	50.4	623
118	Genome-wide RNAi screening identifies human proteins with a regulatory function in the early secretory pathway. <i>Nature Cell Biology</i> , 2012 , 14, 764-74	23.4	141
117	The nucleoporin Nup358/RanBP2 promotes nuclear import in a cargo- and transport receptor-specific manner. <i>Traffic</i> , 2012 , 13, 218-33	5.7	52
116	Live-cell assays to identify regulators of ER-to-Golgi trafficking. <i>Traffic</i> , 2012 , 13, 416-32	5.7	9

115	On target: a public repository for large-scale RNAi experiments. <i>Nature Cell Biology</i> , 2012 , 14, 115	23.4	8
114	MicroRNA-200c represses migration and invasion of breast cancer cells by targeting actin-regulatory proteins FHOD1 and PPM1F. <i>Molecular and Cellular Biology</i> , 2012 , 32, 633-51	4.8	175
113	Strong EGFR signaling in cell line models of ERBB2-amplified breast cancer attenuates response towards ERBB2-targeting drugs. <i>Oncogenesis</i> , 2012 , 1, e16	6.6	55
112	F-box and leucine-rich repeat protein 22 is a cardiac-enriched F-box protein that regulates sarcomeric protein turnover and is essential for maintenance of contractile function in vivo. <i>Circulation Research</i> , 2012 , 111, 1504-16	15.7	45
111	Global microRNA level regulation of EGFR-driven cell-cycle protein network in breast cancer. <i>Molecular Systems Biology</i> , 2012 , 8, 570	12.2	144
110	Identification and characterization of a set of conserved and new regulators of cytoskeletal organization, cell morphology and migration. <i>BMC Biology</i> , 2011 , 9, 54	7.3	108
109	Inferring signalling networks from longitudinal data using sampling based approaches in the R-package QdepnQBMC <i>Bioinformatics</i> , 2011 , 12, 291	3.6	10
108	Mutation and expression analyses of the ribosomal protein gene RPL10 in an extended German sample of patients with autism spectrum disorder. <i>American Journal of Medical Genetics, Part A</i> , 2011 , 155A, 1472-5	2.5	27
107	Time-resolved human kinome RNAi screen identifies a network regulating mitotic-events as early regulators of cell proliferation. <i>PLoS ONE</i> , 2011 , 6, e22176	3.7	8
106	miR-200bc/429 cluster targets PLCgamma1 and differentially regulates proliferation and EGF-driven invasion than miR-200a/141 in breast cancer. <i>Oncogene</i> , 2010 , 29, 4297-306	9.2	175
105	QuantProReloaded: quantitative analysis of microspot immunoassays. <i>Bioinformatics</i> , 2010 , 26, 2480-1	7.2	5
104	Dynamic deterministic effects propagation networks: learning signalling pathways from longitudinal protein array data. <i>Bioinformatics</i> , 2010 , 26, i596-602	7.2	26
103	Myomasp/LRRC39, a heart- and muscle-specific protein, is a novel component of the sarcomeric M-band and is involved in stretch sensing. <i>Circulation Research</i> , 2010 , 107, 1253-64	15.7	43
102	RNAi-based validation of antibodies for reverse phase protein arrays. <i>Proteome Science</i> , 2010 , 8, 69	2.6	15
101	Increasing the sensitivity of reverse phase protein arrays by antibody-mediated signal amplification. <i>Proteome Science</i> , 2010 , 8, 36	2.6	14
100	Localization- and mutation-dependent microRNA (miRNA) expression signatures in gastrointestinal stromal tumours (GISTs), with a cluster of co-expressed miRNAs located at 14q32.31. <i>Journal of Pathology</i> , 2010 , 220, 71-86	9.4	93
99	The completion of the Mammalian Gene Collection (MGC). <i>Genome Research</i> , 2009 , 19, 2324-33	9.7	98
98	KEGGgraph: a graph approach to KEGG PATHWAY in R and bioconductor. <i>Bioinformatics</i> , 2009 , 25, 1470-7	7.2	221

97	Modeling ERBB receptor-regulated G1/S transition to find novel targets for de novo trastuzumab resistance. <i>BMC Systems Biology</i> , 2009 , 3, 1	3.5	175
96	Functional genomics and proteomics approaches to study the ERBB network in cancer. <i>FEBS Letters</i> , 2009 , 583, 1766-71	3.8	4
95	Systematic subcellular localization of novel proteins identified by large-scale cDNA sequencing. <i>EMBO Reports</i> , 2009 , 10, 1363-1363	6.5	2
94	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. <i>Nature Biotechnology</i> , 2008 , 26, 889-96	44.5	417
93	Human Proteinpedia enables sharing of human protein data. <i>Nature Biotechnology</i> , 2008 , 26, 164-7	44.5	138
92	Reduced expression of vacuole membrane protein 1 affects the invasion capacity of tumor cells. <i>Oncogene</i> , 2008 , 27, 1320-6	9.2	39
91	Extending pathways based on gene lists using InterPro domain signatures. <i>BMC Bioinformatics</i> , 2008 , 9, 3	3.6	11
90	Automated production of recombinant human proteins as resource for proteome research. <i>Proteome Science</i> , 2008 , 6, 4	2.6	18
89	Norepinephrine transporter and catecholamine-O-methyltransferase gene variants and attention-deficit/hyperactivity disorder symptoms in adults. <i>Journal of Neural Transmission</i> , 2008 , 115, 323-9	4.3	32
88	Contact spotting of protein microarrays coupled with spike-in of normalizer protein permits time-resolved analysis of ERBB receptor signaling. <i>Proteomics</i> , 2008 , 8, 1586-94	4.8	13
87	Proteinarrays können Nebenwege von Tumor-Wirkstoffen im Brustkrebs aufdecken. <i>Biologie in Unserer Zeit</i> , 2008 , 38, 17-20	0.1	
86	A polymorphism at the 3' untranslated region of the CLOCK gene is associated with adult attention-deficit hyperactivity disorder. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2008 , 147, 333-8	3.5	79
85	The H-Invitational Database (H-InvDB), a comprehensive annotation resource for human genes and transcripts. <i>Nucleic Acids Research</i> , 2008 , 36, D793-9	20.1	52
84	Infrared-based protein detection arrays for quantitative proteomics. <i>Proteomics</i> , 2007 , 7, 558-564	4.8	66
83	The full-ORF clone resource of the German cDNA Consortium. <i>BMC Genomics</i> , 2007 , 8, 399	4.5	22
82	Combinatorial RNAi for quantitative protein network analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 6579-84	11.5	52
81	High-content microscopy identifies new neurite outgrowth regulators. <i>Molecular Biology of the Cell</i> , 2007 , 18, 242-52	3.5	38
80	High-throughput flow cytometry-based assay to identify apoptosis-inducing proteins. <i>Journal of Biomolecular Screening</i> , 2007 , 12, 510-20		6

79	The 3of5 web application for complex and comprehensive pattern matching in protein sequences. <i>BMC Bioinformatics</i> , 2006 , 7, 144	3.6	13
78	CAFTAN: a tool for fast mapping, and quality assessment of cDNAs. <i>BMC Bioinformatics</i> , 2006 , 7, 473	3.6	
77	The systematic functional characterisation of Xq28 genes prioritises candidate disease genes. <i>BMC Genomics</i> , 2006 , 7, 29	4.5	20
76	The LIFEdb database in 2006. <i>Nucleic Acids Research</i> , 2006 , 34, D415-8	20.1	33
75	Large-scale identification and characterization of alternative splicing variants of human gene transcripts using 56,419 completely sequenced and manually annotated full-length cDNAs. <i>Nucleic Acids Research</i> , 2006 , 34, 3917-28	20.1	39
74	Statistical methods and software for the analysis of highthroughput reverse genetic assays using flow cytometry readouts. <i>Genome Biology</i> , 2006 , 7, R77	18.3	19
73	PML-associated repressor of transcription (PAROT), a novel KRAB-zinc finger repressor, is regulated through association with PML nuclear bodies. <i>Experimental Cell Research</i> , 2006 , 312, 901-12	4.2	16
72	Modeling breast cell cycle regulation—overcoming drug resistance. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society</i> , 2006 , 2006, 40-3		
71	An anthropoid-specific segmental duplication on human chromosome 1q22. <i>Genomics</i> , 2006 , 88, 143-51	4.3	22
70	Proteomics and Beyond: a report on the 3rd Annual Spring Workshop of the HUPO-PSI 21-23 April 2006, San Francisco, CA, USA. <i>Proteomics</i> , 2006 , 6, 4439-43	4.8	12
69	Genetic association of the human corticotropin releasing hormone receptor 1 (CRHR1) with binge drinking and alcohol intake patterns in two independent samples. <i>Molecular Psychiatry</i> , 2006 , 11, 594-602	15.1	158
68	Functional profiling: from microarrays via cell-based assays to novel tumor relevant modulators of the cell cycle. <i>Cancer Research</i> , 2005 , 65, 7733-42	10.1	18
67	Gamma-BAR, a novel AP-1-interacting protein involved in post-Golgi trafficking. <i>EMBO Journal</i> , 2005 , 24, 1122-33	13	39
66	Alternative pre-mRNA processing regulates cell-type specific expression of the IL4I1 and NUP62 genes. <i>BMC Biology</i> , 2005 , 3, 16	7.3	19
65	Large-scale protein expression for proteome research. <i>Proteomics</i> , 2005 , 5, 3571-80	4.8	53
64	Systematic comparison of surface coatings for protein microarrays. <i>Proteomics</i> , 2005 , 5, 4705-12	4.8	40
63	Protein microarrays as a discovery tool for studying protein-protein interactions. <i>Expert Review of Proteomics</i> , 2005 , 2, 13-26	4.2	20
62	From ORFeome to biology: a functional genomics pipeline. <i>Genome Research</i> , 2004 , 14, 2136-44	9.7	40

61	High-throughput protein analysis integrating bioinformatics and experimental assays. <i>Nucleic Acids Research</i> , 2004 , 32, 742-8	20.1	15
60	High-content screening microscopy identifies novel proteins with a putative role in secretory membrane traffic. <i>Genome Research</i> , 2004 , 14, 1948-56	9.7	53
59	LIFEdb: a database for functional genomics experiments integrating information from external sources, and serving as a sample tracking system. <i>Nucleic Acids Research</i> , 2004 , 32, D505-8	20.1	40
58	Integrative annotation of 21,037 human genes validated by full-length cDNA clones. <i>PLoS Biology</i> , 2004 , 2, e162	9.7	255
57	SMART amplification combined with cDNA size fractionation in order to obtain large full-length clones. <i>BMC Genomics</i> , 2004 , 5, 36	4.5	59
56	SMP-Cell: Funktionsanalyse am laufenden Band. <i>Biologie in Unserer Zeit</i> , 2004 , 34, 286-287	0.1	
55	The German cDNA network: cDNAs, functional genomics and proteomics. <i>Journal of Structural and Functional Genomics</i> , 2003 , 4, 87-96		12
54	Frequent downregulation of DMBT1 and galectin-3 in epithelial skin cancer. <i>International Journal of Cancer</i> , 2003 , 105, 149-57	7.5	41
53	No association of alcohol dependence with a NMDA-receptor 2B gene variant. <i>Molecular Psychiatry</i> , 2003 , 8, 11-2	15.1	16
52	CDNAs for functional genomics and proteomics: the German Consortium. <i>Comptes Rendus - Biologies</i> , 2003 , 326, 1003-9	1.4	18
51	A microscope-based screening platform for large-scale functional protein analysis in intact cells. <i>FEBS Letters</i> , 2003 , 554, 394-8	3.8	83
50	Analysis of genetic variations of protein tyrosine kinase fyn and their association with alcohol dependence in two independent cohorts. <i>Biological Psychiatry</i> , 2003 , 54, 1422-6	7.9	62
49	An integrative model on the role of DMBT1 in epithelial cancer. <i>Cancer Detection and Prevention</i> , 2002 , 26, 266-74		18
48	Sequential changes of the DMBT1 expression and location in normal lung tissue and lung carcinomas. <i>Genes Chromosomes and Cancer</i> , 2002 , 35, 164-9	5	47
47	The SRCR/SID region of DMBT1 defines a complex multi-allele system representing the major basis for its variability in cancer. <i>Genes Chromosomes and Cancer</i> , 2002 , 35, 242-55	5	36
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