

# Stefan Wiemann

## List of Publications by Citations

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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	X-linked dyskeratosis congenita is caused by mutations in a highly conserved gene with putative nucleolar functions. <i>Nature Genetics</i> , <b>1998</b> , 19, 32-8	36.3	739
203	Dissecting the genomic complexity underlying medulloblastoma. <i>Nature</i> , <b>2012</b> , 488, 100-5	50.4	623
202	Genomic rearrangement in NEMO impairs NF-kappaB activation and is a cause of incontinentia pigmenti. The International Incontinentia Pigmenti (IP) Consortium. <i>Nature</i> , <b>2000</b> , 405, 466-72	50.4	607
201	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. <i>Nature Biotechnology</i> , <b>2008</b> , 26, 889-96	44.5	417
200	DMBT1, a new member of the SRCR superfamily, on chromosome 10q25.3-26.1 is deleted in malignant brain tumours. <i>Nature Genetics</i> , <b>1997</b> , 17, 32-9	36.3	386
199	Enhancer hijacking activates GFI1 family oncogenes in medulloblastoma. <i>Nature</i> , <b>2014</b> , 511, 428-34	50.4	377
198	Complete DNA sequence of yeast chromosome XI. <i>Nature</i> , <b>1994</b> , 369, 371-8	50.4	336
197	Systematic subcellular localization of novel proteins identified by large-scale cDNA sequencing. <i>EMBO Reports</i> , <b>2000</b> , 1, 287-92	6.5	307
196	Integrative annotation of 21,037 human genes validated by full-length cDNA clones. <i>PLoS Biology</i> , <b>2004</b> , 2, e162	9.7	255
195	MicroRNA-520/373 family functions as a tumor suppressor in estrogen receptor negative breast cancer by targeting NF- $\kappa$ B and TGF- $\beta$ signaling pathways. <i>Oncogene</i> , <b>2012</b> , 31, 4150-63	9.2	223
194	KEGGgraph: a graph approach to KEGG PATHWAY in R and bioconductor. <i>Bioinformatics</i> , <b>2009</b> , 25, 1470-1	9.2	221
193	Re-expression of microRNA-375 reverses both tamoxifen resistance and accompanying EMT-like properties in breast cancer. <i>Oncogene</i> , <b>2013</b> , 32, 1173-82	9.2	216
192	miR-200bc/429 cluster targets PLCgamma1 and differentially regulates proliferation and EGF-driven invasion than miR-200a/141 in breast cancer. <i>Oncogene</i> , <b>2010</b> , 29, 4297-306	9.2	175
191	Modeling ERBB receptor-regulated G1/S transition to find novel targets for de novo trastuzumab resistance. <i>BMC Systems Biology</i> , <b>2009</b> , 3, 1	3.5	175
190	MicroRNA-200c represses migration and invasion of breast cancer cells by targeting actin-regulatory proteins FHOD1 and PPM1F. <i>Molecular and Cellular Biology</i> , <b>2012</b> , 32, 633-51	4.8	175
189	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> , <b>2006</b> , 11, 594-602	15.1	158
188	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> , <b>2014</b> , 184, 1209-1218	5.8	155

187	Toward a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs. <i>Genome Research</i> , <b>2001</b> , 11, 422-35	9.7	154
186	Global microRNA level regulation of EGFR-driven cell-cycle protein network in breast cancer. <i>Molecular Systems Biology</i> , <b>2012</b> , 8, 570	12.2	144
185	Genome-wide RNAi screening identifies human proteins with a regulatory function in the early secretory pathway. <i>Nature Cell Biology</i> , <b>2012</b> , 14, 764-74	23.4	141
184	Human Proteinpedia enables sharing of human protein data. <i>Nature Biotechnology</i> , <b>2008</b> , 26, 164-7	44.5	138
183	Aberrant DNA hypermethylation of SDHC: a novel mechanism of tumor development in Carney triad. <i>Endocrine-Related Cancer</i> , <b>2014</b> , 21, 567-77	5.7	130
182	Toward a Catalog of Human Genes and Proteins: Sequencing and Analysis of 500 Novel Complete Protein Coding Human cDNAs. <i>Genome Research</i> , <b>2001</b> , 11, 422-435	9.7	126
181	MicroRNA-31 sensitizes human breast cells to apoptosis by direct targeting of protein kinase C epsilon (PKCepsilon). <i>Journal of Biological Chemistry</i> , <b>2013</b> , 288, 8750-8761	5.4	112
180	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> , <b>2013</b> , 9, e1003373	6	108
179	Identification and characterization of a set of conserved and new regulators of cytoskeletal organization, cell morphology and migration. <i>BMC Biology</i> , <b>2011</b> , 9, 54	7.3	108
178	Advances in CRISPR-Cas9 genome engineering: lessons learned from RNA interference. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, 3407-19	20.1	104
177	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> , <b>2015</b> , 34, 4867-78	9.2	104
176	The completion of the Mammalian Gene Collection (MGC). <i>Genome Research</i> , <b>2009</b> , 19, 2324-33	9.7	98
175	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> , <b>2010</b> , 220, 71-86	9.4	93
174	Enhancer hijacking activates oncogenic transcription factor NR4A3 in acinic cell carcinomas of the salivary glands. <i>Nature Communications</i> , <b>2019</b> , 10, 368	17.4	89
173	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> , <b>2014</b> , 233, 368-79	9.4	89
172	A microscope-based screening platform for large-scale functional protein analysis in intact cells. <i>FEBS Letters</i> , <b>2003</b> , 554, 394-8	3.8	83
171	The ORFeome Collaboration: a genome-scale human ORF-clone resource. <i>Nature Methods</i> , <b>2016</b> , 13, 191-2	21.6	80
170	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> , <b>2008</b> , 147, 333-8	3.5	79

169	The genomic structure of the DMBT1 gene: evidence for a region with susceptibility to genomic instability. <i>Oncogene</i> , <b>1999</b> , 18, 6233-40	9.2	74
168	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> , <b>2016</b> , 238, 700-10	9.4	73
167	Environment-induced epigenetic reprogramming in genomic regulatory elements in smoking mothers and their children. <i>Molecular Systems Biology</i> , <b>2016</b> , 12, 861	12.2	71
166	Primer design for large scale sequencing. <i>Nucleic Acids Research</i> , <b>1998</b> , 26, 3006-12	20.1	69
165	Infrared-based protein detection arrays for quantitative proteomics. <i>Proteomics</i> , <b>2007</b> , 7, 558-564	4.8	66
164	LIMT is a novel metastasis inhibiting lncRNA suppressed by EGF and downregulated in aggressive breast cancer. <i>EMBO Molecular Medicine</i> , <b>2016</b> , 8, 1052-64	12	66
163	Tumor-Stroma-Inflammation Networks Promote Pro-metastatic Chemokines and Aggressiveness Characteristics in Triple-Negative Breast Cancer. <i>Frontiers in Immunology</i> , <b>2019</b> , 10, 757	8.4	63
162	Analysis of genetic variations of protein tyrosine kinase fyn and their association with alcohol dependence in two independent cohorts. <i>Biological Psychiatry</i> , <b>2003</b> , 54, 1422-6	7.9	62
161	MicroRNA-30c-2-3p negatively regulates NF- $\kappa$ B signaling and cell cycle progression through downregulation of TRADD and CCNE1 in breast cancer. <i>Molecular Oncology</i> , <b>2015</b> , 9, 1106-19	7.9	61
160	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> , <b>2016</b> , 17, 566	4.5	61
159	Recurrent Somatic PDGFRB Mutations in Sporadic Infantile/Solitary Adult Myofibromas But Not in Angioleiomyomas and Myopericytomas. <i>American Journal of Surgical Pathology</i> , <b>2017</b> , 41, 195-203	6.7	60
158	SMART amplification combined with cDNA size fractionation in order to obtain large full-length clones. <i>BMC Genomics</i> , <b>2004</b> , 5, 36	4.5	59
157	Dyskerin localizes to the nucleolus and its mislocalization is unlikely to play a role in the pathogenesis of dyskeratosis congenita. <i>Human Molecular Genetics</i> , <b>1999</b> , 8, 2515-24	5.6	59
156	Combinatorial targeting of FGF and ErbB receptors blocks growth and metastatic spread of breast cancer models. <i>Breast Cancer Research</i> , <b>2013</b> , 15, R8	8.3	56
155	Strong EGFR signaling in cell line models of ERBB2-amplified breast cancer attenuates response towards ERBB2-targeting drugs. <i>Oncogenesis</i> , <b>2012</b> , 1, e16	6.6	55
154	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> , <b>2017</b> , 8, e2973	9.8	53
153	High-content screening microscopy identifies novel proteins with a putative role in secretory membrane traffic. <i>Genome Research</i> , <b>2004</b> , 14, 1948-56	9.7	53
152	Large-scale protein expression for proteome research. <i>Proteomics</i> , <b>2005</b> , 5, 3571-80	4.8	53

151	The nucleoporin Nup358/RanBP2 promotes nuclear import in a cargo- and transport receptor-specific manner. <i>Traffic</i> , <b>2012</b> , 13, 218-33	5.7	52
150	Combinatorial RNAi for quantitative protein network analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2007</b> , 104, 6579-84	11.5	52
149	The H-Invitational Database (H-InvDB), a comprehensive annotation resource for human genes and transcripts. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, D793-9	20.1	52
148	Isoform C beta 2, an unusual form of the bovine catalytic subunit of cAMP-dependent protein kinase. <i>Journal of Biological Chemistry</i> , <b>1991</b> , 266, 5140-6	5.4	52
147	Proteomic profiling of breast cancer metabolism identifies SHMT2 and ASCT2 as prognostic factors. <i>Breast Cancer Research</i> , <b>2017</b> , 19, 112	8.3	50
146	EGF induces microRNAs that target suppressors of cell migration: miR-15b targets MTSS1 in breast cancer. <i>Science Signaling</i> , <b>2015</b> , 8, ra29	8.8	50
145	miRNA-1246 induces pro-inflammatory responses in mesenchymal stem/stromal cells by regulating PKA and PP2A. <i>Oncotarget</i> , <b>2017</b> , 8, 43897-43914	3.3	48
144	Sequential changes of the DMBT1 expression and location in normal lung tissue and lung carcinomas. <i>Genes Chromosomes and Cancer</i> , <b>2002</b> , 35, 164-9	5	47
143	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> , <b>2019</b> , 43, 1264-1272	6.7	47
142	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> , <b>2012</b> , 111, 1504-16	15.7	45
141	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> , <b>2010</b> , 107, 1253-64	15.7	43
140	Diurnal suppression of EGFR signalling by glucocorticoids and implications for tumour progression and treatment. <i>Nature Communications</i> , <b>2014</b> , 5, 5073	17.4	42
139	Pore membrane and/or filament interacting like protein 1 (POMFIL1) is predominantly expressed in the nervous system and encodes different protein isoforms. <i>Gene</i> , <b>2002</b> , 290, 73-94	3.8	42
138	Frequent downregulation of DMBT1 and galectin-3 in epithelial skin cancer. <i>International Journal of Cancer</i> , <b>2003</b> , 105, 149-57	7.5	41
137	Synaptojanin 2 is a druggable mediator of metastasis and the gene is overexpressed and amplified in breast cancer. <i>Science Signaling</i> , <b>2015</b> , 8, ra7	8.8	40
136	From ORFeome to biology: a functional genomics pipeline. <i>Genome Research</i> , <b>2004</b> , 14, 2136-44	9.7	40
135	LIFEdb: a database for functional genomics experiments integrating information from external sources, and serving as a sample tracking system. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, D505-8	20.1	40
134	Systematic comparison of surface coatings for protein microarrays. <i>Proteomics</i> , <b>2005</b> , 5, 4705-12	4.8	40

133	Reduced expression of vacuole membrane protein 1 affects the invasion capacity of tumor cells. <i>Oncogene</i> , <b>2008</b> , 27, 1320-6	9.2	39
132	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> , <b>2006</b> , 34, 3917-28	20.1	39
131	Gamma-BAR, a novel AP-1-interacting protein involved in post-Golgi trafficking. <i>EMBO Journal</i> , <b>2005</b> , 24, 1122-33	13	39
130	High-content microscopy identifies new neurite outgrowth regulators. <i>Molecular Biology of the Cell</i> , <b>2007</b> , 18, 242-52	3.5	38
129	Notch-Mediated Tumor-Stroma-Inflammation Networks Promote Invasive Properties and CXCL8 Expression in Triple-Negative Breast Cancer. <i>Frontiers in Immunology</i> , <b>2019</b> , 10, 804	8.4	37
128	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> , <b>2002</b> , 35, 242-55	5	36
127	Simultaneous on-line DNA sequencing on both strands with two fluorescent dyes. <i>Analytical Biochemistry</i> , <b>1995</b> , 224, 117-21	3.1	36
126	Recurrent mutations within the amino-terminal region of Eatenin are probable key molecular driver events in sinonasal hemangiopericytoma. <i>American Journal of Pathology</i> , <b>2015</b> , 185, 563-71	5.8	35
125	PI3K: A master regulator of brain metastasis-promoting macrophages/microglia. <i>Glia</i> , <b>2018</b> , 66, 2438-2455	9.5	34
124	The LIFEdb database in 2006. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, D415-8	20.1	33
123	Norepinephrine transporter and catecholamine-O-methyltransferase gene variants and attention-deficit/hyperactivity disorder symptoms in adults. <i>Journal of Neural Transmission</i> , <b>2008</b> , 115, 323-9	4.3	32
122	High-throughput automated DNA sequencing facility with fluorescent labels at the European Molecular Biology Laboratory. <i>Electrophoresis</i> , <b>1992</b> , 13, 616-9	3.6	32
121	Assembly of a parts list of the human mitotic cell cycle machinery. <i>Journal of Molecular Cell Biology</i> , <b>2019</b> , 11, 703-718	6.3	31
120	Targeting PLK1 overcomes T-DM1 resistance via CDK1-dependent phosphorylation and inactivation of Bcl-2/xL in HER2-positive breast cancer. <i>Oncogene</i> , <b>2018</b> , 37, 2251-2269	9.2	30
119	Impact of clinical exomes in neurodevelopmental and neurometabolic disorders. <i>Molecular Genetics and Metabolism</i> , <b>2017</b> , 121, 297-307	3.7	30
118	Phenotypical and molecular distinctness of sinonasal haemangiopericytoma compared to solitary fibrous tumour of the sinonasal tract. <i>Histopathology</i> , <b>2014</b> , 65, 667-73	7.3	29
117	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> , <b>2017</b> , 27, 1323-1335	9.7	27
116	Genetically coupled receptor-ligand pair NKp80-AICL enables autonomous control of human NK cell responses. <i>Blood</i> , <b>2013</b> , 122, 2380-9	2.2	27

115	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> , <b>2011</b> , 155A, 1472-5	2.5	27
114	Dynamic deterministic effects propagation networks: learning signalling pathways from longitudinal protein array data. <i>Bioinformatics</i> , <b>2010</b> , 26, i596-602	7.2	26
113	Transcription mapping in a medulloblastoma breakpoint interval and Smith-Magenis syndrome candidate region: identification of 53 transcriptional units and new candidate genes. <i>Genomics</i> , <b>1999</b> , 56, 1-11	4.3	26
112	Illuminating the human genome. <i>Histochemistry and Cell Biology</i> , <b>2001</b> , 115, 23-9	2.4	25
111	Navigator-3, a modulator of cell migration, may act as a suppressor of breast cancer progression. <i>EMBO Molecular Medicine</i> , <b>2015</b> , 7, 299-314	12	22
110	The full-ORF clone resource of the German cDNA Consortium. <i>BMC Genomics</i> , <b>2007</b> , 8, 399	4.5	22
109	An anthropoid-specific segmental duplication on human chromosome 1q22. <i>Genomics</i> , <b>2006</b> , 88, 143-51	4.3	22
108	Genomic organization of a 225-kb region in Xq28 containing the gene for X-linked myotubular myopathy (MTM1) and a related gene (MTMR1). <i>Genomics</i> , <b>1998</b> , 54, 256-66	4.3	22
107	Automated low-redundancy large-scale DNA sequencing by primer walking. <i>BioTechniques</i> , <b>1993</b> , 15, 714-21	2.5	22
106	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> , <b>2016</b> , 99, 1009-25	6.5	21
105	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> , <b>2015</b> , 136, 1013-23	7.5	21
104	Differential response to formaldehyde in tamoxifen resistant MCF-7 breast cancer cells. <i>PLoS ONE</i> , <b>2014</b> , 9, e101473	3.7	21
103	Protein signatures of oxidative stress response in a patient specific cell line model for autism. <i>Molecular Autism</i> , <b>2014</b> , 5, 10	6.5	20
102	Co-Inflammatory Roles of TGF $\beta$ in the Presence of TNF $\alpha$ Drive a Pro-inflammatory Fate in Mesenchymal Stem Cells. <i>Frontiers in Immunology</i> , <b>2017</b> , 8, 479	8.4	20
101	The systematic functional characterisation of Xq28 genes prioritises candidate disease genes. <i>BMC Genomics</i> , <b>2006</b> , 7, 29	4.5	20
100	Protein microarrays as a discovery tool for studying protein-protein interactions. <i>Expert Review of Proteomics</i> , <b>2005</b> , 2, 13-26	4.2	20
99	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> , <b>2018</b> , 24, 1987-2001	12.0	19
98	Statistical methods and software for the analysis of highthroughput reverse genetic assays using flow cytometry readouts. <i>Genome Biology</i> , <b>2006</b> , 7, R77	18.3	19

97	Alternative pre-mRNA processing regulates cell-type specific expression of the IL4I1 and NUP62 genes. <i>BMC Biology</i> , <b>2005</b> , 3, 16	7.3	19
96	Nucleotide sequence and analysis of the centromeric region of yeast chromosome IX. <i>Yeast</i> , <b>1995</b> , 11, 61-78	3.4	19
95	TGF $\beta$ 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> , <b>2018</b> , 12, 1447-1463	7.9	18
94	Automated production of recombinant human proteins as resource for proteome research. <i>Proteome Science</i> , <b>2008</b> , 6, 4	2.6	18
93	An integrative model on the role of DMBT1 in epithelial cancer. <i>Cancer Detection and Prevention</i> , <b>2002</b> , 26, 266-74		18
92	CDNAs for functional genomics and proteomics: the German Consortium. <i>Comptes Rendus - Biologies</i> , <b>2003</b> , 326, 1003-9	1.4	18
91	Functional profiling: from microarrays via cell-based assays to novel tumor relevant modulators of the cell cycle. <i>Cancer Research</i> , <b>2005</b> , 65, 7733-42	10.1	18
90	Transcriptional analysis of the candidate region for incontinentia pigmenti (IP2) in Xq28. <i>Genome Research</i> , <b>1996</b> , 6, 922-34	9.7	18
89	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> , <b>2018</b> , 7, e1500671	7.2	18
88	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> , <b>2017</b> ,	3.5	17
87	Reverse phase protein array based tumor profiling identifies a biomarker signature for risk classification of hormone receptor-positive breast cancer. <i>Translational Proteomics</i> , <b>2014</b> , 2, 52-59		16
86	So rare we need to hunt for them: reframing the ethical debate on incidental findings. <i>Genome Medicine</i> , <b>2015</b> , 7, 83	14.4	16
85	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> , <b>2006</b> , 312, 901-12	4.2	16
84	No association of alcohol dependence with a NMDA-receptor 2B gene variant. <i>Molecular Psychiatry</i> , <b>2003</b> , 8, 11-2	15.1	16
83	The protein kinase A catalytic subunit C $\alpha$ : molecular characterization and distribution of the splice variant. <i>Biochemical Journal</i> , <b>2000</b> , 351, 123-132	3.8	16
82	Being in the right location at the right time. <i>Genome Biology</i> , <b>2001</b> , 2, REVIEWS1024	18.3	16
81	Separation of up to 1000 bases on a modified A.L.F. DNA sequencer. <i>Nucleic Acids Research</i> , <b>1993</b> , 21, 6042-4	20.1	16
80	Cloning of the C alpha catalytic subunit of the bovine cAMP-dependent protein kinase. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , <b>1992</b> , 1171, 93-6		16



79	Epigenetic mechanisms underlie the crosstalk between growth factors and a steroid hormone. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, 12681-12699	20.1	15
78	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> , <b>2018</b> , 123, 364-374	3.7	15
77	Epidermal growth-factor-induced transcript isoform variation drives mammary cell migration. <i>PLoS ONE</i> , <b>2013</b> , 8, e80566	3.7	15
76	RNAi-based validation of antibodies for reverse phase protein arrays. <i>Proteome Science</i> , <b>2010</b> , 8, 69	2.6	15
75	High-throughput protein analysis integrating bioinformatics and experimental assays. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, 742-8	20.1	15
74	Increasing the sensitivity of reverse phase protein arrays by antibody-mediated signal amplification. <i>Proteome Science</i> , <b>2010</b> , 8, 36	2.6	14
73	Efficient low redundancy large-scale DNA sequencing at EMBL. <i>Journal of Biotechnology</i> , <b>1995</b> , 41, 121-9	3.7	14
72	Contact spotting of protein microarrays coupled with spike-in of normalizer protein permits time-resolved analysis of ERBB receptor signaling. <i>Proteomics</i> , <b>2008</b> , 8, 1586-94	4.8	13
71	The 3of5 web application for complex and comprehensive pattern matching in protein sequences. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 144	3.6	13
70	Epitopes fused to F-pilin are incorporated into functional recombinant pili. <i>Journal of Molecular Biology</i> , <b>1998</b> , 279, 589-603	6.5	13
69	DelGEF, an RCC1-related protein encoded by a gene on chromosome 11p14 critical for two forms of hereditary deafness. <i>FEBS Letters</i> , <b>1999</b> , 460, 153-60	3.8	13
68	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> , <b>2006</b> , 6, 4439-43	4.8	12
67	The German cDNA network: cDNAs, functional genomics and proteomics. <i>Journal of Structural and Functional Genomics</i> , <b>2003</b> , 4, 87-96		12
66	Coordinated Pulses of mRNA and of Protein Translation or Degradation Produce EGF-Induced Protein Bursts. <i>Cell Reports</i> , <b>2017</b> , 18, 3129-3142	10.6	11
65	Findings made in gene panel to whole genome sequencing: data, knowledge, ethics - and consequences?. <i>Expert Review of Molecular Diagnostics</i> , <b>2016</b> , 16, 1259-1270	3.8	11
64	Extending pathways based on gene lists using InterPro domain signatures. <i>BMC Bioinformatics</i> , <b>2008</b> , 9, 3	3.6	11
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