Manfred Gessler

List of Publications by Year
in descending order

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144 papers	13,942 citations	26630 56 h-index	21540 114 g-index

152 all docs	152 docs citations	152 times ranked	17078 citing authors

#	Article	IF	Citations
1	Homozygous deletion in Wilms tumours of a zinc-finger gene identified by chromosome jumping. Nature, 1990, 343, 774-778.	27.8	1,279
2	The landscape of genomic alterations across childhood cancers. Nature, 2018, 555, 321-327.	27.8	1,068
3	A Murine Model of Holt-Oram Syndrome Defines Roles of the T-Box Transcription Factor Tbx5 in Cardiogenesis and Disease. Cell, 2001, 106, 709-721.	28.9	957
4	The Notch target genes Hey1 and Hey2 are required for embryonic vascular development. Genes and Development, 2004, 18, 901-911.	5.9	576
5	GLI3 zinc-finger gene interrupted by translocations in Greig syndrome families. Nature, 1991, 352, 539-540.	27.8	553
6	Common variants at SCN5A-SCN10A and HEY2 are associated with Brugada syndrome, a rare disease with high risk of sudden cardiac death. Nature Genetics, 2013, 45, 1044-1049.	21.4	467
7	Loss of Fat4 disrupts PCP signaling and oriented cell division and leads to cystic kidney disease. Nature Genetics, 2008, 40, 1010-1015.	21.4	455
8	Delta Notch and then? Protein interactions and proposed modes of repression by Hes and Hey bHLH factors. Nucleic Acids Research, 2007, 35, 4583-4596.	14.5	323
9	Epithelial Notch signaling regulates interstitial fibrosis development in the kidneys of mice and humans. Journal of Clinical Investigation, 2010, 120, 4040-4054.	8.2	306
10	Frasier syndrome is caused by defective alternative splicing of WT1 leading to an altered ratio of WT1 +/-KTS splice isoforms. Human Molecular Genetics, 1998, 7, 709-714.	2.9	303
11	Rationale for the treatment of Wilms tumour in the UMBRELLA SIOPâ€“RTSG 2016 protocol. Nature Reviews Urology, 2017, 14, 743-752.	3.8	249
12	Mutations in the SIX1/2 Pathway and the DROSHA/DGCR8 miRNA Microprocessor Complex Underlie High-Risk Blastemal Type Wilms Tumors. Cancer Cell, 2015, 27, 298-311.	16.8	248
13	Sarcoma classification by DNA methylation profiling. Nature Communications, 2021, 12, 498.	12.8	237
14	Hey2 Regulation by FGF Provides a Notch-Independent Mechanism for Maintaining Pillar Cell Fate in the Organ of Corti. Developmental Cell, 2009, 16, 58-69.	7.0	236
15	Integrated Regulation of Toll-like Receptor Responses by Notch and Interferon-Î³ Pathways. Immunity, 2008, 29, 691-703.	14.3	235
16	Hey genes: a novel subfamily of hairy - and Enhancer of split related genes specifically expressed during mouse embryogenesis. Mechanisms of Development, 1999, 85, 173-177.	1.7	229
17	Comparative Analysis of the Human and Mouse Hey1 Promoter: Hey Genes Are New Notch Target Genes. Biochemical and Biophysical Research Communications, 2000, 275, 652-660.	2.1	214
18	Developmental expression patterns of mouse sFRP genes encoding members of the secreted frizzled related protein family. Mechanisms of Development, 1998, 75, 29-42.	1.7	208

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19	Hypoxia-mediated activation of Dll4-Notch-Hey2 signaling in endothelial progenitor cells and adoption of arterial cell fate. Experimental Cell Research, 2007, 313, 1-9.	2.6	194
20	The UMBRELLA SIOPâ€“RTSG 2016 Wilms tumour pathology and molecular biology protocol. Nature Reviews Urology, 2018, 15, 693-701.	3.8	152
21	Developmental patterning of the cardiac atrioventricular canal by Notch and Hairy-related transcription factors. Development (Cambridge), 2006, 133, 4381-4390.	2.5	147
22	Combined Loss of Hey1 and HeyL Causes Congenital Heart Defects Because of Impaired Epithelial to Mesenchymal Transition. Circulation Research, 2007, 100, 856-863.	4.5	146
23	Multi-omics enrichment analysis using the GeneTrail2 web service. Bioinformatics, 2016, 32, 1502-1508.	4.1	144
24	Mouse gridlock. Current Biology, 2002, 12, 1601-1604.	3.9	142
25	Oscillating Expression of c-Hey2 in the Presomitic Mesoderm Suggests That the Segmentation Clock May Use Combinatorial Signaling through Multiple Interacting bHLH Factors. Developmental Biology, 2000, 227, 91-103.	2.0	139
26	Gain of 1q Is Associated with Adverse Outcome in Favorable Histology Wilmsâ€™ Tumors. American Journal of Pathology, 2001, 158, 393-398.	3.8	127
27	The genomic organization and expression of the WT1 gene. Genomics, 1992, 12, 807-813.	2.9	125
28	Characterization of the chromosomal translocation t(10;17)(q22;p13) in clear cell sarcoma of kidney. Journal of Pathology, 2012, 227, 72-80.	4.5	125
29	Hey Basic Helix-Loop-Helix Transcription Factors Are Repressors of GATA4 and GATA6 and Restrict Expression of the GATA Target Gene ANF in Fetal Hearts. Molecular and Cellular Biology, 2005, 25, 8960-8970.	2.3	109
30	Survival in Patients with High-Risk Prostate Cancer Is Predicted by miR-221, Which Regulates Proliferation, Apoptosis, and Invasion of Prostate Cancer Cells by Inhibiting IRF2 and SOCS3. Cancer Research, 2014, 74, 2591-2603.	0.9	107
31	Gain of 1q As a Prognostic Biomarker in Wilms Tumors (WTs) Treated With Preoperative Chemotherapy in the International Society of Paediatric Oncology (SIOP) WT 2001 Trial: A SIOP Renal Tumours Biology Consortium Study. Journal of Clinical Oncology, 2016, 34, 3195-3203.	1.6	105
32	Deletion of GLI3 supports the homology of the human Greig cephalopolysyndactyly syndrome (GCPS) and the mouse mutant extra toes (Xt). Mammalian Genome, 1992, 3, 461-463.	2.2	104
33	Primary intracranial spindle cell sarcoma with rhabdomyosarcoma-like features share a highly distinct methylation profile and DICER1 mutations. Acta Neuropathologica, 2018, 136, 327-337.	7.7	104
34	Transposable elements as a source of genetic innovation: expression and evolution of a family of retrotransposon-derived neogenes in mammals. Gene, 2005, 345, 101-111.	2.2	101
35	Analysis of HeyL expression in wild-type and Notch pathway mutant mouse embryos. Mechanisms of Development, 2000, 98, 175-178.	1.7	95
36	Gene expression profiles of brain endothelial cells during embryonic development at bulk and single-cell levels. Science Signaling, 2017, 10, .	3.6	91

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37	Expression profiling of Wilms tumors reveals new candidate genes for different clinical parameters. International Journal of Cancer, 2006, 118, 1954-1962.	5.1	85
38	Multiple mechanisms of MYCN dysregulation in Wilms tumour. Oncotarget, 2015, 6, 7232-7243.	1.8	85
39	Target genes of the WNT/Î²-catenin pathway in Wilms tumors. Genes Chromosomes and Cancer, 2006, 45, 565-574.	2.8	82
40	Expression of mousedchs1,fjx1, andfat-jsuggests conservation of the planar cell polarity pathway identified in drosophila. Developmental Dynamics, 2005, 234, 747-755.	1.8	80
41	GATA-dependent regulatory switches establish atrioventricular canal specificity during heart development. Nature Communications, 2014, 5, 3680.	12.8	78
42	Characterization of the Human and Mouse HEY1, HEY2, and HEYL Genes: Cloning, Mapping, and Mutation Screening of a New bHLH Gene Family. Genomics, 2000, 66, 195-203.	2.9	76
43	Physiological Notch Signaling Maintains Bone Homeostasis via RBPjk and Hey Upstream of NFATc1. PLoS Genetics, 2012, 8, e1002577.	3.5	76
44	Array-based DNA-methylation profiling in sarcomas with small blue round cell histology provides valuable diagnostic information. Modern Pathology, 2018, 31, 1246-1256.	5.5	76
45	Wilms tumour. Nature Reviews Disease Primers, 2021, 7, 75.	30.5	75
46	Allele loss in Wilms tumors of chromosome arms 11q, 16q, and 22q correlates with clinicopathological parameters. , 1998, 22, 287-294.		74
47	Identification and Analyses of Extra-Cranial and Cranial Rhabdoid Tumor Molecular Subgroups Reveal Tumors with Cytotoxic T Cell Infiltration. Cell Reports, 2019, 29, 2338-2354.e7.	6.4	74
48	Recurrent intragenic rearrangements of EGFR and BRAF in soft tissue tumors of infants. Nature Communications, 2018, 9, 2378.	12.8	72
49	Human CC10, the homologue of rabbit uteroglobin: genomic cloning, chromosomal localization and expression in endometrial cell lines. Human Molecular Genetics, 1992, 1, 371-378.	2.9	69
50	Subtype-Specific FBXW7 Mutation and MYCN Copy Number Gain in Wilms' Tumor. Clinical Cancer Research, 2010, 16, 2036-2045.	7.0	69
51	Hey bHLH Transcription Factors. Current Topics in Developmental Biology, 2014, 110, 285-315.	2.2	68
52	Target Gene Analysis by Microarrays and Chromatin Immunoprecipitation Identifies HEY Proteins as Highly Redundant bHLH Repressors. PLoS Genetics, 2012, 8, e1002728.	3.5	66
53	Placental Î±2-adrenoceptors control vascular development at the interface between mother and embryo. Nature Genetics, 2002, 31, 311-315.	21.4	65
54	COUP-TFII orchestrates venous and lymphatic endothelial identity by homo- or hetero-dimerisation with PROX1. Journal of Cell Science, 2013, 126, 1164-1175.	2.0	65

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55	The transcriptional repressor Hes1 attenuates inflammation by regulating transcription elongation. Nature Immunology, 2016, 17, 930-937.	14.5	64
56	Combining miRNA and mRNA Expression Profiles in Wilms Tumor Subtypes. International Journal of Molecular Sciences, 2016, 17, 475.	4.1	61
57	A physical map around the WAGR complex on the short arm of chromosome 11. Genomics, 1989, 5, 43-55.	2.9	60
58	Hey Genes in Cardiovascular Development. Trends in Cardiovascular Medicine, 2003, 13, 221-226.	4.9	58
59	Loss of Heterozygosity at 2q37 in Sporadic Wilms' Tumor: Putative Role for miR-562. Clinical Cancer Research, 2009, 15, 5985-5992.	7.0	56
60	Mutually exclusive BCOR internal tandem duplications and YWHAEâ€NUTM2 fusions in clear cell sarcoma of kidney: not the full story. Journal of Pathology, 2016, 238, 617-620.	4.5	56
61	Novel features of boundary cap cells revealed by the analysis of newly identified molecular markers. Glia, 2009, 57, 1450-1457.	4.9	55
62	WTX inactivation is a frequent, but late event in Wilms tumors without apparent clinical impact. Genes Chromosomes and Cancer, 2009, 48, 1102-1111.	2.8	54
63	Expression of Notch pathway genes in the embryonic mouse metanephros suggests a role in proximal tubule development. Gene Expression Patterns, 2003, 3, 595-598.	0.8	53
64	TP53 alterations in Wilms tumour represent progression events with strong intratumour heterogeneity that are closely linked but not limited to anaplasia. Journal of Pathology: Clinical Research, 2017, 3, 234-248.	3.0	53
65	Identification of the human homolog of the imprinted mouse Air non-coding RNA. Genomics, 2008, 92, 464-473.	2.9	52
66	Loss of 11q and 16q in Wilms tumors is associated with anaplasia, tumor recurrence, and poor prognosis. Genes Chromosomes and Cancer, 2007, 46, 163-170.	2.8	51
67	Overlapping expression pattern of the actin organizers Spir-1 and formin-2 in the developing mouse nervous system and the adult brain. Gene Expression Patterns, 2004, 4, 249-255.	0.8	48
68	New prognostic markers revealed by evaluation of genes correlated with clinical parameters in Wilms tumors. Genes Chromosomes and Cancer, 2008, 47, 386-395.	2.8	48
69	Developmental Expression and Biochemical Characterization of Emu Family Members. Developmental Biology, 2002, 249, 204-218.	2.0	45
70	TRIM28 haploinsufficiency predisposes to Wilms tumor. International Journal of Cancer, 2019, 145, 941-951.	5.1	45
71	All-trans retinoic acid treatment of Wilms tumor cells reverses expression of genes associated with high risk and relapse in vivo. Oncogene, 2005, 24, 5246-5251.	5.9	44
72	Differential expression of the cellular oncogenes c-src and c-yes in embryonal and adult chicken tissues. Bioscience Reports, 1984, 4, 757-770.	2.4	41

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73	Further evidence that imbalance of WT1 isoforms may be involved in Denys â€“ Drash syndrome. Human Molecular Genetics, 1993, 2, 1967-1968.	2.9	41
74	ETV6â€“NTRK3 in congenital mesoblastic nephroma: A report of the SIOP/GPOH nephroblastoma study. Pediatric Blood and Cancer, 2018, 65, e26925.	1.5	41
75	Identification of Optimized Target Sequences for the GLI3 Zinc Finger Protein. DNA and Cell Biology, 1995, 14, 629-634.	1.9	39
76	Characterization of hey bHLH genes in teleost fish. Development Genes and Evolution, 2003, 213, 541-553.	0.9	35
77	Distinct molecular origins for Denys-Drash and Frasier syndromes. Human Genetics, 1993, 91, 285-6.	3.8	34
78	Fjx1: A notch-inducible secreted ligand with specific binding sites in developing mouse embryos and adult brain. Developmental Dynamics, 2005, 234, 602-612.	1.8	34
79	The rodent Four-jointed ortholog Fjx1 regulates dendrite extension. Developmental Biology, 2007, 312, 461-470.	2.0	34
80	Cell-autonomous and redundant roles of Hey1 and HeyL in muscle stem cells: HeyL requires Hes1 to bind diverse DNA sites. Development (Cambridge), 2019, 146, .	2.5	34
81	Fjx1, the murine homologue of the Drosophila four-jointed gene, codes for a putative secreted protein expressed in restricted domains of the developing and adult brain. Mechanisms of Development, 1999, 80, 213-217.	1.7	32
82	Phenotypic variability in Hey2 ?/? mice and absence of HEY2 mutations in patients with congenital heart defects or Alagille syndrome. Mammalian Genome, 2004, 15, 711-716.	2.2	32
83	Analysis of WT1 target gene expression in stably transfected cell lines. Oncogene, 1998, 17, 1287-1294.	5.9	31
84	Paediatric renal tumours: perspectives from the SIOPâ€“RTSG. Nature Reviews Urology, 2017, 14, 3-4.	3.8	31
85	Treatment-independent miRNA signature in blood of wilms tumor patients. BMC Genomics, 2012, 13, 379.	2.8	29
86	Defective autophagy through epg5 mutation results in failure to reduce germ plasm and mitochondria. FASEB Journal, 2015, 29, 4145-4161.	0.5	29
87	Homozygous inactivation ofWTI in a Wilms' tumor associated with the WAGR syndrome. Genes Chromosomes and Cancer, 1993, 7, 131-136.	2.8	28
88	The Notch Pathway Inhibits TGFÎ² Signaling in Breast Cancer through HEYL-Mediated Crosstalk. Cancer Research, 2014, 74, 6509-6518.	0.9	27
89	Characteristics and outcome of pediatric renal cell carcinoma patients registered in the International Society of Pediatric Oncology (<scp>SIOP</scp>) 93â€01, 2001 and <scp>UKâ€IMPORT</scp> database: A report of the <scp>SIOPâ€Renal</scp> Tumor Study Group. International Journal of Cancer, 2021, 148, 2724-2735.	5.1	26
90	her7 and hey1, but not lunatic fringe show dynamic expression during somitogenesis in medaka (Oryzias latipes). Gene Expression Patterns, 2004, 4, 553-559.	0.8	25

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91	Characterization of primary wilms tumor cultures as an in vitro model. Genes Chromosomes and Cancer, 2012, 51, 92-104.	2.8	23
92	Mechanisms of epigenetic and cell-type specific regulation of Hey target genes in ES cells and cardiomyocytes. Journal of Molecular and Cellular Cardiology, 2015, 79, 79-88.	1.9	23
93	Hey bHLH Factors in Cardiovascular Development. Pediatric Cardiology, 2010, 31, 363-370.	1.3	22
94	An essential developmental function for murine phosphoglycolate phosphatase in safeguarding cell proliferation. Scientific Reports, 2016, 6, 35160.	3.3	22
95	An Ordered NotI Fragment Map of Human Chromosome Band 11p15. Genomics, 1994, 23, 211-222.	2.9	21
96	Retinoic acid pathway activity in wilms tumors and characterization of biological responses in vitro. Molecular Cancer, 2011, 10, 136.	19.2	21
97	Sequence of the WT1 Upstream Region Including the Wit-1 Gene. Genomics, 1993, 17, 499-501.	2.9	20
98	Screen for genes regulated during early kidney morphogenesis. Genesis, 1999, 24, 273-283.	2.1	20
99	Molecular analysis of E-cadherin and cadherin-11 in Wilms' tumours. , 2000, 191, 162-169.		20
100	Upregulation of Soluble Vascular Endothelial Growth Factor Receptor 1 Contributes to Angiogenesis Defects in the Placenta of Î±2B-Adrenoceptorâ€“Deficient Mice. Circulation Research, 2007, 101, 682-691.	4.5	20
101	A WAGR region gene between PAX-6 and FSHB expressed in fetal brain. Human Genetics, 1994, 94, 658-64.	3.8	19
102	Novel Familial WT1 Read-Through Mutation Associated With Wilms Tumor and Slow Progressive Nephropathy. American Journal of Kidney Diseases, 2005, 45, 1100-1104.	1.9	19
103	The transcription factor Hey and nuclear lamins specify and maintain cell identity. ELife, 2019, 8, .	6.0	19
104	Molecular mapping and cloning of the breakpoints of a chromosome 11p14.1?p13 deletion associated with the AGR syndrome. Genomics, 1988, 3, 117-123.	2.9	18
105	A somatic cell hybrid panel and DNA probes for physical mapping of human chromosome 7p. Genomics, 1991, 11, 737-743.	2.9	18
106	Isolation of a Yeast Artificial Chromosome Contig Spanning the Greig Cephalopolysyndactyly Syndrome (GCPS) Gene Region. Genomics, 1994, 22, 563-568.	2.9	17
107	Cloning and expression analysis of the mouse stroma marker Snep encoding a novel nidogen domain protein. Developmental Dynamics, 2004, 230, 371-377.	1.8	17
108	High-risk blastemal Wilms tumor can be modeled by 3D spheroid cultures in vitro. Oncogene, 2020, 39, 849-861.	5.9	17

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109	cDNA Sequence, Genomic Organization, and Evolutionary Conservation of a Novel Gene from the WAGR Region. Genomics, 1995, 29, 526-532.	2.9	16
110	Expression patterns of the mouse Spir-2 actin nucleator. Gene Expression Patterns, 2010, 10, 345-350.	0.8	16
111	Identification of BOIP, a novel cDNA highly expressed during spermatogenesis that encodes a protein interacting with the orange domain of the hairy-related transcription factor HRT1/Hey1 inXenopus and mouse. Developmental Dynamics, 2003, 228, 716-725.	1.8	14
112	Very-KIND is a novel nervous system specific guanine nucleotide exchange factor for Ras GTPases. Gene Expression Patterns, 2005, 6, 79-85.	0.8	13
113	Chibby, a novel antagonist of the Wnt pathway, is not involved in Wilms tumor development. Cancer Letters, 2005, 220, 115-120.	7.2	13
114	Pericentric intrachromosomal insertion responsible for recurrence of del(11)(p13p14) in a family. Genes Chromosomes and Cancer, 1993, 7, 57-62.	2.8	12
115	Isolation and characterization of a cosmid contig for the GCPS gene region. Human Genetics, 1995, 95, 82-8.	3.8	12
116	Loss or oncogenic mutation of DROSHA impairs kidney development and function, but is not sufficient for Wilms tumor formation. International Journal of Cancer, 2019, 144, 1391-1400.	5.1	12
117	A 7.5 Mb Sequence-Ready PAC Contig and Gene Expression Map of Human Chromosome 11p13-p14.1. Genome Research, 1999, 9, 1074-1086.	5.5	11
118	Identification of limited regions of genetic aberrations in patients affected with Wilms' tumor using a tiling-path chromosome 22 array. International Journal of Cancer, 2006, 119, 571-578.	5.1	10
119	MYCN and MAX alterations in Wilms tumor and identification of novel N-MYC interaction partners as biomarker candidates. Cancer Cell International, 2021, 21, 555.	4.1	10
120	Mosaic variegated aneuploidy in mouse BubR1 deficient embryos and pregnancy loss in human. Chromosome Research, 2014, 22, 375-392.	2.2	9
121	Transcript Map of a 900-kb Genomic Region in Xp22.1â€“p22.2: Identification of 12 Novel Genes. Genomics, 1998, 51, 59-67.	2.9	8
122	A Sequence-Ready 3-Mb PAC Contig Covering 16 Breakpoints of the Wilms Tumor/Anirida Region of Human Chromosome 11p13. Genomics, 1998, 53, 155-163.	2.9	8
123	Drug<scp>T</scp>arget<scp>I</scp>nspector: An assistance tool for patient treatment stratification. International Journal of Cancer, 2016, 138, 1765-1776.	5.1	8
124	REGGAE: a novel approach for the identification of key transcriptional regulators. Bioinformatics, 2018, 34, 3503-3510.	4.1	8
125	The potassium channel gene HK1 maps to human chromosome 11p14.1, close to the FSHB gene. Human Genetics, 1992, 90, 319-21.	3.8	7
126	Hey bHLH Proteins Interact with a FBXO45 Containing SCF Ubiquitin Ligase Complex and Induce Its Translocation into the Nucleus. PLoS ONE, 2015, 10, e0130288.	2.5	7

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127	Nierentumoren. , 2006, , 847-864.		7
128	The human MyoD1 (MYF3) gene maps on the short arm of chromosome 11 but is not associated with the WAGR locus or the region for the Beckwith-Wiedemann syndrome. Human Genetics, 1990, 86, 135-8.	3.8	6
129	Dll1 and Dll4: similar, but not the same. Blood, 2009, 113, 5375-5376.	1.4	6
130	HEYL Regulates Neoangiogenesis Through Overexpression in Both Breast Tumor Epithelium and Endothelium. Frontiers in Oncology, 2020, 10, 581459.	2.8	6
131	Characteristics of Nephroblastoma/Nephroblastomatosis in Children with a Clinically Reported Underlying Malformation or Cancer Predisposition Syndrome. Cancers, 2021, 13, 5016.	3.7	6
132	The DGCR8 E518K mutation found in Wilms tumors leads to a partial miRNA processing defect that alters gene expression patterns and biological processes. Carcinogenesis, 2022, 43, 82-93.	2.8	6
133	An Integrated YAC Clone Contig for the WAGR Region on Human Chromosome 11p13â€“p14.1. Genomics, 1995, 30, 37-45.	2.9	5
134	Autoantibody Signature Differentiates Wilms Tumor Patients from Neuroblastoma Patients. PLoS ONE, 2011, 6, e28951.	2.5	5
135	Confirmation of the localization of the human recombination activating gene 1 (RAG1) to chromosome 11p13. Human Genetics, 1994, 93, 215-7.	3.8	4
136	CpG island clones for Chromosome 11p?a resource for mapping and gene identification. Mammalian Genome, 1995, 6, 421-425.	2.2	4
137	Multicenter study identified molecular bloodâ€born protein signatures for Wilms Tumor. International Journal of Cancer, 2012, 131, 673-682.	5.1	4
138	1q gain is a frequent finding in preoperatively treated Wilms tumors, but of limited prognostic value for risk stratification in the SIOP2001/GPOH trial. Genes Chromosomes and Cancer, 2014, 53, 960-962.	2.8	4
139	The role of TCF3 as potential master regulator in blastemal Wilms tumors. International Journal of Cancer, 2019, 144, 1432-1443.	5.1	4
140	The genomic landscape of pediatric renal cell carcinomas. IScience, 2022, 25, 104167.	4.1	3
141	Less may be more for stage I epithelial Wilms tumors. Cancer, 2020, 126, 2762-2764.	4.1	2
142	Abstract A1-59: Multiple mechanisms of MYCN dysregulation in Wilms tumor. , 2015, , .		1
143	Abstract A1-67: Prognostic significance of copy number aberrations in Wilms tumor. , 2015, , .		0
144	Six new polymorphic microsatellite markers used for the integration of genetic and physical maps of human chromosome 7. Human Genetics, 1996, 97, 842-844.	3.8	0