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	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
2	The genomic landscape of pediatric renal cell carcinomas. IScience, 2022, 25, 104167.	4.1	3
3	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
4	Sarcoma classification by DNA methylation profiling. Nature Communications, 2021, 12, 498.	12.8	237
5	Characteristics of Nephroblastoma/Nephroblastomatosis in Children with a Clinically Reported Underlying Malformation or Cancer Predisposition Syndrome. Cancers, 2021, 13, 5016.	3.7	6
6	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
7	Wilms tumour. Nature Reviews Disease Primers, 2021, 7, 75.	30.5	75
8	High-risk blastemal Wilms tumor can be modeled by 3D spheroid cultures in vitro. Oncogene, 2020, 39, 849-861.	5.9	17
9	Less may be more for stage I epithelial Wilms tumors. Cancer, 2020, 126, 2762-2764.	4.1	2
10	HEYL Regulates Neoangiogenesis Through Overexpression in Both Breast Tumor Epithelium and Endothelium. Frontiers in Oncology, 2020, 10, 581459.	2.8	6
11	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
12	TRIM28 haploinsufficiency predisposes to Wilms tumor. International Journal of Cancer, 2019, 145, 941-951.	5.1	45
13	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
14	The role of TCF3 as potential master regulator in blastemal Wilms tumors. International Journal of Cancer, 2019, 144, 1432-1443.	5.1	4
15	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
16	The transcription factor Hey and nuclear lamins specify and maintain cell identity. ELife, 2019, 8, .	6.0	19
17	The landscape of genomic alterations across childhood cancers. Nature, 2018, 555, 321-327.	27.8	1,068
18	ETV6â€“NTRK3 in congenital mesoblastic nephroma: A report of the SIOP/GPOH nephroblastoma study. Pediatric Blood and Cancer, 2018, 65, e26925.	1.5	41

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19	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
20	The UMBRELLA SIOPâ€“RTSG 2016 Wilms tumour pathology and molecular biology protocol. Nature Reviews Urology, 2018, 15, 693-701.	3.8	152
21	REGGAE: a novel approach for the identification of key transcriptional regulators. Bioinformatics, 2018, 34, 3503-3510.	4.1	8
22	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
23	Recurrent intragenic rearrangements of EGFR and BRAF in soft tissue tumors of infants. Nature Communications, 2018, 9, 2378.	12.8	72
24	Paediatric renal tumours: perspectives from the SIOPâ€“RTSG. Nature Reviews Urology, 2017, 14, 3-4.	3.8	31
25	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
26	Rationale for the treatment of Wilms tumour in the UMBRELLA SIOPâ€“RTSG 2016 protocol. Nature Reviews Urology, 2017, 14, 743-752.	3.8	249
27	Gene expression profiles of brain endothelial cells during embryonic development at bulk and single-cell levels. Science Signaling, 2017, 10, .	3.6	91
28	Combining miRNA and mRNA Expression Profiles in Wilms Tumor Subtypes. International Journal of Molecular Sciences, 2016, 17, 475.	4.1	61
29	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
30	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
31	An essential developmental function for murine phosphoglycolate phosphatase in safeguarding cell proliferation. Scientific Reports, 2016, 6, 35160.	3.3	22
32	The transcriptional repressor Hes1 attenuates inflammation by regulating transcription elongation. Nature Immunology, 2016, 17, 930-937.	14.5	64
33	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
34	Multi-omics enrichment analysis using the GeneTrail2 web service. Bioinformatics, 2016, 32, 1502-1508.	4.1	144
35	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
36	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

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37	Defective autophagy through epg5 mutation results in failure to reduce germ plasm and mitochondria. FASEB Journal, 2015, 29, 4145-4161.	0.5	29
38	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
39	Multiple mechanisms of MYCN dysregulation in Wilms tumour. Oncotarget, 2015, 6, 7232-7243.	1.8	85
40	Abstract A1-59: Multiple mechanisms of MYCN dysregulation in Wilms tumor. , 2015, , .		1
41	Abstract A1-67: Prognostic significance of copy number aberrations in Wilms tumor. , 2015, , .		0
42	The Notch Pathway Inhibits TGFÎ² Signaling in Breast Cancer through HEYL-Mediated Crosstalk. Cancer Research, 2014, 74, 6509-6518.	0.9	27
43	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
44	GATA-dependent regulatory switches establish atrioventricular canal specificity during heart development. Nature Communications, 2014, 5, 3680.	12.8	78
45	Hey bHLH Transcription Factors. Current Topics in Developmental Biology, 2014, 110, 285-315.	2.2	68
46	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
47	Mosaic variegated aneuploidy in mouse BubR1 deficient embryos and pregnancy loss in human. Chromosome Research, 2014, 22, 375-392.	2.2	9
48	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
49	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
50	Physiological Notch Signaling Maintains Bone Homeostasis via RBPjk and Hey Upstream of NFATc1. PLoS Genetics, 2012, 8, e1002577.	3.5	76
51	Target Gene Analysis by Microarrays and Chromatin Immunoprecipitation Identifies HEY Proteins as Highly Redundant bHLH Repressors. PLoS Genetics, 2012, 8, e1002728.	3.5	66
52	Treatment-independent miRNA signature in blood of wilms tumor patients. BMC Genomics, 2012, 13, 379.	2.8	29
53	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
54	Multicenter study identified molecular bloodâ€born protein signatures for Wilms Tumor. International Journal of Cancer, 2012, 131, 673-682.	5.1	4

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55	Characterization of primary wilms tumor cultures as an in vitro model. Genes Chromosomes and Cancer, 2012, 51, 92-104.	2.8	23
56	Autoantibody Signature Differentiates Wilms Tumor Patients from Neuroblastoma Patients. PLoS ONE, 2011, 6, e28951.	2.5	5
57	Retinoic acid pathway activity in wilms tumors and characterization of biological responses in vitro. Molecular Cancer, 2011, 10, 136.	19.2	21
58	Hey bHLH Factors in Cardiovascular Development. Pediatric Cardiology, 2010, 31, 363-370.	1.3	22
59	Expression patterns of the mouse Spir-2 actin nucleator. Gene Expression Patterns, 2010, 10, 345-350.	0.8	16
60	Subtype-Specific FBXW7 Mutation and MYCN Copy Number Gain in Wilms' Tumor. Clinical Cancer Research, 2010, 16, 2036-2045.	7.0	69
61	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
62	Loss of Heterozygosity at 2q37 in Sporadic Wilms' Tumor: Putative Role for miR-562. Clinical Cancer Research, 2009, 15, 5985-5992.	7.0	56
63	Novel features of boundary cap cells revealed by the analysis of newly identified molecular markers. Glia, 2009, 57, 1450-1457.	4.9	55
64	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
65	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
66	Dll1 and Dll4: similar, but not the same. Blood, 2009, 113, 5375-5376.	1.4	6
67	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
68	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
69	Integrated Regulation of Toll-like Receptor Responses by Notch and Interferon-Î³ Pathways. Immunity, 2008, 29, 691-703.	14.3	235
70	Identification of the human homolog of the imprinted mouse Air non-coding RNA. Genomics, 2008, 92, 464-473.	2.9	52
71	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
72	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

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73	The rodent Four-jointed ortholog Fjx1 regulates dendrite extension. Developmental Biology, 2007, 312, 461-470.	2.0	34
74	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
75	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
76	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
77	Target genes of the WNT/Î²-catenin pathway in Wilms tumors. Genes Chromosomes and Cancer, 2006, 45, 565-574.	2.8	82
78	Expression profiling of Wilms tumors reveals new candidate genes for different clinical parameters. International Journal of Cancer, 2006, 118, 1954-1962.	5.1	85
79	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
80	Developmental patterning of the cardiac atrioventricular canal by Notch and Hairy-related transcription factors. Development (Cambridge), 2006, 133, 4381-4390.	2.5	147
81	Nierentumoren. , 2006, , 847-864.		7
82	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
83	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
84	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
85	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
86	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
87	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
88	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
89	Chibby, a novel antagonist of the Wnt pathway, is not involved in Wilms tumor development. Cancer Letters, 2005, 220, 115-120.	7.2	13
90	The Notch target genes Hey1 and Hey2 are required for embryonic vascular development. Genes and Development, 2004, 18, 901-911.	5.9	576

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91	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
92	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
93	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
94	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
95	Characterization of hey bHLH genes in teleost fish. Development Genes and Evolution, 2003, 213, 541-553.	0.9	35
96	Hey Genes in Cardiovascular Development. Trends in Cardiovascular Medicine, 2003, 13, 221-226.	4.9	58
97	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
98	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
99	Developmental Expression and Biochemical Characterization of Emu Family Members. Developmental Biology, 2002, 249, 204-218.	2.0	45
100	Mouse gridlock. Current Biology, 2002, 12, 1601-1604.	3.9	142
101	Placental Î±2-adrenoceptors control vascular development at the interface between mother and embryo. Nature Genetics, 2002, 31, 311-315.	21.4	65
102	Gain of 1q Is Associated with Adverse Outcome in Favorable Histology Wilmsâ€™ Tumors. American Journal of Pathology, 2001, 158, 393-398.	3.8	127
103	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
104	Molecular analysis of E-cadherin and cadherin-11 in Wilms' tumours. , 2000, 191, 162-169.		20
105	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
106	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
107	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
108	Analysis of HeyL expression in wild-type and Notch pathway mutant mouse embryos. Mechanisms of Development, 2000, 98, 175-178.	1.7	95

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109	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
110	Screen for genes regulated during early kidney morphogenesis. Genesis, 1999, 24, 273-283.	2.1	20
111	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
112	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
113	Analysis of WT1 target gene expression in stably transfected cell lines. Oncogene, 1998, 17, 1287-1294.	5.9	31
114	Allele loss in Wilms tumors of chromosome arms 11q, 16q, and 22q correlates with clinicopathological parameters. , 1998, 22, 287-294.		74
115	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
116	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
117	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
118	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
119	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
120	CpG island clones for Chromosome 11p?a resource for mapping and gene identification. Mammalian Genome, 1995, 6, 421-425.	2.2	4
121	Isolation and characterization of a cosmid contig for the GCPS gene region. Human Genetics, 1995, 95, 82-8.	3.8	12
122	Identification of Optimized Target Sequences for the GLI3 Zinc Finger Protein. DNA and Cell Biology, 1995, 14, 629-634.	1.9	39
123	An Integrated YAC Clone Contig for the WAGR Region on Human Chromosome 11p13â€“p14.1. Genomics, 1995, 30, 37-45.	2.9	5
124	cDNA Sequence, Genomic Organization, and Evolutionary Conservation of a Novel Gene from the WAGR Region. Genomics, 1995, 29, 526-532.	2.9	16
125	A WAGR region gene between PAX-6 and FSHB expressed in fetal brain. Human Genetics, 1994, 94, 658-64.	3.8	19
126	Confirmation of the localization of the human recombination activating gene 1 (RAG1) to chromosome 11p13. Human Genetics, 1994, 93, 215-7.	3.8	4

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127	Isolation of a Yeast Artificial Chromosome Contig Spanning the Greig Cephalopolysyndactyly Syndrome (GCPS) Gene Region. Genomics, 1994, 22, 563-568.	2.9	17
128	An Ordered NotI Fragment Map of Human Chromosome Band 11p15. Genomics, 1994, 23, 211-222.	2.9	21
129	Pericentric intrachromosomal insertion responsible for recurrence of del(11)(p13p14) in a family. Genes Chromosomes and Cancer, 1993, 7, 57-62.	2.8	12
130	Homozygous inactivation ofWTI in a Wilms' tumor associated with the WAGR syndrome. Genes Chromosomes and Cancer, 1993, 7, 131-136.	2.8	28
131	Distinct molecular origins for Denys-Drash and Frasier syndromes. Human Genetics, 1993, 91, 285-6.	3.8	34
132	Sequence of the WT1 Upstream Region Including the Wit-1 Gene. Genomics, 1993, 17, 499-501.	2.9	20
133	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
134	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
135	The genomic organization and expression of the WT1 gene. Genomics, 1992, 12, 807-813.	2.9	125
136	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
137	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
138	A somatic cell hybrid panel and DNA probes for physical mapping of human chromosome 7p. Genomics, 1991, 11, 737-743.	2.9	18
139	GLI3 zinc-finger gene interrupted by translocations in Greig syndrome families. Nature, 1991, 352, 539-540.	27.8	553
140	Homozygous deletion in Wilms tumours of a zinc-finger gene identified by chromosome jumping. Nature, 1990, 343, 774-778.	27.8	1,279
141	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
142	A physical map around the WAGR complex on the short arm of chromosome 11. Genomics, 1989, 5, 43-55.	2.9	60
143	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
144	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