Wendy A Bickmore

List of Publications by Year
in descending order

180 papers	22,040 citations	9234 74 h-index	9839 141 g-index
237 all docs	237 docs citations	237 times ranked	19053 citing authors

#	Article	IF	Citations
1	The sight of transcription. Nature Cell Biology, 2022, 24, 284-285.	4.6	0
2	TADs do not stay in the loop. Molecular Cell, 2022, 82, 2188-2189.	4.5	0
3	From bedside to bench: regulation of host factors in SARS-CoV-2 infection. Experimental and Molecular Medicine, 2021, 53, 483-494.	3.2	6
4	CorneliaÂde Lange syndrome-associated mutations cause a DNA damage signalling and repair defect. Nature Communications, 2021, 12, 3127.	5.8	18
5	Nuclear organisation and replication timing are coupled through RIF1â€“PP1 interaction. Nature Communications, 2021, 12, 2910.	5.8	29
6	Extensive pleiotropism and allelic heterogeneity mediate metabolic effects of <i>IRX3</i> and <i>IRX5</i>. Science, 2021, 372, 1085-1091.	6.0	66
7	Linking the <i>FTO</i> obesity rs1421085 variant circuitry to cellular, metabolic, and organismal phenotypes in vivo. Science Advances, 2021, 7, .	4.7	19
8	MUC4 is not expressed in cell lines used for live cell imaging. Wellcome Open Research, 2021, 6, 265.	0.9	2
9	Quantitative spatial and temporal assessment of regulatory element activity in zebrafish. ELife, 2021, 10, .	2.8	14
10	Fine-mapping and cell-specific enrichment at corneal resistance factor loci prioritize candidate causal regulatory variants. Communications Biology, 2020, 3, 762.	2.0	6
11	Bivalent promoter hypermethylation in cancer is linked to the H327me3/H3K4me3 ratio in embryonic stem cells. BMC Biology, 2020, 18, 25.	1.7	35
12	Recent advances in the spatial organization of the mammalian genome. Journal of Biosciences, 2020, 45, 1.	0.5	12
13	<i>Coolpup.py:</i> versatile pile-up analysis of Hi-C data. Bioinformatics, 2020, 36, 2980-2985.	1.8	111
14	A central role for canonical PRC1 in shaping the 3D nuclear landscape. Genes and Development, 2020, 34, 931-949.	2.7	100
15	Developmentally regulated <i>Shh</i> expression is robust to TAD perturbations. Development (Cambridge), 2019, 146, .	1.2	111
16	Chromatin topology, condensates and gene regulation: shifting paradigms or just a phase?. Development (Cambridge), 2019, 146, .	1.2	93
17	DNA Methylation Directs Polycomb-Dependent 3D Genome Re-organization in Naive Pluripotency. Cell Reports, 2019, 29, 1974-1985.e6.	2.9	76
18	Decreased Enhancer-Promoter Proximity Accompanying Enhancer Activation. Molecular Cell, 2019, 76, 473-484.e7.	4.5	223

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19	EvoChromo: towards a synthesis of chromatin biology and evolution. Development (Cambridge), 2019, 146, .	1.2	16
20	Editorial overview: Genome architecture and expression. Current Opinion in Genetics and Development, 2019, 55, iii-iv.	1.5	4
21	Nuclear pore density controls heterochromatin reorganization during senescence. Genes and Development, 2019, 33, 144-149.	2.7	73
22	Patterns in the genome. Heredity, 2019, 123, 50-57.	1.2	7
23	BRD4 interacts with NIPBL and BRD4 is mutated in a Cornelia de Langeâ€"like syndrome. Nature Genetics, 2018, 50, 329-332.	9.4	96
24	PRC1 Fine-tunes Gene Repression and Activation to Safeguard Skin Development and Stem Cell Specification. Cell Stem Cell, 2018, 22, 726-739.e7.	5.2	106
25	Challenges and guidelines toward 4D nucleome data and model standards. Nature Genetics, 2018, 50, 1352-1358.	9.4	47
26	Repo-Man/PP1 regulates heterochromatin formation in interphase. Nature Communications, 2017, 8, 14048.	5.8	46
27	Expression of progerin does not result in an increased mutation rate. Chromosome Research, 2017, 25, 227-239.	1.0	5
28	A mechanism of cohesinâ€dependent loop extrusion organizes zygotic genome architecture. EMBO Journal, 2017, 36, 3600-3618.	3.5	291
29	Glucocorticoid Receptor Binding Induces Rapid and Prolonged Large-Scale Chromatin Decompaction at Multiple Target Loci. Cell Reports, 2017, 21, 3022-3031.	2.9	43
30	Psip1/p52 regulates posterior Hoxa genes through activation of lncRNA Hottip. PLoS Genetics, 2017, 13, e1006677.	1.5	30
31	Bidirectional transcription initiation marks accessible chromatin and is not specific to enhancers. Genome Biology, 2017, 18, 242.	3.8	52
32	Histone H3 globular domain acetylation identifies a new class of enhancers. Nature Genetics, 2016, 48, 681-686.	9.4	184
33	Condensin II mutation causes T-cell lymphoma through tissue-specific genome instability. Genes and Development, 2016, 30, 2173-2186.	2.7	41
34	<i>Shh</i> and ZRS enhancer co-localisation is specific to the zone of polarizing activity. Development (Cambridge), 2016, 143, 2994-3001.	1.2	107
35	Polycomb-mediated chromatin compaction weathers the STORM. Genome Biology, 2016, 17, 35.	3.8	2
36	Enhancer Turnover Is Associated with a Divergent Transcriptional Response to Glucocorticoid in Mouse and Human Macrophages. Journal of Immunology, 2016, 196, 813-822.	0.4	89

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37	SBE6: a novel long-range enhancer involved in driving sonic hedgehog expression in neural progenitor cells. Open Biology, 2016, 6, 160197.	1.5	17
38	A Hox-Embedded Long Noncoding RNA: Is It All Hot Air?. PLoS Genetics, 2016, 12, e1006485.	1.5	38
39	Polycomb enables primitive endoderm lineage priming in embryonic stem cells. ELife, 2016, 5, .	2.8	28
40	Regulatory Domains and Their Mechanisms. Cold Spring Harbor Symposia on Quantitative Biology, 2015, 80, 45-51.	2.0	29
41	PRC2-independent chromatin compaction and transcriptional repression in cancer. Oncogene, 2015, 34, 741-751.	2.6	10
42	The frequent evolutionary birth and death of functional promoters in mouse and human. Genome Research, 2015, 25, 1546-1557.	2.4	55
43	Chromatin at the nuclear periphery and the regulation of genome functions. Histochemistry and Cell Biology, 2015, 144, 111-122.	0.8	69
44	A TAD Closer to Understanding Dosage Compensation. Developmental Cell, 2015, 33, 498-499.	3.1	2
45	Divergent transcriptional activation by glucocorticoids in mouse and human macrophages. Lancet, The, 2015, 385, S54.	6.3	4
46	The E3 ubiquitin ligase activity of RING1B is not essential for early mouse development. Genes and Development, 2015, 29, 1897-1902.	2.7	142
47	An Overview of Genome Organization and How We Got There: from FISH to Hi-C. Microbiology and Molecular Biology Reviews, 2015, 79, 347-372.	2.9	190
48	Estrogen-induced chromatin decondensation and nuclear re-organization linked to regional epigenetic regulation in breast cancer. Genome Biology, 2015, 16, 145.	3.8	49
49	The Hierarchy of Transcriptional Activation: From Enhancer to Promoter. Trends in Genetics, 2015, 31, 696-708.	2.9	127
50	Reed-Sternberg Cells Form by Abscission Failure in the Presence of Functional Aurora B Kinase. PLoS ONE, 2015, 10, e0124629.	1.1	11
51	Chromatin decondensation is sufficient to alter nuclear organization in embryonic stem cells. Science, 2014, 346, 1238-1242.	6.0	267
52	Psip1/Ledgf p75 restrains<i>Hox</i>gene expression by recruiting both trithorax and polycomb group proteins. Nucleic Acids Research, 2014, 42, 9021-9032.	6.5	26
53	Spatial genome organization: contrasting views from chromosome conformation capture and fluorescence in situ hybridization. Genes and Development, 2014, 28, 2778-2791.	2.7	230
54	Redistribution of H3K27me3 upon DNA hypomethylation results in de-repression of Polycomb target genes. Genome Biology, 2013, 14, R25.	13.9	200

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55	Specific nuclear envelope transmembrane proteins can promote the location of chromosomes to and from the nuclear periphery. Genome Biology, 2013, 14, R14.	13.9	116
56	The Spatial Organization of the Human Genome. Annual Review of Genomics and Human Genetics, 2013, 14, 67-84.	2.5	358
57	Flashing a Light on the Spatial Organization of Transcription. Science, 2013, 341, 621-622.	6.0	4
58	H4K16 acetylation marks active genes and enhancers of embryonic stem cells, but does not alter chromatin compaction. Genome Research, 2013, 23, 2053-2065.	2.4	158
59	Enhancers: five essential questions. Nature Reviews Genetics, 2013, 14, 288-295.	7.7	455
60	Genome Architecture: Domain Organization of Interphase Chromosomes. Cell, 2013, 152, 1270-1284.	13.5	659
61	Single-Cell Dynamics of Genome-Nuclear Lamina Interactions. Cell, 2013, 153, 178-192.	13.5	609
62	Divergence of Mammalian Higher Order Chromatin Structure Is Associated with Developmental Loci. PLoS Computational Biology, 2013, 9, e1003017.	1.5	36
63	FGF Signalling Regulates Chromatin Organisation during Neural Differentiation via Mechanisms that Can Be Uncoupled from Transcription. PLoS Genetics, 2013, 9, e1003614.	1.5	50
64	Regulation from a distance: long-range control of gene expression in development and disease. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20120372.	1.8	22
65	Regional chromatin decompaction in Cornelia de Lange syndrome associated with NIPBL disruption can be uncoupled from cohesin and CTCF. Human Molecular Genetics, 2013, 22, 4180-4193.	1.4	35
66	Higherâ€order chromatin folding and gene regulation. FASEB Journal, 2013, 27, 456.1.	0.2	0
67	Histone H2A Mono-Ubiquitination Is a Crucial Step to Mediate PRC1-Dependent Repression of Developmental Genes to Maintain ES Cell Identity. PLoS Genetics, 2012, 8, e1002774.	1.5	233
68	Psip1/Ledgf p52 Binds Methylated Histone H3K36 and Splicing Factors and Contributes to the Regulation of Alternative Splicing. PLoS Genetics, 2012, 8, e1002717.	1.5	296
69	Anterior-posterior differences in HoxD chromatin topology in limb development. Development (Cambridge), 2012, 139, 3157-3167.	1.2	62
70	Chromosome organization in the nucleus â€“ charting new territory across the Hi-Cs. Current Opinion in Genetics and Development, 2012, 22, 125-131.	1.5	52
71	ENCODE explained. Nature, 2012, 489, 52-54.	13.7	245
72	PRC1 and PRC2 Are Not Required for Targeting of H2A.Z to Developmental Genes in Embryonic Stem Cells. PLoS ONE, 2012, 7, e34848.	1.1	40

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73	Enhancers: From Developmental Genetics to the Genetics of Common Human Disease. Developmental Cell, 2011, 21, 17-19.	3.1	60
74	A condensed view of chromatin during T cell development. EMBO Journal, 2011, 30, 235-236.	3.5	4
75	Fluorescence in situ hybridization with high-complexity repeat-free oligonucleotide probes generated by massively parallel synthesis. Chromosome Research, 2011, 19, 901-909.	1.0	140
76	A wake-up call to delve deeper into the cell. Development (Cambridge), 2011, 138, 5275-5276.	1.2	0
77	Changes in chromatin structure during processing of wax-embedded tissue sections. Chromosome Research, 2010, 18, 677-688.	1.0	6
78	Stable Morphology, but Dynamic Internal Reorganisation, of Interphase Human Chromosomes in Living Cells. PLoS ONE, 2010, 5, e11560.	1.1	54
79	The effect of translocation-induced nuclear reorganization on gene expression. Genome Research, 2010, 20, 554-564.	2.4	100
80	Bone Marrow Stem Cells Contribute to Alcohol Liver Fibrosis in Humans. Stem Cells and Development, 2010, 19, 1417-1425.	1.1	40
81	Activation of Estrogen-Responsive Genes Does Not Require Their Nuclear Co-Localization. PLoS Genetics, 2010, 6, e1000922.	1.5	64
82	Ring1B Compacts Chromatin Structure and Represses Gene Expression Independent of Histone Ubiquitination. Molecular Cell, 2010, 38, 452-464.	4.5	485
83	Altered states: how gene expression is changed during differentiation. Current Opinion in Genetics and Development, 2010, 20, 467-469.	1.5	6
84	KRAB zinc-finger proteins localise to novel KAP1-containing foci that are adjacent to PML nuclear bodies. Journal of Cell Science, 2009, 122, 937-946.	1.2	23
85	Lack of bystander activation shows that localization exterior to chromosome territories is not sufficient to up-regulate gene expression. Genome Research, 2009, 19, 1184-1194.	2.4	60
86	Transcription factories: gene expression in unions?. Nature Reviews Genetics, 2009, 10, 457-466.	7.7	336
87	Transcription and the nuclear periphery: edge of darkness?. Current Opinion in Genetics and Development, 2009, 19, 187-191.	1.5	55
88	Porin new light onto chromatin and nuclear organization. Genome Biology, 2008, 9, 222.	13.9	6
89	Characterization of chromatin texture by contour complexity for cancer cell classification. , 2008, , .		7
90	G9a Histone Methyltransferase Contributes to Imprinting in the Mouse Placenta. Molecular and Cellular Biology, 2008, 28, 1104-1113.	1.1	172

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91	Recruitment to the Nuclear Periphery Can Alter Expression of Genes in Human Cells. PLoS Genetics, 2008, 4, e1000039.	1.5	494
92	Ectopic nuclear reorganisation driven by a<i>Hoxb1</i>transgene transposed into<i>Hoxd</i>. Journal of Cell Science, 2008, 121, 571-577.	1.2	42
93	Chromosome territory reorganization in a human disease with altered DNA methylation. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 16546-16551.	3.3	64
94	Epigenetic disruption of ribosomal RNA genes and nucleolar architecture in DNA methyltransferase 1 (Dnmt1) deficient cells. Nucleic Acids Research, 2007, 35, 2191-2198.	6.5	128
95	DNA methylation affects nuclear organization, histone modifications, and linker histone binding but not chromatin compaction. Journal of Cell Biology, 2007, 177, 401-411.	2.3	107
96	Nuclear reorganisation and chromatin decondensation are conserved, but distinct, mechanisms linked to Hox gene activation. Development (Cambridge), 2007, 134, 909-919.	1.2	182
97	Mutations in TOPORS Cause Autosomal Dominant Retinitis Pigmentosa with Perivascular Retinal Pigment Epithelium Atrophy. American Journal of Human Genetics, 2007, 81, 1098-1103.	2.6	77
98	Role of PSIP1/LEDGF/p75 in Lentiviral Infectivity and Integration Targeting. PLoS ONE, 2007, 2, e1340.	1.1	209
99	Nuclear organization of the genome and the potential for gene regulation. Nature, 2007, 447, 413-417.	13.7	683
100	Chromatin structure and evolution in the human genome. BMC Evolutionary Biology, 2007, 7, 72.	3.2	80
101	The ins and outs of gene regulation and chromosome territory organisation. Current Opinion in Cell Biology, 2007, 19, 311-316.	2.6	125
102	Developmental timing in Dictyostelium is regulated by the Set1 histone methyltransferase. Developmental Biology, 2006, 292, 519-532.	0.9	37
103	Sealed with a X. Nature Cell Biology, 2006, 8, 207-209.	4.6	4
104	Disruption of Ledgf/Psip1 Results in Perinatal Mortality and HomeoticSkeletal Transformations. Molecular and Cellular Biology, 2006, 26, 7201-7210.	1.1	96
105	The relationship between higher-order chromatin structure and transcription. Biochemical Society Symposia, 2006, 73, 59-66.	2.7	11
106	The role of chromatin structure in regulating the expression of clustered genes. Nature Reviews Genetics, 2005, 6, 775-781.	7.7	263
107	The effects of histone deacetylase inhibitors on heterochromatin: implications for anticancer therapy?. EMBO Reports, 2005, 6, 520-524.	2.0	109
108	Does radial nuclear organisation influence DNA damage?. Chromosome Research, 2005, 13, 377-388.	1.0	29

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109	Distinctive nuclear organisation of centromeres and regions involved in pluripotency in human embryonic stem cells. Journal of Cell Science, 2005, 118, 3861-3868.	1.2	147
110	Bone marrow-derived SP cells can contribute to the respiratory tract of mice in vivo. Journal of Cell Science, 2005, 118, 2441-2450.	1.2	79
111	Nuclear re-organisation of the Hoxb complex during mouse embryonic development. Development (Cambridge), 2005, 132, 2215-2223.	1.2	181
112	The SOD1 transgene in the G93A mouse model of amyotrophic lateral sclerosis lies on distal mouse chromosome 12. Amyotrophic Lateral Sclerosis and Other Motor Neuron Disorders, 2005, 6, 111-114.	2.3	19
113	Chromatin decondensation and nuclear reorganization of the HoxB locus upon induction of transcription. Genes and Development, 2004, 18, 1119-1130.	2.7	562
114	The Radial Positioning of Chromatin Is Not Inherited through Mitosis but Is Established De Novo in Early G1. Current Biology, 2004, 14, 166-172.	1.8	168
115	Does looping and clustering in the nucleus regulate gene expression?. Current Opinion in Cell Biology, 2004, 16, 256-262.	2.6	104
116	Nuclear organization of centromeric domains is not perturbed by inhibition of histone deacetylases. Chromosome Research, 2004, 12, 505-516.	1.0	47
117	Altered protein dynamics of disease-associated lamin A mutants. BMC Cell Biology, 2004, 5, 46.	3.0	46
118	Chromatin Organization in the Mammalian Nucleus. International Review of Cytology, 2004, 242, 283-336.	6.2	125
119	Chromatin Architecture of the Human Genome. Cell, 2004, 118, 555-566.	13.5	452
120	3D3/lyric: a novel transmembrane protein of the endoplasmic reticulum and nuclear envelope, which is also present in the nucleolus. Experimental Cell Research, 2004, 294, 94-105.	1.2	86
121	Do Higher-Order Chromatin Structure and Nuclear Reorganization Play a Role in Regulating Hox Gene Expression during Development?. Cold Spring Harbor Symposia on Quantitative Biology, 2004, 69, 251-258.	2.0	13
122	Formation of facultative heterochromatin in the absence of HP1. EMBO Journal, 2003, 22, 5540-5550.	3.5	102
123	Chromosome Position: Now, Where Was I?. Current Biology, 2003, 13, R357-R359.	1.8	29
124	Human cord blood-derived cells can differentiate into hepatocytes in the mouse liver with no evidence of cellular fusion. Gastroenterology, 2003, 124, 1891-1900.	0.6	303
125	Considering Nuclear Compartmentalization in the Light of Nuclear Dynamics. Cell, 2003, 112, 403-406.	13.5	119
126	Perturbations of chromatin structure in human genetic disease: recent advances. Human Molecular Genetics, 2003, 12, R207-R213.	1.4	51

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127	Spatial organization of active and inactive genes and noncoding DNA within chromosome territories. Journal of Cell Biology, 2002, 157, 579-589.	2.3	207
128	Mammalian PRP4 Kinase Copurifies and Interacts with Components of Both the U5 snRNP and the N-CoR Deacetylase Complexes. Molecular and Cellular Biology, 2002, 22, 5141-5156.	1.1	76
129	Gene density and transcription influence the localization of chromatin outside of chromosome territories detectable by FISH. Journal of Cell Biology, 2002, 159, 753-763.	2.3	264
130	Chromatin Motion Is Constrained by Association with Nuclear Compartments in Human Cells. Current Biology, 2002, 12, 439-445.	1.8	533
131	The plasticity of cell fate and gene expression â€" ewe perspectives. Current Opinion in Cell Biology, 2002, 14, 739-740.	2.6	0
132	Influences of chromosome size, gene density and nuclear position on the frequency of constitutional translocations in the human population. Chromosome Research, 2002, 10, 707-715.	1.0	78
133	Addressing protein localization within the nucleus. EMBO Journal, 2002, 21, 1248-1254.	3.5	62
134	The spatial organization of human chromosomes within the nuclei of normal and emerin-mutant cells. Human Molecular Genetics, 2001, 10, 211-219.	1.4	592
135	Comment on Frank Gannon's article â€˜Searching for discriminationâ€™ in EMBO reports , August 2001. EMBO Reports, 2001, 2, 860-860.	2.0	0
136	Human acrocentric chromosomes with transcriptionally silent nucleolar organizer regions associate with nucleoli. EMBO Journal, 2001, 20, 2867-2877.	3.5	120
137	Dual Y-chromosome Painting and Immunofluorescence Staining of Archival Human Liver Transplant Biopsies. Journal of Histochemistry and Cytochemistry, 2001, 49, 1321-1322.	1.3	18
138	Human diseases with underlying defects in chromatin structure and modification. Human Molecular Genetics, 2001, 10, 2233-2242.	1.4	84
139	Large-scale identification of mammalian proteins localized to nuclear sub-compartments. Human Molecular Genetics, 2001, 10, 1995-2011.	1.4	108
140	Re-modelling of nuclear architecture in quiescent and senescent human fibroblasts. Current Biology, 2000, 10, 149-152.	1.8	291
141	HuCHRAC, a human ISWI chromatin remodelling complex contains hACF1 and two novel histone-fold proteins. EMBO Journal, 2000, 19, 3377-3387.	3.5	196
142	CpG island libraries from human Chromosomes 18 and 22: landmarks for novel genes. Mammalian Genome, 2000, 11, 373-383.	1.0	27
143	Unusual chromosome architecture and behaviour at an HSR. Chromosoma, 2000, 109, 181-189.	1.0	3
144	Pausing for Thought on the Boundaries of Imprinting. Cell, 2000, 102, 705-708.	13.5	25

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145	Differences in the Localization and Morphology of Chromosomes in the Human Nucleus. Journal of Cell Biology, 1999, 145, 1119-1131.	2.3	823
146	Localization of a putative transcriptional regulator (ATRX) at pericentromeric heterochromatin and the short arms of acrocentric chromosomes. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 13983-13988.	3.3	233
147	Fluorescence in situ hybridization analysis of chromosome and chromatin structure. Methods in Enzymology, 1999, 304, 650-662.	0.4	9
148	Putting the genome on the map. Trends in Genetics, 1998, 14, 403-409.	2.9	59
149	The Chromosomal Distribution of CpG Islands in the Mouse: Evidence for Genome Scrambling in the Rodent Lineage. Genomics, 1997, 40, 454-461.	1.3	42
150	The Reticulocalbin Gene Maps to the WAGR Region in Human and to the Small Eye Harwell Deletion in Mouse. Genomics, 1997, 42, 260-267.	1.3	44
151	The Metaphase Chromosome as a Reporter of Nuclear Activity. Experimental Cell Research, 1996, 229, 198-200.	1.2	2
152	Visualizing the Spatial Relationships between Defined DNA Sequences and the Axial Region of Extracted Metaphase Chromosomes. Cell, 1996, 84, 95-104.	13.5	75
153	Imprinting mutation in the Beckwith-Wiedemann syndrome leads to biallelic IGF2 expression through an H19-independent pathway. Human Molecular Genetics, 1996, 5, 2027-2032.	1.4	103
154	Models of DNA Replication Timing in Interphase Nuclei: An Exercise in Inferring Process from State. Biometrics, 1995, 51, 750.	0.8	4
155	Aniridia-associated cytogenetic rearrangements suggest that a position effect may cause the mutant phenotype. Human Molecular Genetics, 1995, 4, 415-422.	1.4	195
156	DNA binding capacity of the WT1 protein is abolished by Denysâ€"Drash syndrome WT1 point mutations. Human Molecular Genetics, 1995, 4, 351-358.	1.4	98
157	A high-resolution integrated physical, cytogenetic, and genetic map of human chromosome 11: distal p13 to proximal p15.1. Genomics, 1995, 25, 447-461.	1.3	58
158	Imprinting mutations in the Beckwithâ€"Wiedemann syndrome suggested by an altered imprinting pattern in the IGF2â€"H19 domain. Human Molecular Genetics, 1995, 4, 2379-2385.	1.4	235
159	The distribution of CpG islands in mammalian chromosomes. Nature Genetics, 1994, 7, 376-382.	9.4	251
160	The Human Serum Amyloid A Protein (SAA) Superfamily Gene Cluster: Mapping to Chromosome 11p15.1 by Physical and Genetic Linkage Analysis. Genomics, 1994, 19, 221-227.	1.3	50
161	Organization of the Region Encompassing the Human Serum Amyloid A (SAA) Gene Family on Chromosome 11p15.1. Genomics, 1994, 23, 492-495.	1.3	32
162	Regional Physical Mapping: Genome Analysis, vol. 5. Edited by K. E. Davies, and S. M. Tilghman. Cold Spring Harbor Laboratory Press. 1993. 140 pages. Cloth. $49.00. ISBN 0 87969 413 0.. Genetical Research, 1994, 64, 78-79.	0.3	0

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163	Chromosomes: A Synthesis. By Robert P. Wagner, Marjory P. Maguire, and Raymond L. Stallings. Wiley-Liss. 1993. 523 pages. Hard cover. Price $89.95. ISBN 0 471 56124 X.. Genetical Research, 1994, 64, 83-83.	0.3	0
164	Genes and genomes: Chromosome bands - flavours to savour. BioEssays, 1993, 15, 349-354.	1.2	178
165	Colocalization of the Human CD59 Gene to 11p13 with the MIC11 Cell Surface Antigen. Genomics, 1993, 17, 129-135.	1.3	34
166	The expression of the Wilms' tumour gene, WT1, in the developing mammalian embryo. Mechanisms of Development, 1993, 40, 85-97.	1.7	530
167	A Y chromosome gene family with RNA-binding protein homology: Candidates for the azoospermia factor AZF controlling human spermatogenesis. Cell, 1993, 75, 1287-1295.	13.5	510
168	Modulation of DNA binding specificity by alternative splicing of the Wilms tumor wt1 gene transcript. Science, 1992, 257, 235-237.	6.0	236
169	[22] Use of restriction endonucleases to detect and isolate genes from mammalian cells. Methods in Enzymology, 1992, 216, 224-244.	0.4	54
170	The candidate Wilms' tumour gene is involved in genitourinary development. Nature, 1990, 346, 194-197.	13.7	814
171	Role for the Wilms tumor gene in genital development?. Proceedings of the National Academy of Sciences of the United States of America, 1990, 87, 5383-5386.	3.3	86
172	Close linkage of the human cytochrome P450IIA and P450IIB gene subfamilies: implications for the assignment of substrate specificity. Nucleic Acids Research, 1989, 17, 2907-2917.	6.5	47
173	Aniridia, Wilms' tumor and human chromosome 11. Ophthalmic Paediatrics and Genetics, 1989, 10, 229-248.	0.4	7
174	Long-range structure of H-ras 1-selected transgenomes. Somatic Cell and Molecular Genetics, 1989, 15, 229-235.	0.7	8
175	Mammalian chromosome banding â€” an expression of genome organization. Trends in Genetics, 1989, 5, 144-148.	2.9	175
176	CpG islands surround a DNA segment located between translocation breakpoints associated with genitourinary dysplasia and aniridia. Genomics, 1989, 5, 685-693.	1.3	23
177	Hitch-hiking from HRAS1 to the WAGR locus with CMGT markers. Nucleic Acids Research, 1988, 16, 51-60.	6.5	41
178	Evolution of homologous sequences on the human X and Y chromosomes, outside of the meiotic pairing segment. Nucleic Acids Research, 1987, 15, 6261-6271.	6.5	41
179	HRAS1-selected chromosome transfer generates markers that colocalize aniridia- and genitourinary dysplasia-associated translocation breakpoints and the Wilms tumor gene within band 11p13.. Proceedings of the National Academy of Sciences of the United States of America, 1987, 84, 5355-5359.	3.3	68
180	MUC4 is not expressed in cell lines used for live cell imaging. Wellcome Open Research, 0, 6, 265.	0.9	2