Ingo Schubert

List of Publications by Year
in descending order

162 papers	11,534 citations	25034 57 h-index	33894 99 g-index
164 all docs	164 docs citations	164 times ranked	8241 citing authors

#	Article	IF	Citations
1	The Ribosomal DNA Loci of the Ancient Monocot Pistia stratiotes L. (Araceae) Contain Different Variants of the 35S and 5S Ribosomal RNA Gene Units. Frontiers in Plant Science, 2022, 13, 819750.	3.6	6
2	Boon and Bane of DNA Double-Strand Breaks. International Journal of Molecular Sciences, 2021, 22, 5171.	4.1	10
3	Return of the Lemnaceae: duckweed as a model plant system in the genomics and postgenomics era. Plant Cell, 2021, 33, 3207-3234.	6.6	111
4	Limitation of current probe design for oligo-cross-FISH, exemplified by chromosome evolution studies in duckweeds. Chromosoma, 2021, 130, 15-25.	2.2	9
5	Comparative analysis of epigenetic inhibitors reveals different degrees of interference with transcriptional gene silencing and induction of DNA damage. Plant Journal, 2020, 102, 68-84.	5.7	22
6	Chromosome-scale genome assembly for the duckweed Spirodela intermedia, integrating cytogenetic maps, PacBio and Oxford Nanopore libraries. Scientific Reports, 2020, 10, 19230.	3.3	23
7	Super-Resolution Microscopy Reveals Diversity of Plant Centromere Architecture. International Journal of Molecular Sciences, 2020, 21, 3488.	4.1	42
8	A taxonomic revision of <i>Lemna</i> sect. <i>Uninerves</i> (Lemnaceae). Taxon, 2020, 69, 56-66.	0.7	46
9	Variation in genome size, cell and nucleus volume, chromosome number and rDNA loci among duckweeds. Scientific Reports, 2019, 9, 3234.	3.3	49
10	Satellite DNA in Vicia faba is characterized by remarkable diversity in its sequence composition, association with centromeres, and replication timing. Scientific Reports, 2018, 8, 5838.	3.3	66
11	What is behind â€œcentromere repositioningâ€?. Chromosoma, 2018, 127, 229-234.	2.2	29
12	Generating a highâ€confidence reference genome map of the Greater Duckweed by integration of cytogenomic, optical mapping, and Oxford Nanopore technologies. Plant Journal, 2018, 96, 670-684.	5.7	64
13	Chromosome identification for the carnivorous plant Genlisea margaretae. Chromosoma, 2017, 126, 389-397.	2.2	7
14	Non-random chromosome arrangement in triploid endosperm nuclei. Chromosoma, 2017, 126, 115-124.	2.2	16
15	Deletionâ€bias in <scp>DNA</scp> doubleâ€strand break repair differentially contributes to plant genome shrinkage. New Phytologist, 2017, 214, 1712-1721.	7.3	34
16	Some past developments and open questions in understanding the biology of nucleus. Nucleus (India), 2017, 60, 247-249.	2.2	2
17	Endogenous sequence patterns predispose the repair modes of <scp>CRISPR</scp>/Cas9â€induced <scp>DNA</scp> doubleâ€stranded breaks in <i>Arabidopsis thaliana</i>. Plant Journal, 2017, 92, 57-67.	5.7	34
18	Reconstruction of chromosome rearrangements between the two most ancestral duckweed species Spirodela polyrhiza and S. intermedia. Chromosoma, 2017, 126, 729-739.	2.2	27

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19	We Have an Inflation of Review Papersâ€"for what Are Reviews Good?. Frontiers in Plant Science, 2016, 7, 88.	3.6	0
20	The mapâ€based genome sequence of <i><scp>S</scp>pirodela polyrhiza</i> aligned with its chromosomes, a reference for karyotype evolution. New Phytologist, 2016, 209, 354-363.	7.3	40
21	Molecular, genetic and evolutionary analysis of a paracentric inversion in <i>Arabidopsis thaliana</i>. Plant Journal, 2016, 88, 159-178.	5.7	81
22	Genome Stability and Evolution: Attempting a Holistic View. Trends in Plant Science, 2016, 21, 749-757.	8.8	125
23	Stable gene replacement in barley by targeted double-strand break induction. Journal of Experimental Botany, 2016, 67, 1433-1445.	4.8	49
24	Centromere and telomere sequence alterations reflect the rapid genome evolution within the carnivorous plant genus <i>Genlisea</i>. Plant Journal, 2015, 84, 1087-1099.	5.7	41
25	Recurrent sequence exchange between homeologous grass chromosomes. Plant Journal, 2015, 84, 747-759.	5.7	5
26	Comparative Genome Analysis Reveals Divergent Genome Size Evolution in a Carnivorous Plant Genus. Plant Genome, 2015, 8, eplantgenome2015.04.0021.	2.8	45
27	Metatranscriptome analysis reveals host-microbiome interactions in traps of carnivorous Genlisea species. Frontiers in Microbiology, 2015, 6, 526.	3.5	23
28	Chromatin organization and cytological features of carnivorous Genlisea species with large genome size differences. Frontiers in Plant Science, 2015, 6, 613.	3.6	5
29	Chromatin associations in Arabidopsis interphase nuclei. Frontiers in Genetics, 2014, 5, 389.	2.3	25
30	Repair of Site-Specific DNA Double-Strand Breaks in Barley Occurs via Diverse Pathways Primarily Involving the Sister Chromatid. Plant Cell, 2014, 26, 2156-2167.	6.6	55
31	Loading of the centromeric histone H3 variant during meiosisâ€"how does it differ from mitosis?. Chromosoma, 2014, 123, 491-497.	2.2	29
32	De novo generation of plant centromeres at tandem repeats. Chromosoma, 2013, 122, 233-241.	2.2	18
33	<i>Arabidopsis</i> KINETOCHORE NULL2 Is an Upstream Component for Centromeric Histone H3 Variant cenH3 Deposition at Centromeres. Plant Cell, 2013, 25, 3389-3404.	6.6	80
34	Structureâ€function relationships during transgenic telomerase expression in <i>Arabidopsis</i>. Physiologia Plantarum, 2013, 149, 114-126.	5.2	22
35	Mechanisms of Chromosome Rearrangements. , 2013, , 137-147.		36
36	Patterns of nucleotide asymmetries in plant and animal genomes. BioSystems, 2013, 111, 181-189.	2.0	17

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37	The Arabidopsis CAP-D proteins are required for correct chromatin organisation, growth and fertility. Chromosoma, 2013, 122, 517-533.	2.2	42
38	Engineered plant minichromosomes. International Journal of Developmental Biology, 2013, 57, 651-657.	0.6	5
39	Chromosomal Distribution and Functional Interpretation of Epigenetic Histone Marks in Plants. , 2012, , 231-253.		19
40	Telomere-mediated truncation of barley chromosomes. Chromosoma, 2012, 121, 181-190.	2.2	41
41	Organization and dynamics of plant interphase chromosomes. Trends in Plant Science, 2011, 16, 273-281.	8.8	77
42	No Evidence for â€œBreak-Induced Replicationâ€•in a Higher Plant â€“ But Break-Induced Conversion May Occur. Frontiers in Plant Science, 2011, 2, 8.	3.6	11
43	Between Genes and Genomes â€“ Future Challenges for Cytogenetics. Frontiers in Genetics, 2011, 2, 30.	2.3	1
44	'Sex and crime' in evolution - why sexuality was so successful. Genes and Genetic Systems, 2011, 86, 1-6.	0.7	6
45	Induction of telomereâ€mediated chromosomal truncation and stability of truncated chromosomes in <i>Arabidopsis thaliana</i>. Plant Journal, 2011, 68, 28-39.	5.7	44
46	Knockdown of CENH3 in Arabidopsis reduces mitotic divisions and causes sterility by disturbed meiotic chromosome segregation. Plant Journal, 2011, 68, 40-50.	5.7	94
47	The E2F transcription factor family regulates <i>CENH3</i> expression in <i>Arabidopsis thaliana</i>. Plant Journal, 2011, 68, 646-656.	5.7	40
48	Interpretation of karyotype evolution should consider chromosome structural constraints. Trends in Genetics, 2011, 27, 207-216.	6.7	252
49	Recognition of A. thaliana centromeres by heterologous CENH3 requires high similarity to the endogenous protein. Plant Molecular Biology, 2011, 75, 253-261.	3.9	36
50	Pairing of lacO tandem repeats in Arabidopsis thaliana nuclei requires the presence of hypermethylated, large arrays at two chromosomal positions, but does not depend on H3-lysine-9-dimethylation. Chromosoma, 2011, 120, 609-619.	2.2	17
51	Deposition, turnover, and release of CENH3 at Arabidopsis centromeres. Chromosoma, 2011, 120, 633-640.	2.2	32
52	Synteny between Brachypodium distachyon and Hordeum vulgare as revealed by FISH. Chromosome Research, 2010, 18, 841-850.	2.2	50
53	Dynamics of a novel centromeric histone variant CenH3 reveals the evolutionary ancestral timing of centromere biogenesis. Nucleic Acids Research, 2010, 38, 7526-7537.	14.5	52
54	The MCM-Binding Protein ETG1 Aids Sister Chromatid Cohesion Required for Postreplicative Homologous Recombination Repair. PLoS Genetics, 2010, 6, e1000817.	3.5	58

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55	The STRUCTURAL MAINTENANCE OF CHROMOSOMES 5/6 Complex Promotes Sister Chromatid Alignment and Homologous Recombination after DNA Damage in<i>Arabidopsis thaliana</i>Â Â. Plant Cell, 2009, 21, 2688-2699.	6.6	98
56	Cohesin gene defects may impair sister chromatid alignment and genome stability in Arabidopsis thaliana. Chromosoma, 2009, 118, 591-605.	2.2	45
57	The chromosomal distribution of histone methylation marks in gymnosperms differs from that of angiosperms. Chromosome Research, 2008, 16, 891-898.	2.2	41
58	Arabidopsis sister chromatids often show complete alignment or separation along a 1.2-Mb euchromatic region but no cohesion â€œhot spotsâ€. Chromosoma, 2008, 117, 261-266.	2.2	13
59	Size and number of tandem repeat arrays can determine somatic homologous pairing of transgene loci mediated by epigenetic modifications in Arabidopsis thaliana nuclei. Chromosoma, 2008, 117, 267-276.	2.2	27
60	Hypomethylation and hypermethylation of the tandem repetitive 5SÂrRNA genes in Arabidopsis. Plant Journal, 2008, 54, 299-309.	5.7	15
61	Engineered Plant Minichromosomes: A Bottom-Up Success?. Plant Cell, 2008, 20, 8-10.	6.6	31
62	The Arabidopsis checkpoint protein Bub3.1 is essential for gametophyte development. Frontiers in Bioscience - Landmark, 2008, Volume, 5202.	3.0	19
63	The Triploid Endosperm Genome of Arabidopsis Adopts a Peculiar, Parental-Dosage-Dependent Chromatin Organization. Plant Cell, 2007, 19, 1782-1794.	6.6	85
64	Engineered Plant Minichromosomes: A Resurrection of B Chromosomes?. Plant Cell, 2007, 19, 2323-2327.	6.6	27
65	Interphase Chromosome Arrangement in <i>Arabidopsis thaliana</i> Is Similar in Differentiated and Meristematic Tissues and Shows a Transient Mirror Symmetry After Nuclear Division. Genetics, 2007, 176, 853-863.	2.9	67
66	Regulation of Arabidopsis thaliana 5S rRNA Genes. Plant and Cell Physiology, 2007, 48, 745-752.	3.1	34
67	The Catalytically Active Tyrosine Residues of Both SPO11-1 and SPO11-2 Are Required for Meiotic Double-Strand Break Induction in <i>Arabidopsis</i>. Plant Cell, 2007, 19, 3090-3099.	6.6	125
68	Impact of environmental and endogenous factors on endopolyploidization in angiosperms. Environmental and Experimental Botany, 2007, 60, 404-411.	4.2	21
69	Chromosome evolution. Current Opinion in Plant Biology, 2007, 10, 109-115.	7.1	181
70	Arabidopsis CBF5 interacts with the H/ACA snoRNP assembly factor NAF1. Plant Molecular Biology, 2007, 65, 615-626.	3.9	33
71	The cytogenetics and genomics of crop plants. Chromosome Research, 2007, 15, 1-2.	2.2	2
72	Random homologous pairing and incomplete sister chromatid alignment are common in angiosperm interphase nuclei. Molecular Genetics and Genomics, 2007, 278, 167-176.	2.1	24

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73	Loading time of the centromeric histone H3 variant differs between plants and animals. Chromosoma, 2007, 116, 507-510.	2.2	38
74	Mechanisms of chromosome number reduction in<i>Arabidopsis thaliana</i>and related Brassicaceae species. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 5224-5229.	7.1	360
75	Cytogenetic Analyses of <i>Arabidopsis</i>. , 2006, 323, 173-186.		52
76	Chromosomal histone modification patterns â€“ from conservation to diversity. Trends in Plant Science, 2006, 11, 199-208.	8.8	338
77	Direct labelling of BAC-DNA by rolling-circle amplification. Plant Journal, 2006, 45, 857-862.	5.7	22
78	Chromosome arrangement and nuclear architecture but not centromeric sequences are conserved between <i>Arabidopsis thaliana</i> and <i>Arabidopsis lyrata</i>. Plant Journal, 2006, 48, 771-783.	5.7	61
79	MOM1 mediates DNAâ€methylationâ€independent silencing of repetitive sequences in Arabidopsis. EMBO Reports, 2006, 7, 1273-1278.	4.5	102
80	Sister Chromatids Are Often Incompletely Aligned in Meristematic and Endopolyploid Interphase Nuclei of <i>Arabidopsis thaliana</i>. Genetics, 2006, 172, 467-475.	2.9	58
81	Loading of <i>Arabidopsis</i> Centromeric Histone CENH3 Occurs Mainly during G2 and Requires the Presence of the Histone Fold Domain. Plant Cell, 2006, 18, 2443-2451.	6.6	181
82	DNA hypomethylation reduces homologous pairing of inserted tandem repeat arrays in somatic nuclei of Arabidopsis thaliana. Plant Journal, 2005, 44, 531-540.	5.7	27
83	Chromosome triplication found across the tribe <i>Brassiceae</i>. Genome Research, 2005, 15, 516-525.	5.5	598
84	The Inheritance of Apomixis in Poa pratensis Confirms a Five Locus Model with Differences in Gene Expressivity and Penetrance. Plant Cell, 2005, 17, 13-24.	6.6	88
85	The Arabidopsis HETEROCHROMATIN PROTEIN1 Homolog (TERMINAL FLOWER2) Silences Genes Within the Euchromatic Region but not Genes Positioned in Heterochromatin. Plant and Cell Physiology, 2005, 46, 1747-1756.	3.1	98
86	Tandem repetitive transgenes and fluorescent chromatin tags alter local interphase chromosome arrangement in Arabidopsis thaliana. Journal of Cell Science, 2005, 118, 3751-3758.	2.0	59
87	Chromosomal localization of rDNA in the Brassicaceae. Genome, 2005, 48, 341-346.	2.0	42
88	Genomic in situ hybridization in plants with small genomes is feasible and elucidates the chromosomal parentage in interspecific <i>Arabidopsis</i> hybrids. Genome, 2004, 47, 954-960.	2.0	31
89	Dual histone H3 methylation marks at lysines 9 and 27 required for interaction with CHROMOMETHYLASE3. EMBO Journal, 2004, 23, 4146-4155.	7.8	359
90	A Specific Î±-Tubulin is Associated with the Initiation of Parthenogenesis in â€˜Salmonâ€™ Wheat Lines. Hereditas, 2004, 126, 219-224.	1.4	9

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91	Dimethylation of histone H3 lysine 9 is a critical mark for DNA methylation and gene silencing in Arabidopsis thaliana. Chromosoma, 2004, 112, 308-315.	2.2	289
92	Chromosome territory arrangement and homologous pairing in nuclei of Arabidopsis thaliana are predominantly random except for NOR-bearing chromosomes. Chromosoma, 2004, 113, 258-269.	2.2	206
93	Chromosome Structure and Evolution. , 2004, , 273-277.		1
94	Comparative analysis of the functional genome architecture of animal and plant cell nuclei. Chromosome Research, 2003, 11, 471-484.	2.2	30
95	Recent progress in chromosome painting of Arabidopsis and related species. Chromosome Research, 2003, 11, 195-204.	2.2	92
96	Coevolution of apomixis and genome size within the genus Hypericum. Sexual Plant Reproduction, 2003, 16, 51-58.	2.2	70
97	DNA and proteins of plant centromeres. Current Opinion in Plant Biology, 2003, 6, 554-560.	7.1	99
98	Histone modifications in <i>Arabidopsis</i>â€" high methylation of H3 lysine 9 is dispensable for constitutive heterochromatin. Plant Journal, 2003, 33, 471-480.	5.7	144
99	Methylation of histone H3 in euchromatin of plant chromosomes depends on basic nuclear DNA content. Plant Journal, 2003, 33, 967-973.	5.7	186
100	The transcriptional response ofArabidopsisto genotoxic stress - a high-density colony array study (HDCA). Plant Journal, 2003, 35, 771-786.	5.7	91
101	Changes in 5S rDNA Chromatin Organization and Transcription during Heterochromatin Establishment in Arabidopsis. Plant Cell, 2003, 15, 2929-2939.	6.6	120
102	Interphase chromosomes in <i>Arabidopsis</i> are organized as well defined chromocenters from which euchromatin loops emanate. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 14584-14589.	7.1	429
103	Science and politics: Hans Stubbe and the Institute of Plant Genetics and Crop Plant Research at Gatersleben. Trends in Plant Science, 2002, 7, 418-420.	8.8	0
104	A comparison of N-methyl-N-nitrosourea-induced chromatid aberrations and micronuclei in barley meristems using FISH techniques. Mutation Research - Genetic Toxicology and Environmental Mutagenesis, 2002, 517, 47-51.	1.7	27
105	An Archaebacterial Topoisomerase Homolog Not Present in Other Eukaryotes Is Indispensable for Cell Proliferation of Plants. Current Biology, 2002, 12, 1787-1791.	3.9	113
106	Transient CENP-E-like kinetochore proteins in plants. Chromosome Research, 2002, 10, 561-570.	2.2	13
107	DNA methylation controls histone H3 lysine 9 methylation and heterochromatin assembly in Arabidopsis. EMBO Journal, 2002, 21, 6549-6559.	7.8	439
108	DNA damage and repair in Arabidopsis thaliana as measured by the comet assay after treatment with different classes of genotoxins. Mutation Research - Genetic Toxicology and Environmental Mutagenesis, 2001, 493, 87-93.	1.7	142

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109	The comet assay detects adaptation to MNU-induced DNA damage in barley. Mutation Research - Genetic Toxicology and Environmental Mutagenesis, 2001, 493, 95-100.	1.7	38
110	Chromatin organization and its relation to replication and histone acetylation during the cell cycle in barley. Chromosoma, 2001, 110, 83-92.	2.2	113
111	Reconstruction of reproductive diversity in Hypericum perforatum L. opens novel strategies to manage apomixis. Plant Journal, 2001, 26, 275-282.	5.7	99
112	Chromosome painting in plants. Cytotechnology, 2001, 23, 57-69.	0.7	123
113	Chromosome painting in plants. , 2001, , 57-69.		9
114	Chromosome painting in <i>Arabidopsis thaliana</i>. Plant Journal, 2001, 28, 689-697.	5.7	156
115	Detection of specific DNA lesions by a combination of comet assay and FISH in plants. , 2000, 35, 132-138.		37
116	Adaptation to alkylation damage in DNA measured by the comet assay. Environmental and Molecular Mutagenesis, 2000, 36, 146-150.	2.2	74
117	An efficient screen for reproductive pathways using mature seeds of monocots and dicots. Plant Journal, 2000, 21, 97-108.	5.7	330
118	Opportunism knocks?. Nature, 2000, 404, 120-120.	27.8	244
119	People must be judged in the context of their time. Nature, 2000, 404, 330-330.	27.8	3
120	Localization of 5S RNA genes on tobacco chromosomes. Chromosome Research, 2000, 8, 85-87.	2.2	12
121	Evolutionary conservation of kinetochore protein sequences in plants. Chromosoma, 2000, 109, 482-489.	2.2	33
122	Histone H4 Acetylation of Euchromatin and Heterochromatin Is Cell Cycle Dependent and Correlated with Replication Rather Than with Transcription. Plant Cell, 2000, 12, 2087.	6.6	1
123	Histone H4 Acetylation of Euchromatin and Heterochromatin Is Cell Cycle Dependent and Correlated with Replication Rather Than with Transcription. Plant Cell, 2000, 12, 2087-2100.	6.6	163
124	DNA content, rDNA loci, and DAPI bands reflect the phylogenetic distance between <i>Lathyrus </i>species. Genome, 2000, 43, 1027-1032.	2.0	5
125	The cell cycle dependent phosphorylation of histone H3 is correlated with the condensation of plant mitotic chromosomes. Plant Journal, 1999, 18, 675-679.	5.7	116
126	Molecular-cytogenetic characterization of the Vicia faba genome--heterochromatin differentiation, replication patterns and sequence localization. Chromosome Research, 1998, 6, 219-230.	2.2	63

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127	Terminal heterochromatin and alternative telomeric sequences in Allium cepa. , 1998, 6, 315-321.		91
128	Late-replicating satellites: something for all centromeres?. Trends in Genetics, 1998, 14, 385-386.	6.7	25
129	Assignment of linkage groups to pea chromosomes after karyotyping and gene mapping by fluorescent in situ hybridization. Chromosoma, 1998, 107, 272-276.	2.2	61
130	An efficient screening for terminal deletions and translocations of barley chromosomes added to common wheat. Plant Journal, 1998, 14, 489-495.	5.7	78
131	A<i>TY3/GYPSY</i>retrotransposonâ€‘like sequence localizes to the centromeric regions of cereal chromosomes. Plant Journal, 1998, 16, 721-728.	5.7	231
132	Karyotype analysis of Helianthus annuus using Giemsa banding and fluorescence in situ hybridization. Chromosome Research, 1997, 5, 451-456.	2.2	27
133	Histone H4 acetylation in plant heterochromatin is altered during the cell cycle. Chromosoma, 1997, 106, 193-197.	2.2	40
134	Formation and repair ofO6-methylguanine in recombination hot spots of plant chromosomes. Environmental and Molecular Mutagenesis, 1997, 29, 394-399.	2.2	13
135	Removal ofO6-methylguanine from plant DNA in vivo is accelerated under conditions of clastogenic adaptation. , 1997, 29, 400-405.		15
136	Chromosome ?painting? in plants ? a feasible technique?. Chromosoma, 1996, 104, 315-320.	2.2	72
137	Differential immunostaining of plant chromosomes by antibodies recognizing acetylated histone H4 variants. Chromosome Research, 1996, 4, 191-194.	2.2	42
138	How do Alliaceae stabilize their chromosome ends in the absence of TTTAGGG sequences?. Chromosome Research, 1996, 4, 207-213.	2.2	144
139	TheTy1-copia group retrotransposons ofAllium cepa are distributed throughout the chromosomes but are enriched in the terminal heterochromatin. Chromosome Research, 1996, 4, 357-364.	2.2	124
140	In situ localization of yeast artificial chromosome sequences on tomato and potato metaphase chromosomes. Chromosome Research, 1996, 4, 277-281.	2.2	25
141	Aneuploids as a key for new molecular cloning strategies: development of DNA markers by microdissection using Triticum aestivum-Aegilops markgrafii chromosome addition line B. Euphytica, 1996, 89, 41-47.	1.2	17
142	Chromosome ?painting? in plants ? a feasible technique?. Chromosoma, 1996, 104, 315-320.	2.2	58
143	Primed in situ labelling facilitates flow sorting of similar sized chromosomes. Plant Journal, 1995, 7, 1039-1044.	5.7	44
144	The nodule-specific VfENOD-GRP3 gene encoding a glycine-rich early nodulin is located on chromosome I of Vicia faba L. and is predominantly expressed in the interzone II-III of root nodules. Plant Molecular Biology, 1995, 28, 405-421.	3.9	29

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145	Alteration of basic chromosome number by fusionâ€“fission cycles. Genome, 1995, 38, 1289-1292.	2.0	28
146	Utility of DNA amplified by degenerate oligonucleotide-primed PCR (DOP-PCR) from the total genome and defined chromosomal regions of field bean. Molecular Genetics and Genomics, 1994, 243, 173-177.	2.4	46
147	Plant Chromosome Analysis and Sorting by Flow Cytometry. Critical Reviews in Plant Sciences, 1994, 13, 275-309.	5.7	81
148	Localization of seed protein genes on flow-sorted field bean chromosomes. Chromosome Research, 1993, 1, 107-115.	2.2	76
149	Localization of vicilin genes via polymerase chain reaction on microisolated field bean chromosomes. Plant Journal, 1993, 3, 883-886.	5.7	28
150	Midiprep method for isolation of DNA from plants with a high content of polyphenolics. Nucleic Acids Research, 1993, 21, 3328-3330.	14.5	80
151	Karyotype Reconstruction in Plants with Special Emphasis on Vicia faba L.. Developments in Plant Genetics and Breeding, 1991, 2, 113-140.	0.6	5
152	Position-dependent NOR activity in barley. Chromosoma, 1990, 99, 352-359.	2.2	68
153	Restriction Endonuclease (Re-) Banding of Plant Chromosomes. Caryologia, 1990, 43, 117-130.	0.3	9
154	Are SCE frequencies indicative of adaptive response of plant cells?. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 1989, 211, 301-306.	1.0	9
155	Silver Staining of Nucleolus Organizing Regions inZea Mays. Caryologia, 1985, 38, 331-334.	0.3	2
156	Mobile nucleolus organizing regions (NORs) inAllium (Liliaceae s. lat.)? ? Inferences from the specifity of silver staining. Plant Systematics and Evolution, 1984, 144, 291-305.	0.9	74
157	On the origin of hydroxyurea-induced chromatid aberrations in G2 chromosomes with BrdUrd in only one of the sister chromatids. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 1983, 108, 301-316.	1.0	15
158	Phylogenetic conclusions from Giemsa banding and NOR staining in top onions (Liliaceae). Plant Systematics and Evolution, 1983, 143, 245-256.	0.9	38
159	Sister chromatid exchanges and heterochromatin. Human Genetics, 1981, 57, 119-30.	3.8	28
160	Distribution of heterochromatin in a reconstructed karyotype of Vicia faba as identified by banding- and DNA-late replication patterns. Chromosoma, 1978, 69, 193-209.	2.2	80
161	Organization of 5 S RNA genes in vicia faba. FEBS Letters, 1978, 96, 19-22.	2.8	3
162	Non-random intrachromosomal distribution of radiation-induced chromatid aberrations in Vicia faba. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 1976, 35, 79-90.	1.0	16