

Petr Novak

List of Publications by Year in descending order

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75
papers

6,481
citations

57719

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docs citations

79
times ranked

8586
citing authors

#	ARTICLE	IF	CITATIONS
1	Impact of parasitic lifestyle and different types of centromere organization on chromosome and genome evolution in the plant genus <i>Cuscuta</i> . <i>New Phytologist</i> , 2021, 229, 2365-2377.	3.5	22
2	Complex sequence organization of heterochromatin in the holocentric plant <i>Cuscuta europaea</i> elucidated by the computational analysis of nanopore reads. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 2179-2189.	1.9	9
3	Characterization of repeat arrays in ultra-long nanopore reads reveals frequent origin of satellite DNA from retrotransposon-derived tandem repeats. <i>Plant Journal</i> , 2020, 101, 484-500.	2.8	76
4	Repeat-sequence turnover shifts fundamentally in species with large genomes. <i>Nature Plants</i> , 2020, 6, 1325-1329.	4.7	87
5	Global analysis of repetitive DNA from unassembled sequence reads using RepeatExplorer2. <i>Nature Protocols</i> , 2020, 15, 3745-3776.	5.5	144
6	Chromosome-scale genome assembly for the duckweed <i>Spirodela intermedia</i> , integrating cytogenetic maps, PacBio and Oxford Nanopore libraries. <i>Scientific Reports</i> , 2020, 10, 19230.	1.6	23
7	Extraordinary Sequence Diversity and Promiscuity of Centromeric Satellites in the Legume Tribe Fabae. <i>Molecular Biology and Evolution</i> , 2020, 37, 2341-2356.	3.5	42
8	Differential Genome Size and Repetitive DNA Evolution in Diploid Species of <i>Melampodium</i> sect. <i>Melampodium</i> (Asteraceae). <i>Frontiers in Plant Science</i> , 2020, 11, 362.	1.7	37
9	The Repetitive Content in Lupin Genomes. <i>Compendium of Plant Genomes</i> , 2020, , 161-186.	0.3	2
10	A reference genome for pea provides insight into legume genome evolution. <i>Nature Genetics</i> , 2019, 51, 1411-1422.	9.4	363
11	The Dark Matter of Large Cereal Genomes: Long Tandem Repeats. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2483.	1.8	19
12	Accessing a Russian Wheat Aphid Resistance Gene in Bread Wheat by Long-Read Technologies. <i>Plant Genome</i> , 2019, 12, 180065.	1.6	15
13	Genome invasion by a hypomethylated satellite repeat in Australian crucifer <i>Ballantinia antipoda</i> . <i>Plant Journal</i> , 2019, 99, 1066-1079.	2.8	3
14	Nondisjunction and unequal spindle organization accompany the drive of <i>Aegilops speltoides</i> B chromosomes. <i>New Phytologist</i> , 2019, 223, 1340-1352.	3.5	26
15	Systematic survey of plant LTR-retrotransposons elucidates phylogenetic relationships of their polyprotein domains and provides a reference for element classification. <i>Mobile DNA</i> , 2019, 10, 1.	1.3	265
16	Satellite DNA in <i>Vicia faba</i> is characterized by remarkable diversity in its sequence composition, association with centromeres, and replication timing. <i>Scientific Reports</i> , 2018, 8, 5838.	1.6	66
17	Dating the Species Network: Allopolyploidy and Repetitive DNA Evolution in American Daisies (<i>Melampodium</i> sect. <i>Melampodium</i> , Asteraceae). <i>Systematic Biology</i> , 2018, 67, 1010-1024.	2.7	54
18	Impaired N-linked glycosylation of uptake and efflux transporters in human non-alcoholic fatty liver disease. <i>Liver International</i> , 2017, 37, 1074-1081.	1.9	68

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19	TAREAN: a computational tool for identification and characterization of satellite DNA from unassembled short reads. <i>Nucleic Acids Research</i> , 2017, 45, e111-e111.	6.5	222
20	Metabolomic profiling distinction of human nonalcoholic fatty liver disease progression from a common rat model. <i>Obesity</i> , 2017, 25, 1069-1076.	1.5	41
21	Karyotypes and Distribution of Tandem Repeat Sequences in <i>Brassica nigra</i> ; Determined by Fluorescence in situ Hybridization. <i>Cytogenetic and Genome Research</i> , 2017, 152, 158-165.	0.6	10
22	Centromeric and non-centromeric satellite DNA organisation differs in holocentric <i>Rhynchospora</i> species. <i>Chromosoma</i> , 2017, 126, 325-335.	1.0	59
23	Transcription factor binding site enrichment analysis predicts drivers of altered gene expression in nonalcoholic steatohepatitis. <i>Biochemical Pharmacology</i> , 2016, 122, 62-71.	2.0	16
24	Characterization of a novel radiation-induced sarcoma cell line. <i>Journal of Surgical Oncology</i> , 2015, 111, 669-682.	0.8	2
25	Centromere and telomere sequence alterations reflect the rapid genome evolution within the carnivorous plant genus <i>Genlisea</i> . <i>Plant Journal</i> , 2015, 84, 1087-1099.	2.8	41
26	Analysis of the giant genomes of <i>Fritillaria</i> (<i>Liliaceae</i>) indicates that a lack of DNA removal characterizes extreme expansions in genome size. <i>New Phytologist</i> , 2015, 208, 596-607.	3.5	122
27	Comparative Genome Analysis Reveals Divergent Genome Size Evolution in a Carnivorous Plant Genus. <i>Plant Genome</i> , 2015, 8, eplantgenome2015.04.0021.	1.6	45
28	Chromatin organization and cytological features of carnivorous <i>Genlisea</i> species with large genome size differences. <i>Frontiers in Plant Science</i> , 2015, 6, 613.	1.7	5
29	Centromeres Off the Hook: Massive Changes in Centromere Size and Structure Following Duplication of <i>CenH3</i> Gene in <i>Fabeae</i> Species. <i>Molecular Biology and Evolution</i> , 2015, 32, 1862-1879.	3.5	69
30	Holocentromeres in <i>Rhynchospora</i> are associated with genome-wide centromere-specific repeat arrays interspersed among euchromatin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13633-13638.	3.3	96
31	Branched chain amino acid metabolism profiles in progressive human nonalcoholic fatty liver disease. <i>Amino Acids</i> , 2015, 47, 603-615.	1.2	175
32	Expression profiling of circulating tumor cells in metastatic breast cancer. <i>Breast Cancer Research and Treatment</i> , 2015, 149, 121-131.	1.1	48
33	Genomic Repeat Abundances Contain Phylogenetic Signal. <i>Systematic Biology</i> , 2015, 64, 112-126.	2.7	126
34	In Depth Characterization of Repetitive DNA in 23 Plant Genomes Reveals Sources of Genome Size Variation in the Legume Tribe <i>Fabeae</i> . <i>PLoS ONE</i> , 2015, 10, e0143424.	1.1	172
35	Differential amplification of satellite PaB6 in chromosomally hypervariable <i>Prospero autumnale</i> complex (<i>Hyacinthaceae</i>). <i>Annals of Botany</i> , 2014, 114, 1597-1608.	1.4	58
36	Immortalization of normal human mammary epithelial cells in two steps by direct targeting of senescence barriers does not require gross genomic alterations. <i>Cell Cycle</i> , 2014, 13, 3423-3435.	1.3	60

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37	Characterization of Hepatocellular Carcinoma Related Genes and Metabolites in Human Nonalcoholic Fatty Liver Disease. <i>Digestive Diseases and Sciences</i> , 2014, 59, 365-374.	1.1	39
38	Expression of selected pathway-marker genes in human urothelial cells exposed chronically to a non-cytotoxic concentration of monomethylarsonous acid. <i>Toxicology Reports</i> , 2014, 1, 421-434.	1.6	3
39	Boom-Bust Turnovers of Megabase-Sized Centromeric DNA in <i>Solanum</i> Species: Rapid Evolution of DNA Sequences Associated with Centromeres. <i>Plant Cell</i> , 2014, 26, 1436-1447.	3.1	73
40	The Adaptive Endoplasmic Reticulum Stress Response to Lipotoxicity in Progressive Human Nonalcoholic Fatty Liver Disease. <i>Toxicological Sciences</i> , 2014, 137, 26-35.	1.4	121
41	Genome-Wide Analysis of Repeat Diversity across the Family Musaceae. <i>PLoS ONE</i> , 2014, 9, e98918.	1.1	54
42	Abstract 1200: Characterization of a novel radiation-induced sarcoma cell line. , 2014, , .		0
43	The holocentric species <i>Caenorhabditis elegans</i> shows interplay between centromere and large-scale genome organization. <i>Plant Journal</i> , 2013, 73, 555-565.	2.8	86
44	Decreased hepatotoxic bile acid composition and altered synthesis in progressive human nonalcoholic fatty liver disease. <i>Toxicology and Applied Pharmacology</i> , 2013, 268, 132-140.	1.3	153
45	Diploidization and genome size change in allopolyploids is associated with differential dynamics of low- and high-copy sequences. <i>Plant Journal</i> , 2013, 74, 829-839.	2.8	112
46	High-copy sequences reveal distinct evolution of the rye B chromosome. <i>New Phytologist</i> , 2013, 199, 550-558.	3.5	75
47	Flow Sorting and Sequencing Meadow Fescue Chromosome 4F. <i>Plant Physiology</i> , 2013, 163, 1323-1337.	2.3	27
48	RepeatExplorer: a Galaxy-based web server for genome-wide characterization of eukaryotic repetitive elements from next-generation sequence reads. <i>Bioinformatics</i> , 2013, 29, 792-793.	1.8	619
49	Contrasting Patterns of Transposable Element and Satellite Distribution on Sex Chromosomes (XY1Y2) in the Dioecious Plant <i>Rumex acetosa</i> . <i>Genome Biology and Evolution</i> , 2013, 5, 769-782.	1.1	55
50	Stretching the Rules: Monocentric Chromosomes with Multiple Centromere Domains. <i>PLoS Genetics</i> , 2012, 8, e1002777.	1.5	127
51	Selfish supernumerary chromosome reveals its origin as a mosaic of host genome and organellar sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13343-13346.	3.3	173
52	Next-Generation Sequencing Reveals the Impact of Repetitive DNA Across Phylogenetically Closely Related Genomes of Orobanchaceae. <i>Molecular Biology and Evolution</i> , 2012, 29, 3601-3611.	3.5	82
53	Survey Sequencing Reveals Elevated DNA Transposon Activity, Novel Elements, and Variation in Repetitive Landscapes among Vesper Bats. <i>Genome Biology and Evolution</i> , 2012, 4, 575-585.	1.1	38
54	Repeatless and Repeat-Based Centromeres in Potato: Implications for Centromere Evolution. <i>Plant Cell</i> , 2012, 24, 3559-3574.	3.1	221

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55	Cell-Type Specific DNA Methylation Patterns Define Human Breast Cellular Identity. PLoS ONE, 2012, 7, e52299.	1.1	22
56	Global gene expression changes in human urothelial cells exposed to low-level monomethylarsonous acid. Toxicology, 2012, 291, 102-112.	2.0	20
57	Independent, Rapid and Targeted Loss of Highly Repetitive DNA in Natural and Synthetic Allopolyploids of <i>Nicotiana tabacum</i> . PLoS ONE, 2012, 7, e36963.	1.1	77
58	Analysis of Global and Absorption, Distribution, Metabolism, and Elimination Gene Expression in the Progressive Stages of Human Nonalcoholic Fatty Liver Disease. Drug Metabolism and Disposition, 2011, 39, 1954-1960.	1.7	141
59	Next Generation Sequencing-Based Analysis of Repetitive DNA in the Model Dioecious Plant <i>Silene latifolia</i> . PLoS ONE, 2011, 6, e27335.	1.1	97
60	Organization and Evolution of Subtelomeric Satellite Repeats in the Potato Genome. G3: Genes, Genomes, Genetics, 2011, 1, 85-92.	0.8	75
61	A widespread occurrence of extra open reading frames in plant Ty3/gypsy retrotransposons. Genetica, 2011, 139, 1543-1555.	0.5	23
62	Next Generation Sequencing Reveals Genome Downsizing in Allotetraploid <i>Nicotiana tabacum</i> , Predominantly through the Elimination of Paternally Derived Repetitive DNAs. Molecular Biology and Evolution, 2011, 28, 2843-2854.	3.5	150
63	Graph-based clustering and characterization of repetitive sequences in next-generation sequencing data. BMC Bioinformatics, 2010, 11, 378.	1.2	403
64	Global sequence characterization of rice centromeric satellite based on oligomer frequency analysis in large-scale sequencing data. Bioinformatics, 2010, 26, 2101-2108.	1.8	43
65	Stepwise DNA Methylation Changes Are Linked to Escape from Defined Proliferation Barriers and Mammary Epithelial Cell Immortalization. Cancer Research, 2009, 69, 5251-5258.	0.4	113
66	Arsenicals produce stable progressive changes in DNA methylation patterns that are linked to malignant transformation of immortalized urothelial cells. Toxicology and Applied Pharmacology, 2009, 241, 221-229.	1.3	44
67	p53 induces distinct epigenetic states at its direct target promoters. BMC Genomics, 2008, 9, 486.	1.2	49
68	Epigenetic remodeling during arsenical-induced malignant transformation. Carcinogenesis, 2008, 29, 1500-1508.	1.3	113
69	Agglomerative Epigenetic Aberrations Are a Common Event in Human Breast Cancer. Cancer Research, 2008, 68, 8616-8625.	0.4	146
70	Chalcone synthase homologues from <i>Humulus lupulus</i> : some enzymatic properties and expression. Biologia Plantarum, 2006, 50, 48-54.	1.9	27
71	Epigenetic Inactivation of the HOXA Gene Cluster in Breast Cancer. Cancer Research, 2006, 66, 10664-10670.	0.4	109
72	THE ESTABLISHMENT AND SCREENING OF HOP GENOMIC AND CDNA LIBRARIES FOR GENES DETERMINING LUPULIN PRODUCTION. Acta Horticulturae, 2005, , 81-84.	0.1	0

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73	Cloning and Molecular Analysis of the Regulatory Factor HlMyb1 in Hop (<i>Humulus lupulus</i> L.) and the Potential of Hop To Produce Bioactive Prenylated Flavonoids. <i>Journal of Agricultural and Food Chemistry</i> , 2005, 53, 4793-4798.	2.4	26
74	Valerophenone synthase-like chalcone synthase homologues in <i>Humulus lupulus</i> . <i>Biologia Plantarum</i> , 2003, 46, 375-381.	1.9	20
75	Cloning and characterisation of chs-specific DNA and cDNA sequences from hop (<i>Humulus lupulus</i> L.). <i>Plant Science</i> , 2002, 162, 1007-1018.	1.7	34