

# Petr Novak

## List of Publications by Year in descending order

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75  
papers

6,481  
citations

57758

44  
h-index

79698

73  
g-index

79  
all docs

79  
docs citations

79  
times ranked

8586  
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	4.1	619
2	Graph-based clustering and characterization of repetitive sequences in next-generation sequencing data. <i>BMC Bioinformatics</i> , 2010, 11, 378.	2.6	403
3	A reference genome for pea provides insight into legume genome evolution. <i>Nature Genetics</i> , 2019, 51, 1411-1422.	21.4	363
4	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.	3.6	265
5	TAREAN: a computational tool for identification and characterization of satellite DNA from unassembled short reads. <i>Nucleic Acids Research</i> , 2017, 45, e111-e111.	14.5	222
6	Repeatless and Repeat-Based Centromeres in Potato: Implications for Centromere Evolution. <i>Plant Cell</i> , 2012, 24, 3559-3574.	6.6	221
7	Branched chain amino acid metabolism profiles in progressive human nonalcoholic fatty liver disease. <i>Amino Acids</i> , 2015, 47, 603-615.	2.7	175
8	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.	7.1	173
9	In Depth Characterization of Repetitive DNA in 23 Plant Genomes Reveals Sources of Genome Size Variation in the Legume Tribe Fabaeae. <i>PLoS ONE</i> , 2015, 10, e0143424.	2.5	172
10	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.	2.8	153
11	Next Generation Sequencing Reveals Genome Downsizing in Allotetraploid <i>Nicotiana tabacum</i> , Predominantly through the Elimination of Paternally Derived Repetitive DNAs. <i>Molecular Biology and Evolution</i> , 2011, 28, 2843-2854.	8.9	150
12	Agglomerative Epigenetic Aberrations Are a Common Event in Human Breast Cancer. <i>Cancer Research</i> , 2008, 68, 8616-8625.	0.9	146
13	Global analysis of repetitive DNA from unassembled sequence reads using RepeatExplorer2. <i>Nature Protocols</i> , 2020, 15, 3745-3776.	12.0	144
14	Analysis of Global and Absorption, Distribution, Metabolism, and Elimination Gene Expression in the Progressive Stages of Human Nonalcoholic Fatty Liver Disease. <i>Drug Metabolism and Disposition</i> , 2011, 39, 1954-1960.	3.3	141
15	Stretching the Rules: Monocentric Chromosomes with Multiple Centromere Domains. <i>PLoS Genetics</i> , 2012, 8, e1002777.	3.5	127
16	Genomic Repeat Abundances Contain Phylogenetic Signal. <i>Systematic Biology</i> , 2015, 64, 112-126.	5.6	126
17	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.	7.3	122
18	The Adaptive Endoplasmic Reticulum Stress Response to Lipotoxicity in Progressive Human Nonalcoholic Fatty Liver Disease. <i>Toxicological Sciences</i> , 2014, 137, 26-35.	3.1	121

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19	Epigenetic remodeling during arsenical-induced malignant transformation. <i>Carcinogenesis</i> , 2008, 29, 1500-1508.	2.8	113
20	Stepwise DNA Methylation Changes Are Linked to Escape from Defined Proliferation Barriers and Mammary Epithelial Cell Immortalization. <i>Cancer Research</i> , 2009, 69, 5251-5258.	0.9	113
21	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.	5.7	112
22	Epigenetic Inactivation of the HOXA Gene Cluster in Breast Cancer. <i>Cancer Research</i> , 2006, 66, 10664-10670.	0.9	109
23	Next Generation Sequencing-Based Analysis of Repetitive DNA in the Model Dioecious Plant <i>Silene latifolia</i> . <i>PLoS ONE</i> , 2011, 6, e27335.	2.5	97
24	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.	7.1	96
25	Repeat-sequence turnover shifts fundamentally in species with large genomes. <i>Nature Plants</i> , 2020, 6, 1325-1329.	9.3	87
26	The holocentric species <i>Caenorhabditis elegans</i> shows interplay between centromere and large-scale genome organization. <i>Plant Journal</i> , 2013, 73, 555-565.	5.7	86
27	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.	8.9	82
28	Independent, Rapid and Targeted Loss of Highly Repetitive DNA in Natural and Synthetic Allopolyploids of <i>Nicotiana glauca</i> . <i>PLoS ONE</i> , 2012, 7, e36963.	2.5	77
29	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.	5.7	76
30	Organization and Evolution of Subtelomeric Satellite Repeats in the Potato Genome. <i>G3: Genes, Genomes, Genetics</i> , 2011, 1, 85-92.	1.8	75
31	High-copy sequences reveal distinct evolution of the rye B chromosome. <i>New Phytologist</i> , 2013, 199, 550-558.	7.3	75
32	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.	6.6	73
33	Centromeres Off the Hook: Massive Changes in Centromere Size and Structure Following Duplication of <i>CenH3</i> Gene in <i>Fabaceae</i> Species. <i>Molecular Biology and Evolution</i> , 2015, 32, 1862-1879.	8.9	69
34	Impaired N-linked glycosylation of uptake and efflux transporters in human non-alcoholic fatty liver disease. <i>Liver International</i> , 2017, 37, 1074-1081.	3.9	68
35	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.	3.3	66
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.	2.6	60

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37	Centromeric and non-centromeric satellite DNA organisation differs in holocentric <i>Rhynchospora</i> species. <i>Chromosoma</i> , 2017, 126, 325-335.	2.2	59
38	Differential amplification of satellite PaB6 in chromosomally hypervariable <i>Prospero autumnale</i> complex (Hyacinthaceae). <i>Annals of Botany</i> , 2014, 114, 1597-1608.	2.9	58
39	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.	2.5	55
40	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.	5.6	54
41	Genome-Wide Analysis of Repeat Diversity across the Family Musaceae. <i>PLoS ONE</i> , 2014, 9, e98918.	2.5	54
42	p53 induces distinct epigenetic states at its direct target promoters. <i>BMC Genomics</i> , 2008, 9, 486.	2.8	49
43	Expression profiling of circulating tumor cells in metastatic breast cancer. <i>Breast Cancer Research and Treatment</i> , 2015, 149, 121-131.	2.5	48
44	Comparative Genome Analysis Reveals Divergent Genome Size Evolution in a Carnivorous Plant Genus. <i>Plant Genome</i> , 2015, 8, eplantgenome2015.04.0021.	2.8	45
45	Arsenicals produce stable progressive changes in DNA methylation patterns that are linked to malignant transformation of immortalized urothelial cells. <i>Toxicology and Applied Pharmacology</i> , 2009, 241, 221-229.	2.8	44
46	Global sequence characterization of rice centromeric satellite based on oligomer frequency analysis in large-scale sequencing data. <i>Bioinformatics</i> , 2010, 26, 2101-2108.	4.1	43
47	Extraordinary Sequence Diversity and Promiscuity of Centromeric Satellites in the Legume Tribe Fabaeae. <i>Molecular Biology and Evolution</i> , 2020, 37, 2341-2356.	8.9	42
48	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.	5.7	41
49	Metabolomic profiling distinction of human nonalcoholic fatty liver disease progression from a common rat model. <i>Obesity</i> , 2017, 25, 1069-1076.	3.0	41
50	Characterization of Hepatocellular Carcinoma Related Genes and Metabolites in Human Nonalcoholic Fatty Liver Disease. <i>Digestive Diseases and Sciences</i> , 2014, 59, 365-374.	2.3	39
51	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.	2.5	38
52	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.	3.6	37
53	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.	3.6	34
54	Chalcone synthase homologues from <i>Humulus lupulus</i> : some enzymatic properties and expression. <i>Biologia Plantarum</i> , 2006, 50, 48-54.	1.9	27

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55	Flow Sorting and Sequencing Meadow Fescue Chromosome 4F. <i>Plant Physiology</i> , 2013, 163, 1323-1337.	4.8	27
56	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.	5.2	26
57	Nondisjunction and unequal spindle organization accompany the drive of <i>Aegilops speltoides</i> B chromosomes. <i>New Phytologist</i> , 2019, 223, 1340-1352.	7.3	26
58	A widespread occurrence of extra open reading frames in plant Ty3/gypsy retrotransposons. <i>Genetica</i> , 2011, 139, 1543-1555.	1.1	23
59	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.	3.3	23
60	Cell-Type Specific DNA Methylation Patterns Define Human Breast Cellular Identity. <i>PLoS ONE</i> , 2012, 7, e52299.	2.5	22
61	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.	7.3	22
62	Valerophenone synthase-like chalcone synthase homologues in <i>Humulus lupulus</i> . <i>Biologia Plantarum</i> , 2003, 46, 375-381.	1.9	20
63	Global gene expression changes in human urothelial cells exposed to low-level monomethylarsonous acid. <i>Toxicology</i> , 2012, 291, 102-112.	4.2	20
64	The Dark Matter of Large Cereal Genomes: Long Tandem Repeats. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2483.	4.1	19
65	Transcription factor binding site enrichment analysis predicts drivers of altered gene expression in nonalcoholic steatohepatitis. <i>Biochemical Pharmacology</i> , 2016, 122, 62-71.	4.4	16
66	Accessing a Russian Wheat Aphid Resistance Gene in Bread Wheat by Long-Read Technologies. <i>Plant Genome</i> , 2019, 12, 180065.	2.8	15
67	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.	1.1	10
68	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.	4.1	9
69	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.	3.6	5
70	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.	3.3	3
71	Genome invasion by a hypomethylated satellite repeat in Australian crucifer <i>Ballantinia antipoda</i> . <i>Plant Journal</i> , 2019, 99, 1066-1079.	5.7	3
72	Characterization of a novel radiation-induced sarcoma cell line. <i>Journal of Surgical Oncology</i> , 2015, 111, 669-682.	1.7	2

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73	The Repetitive Content in Lupin Genomes. <i>Compendium of Plant Genomes</i> , 2020, , 161-186.	0.5	2
74	THE ESTABLISHMENT AND SCREENING OF HOP GENOMIC AND CDNA LIBRARIES FOR GENES DETERMINING LUPULIN PRODUCTION. <i>Acta Horticulturae</i> , 2005, , 81-84.	0.2	0
75	Abstract 1200: Characterization of a novel radiation-induced sarcoma cell line. , 2014, , .		0