

# Pavel Neumann

## List of Publications by Year in descending order

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59  
papers

5,773  
citations

81839

39  
h-index

133188

59  
g-index

62  
all docs

62  
docs citations

62  
times ranked

4196  
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	Mitotic Spindle Attachment to the Holocentric Chromosomes of <i>Cuscuta europaea</i> Does Not Correlate With the Distribution of CENH3 Chromatin. <i>Frontiers in Plant Science</i> , 2020, 10, 1799.	1.7	37
5	Repeat-sequence turnover shifts fundamentally in species with large genomes. <i>Nature Plants</i> , 2020, 6, 1325-1329.	4.7	87
6	Global analysis of repetitive DNA from unassembled sequence reads using RepeatExplorer2. <i>Nature Protocols</i> , 2020, 15, 3745-3776.	5.5	144
7	Super-Resolution Microscopy Reveals Diversity of Plant Centromere Architecture. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3488.	1.8	42
8	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
9	A reference genome for pea provides insight into legume genome evolution. <i>Nature Genetics</i> , 2019, 51, 1411-1422.	9.4	363
10	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
11	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
12	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
13	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
14	Epigenetic Histone Marks of Extended Meta-Polycentric Centromeres of <i>Lathyrus</i> and <i>Pisum</i> Chromosomes. <i>Frontiers in Plant Science</i> , 2016, 7, 234.	1.7	31
15	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
16	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
17	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
18	Centromeres Off the Hook: Massive Changes in Centromere Size and Structure Following Duplication of <i>CenH3</i> Gene in <i>Fabae</i> Species. <i>Molecular Biology and Evolution</i> , 2015, 32, 1862-1879.	3.5	69

#	ARTICLE	IF	CITATIONS
19	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
20	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.	1.1	172
21	Genome-Wide Analysis of Repeat Diversity across the Family Musaceae. <i>PLoS ONE</i> , 2014, 9, e98918.	1.1	54
22	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
23	Flow Sorting and Sequencing Meadow Fescue Chromosome 4F. <i>Plant Physiology</i> , 2013, 163, 1323-1337.	2.3	27
24	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
25	Stretching the Rules: Monocentric Chromosomes with Multiple Centromere Domains. <i>PLoS Genetics</i> , 2012, 8, e1002777.	1.5	127
26	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
27	Repeatless and Repeat-Based Centromeres in Potato: Implications for Centromere Evolution. <i>Plant Cell</i> , 2012, 24, 3559-3574.	3.1	221
28	Pea ( <i>Pisum sativum</i> L.) in the Genomic Era. <i>Agronomy</i> , 2012, 2, 74-115.	1.3	172
29	Next Generation Sequencing-Based Analysis of Repetitive DNA in the Model Dioecious Plant <i>Silene latifolia</i> . <i>PLoS ONE</i> , 2011, 6, e27335.	1.1	97
30	A widespread occurrence of extra open reading frames in plant Ty3/gypsy retrotransposons. <i>Genetica</i> , 2011, 139, 1543-1555.	0.5	23
31	Plant centromeric retrotransposons: a structural and cytogenetic perspective. <i>Mobile DNA</i> , 2011, 2, 4.	1.3	186
32	Diverse retrotransposon families and an AT-rich satellite DNA revealed in giant genomes of <i>Fritillaria</i> lilies. <i>Annals of Botany</i> , 2011, 107, 255-268.	1.4	78
33	Graph-based clustering and characterization of repetitive sequences in next-generation sequencing data. <i>BMC Bioinformatics</i> , 2010, 11, 378.	1.2	403
34	Repetitive part of the banana ( <i>Musa acuminata</i> ) genome investigated by low-depth 454 sequencing. <i>BMC Plant Biology</i> , 2010, 10, 204.	1.6	90
35	Genome-wide mapping of cytosine methylation revealed dynamic DNA methylation patterns associated with genes and centromeres in rice. <i>Plant Journal</i> , 2010, 63, 353-365.	2.8	112
36	Global sequence characterization of rice centromeric satellite based on oligomer frequency analysis in large-scale sequencing data. <i>Bioinformatics</i> , 2010, 26, 2101-2108.	1.8	43

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37	Hypervariable 3' UTR region of plant LTR-retrotransposons as a source of novel satellite repeats. <i>Gene</i> , 2009, 448, 198-206.	1.0	70
38	Experimental evidence for splicing of intron-containing transcripts of plant LTR retrotransposon Ogr1. <i>Molecular Genetics and Genomics</i> , 2008, 280, 427-36.	1.0	9
39	Sgt1, but not Rar1, is essential for the RB-mediated broad-spectrum resistance to potato late blight. <i>BMC Plant Biology</i> , 2008, 8, 8.	1.6	65
40	The Centromeric Retrotransposons of Rice Are Transcribed and Differentially Processed by RNA Interference. <i>Genetics</i> , 2007, 176, 749-761.	1.2	63
41	Ogr1 elements – A distinct group of plant Ty3/gypsy-like retrotransposons. <i>Gene</i> , 2007, 390, 108-116.	1.0	55
42	Repetitive DNA in the pea ( <i>Pisum sativum</i> L.) genome: comprehensive characterization using 454 sequencing and comparison to soybean and <i>Medicago truncatula</i> . <i>BMC Genomics</i> , 2007, 8, 427.	1.2	256
43	Transcription and Evolutionary Dynamics of the Centromeric Satellite Repeat CentO in Rice. <i>Molecular Biology and Evolution</i> , 2006, 23, 2505-2520.	3.5	62
44	Significant Expansion of <i>Vicia pannonica</i> Genome Size Mediated by Amplification of a Single Type of Giant Retroelement. <i>Genetics</i> , 2006, 173, 1047-1056.	1.2	119
45	PIGY, a new plant envelope-class LTR retrotransposon. <i>Molecular Genetics and Genomics</i> , 2005, 273, 43-53.	1.0	19
46	Structure, Divergence, and Distribution of the CRR Centromeric Retrotransposon Family in Rice. <i>Molecular Biology and Evolution</i> , 2005, 22, 845-855.	3.5	91
47	Characterization of Stowaway MITEs in pea ( <i>Pisum sativum</i> L.) and identification of their potential master elements. <i>Genome</i> , 2005, 48, 831-839.	0.9	24
48	Long-range organization of plant satellite repeats investigated using strand-specific FISH. <i>Cytogenetic and Genome Research</i> , 2005, 109, 58-62.	0.6	6
49	Highly abundant pea LTR retrotransposon Ogr1 is constitutively transcribed and partially spliced. <i>Plant Molecular Biology</i> , 2003, 53, 399-410.	2.0	92
50	Zaba: a novel miniature transposable element present in genomes of legume plants. <i>Molecular Genetics and Genomics</i> , 2003, 269, 624-631.	1.0	14
51	Karyotype Analysis of Four <i>Vicia</i> Species using In Situ Hybridization with Repetitive Sequences. <i>Annals of Botany</i> , 2003, 91, 921-926.	1.4	61
52	Chromosome sorting and PCR-based physical mapping in pea ( <i>Pisum sativum</i> L.). <i>Chromosome Research</i> , 2002, 10, 63-71.	1.0	69
53	Molecular and cytogenetic analysis of repetitive DNA in pea ( <i>Pisum sativum</i> L.). <i>Genome</i> , 2001, 44, 716-728.	0.9	46
54	Microarray-based survey of repetitive genomic sequences in <i>Vicia</i> spp. <i>Plant Molecular Biology</i> , 2001, 45, 229-244.	2.0	37

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55	Molecular and cytogenetic analysis of repetitive DNA in pea ( <i>Pisum sativum</i> L.). <i>Genome</i> , 2001, 44, 716-728.	0.9	28
56	Two new families of tandem repeats isolated from genus <i>Vicia</i> using genomic self-priming PCR. <i>Molecular Genetics and Genomics</i> , 2000, 263, 741-751.	2.4	49
57	Cloning and Characterization of New Repetitive Sequences in Field Bean ( <i>Vicia faba</i> L.). <i>Annals of Botany</i> , 2000, 85, 157.	1.4	0
58	Cloning and Characterization of New Repetitive Sequences in Field Bean ( <i>Vicia faba</i> L.). <i>Annals of Botany</i> , 1999, 83, 535-541.	1.4	21
59	Isolation of chromosomes from <i>Pisum sativum</i> L. hairy root cultures and their analysis by flow cytometry. <i>Plant Science</i> , 1998, 137, 205-215.	1.7	40