Frank R Blattner

List of Publications by Year
in descending order

101 papers	5,102 citations	66343 42 h-index	95266 68 g-index
104 all docs	104 docs citations	104 times ranked	5645 citing authors

#	Article	IF	Citations
1	Direct Amplification of the Entire ITS Region from Poorly Preserved Plant Material Using Recombinant PCR. BioTechniques, 1999, 27, 1180-1186.	1.8	288
2	Phylogeny and New Intrageneric Classification of Allium (Alliaceae) Based on Nuclear Ribosomal DNA ITS Sequences. Aliso, 2006, 22, 372-395.	0.2	275
3	Barley whole exome capture: a tool for genomic research in the genus <i>Hordeum</i> and beyond. Plant Journal, 2013, 76, 494-505.	5.7	260
4	A Chloroplast Genealogy of Hordeum (Poaceae): Long-Term Persisting Haplotypes, Incomplete Lineage Sorting, Regional Extinction, and the Consequences for Phylogenetic Inference. Molecular Biology and Evolution, 2006, 23, 1602-1612.	8.9	192
5	Selfish supernumerary chromosome reveals its origin as a mosaic of host genome and organellar sequences. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 13343-13346.	7.1	173
6	Molecular Analysis of Phylogenetic Relationships among Myrmecophytic Macaranga Species (Euphorbiaceae). Molecular Phylogenetics and Evolution, 2001, 19, 331-344.	2.7	138
7	Identification and Dynamics of Two Classes of Aurora-Like Kinases in Arabidopsis and Other Plants. Plant Cell, 2005, 17, 836-848.	6.6	135
8	Nunatak survival of the high Alpine plant Eritrichium nanum (L.) Gaudin in the central Alps during the ice ages. Molecular Ecology, 2002, 11, 2027-2036.	3.9	128
9	The Considerable Genome Size Variation of Hordeum Species (Poaceae) Is Linked to Phylogeny, Life Form, Ecology, and Speciation Rates. Molecular Biology and Evolution, 2004, 21, 860-869.	8.9	121
10	Phylogenetic analysis of Hordeum (Poaceae) as inferred by nuclear rDNA ITS sequences. Molecular Phylogenetics and Evolution, 2004, 33, 289-299.	2.7	119
11	Phylogeographic Analyses and Paleodistribution Modeling Indicate Pleistocene In Situ Survival of Hordeum Species (Poaceae) in Southern Patagonia without Genetic or Spatial Restriction. Molecular Biology and Evolution, 2009, 26, 907-923.	8.9	107
12	Combined ecological niche modelling and molecular phylogeography revealed the evolutionary history ofHordeum marinum(Poaceae) - niche differentiation, loss of genetic diversity, and speciation in Mediterranean Quaternary refugia. Molecular Ecology, 2007, 16, 1713-1727.	3.9	102
13	Identification and genetic analysis of the APOSPORY locus in Hypericum perforatum L.. Plant Journal, 2010, 62, 773-784.	5.7	92
14	Phylogeny of Crocus (Iridaceae) based on one chloroplast and two nuclear loci: Ancient hybridization and chromosome number evolution. Molecular Phylogenetics and Evolution, 2013, 66, 617-627.	2.7	92
15	Species-Level Phylogeny and Polyploid Relationships in<i>Hordeum</i>(Poaceae) Inferred by Next-Generation Sequencing and<i>In Silico</i>Cloning of Multiple Nuclear Loci. Systematic Biology, 2015, 64, 792-808.	5.6	90
16	Molecular phylogenetics and morphological evolution of St. Johnâ€™s wort (Hypericum; Hypericaceae). Molecular Phylogenetics and Evolution, 2013, 66, 1-16.	2.7	86
17	Multiple intercontinental dispersals shaped the distribution area of Hordeum (Poaceae). New Phytologist, 2006, 169, 603-614.	7.3	85
18	Dated tribe-wide whole chloroplast genome phylogeny indicates recurrent hybridizations within Triticeae. BMC Evolutionary Biology, 2017, 17, 141.	3.2	78

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19	A chloroplast genealogy of myrmecophytic Macaranga species (Euphorbiaceae) in Southeast Asia reveals hybridization, vicariance and long-distance dispersals. Molecular Ecology, 2006, 15, 4409-4424.	3.9	72
20	Storage and mobilization as antagonistic functional constraints on seed storage globulin evolution. Journal of Experimental Botany, 2003, 54, 1645-1654.	4.8	71
21	Data Congruence and Phylogeny of the Papaveraceae s.l. Based on Four Data Sets: atpB and rbcL Sequences, trnK Restriction Sites, and Morphological Characters. Systematic Botany, 1997, 22, 575.	0.5	69
22	Progress in phylogenetic analysis and a new infrageneric classification of the barley genus Hordeum (Poaceae: Triticeae). Breeding Science, 2009, 59, 471-480.	1.9	69
23	Molecular and Morphological Evidence for an Origin of the Aberrant Genus Milula within Himalayan Species of Allium (Alliacae). Molecular Phylogenetics and Evolution, 2000, 17, 209-218.	2.7	68
24	Evolutionary History of Wild Barley (Hordeum vulgare subsp. spontaneum) Analyzed Using Multilocus Sequence Data and Paleodistribution Modeling. Genome Biology and Evolution, 2014, 6, 685-702.	2.5	64
25	Saffron (Crocus sativus) is an autotriploid that evolved in Attica (Greece) from wild Crocus cartwrightianus. Molecular Phylogenetics and Evolution, 2019, 136, 14-20.	2.7	62
26	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
27	Flow cytometric analysis in Lagenaria siceraria (Cucurbitaceae) indicates correlation of genome size with usage types and growing elevation. Plant Systematics and Evolution, 2008, 276, 9-19.	0.9	61
28	Minisatellite telomeres occur in the family Alliaceae but are lost in <i>Allium</i>. American Journal of Botany, 2006, 93, 814-823.	1.7	58
29	Phylogenetic analysis of Allium subg. Melanocrommyum infers cryptic species and demands a new sectional classification. Molecular Phylogenetics and Evolution, 2008, 49, 997-1007.	2.7	58
30	Population demography influences climatic niche evolution: evidence from diploid American <i>Hordeum</i> species (Poaceae). Molecular Ecology, 2010, 19, 1423-1438.	3.9	57
31	Speciesâ€“level phylogeny of <i>Allium</i> subgenus <i>Melanocrommyum</i>: Incomplete lineage sorting, hybridization and <i>trnF</i> gene duplication. Taxon, 2010, 59, 829-840.	0.7	56
32	Oligocene niche shift, Miocene diversification â€“ cold tolerance and accelerated speciation rates in the St. Johnâ€™s Worts (Hypericum, Hypericaceae). BMC Evolutionary Biology, 2015, 15, 80.	3.2	56
33	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
34	Legumains - a family of asparagine-specific cysteine endopeptidases involved in propolypeptide processing and protein breakdown in plants. Journal of Plant Physiology, 2002, 159, 1281-1293.	3.5	54
35	Application of non-coding DNA regions in intraspecific analyses. Plant Systematics and Evolution, 2009, 282, 281-294.	0.9	53
36	RAPD data do not support a second centre of barley domestication in Morocco. Genetic Resources and Crop Evolution, 2001, 48, 13-19.	1.6	51

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37	Phylogenetic relationships of wild and cultivated species of Allium section Cepa inferred by nuclear rDNA ITS sequence analysis. Plant Systematics and Evolution, 2007, 269, 259-269.	0.9	50
38	RAPDs and noncoding chloroplast DNA reveal a single origin of the cultivatedAllium fistulosumfromA. altaicum(Alliaceae). American Journal of Botany, 1999, 86, 554-562.	1.7	48
39	AFLP diversity in the common vetch (Vicia sativa L.) on the world scale. Theoretical and Applied Genetics, 2002, 105, 58-67.	3.6	48
40	SSRâ€seq: Genotyping of microsatellites using nextâ€generation sequencing reveals higher level of polymorphism as compared to traditional fragment size scoring. Ecology and Evolution, 2018, 8, 10817-10833.	1.9	48
41	Molecular phylogeny and divergence times of Astragalus section Hymenostegis: An analysis of a rapidly diversifying species group in Fabaceae. Scientific Reports, 2017, 7, 14033.	3.3	47
42	A putative role for amino acid permeases in sink-source communication of barley tissues uncovered by RNA-seq. BMC Plant Biology, 2012, 12, 154.	3.6	46
43	Two extinct diploid progenitors were involved in allopolyploid formation in the Hordeum murinum (Poaceae: Triticeae) taxon complex. Molecular Phylogenetics and Evolution, 2010, 55, 650-659.	2.7	45
44	Comparative Genome Analysis Reveals Divergent Genome Size Evolution in a Carnivorous Plant Genus. Plant Genome, 2015, 8, eplantgenome2015.04.0021.	2.8	45
45	Morphological evolution and ecological diversification of the forest-dwelling poppies (Papaveraceae:) Tj ETQq1 1 0.784314 rgBT /Overlo Evolution, 1999, 219, 181-197.	0.9	42
46	Phylogeny, karyotype evolution and taxonomy of Crocus series Verni (Iridaceae). Plant Systematics and Evolution, 2015, 301, 309-325.	0.9	42
47	Progenitor-Derivative Relationships of Hordeum Polyploids (Poaceae, Triticeae) Inferred from Sequences of TOPO6, a Nuclear Low-Copy Gene Region. PLoS ONE, 2012, 7, e33808.	2.5	42
48	The evolution of the hexaploid grass Zingeria kochii (Mez) Tzvel. (2n=12) was accompanied by complex hybridization and uniparental loss of ribosomal DNA. Molecular Phylogenetics and Evolution, 2010, 56, 146-155.	2.7	41
49	Molecular data indicate multiple independent colonizations of former lignite mining areas in Eastern Germany by Epipactis palustris (Orchidaceae). Biodiversity and Conservation, 2008, 17, 2441-2453.	2.6	40
50	Genomeâ€wide sequence information reveals recurrent hybridization among diploid wheat wild relatives. Plant Journal, 2020, 102, 493-506.	5.7	40
51	Sex-specific SCAR markers in the dioecious plant Rumex nivalis (Polygonaceae) and implications for the evolution of sex chromosomes. Theoretical and Applied Genetics, 2004, 108, 238-242.	3.6	39
52	Genetic diversity and relationships in Corchorus olitorius (Malvaceae s.l.) inferred from molecular and morphological data. Genetic Resources and Crop Evolution, 2012, 59, 1125-1146.	1.6	39
53	Intron gain and loss in the evolution of the conserved eukaryotic recombination machinery. Nucleic Acids Research, 2002, 30, 5175-5181.	14.5	37
54	Collection and ethnobotanical investigation of Corchorus species in Ethiopia: potential leafy vegetables for dry regions. Genetic Resources and Crop Evolution, 2010, 57, 293-306.	1.6	34

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55	Genome size variation in<i>Corchorus olitorius</i>(Malvaceae s.l.) and its correlation with elevation and phenotypic traits. Genome, 2011, 54, 575-585.	2.0	34
56	Phenetic characterization of Citrullus spp. (Cucurbitaceae) and differentiation of egusi-type (C.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 70	1.6	34
57	Multiple horizontal transfers of nuclear ribosomal genes between phylogenetically distinct grass lineages. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 1726-1731.	7.1	34
58	Phylogeny, geographic distribution, and new taxonomic circumscription of the Crocus reticulatus species group (Iridaceae). Turkish Journal of Botany, 2014, 38, 1182-1198.	1.2	32
59	Cladistic analysis of morphological characters in <i>Hypericum</i> (Hypericaceae). Taxon, 2010, 59, 1495-1507.	0.7	30
60	Genetic diversity of Vitis vinifera in Georgia: relationships between local cultivars and wild grapevine, V. vinifera L. subsp. sylvestris. Genetic Resources and Crop Evolution, 2014, 61, 1507-1521.	1.6	30
61	AtHaspin phosphorylates histone H3 at threonine 3 during mitosis and contributes to embryonic patterning in Arabidopsis. Plant Journal, 2011, 68, 443-454.	5.7	28
62	TOPO6: a nuclear single-copy gene for plant phylogenetic inference. Plant Systematics and Evolution, 2016, 302, 239-244.	0.9	28
63	The Evolution of Genome Size Variation in Drumstick Onions (<I>Allium</I> subgenus) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 42	0.5	26
64	Phylogeny and genetic diversity of D-genome species of Aegilops and Triticum (Triticeae, Poaceae) from Iran based on microsatellites, ITS, and trnL-F. Plant Systematics and Evolution, 2011, 291, 117-131.	0.9	25
65	Comparative molecular and phytochemical investigation of Leontodon autumnalis (Asteraceae,) Tj ETQq1 1 0.784314 rgBT /Overlock 1(	2.9	24
66	Resolving relationships in an exceedingly young Neotropical orchid lineage using Genotyping-by-sequencing data. Molecular Phylogenetics and Evolution, 2020, 144, 106672.	2.7	23
67	B chromosomes of rye are highly conserved and accompanied the development of early agriculture. Annals of Botany, 2013, 112, 527-534.	2.9	22
68	Phylogeny of the saffron-crocus species group, Crocus series Crocus (Iridaceae). Molecular Phylogenetics and Evolution, 2018, 127, 891-897.	2.7	22
69	RAPD Analysis Reveals Geographic Differentiations within Allium schoenoprasum L. (Alliaceae). Plant Biology, 2000, 2, 297-305.	3.8	21
70	Evolution and function of B chromosome 45S rDNA sequences in Brachycome dichromosomatica. Genome, 2007, 50, 638-644.	2.0	21
71	Development of microsatellite markers and assembly of the plastid genome in Cistanthe longiscapa (Montiaceae) based on low-coverage whole genome sequencing. PLoS ONE, 2017, 12, e0178402.	2.5	19
72	Elucidation of the origin of â€˜ agriocrithon â€™ based on domestication genes questions the hypothesis that Tibet is one of the centers of barley domestication. Plant Journal, 2018, 94, 525-534.	5.7	17

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73	Evolution of a conserved protein module from Archaea to plants. Trends in Genetics, 1999, 15, 348-349.	6.7	16
74	Phylogeographic implications of an AFLP phylogeny of the American diploid <i>Hordeum</i> species (Poaceae: Triticeae). Taxon, 2008, 57, 875-881.	0.7	16
75	Comparative chloroplast DNA phylogeography of two tropical pioneer trees, Macaranga gigantea and Macaranga pearsonii (Euphorbiaceae). Tree Genetics and Genomes, 2011, 7, 573-585.	1.6	16
76	Taxonomy of the Genus Hordeum and Barley (Hordeum vulgare). Compendium of Plant Genomes, 2018, , 11-23.	0.5	13
77	Ecotypes and genetic structure of Rhinanthus alectorolophus (Orobanchaceae) in southwestern Germany. Plant Systematics and Evolution, 2013, 299, 1523-1535.	0.9	11
78	Single nucleotide sequence analysis: a cost- and time-effective protocol for the analysis of microsatellite- and indel-rich chloroplast DNA regions. Molecular Ecology Resources, 2008, 8, 62-65.	4.8	10
79	The phylogeographic history of Krascheninnikovia reflects the development of dry steppes and semi-deserts in Eurasia. Scientific Reports, 2021, 11, 6645.	3.3	10
80	Microsatellite markers for the palaeotropic pioneer tree genus Macaranga (Euphorbiaceae) and their cross-species transferability. Molecular Ecology Notes, 2006, 6, 245-248.	1.7	9
81	New aspects of the molecular evolution of legumains, Asn-specific cysteine proteinases. Journal of Plant Physiology, 2012, 169, 319-321.	3.5	9
82	Plant migration under longâ€lasting hyperaridity â€" phylogenomics unravels recent biogeographic history in one of the oldest deserts on Earth. New Phytologist, 2022, 234, 1863-1875.	7.3	9
83	Pollen morphology of <i>Astragalus</i> section <i>Hymenostegis</i> (Fabaceae) and evaluation of its systematic implications. Grana, 2019, 58, 328-336.	0.8	8
84	Pleistocene dynamics of the Eurasian steppe as a driving force of evolution: Phylogenetic history of the genus <i>Capsella</i> (Brassicaceae). Ecology and Evolution, 2021, 11, 12697-12713.	1.9	8
85	Three intercontinental disjunctions in Papaveraceae subfamily Chelidonioideae: evidence from chloroplast DNA. , 1995, , 147-157.		8
86	Phylogenetic Analysis of Microseris (Asteraceae), Including a Newly Discovered Andean Population from Peru. Systematic Botany, 2004, 29, 774-780.	0.5	7
87	Interspecific Relationships in <I>Allium</I> subgenus <I>Melanocrommyum</I> sections <I>Acanthoprason</I> and <I>Asteroprason</I> (Amaryllidaceae) Revealed Using ISSR Markers. Systematic Botany, 2015, 40, 706-715.	0.5	7
88	Rapid Radiation in the Barley Genus Hordeum (Poaceae) During the Pleistocene in the Americas. , 2010, , 17-33.		6
89	Molecular Phylogeny and Morphological Analysis Support a New Species and New Synonymy in Iranian Astragalus (Leguminosae). PLoS ONE, 2016, 11, e0149726.	2.5	5
90	Isolation and characterization of 11 new microsatellite markers for <i>Macaranga</i> (Euphorbiaceae). Molecular Ecology Resources, 2009, 9, 1049-1052.	4.8	4

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91	Nine New Species of the Species-rich GenusAstragalus(Leguminosae). Novon, 2017, 25, 266-281.	0.3	4
92	Georeferenced phylogenetic analysis of a global collection of wild and cultivated Citrullus species. Ecology and Evolution, 2021, 11, 1918-1936.	1.9	4
93	Mechanisms of Speciation in Southeast Asian Ant-Plants of the Genus Macaranga (Euphorbiaceae). , 2010, , 169-191.		4
94	<i>Astragalus trifoliastrum</i> (Fabaceae), a revived species for the flora of Turkey. Nordic Journal of Botany, 2015, 33, 532-539.	0.5	3
95	Landscape genetics of the endangered Atacama Desert shrub Balsamocarpon brevifolium in the context of habitat fragmentation. Global and Planetary Change, 2020, 184, 103059.	3.5	3
96	Genomic, karyological and morphological changes of South American garlics (Ipheion) provide insights into mechanisms of speciation in the Pampean region. Molecular Ecology, 2021, 30, 3716-3729.	3.9	3
97	Allium gilanense, a new species of Allium sect. Codonoprasum (Amaryllidaceae) from Iran: evidence from morphological and molecular data . Phytotaxa, 2020, 474, 283-292.	0.3	3
98	Horizontally Acquired nrDNAs Persist in Low Amounts in Host Hordeum Genomes and Evolve Independently of Native nrDNA. Frontiers in Plant Science, 2021, 12, 672879.	3.6	2
99	First Glimpse on Spring Starflower Domestication. Genes, 2022, 13, 243.	2.4	2
100	Genome Size and Chromosome Number Evaluation of Astragalus L. sect. Hymenostegis Bunge (Fabaceae). Plants, 2022, 11, 435.	3.5	1
101	Astragalus sect. Elvendia (Fabaceae), a new tragacanthic section recorded from Mt. Alvand, a center of endemism in W Iran. Plant Biosystems, 0, , 1-9.	1.6	1