

# Andrew G Sharpe

## List of Publications by Year in descending order

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73  
papers

14,458  
citations

66343

42  
h-index

79698

73  
g-index

75  
all docs

75  
docs citations

75  
times ranked

10721  
citing authors

#	ARTICLE	IF	CITATIONS
1	Early allopolyploid evolution in the post-Neolithic <i>Brassica napus</i> oilseed genome. <i>Science</i> , 2014, 345, 950-953.	12.6	2,089
2	The genome of the mesopolyploid crop species <i>Brassica rapa</i> . <i>Nature Genetics</i> , 2011, 43, 1035-1039.	21.4	1,893
3	Draft genome sequence of chickpea ( <i>Cicer arietinum</i> ) provides a resource for trait improvement. <i>Nature Biotechnology</i> , 2013, 31, 240-246.	17.5	1,049
4	The <i>Brassica oleracea</i> genome reveals the asymmetrical evolution of polyploid genomes. <i>Nature Communications</i> , 2014, 5, 3930.	12.8	918
5	Wild emmer genome architecture and diversity elucidate wheat evolution and domestication. <i>Science</i> , 2017, 357, 93-97.	12.6	781
6	The transcriptional landscape of polyploid wheat. <i>Science</i> , 2018, 361, .	12.6	768
7	Durum wheat genome highlights past domestication signatures and future improvement targets. <i>Nature Genetics</i> , 2019, 51, 885-895.	21.4	576
8	Segmental Structure of the <i>Brassica napus</i> Genome Based on Comparative Analysis With <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2005, 171, 765-781.	2.9	516
9	Multiple wheat genomes reveal global variation in modern breeding. <i>Nature</i> , 2020, 588, 277-283.	27.8	513
10	Transcriptome and methylome profiling reveals relics of genome dominance in the mesopolyploid <i>Brassica oleracea</i> . <i>Genome Biology</i> , 2014, 15, R77.	9.6	456
11	The genome of flax ( <i>Linum usitatissimum</i> ) assembled <i>de novo</i> from short shotgun sequence reads. <i>Plant Journal</i> , 2012, 72, 461-473.	5.7	415
12	The pangenome of an agronomically important crop plant <i>Brassica oleracea</i> . <i>Nature Communications</i> , 2016, 7, 13390.	12.8	375
13	Molecular characterization of <i>Brassica napus</i> NAC domain transcriptional activators induced in response to biotic and abiotic stress. <i>Plant Molecular Biology</i> , 2003, 53, 383-397.	3.9	271
14	Comparison of Flowering Time Genes in <i>Brassica rapa</i> , <i>B. napus</i> and <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 1997, 146, 1123-1129.	2.9	263
15	A haplotype map of allohexaploid wheat reveals distinct patterns of selection on homoeologous genomes. <i>Genome Biology</i> , 2015, 16, 48.	8.8	216
16	A high-density SNP genotyping array for <i>Brassica napus</i> and its ancestral diploid species based on optimised selection of single-locus markers in the allotetraploid genome. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1887-1899.	3.6	205
17	Long-read sequence assembly: a technical evaluation in barley. <i>Plant Cell</i> , 2021, 33, 1888-1906.	6.6	180
18	Polyloid Evolution of the Brassicaceae during the Cenozoic Era. <i>Plant Cell</i> , 2014, 26, 2777-2791.	6.6	165

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19	Patterns of differential gene expression in <i>Brassica napus</i> cultivars infected with <i>Sclerotinia sclerotiorum</i> . <i>Molecular Plant Pathology</i> , 2009, 10, 635-649.	4.2	140
20	Chromosome-scale genome assembly provides insights into rye biology, evolution and agronomic potential. <i>Nature Genetics</i> , 2021, 53, 564-573.	21.4	138
21	Detection and Effects of a Homeologous Reciprocal Transposition in <i>Brassica napus</i> . <i>Genetics</i> , 2003, 165, 1569-1577.	2.9	131
22	Desaturase multigene families of <i>Brassica napus</i> arose through genome duplication. <i>Theoretical and Applied Genetics</i> , 1997, 94, 583-591.	3.6	127
23	Independent deletions of a pathogen-resistance gene in <i>Brassica</i> and <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 15843-15848.	7.1	124
24	Gene expression analysis of flax seed development. <i>BMC Plant Biology</i> , 2011, 11, 74.	3.6	112
25	Alignment of the conserved C genomes of <i>Brassica oleracea</i> and <i>Brassica napus</i> . <i>Theoretical and Applied Genetics</i> , 1996, 93-93, 833-839.	3.6	107
26	Conserved structure and function of the <i>Arabidopsis</i> flowering time gene <i>CONSTANS</i> in <i>Brassica napus</i> . <i>Plant Molecular Biology</i> , 1998, 37, 763-772.	3.9	103
27	A high-contiguity <i>Brassica nigra</i> genome localizes active centromeres and defines the ancestral <i>Brassica</i> genome. <i>Nature Plants</i> , 2020, 6, 929-941.	9.3	94
28	Interaction of <i>Sclerotinia sclerotiorum</i> with <i>Brassica napus</i> : cloning and characterization of endo- and exo-polygalacturonases expressed during saprophytic and parasitic modes. <i>Fungal Genetics and Biology</i> , 2004, 41, 754-765.	2.1	93
29	Characterisation of resistance to turnip mosaic virus in oilseed rape ( <i>Brassica napus</i> ) and genetic mapping of TuRB01. <i>Theoretical and Applied Genetics</i> , 1999, 99, 1149-1154.	3.6	91
30	Comprehensive Transcriptome Assembly of Chickpea ( <i>Cicer arietinum</i> L.) Using Sanger and Next Generation Sequencing Platforms: Development and Applications. <i>PLoS ONE</i> , 2014, 9, e86039.	2.5	87
31	Molecular cloning of a cDNA from <i>Brassica napus</i> L. for a homologue of acyl-CoA-binding protein. <i>Plant Molecular Biology</i> , 1994, 25, 917-920.	3.9	84
32	Gene-based SNP discovery and genetic mapping in pea. <i>Theoretical and Applied Genetics</i> , 2014, 127, 2225-2241.	3.6	74
33	Two <i>Brassica napus</i> polygalacturonase inhibitory protein genes are expressed at different levels in response to biotic and abiotic stresses. <i>Planta</i> , 2003, 217, 299-308.	3.2	70
34	Inheritance of Race-Specific Resistance to <i>Xanthomonas campestris</i> pv. <i>campestris</i> in <i>Brassica</i> Genomes. <i>Phytopathology</i> , 2002, 92, 1134-1141.	2.2	69
35	Interaction of <i>Sclerotinia sclerotiorum</i> with a resistant <i>Brassica napus</i> cultivar: expressed sequence tag analysis identifies genes associated with fungal pathogenesis. <i>Fungal Genetics and Biology</i> , 2004, 41, 735-753.	2.1	67
36	Genetic mapping of the novel Turnip mosaic virus resistance gene TuRB03 in <i>Brassica napus</i> . <i>Theoretical and Applied Genetics</i> , 2003, 107, 1169-1173.	3.6	60

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37	The developmental transcriptome atlas of the biofuel crop <i>Camelina sativa</i> . <i>Plant Journal</i> , 2016, 88, 879-894.	5.7	60
38	A Mutant <i>Brassica napus</i> (Canola) Population for the Identification of New Genetic Diversity via TILLING and Next Generation Sequencing. <i>PLoS ONE</i> , 2013, 8, e84303.	2.5	59
39	The Transcriptional Landscape of Polyploid Wheats and Their Diploid Ancestors during Embryogenesis and Grain Development. <i>Plant Cell</i> , 2019, 31, 2888-2911.	6.6	57
40	Analysis of B-Genome Chromosome Introgression in Interspecific Hybrids of <i>Brassica napus</i> and <i>B. carinata</i> . <i>Genetics</i> , 2011, 187, 659-673.	2.9	48
41	Diversity Array Technology Markers: Genetic Diversity Analyses and Linkage Map Construction in Rapeseed ( <i>Brassica napus</i> L.). <i>DNA Research</i> , 2012, 19, 51-65.	3.4	47
42	Mapping the Brassica Genome. <i>Outlook on Agriculture</i> , 1993, 22, 85-92.	3.4	45
43	Identification of a peptide methionine sulfoxide reductase gene in an oleosin promoter from <i>Brassica napus</i> . <i>Plant Journal</i> , 1996, 10, 235-242.	5.7	41
44	Introgression of <i>Brassica rapa</i> subsp. <i>sylvestris</i> blackleg resistance into <i>B. napus</i> . <i>Molecular Breeding</i> , 2012, 30, 1495-1506.	2.1	41
45	Optical and physical mapping with local finishing enables megabase-scale resolution of agronomically important regions in the wheat genome. <i>Genome Biology</i> , 2018, 19, 112.	8.8	41
46	Buthionine sulfoximine (BSO)-mediated improvement in cultured embryo quality in vitro entails changes in ascorbate metabolism, meristem development and embryo maturation. <i>Planta</i> , 2008, 228, 255-272.	3.2	40
47	Genomic DNA Enrichment Using Sequence Capture Microarrays: a Novel Approach to Discover Sequence Nucleotide Polymorphisms (SNP) in <i>Brassica napus</i> L. <i>PLoS ONE</i> , 2013, 8, e81992.	2.5	40
48	Conservation of NON-EXPRESSOR OF PATHOGENESIS-RELATED GENES1 function between <i>Arabidopsis thaliana</i> and <i>Brassica napus</i> . <i>Physiological and Molecular Plant Pathology</i> , 2007, 71, 174-183.	2.5	33
49	Genetic mapping of SrCad and SNP marker development for marker-assisted selection of Ug99 stem rust resistance in wheat. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1373-1382.	3.6	33
50	Assessing Diversity in the <i>Camelina</i> Genus Provides Insights into the Genome Structure of <i>Camelina sativa</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1297-1308.	1.8	33
51	High-density single nucleotide polymorphism (SNP) array mapping in <i>Brassica oleracea</i> : identification of QTL associated with carotenoid variation in broccoli florets. <i>Theoretical and Applied Genetics</i> , 2014, 127, 2051-2064.	3.6	30
52	Quantitative trait loci for resistance to stripe rust of wheat revealed using global field nurseries and opportunities for stacking resistance genes. <i>Theoretical and Applied Genetics</i> , 2017, 130, 2617-2635.	3.6	27
53	Transcripts of sulphur metabolic genes are co-ordinately regulated in developing seeds of common bean lacking phaseolin and major lectins. <i>Journal of Experimental Botany</i> , 2012, 63, 6283-6295.	4.8	25
54	Mapping quantitative trait loci associated with leaf rust resistance in five spring wheat populations using single nucleotide polymorphism markers. <i>PLoS ONE</i> , 2020, 15, e0230855.	2.5	25

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55	Mapping Seed Phytic Acid Concentration and Iron Bioavailability in a Pea Recombinant Inbred Line Population. <i>Crop Science</i> , 2015, 55, 828-836.	1.8	23
56	High density mapping and haplotype analysis of the major stem-solidness locus SSt1 in durum and common wheat. <i>PLoS ONE</i> , 2017, 12, e0175285.	2.5	23
57	Alternative splicing dynamics and evolutionary divergence during embryogenesis in wheat species. <i>Plant Biotechnology Journal</i> , 2021, 19, 1624-1643.	8.3	23
58	Transcriptome Profiling Identifies Candidate Genes Associated with the Accumulation of Distinct Sulfur $\text{I}^3$ -Glutamyl Dipeptides in <i>Phaseolus vulgaris</i> and <i>Vigna mungo</i> Seeds. <i>Frontiers in Plant Science</i> , 2013, 4, 60.	3.6	21
59	Genome resequencing and simple sequence repeat markers reveal the existence of divergent lineages in the Canadian <i>Puccinia striiformis</i> f. sp. <i>tritici</i> population with extensive DNA methylation. <i>Environmental Microbiology</i> , 2018, 20, 1498-1515.	3.8	21
60	Isolation and characterization of a GCN5-interacting protein from <i>Arabidopsis thaliana</i> . <i>Planta</i> , 2007, 225, 1367-1379.	3.2	20
61	Development and Validation of <i>Thinopyrum elongatum</i> "Expressed Molecular Markers Specific for the Long Arm of Chromosome 7E. <i>Crop Science</i> , 2016, 56, 354-364.	1.8	20
62	High-density genetic mapping of a major QTL for resistance to multiple races of loose smut in a tetraploid wheat cross. <i>PLoS ONE</i> , 2018, 13, e0192261.	2.5	18
63	Structural features of two major nucleolar organizer regions (NORs), <i>NorB1</i> and <i>NorB2</i> , and chromosome-specific rRNA gene expression in wheat. <i>Plant Journal</i> , 2018, 96, 1148-1159.	5.7	17
64	Genetic analysis of resistance to stripe rust in durum wheat ( <i>Triticum turgidum</i> L. var. durum). <i>PLoS ONE</i> , 2018, 13, e0203283.	2.5	17
65	Mapping quantitative trait loci associated with common bunt resistance in a spring wheat ( <i>Triticum</i> ) Tj ETQq1 1 0.784314 rgBT / Over	3.6	17
66	A saturated SNP linkage map for the orange wheat blossom midge resistance gene Sm1. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1507-1517.	3.6	15
67	Deep neural networks for genomic prediction do not estimate marker effects. <i>Plant Genome</i> , 2021, 14, e20147.	2.8	15
68	High Density Mapping of Quantitative Trait Loci Conferring Gluten Strength in Canadian Durum Wheat. <i>Frontiers in Plant Science</i> , 2020, 11, 170.	3.6	14
69	Machine learning analyses of methylation profiles uncovers tissue-specific gene expression patterns in wheat. <i>Plant Genome</i> , 2020, 13, e20027.	2.8	13
70	Comparison of Five Major Trichome Regulatory Genes in <i>Brassica villosa</i> with Orthologues within the Brassicaceae. <i>PLoS ONE</i> , 2014, 9, e95877.	2.5	8
71	The biochemical composition and transcriptome of cotyledons from <i>Brassica napus</i> lines expressing the AtGL3 transcription factor and exhibiting reduced flea beetle feeding. <i>BMC Plant Biology</i> , 2018, 18, 64.	3.6	8
72	Conditional Mapping Identified Quantitative Trait Loci for Grain Protein Concentration Expressing Independently of Grain Yield in Canadian Durum Wheat. <i>Frontiers in Plant Science</i> , 2021, 12, 642955.	3.6	6

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73	Sources of genomic diversity in the self-fertile plant pathogen, <i>Sclerotinia sclerotiorum</i> , and consequences for resistance breeding. PLoS ONE, 2022, 17, e0262891.	2.5	3