

# Andrew G Sharpe

## List of Publications by Year in descending order

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Version: 2024-02-01

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  | Sources of genomic diversity in the self-fertile plant pathogen, <i>Sclerotinia sclerotiorum</i> , and consequences for resistance breeding. <i>PLoS ONE</i> , 2022, 17, e0262891.  | 2.5  | 3         |
| 2  | Chromosome-scale genome assembly provides insights into rye biology, evolution and agronomic potential. <i>Nature Genetics</i> , 2021, 53, 564-573.   | 21.4 | 138       |
| 3  | 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         |
| 4  | Alternative splicing dynamics and evolutionary divergence during embryogenesis in wheat species. <i>Plant Biotechnology Journal</i> , 2021, 19, 1624-1643.  | 8.3  | 23        |
| 5  | Long-read sequence assembly: a technical evaluation in barley. <i>Plant Cell</i> , 2021, 33, 1888-1906.   | 6.6  | 180       |
| 6  | Deep neural networks for genomic prediction do not estimate marker effects. <i>Plant Genome</i> , 2021, 14, e20147.   | 2.8  | 15        |
| 7  | Multiple wheat genomes reveal global variation in modern breeding. <i>Nature</i> , 2020, 588, 277-283.  | 27.8 | 513       |
| 8  | 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        |
| 9  | 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        |
| 10 | Machine learning analyses of methylation profiles uncovers tissue-specific gene expression patterns in wheat. <i>Plant Genome</i> , 2020, 13, e20027.   | 2.8  | 13        |
| 11 | 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        |
| 12 | 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        |
| 13 | 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        |
| 14 | Mapping quantitative trait loci associated with common bunt resistance in a spring wheat ( <i>Triticum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5  | 3.8  | 17        |
| 15 | Durum wheat genome highlights past domestication signatures and future improvement targets. <i>Nature Genetics</i> , 2019, 51, 885-895.   | 21.4 | 576       |
| 16 | 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        |
| 17 | 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         |
| 18 | Structural features of two major nucleolar organizer regions (NORs), <i>Norâ€1</i> and <i>Norâ€2</i> , and chromosome-specific rRNA gene expression in wheat. <i>Plant Journal</i> , 2018, 96, 1148-1159.   | 5.7  | 17        |

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|----|---|------|-----------|
| 19 | Genetic analysis of resistance to stripe rust in durum wheat ( <i>Triticum turgidum</i> L. var. durum). PLoS ONE, 2018, 13, e0203283.   | 2.5  | 17        |
| 20 | Optical and physical mapping with local finishing enables megabase-scale resolution of agronomically important regions in the wheat genome. Genome Biology, 2018, 19, 112.  | 8.8  | 41        |
| 21 | The transcriptional landscape of polyploid wheat. Science, 2018, 361, .   | 12.6 | 768       |
| 22 | High-density genetic mapping of a major QTL for resistance to multiple races of loose smut in a tetraploid wheat cross. PLoS ONE, 2018, 13, e0192261.   | 2.5  | 18        |
| 23 | Wild emmer genome architecture and diversity elucidate wheat evolution and domestication. Science, 2017, 357, 93-97.  | 12.6 | 781       |
| 24 | Quantitative trait loci for resistance to stripe rust of wheat revealed using global field nurseries and opportunities for stacking resistance genes. Theoretical and Applied Genetics, 2017, 130, 2617-2635.                       | 3.6  | 27        |
| 25 | High density mapping and haplotype analysis of the major stem-solidness locus SSt1 in durum and common wheat. PLoS ONE, 2017, 12, e0175285.   | 2.5  | 23        |
| 26 | A high-density SNP genotyping array for Brassica napus and its ancestral diploid species based on optimised selection of single-locus markers in the allotetraploid genome. Theoretical and Applied Genetics, 2016, 129, 1887-1899. | 3.6  | 205       |
| 27 | Development and Validation of <i>Thinopyrum elongatum</i> “Expressed Molecular Markers Specific for the Long Arm of Chromosome 7E. Crop Science, 2016, 56, 354-364.   | 1.8  | 20        |
| 28 | Genetic mapping of SrCad and SNP marker development for marker-assisted selection of Ug99 stem rust resistance in wheat. Theoretical and Applied Genetics, 2016, 129, 1373-1382.  | 3.6  | 33        |
| 29 | The developmental transcriptome atlas of the biofuel crop <i>Camelina sativa</i> . Plant Journal, 2016, 88, 879-894.  | 5.7  | 60        |
| 30 | The pangenome of an agronomically important crop plant Brassica oleracea. Nature Communications, 2016, 7, 13390.  | 12.8 | 375       |
| 31 | A saturated SNP linkage map for the orange wheat blossom midge resistance gene Sm1. Theoretical and Applied Genetics, 2016, 129, 1507-1517.   | 3.6  | 15        |
| 32 | Mapping Seed Phytic Acid Concentration and Iron Bioavailability in a Pea Recombinant Inbred Line Population. Crop Science, 2015, 55, 828-836.   | 1.8  | 23        |
| 33 | A haplotype map of allohexaploid wheat reveals distinct patterns of selection on homoeologous genomes. Genome Biology, 2015, 16, 48.  | 8.8  | 216       |
| 34 | Comparison of Five Major Trichome Regulatory Genes in Brassica villosa with Orthologues within the Brassicaceae. PLoS ONE, 2014, 9, e95877.   | 2.5  | 8         |
| 35 | Gene-based SNP discovery and genetic mapping in pea. Theoretical and Applied Genetics, 2014, 127, 2225-2241.  | 3.6  | 74        |
| 36 | High-density single nucleotide polymorphism (SNP) array mapping in Brassica oleracea: identification of QTL associated with carotenoid variation in broccoli florets. Theoretical and Applied Genetics, 2014, 127, 2051-2064.       | 3.6  | 30        |

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|----|---|------|-----------|
| 37 | Early allopolyploid evolution in the post-Neolithic <i>Brassica napus</i> oilseed genome. <i>Science</i> , 2014, 345, 950-953.  | 12.6 | 2,089     |
| 38 | Polyploid Evolution of the Brassicaceae during the Cenozoic Era. <i>Plant Cell</i> , 2014, 26, 2777-2791.   | 6.6  | 165       |
| 39 | The <i>Brassica oleracea</i> genome reveals the asymmetrical evolution of polyploid genomes. <i>Nature Communications</i> , 2014, 5, 3930.  | 12.8 | 918       |
| 40 | 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        |
| 41 | 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       |
| 42 | 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     |
| 43 | Transcriptome Profiling Identifies Candidate Genes Associated with the Accumulation of Distinct Sulfur <sup>13</sup> -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        |
| 44 | 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        |
| 45 | 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        |
| 46 | 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        |
| 47 | 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        |
| 48 | 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       |
| 49 | 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        |
| 50 | The genome of the mesopolyploid crop species <i>Brassica rapa</i> . <i>Nature Genetics</i> , 2011, 43, 1035-1039.   | 21.4 | 1,893     |
| 51 | Gene expression analysis of flax seed development. <i>BMC Plant Biology</i> , 2011, 11, 74.   | 3.6  | 112       |
| 52 | 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        |
| 53 | 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       |
| 54 | Buthionine sulfoximine (BSO)-mediated improvement in cultured embryo quality <i>in vitro</i> entails changes in ascorbate metabolism, meristem development and embryo maturation. <i>Planta</i> , 2008, 228, 255-272.                                 | 3.2  | 40        |

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|----|--|-----|-----------|
| 55 | 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        |
| 56 | Isolation and characterization of a GCN5-interacting protein from <i>Arabidopsis thaliana</i> . <i>Planta</i> , 2007, 225, 1367-1379.  | 3.2 | 20        |
| 57 | 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       |
| 58 | 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        |
| 59 | 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        |
| 60 | 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       |
| 61 | 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        |
| 62 | 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        |
| 63 | Detection and Effects of a Homeologous Reciprocal Transposition in <i>Brassica napus</i> . <i>Genetics</i> , 2003, 165, 1569-1577.   | 2.9 | 131       |
| 64 | 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        |
| 65 | 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        |
| 66 | Conserved structure and function of the <i>Arabidopsis</i> flowering time gene CONSTANS in <i>Brassica napus</i> . <i>Plant Molecular Biology</i> , 1998, 37, 763-772.   | 3.9 | 103       |
| 67 | 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       |
| 68 | 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       |
| 69 | 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       |
| 70 | Identification of a peptide methionine sulphoxide reductase gene in an oleosin promoter from <i>Brassica napus</i> . <i>Plant Journal</i> , 1996, 10, 235-242.   | 5.7 | 41        |
| 71 | 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       |
| 72 | 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        |

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|----|---|-----|-----------|
| 73 | Mapping the Brassica Genome. Outlook on Agriculture, 1993, 22, 85-92. | 3.4 | 45        |