# Kassa Semagn

List of Publications by Year
in descending order

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|---|---|---|---|
| 76 papers | 4,742 citations | 147801<br>31 h-index | 106344<br>65 g-index |
| 77 all docs | 77 docs citations | 77 times ranked | 4707 citing authors |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 1 | Single nucleotide polymorphism genotyping using Kompetitive Allele Specific PCR (KASP): overview of the technology and its application in crop improvement. Molecular Breeding, 2014, 33, 1-14. | 2.1 | 784 |
| 2 | Genetic Gains in Grain Yield Through Genomic Selection in Eight Bi‐parental Maize Populations under Drought Stress. Crop Science, 2015, 55, 154-163. | 1.8 | 253 |
| 3 | Effectiveness of Genomic Prediction of Maize Hybrid Performance in Different Breeding Populations and Environments. G3: Genes, Genomes, Genetics, 2012, 2, 1427-1436. | 1.8 | 242 |
| 4 | Genomic Prediction in Maize Breeding Populations with Genotyping-by-Sequencing. G3: Genes, Genomes, Genetics, 2013, 3, 1903-1926. | 1.8 | 235 |
| 5 | High-resolution genetic mapping of maize pan-genome sequence anchors. Nature Communications, 2015, 6, 6914. | 12.8 | 213 |
| 6 | Genomic prediction in biparental tropical maize populations in water-stressed and well-watered environments using low-density and GBS SNPs. Heredity, 2015, 114, 291-299. | 2.6 | 187 |
| 7 | Distribution of DArT, AFLP, and SSR markers in a genetic linkage map of a doubled-haploid hexaploid wheat population. Genome, 2006, 49, 545-555. | 2.0 | 152 |
| 8 | Genome-wide association and genomic prediction of resistance to maize lethal necrosis disease in tropical maize germplasm. Theoretical and Applied Genetics, 2015, 128, 1957-1968. | 3.6 | 145 |
| 9 | Effect of Trait Heritability, Training Population Size and Marker Density on Genomic Prediction Accuracy Estimation in 22 bi-parental Tropical Maize Populations. Frontiers in Plant Science, 2017, 8, 1916. | 3.6 | 145 |
| 10 | Meta-analyses of QTL for grain yield and anthesis silking interval in 18 maize populations evaluated under water-stressed and well-watered environments. BMC Genomics, 2013, 14, 313. | 2.8 | 129 |
| 11 | Molecular characterization of diverse CIMMYT maize inbred lines from eastern and southern Africa using single nucleotide polymorphic markers. BMC Genomics, 2012, 13, 113. | 2.8 | 109 |
| 12 | Optimal Design of Preliminary Yield Trials with Genome‐Wide Markers. Crop Science, 2014, 54, 48-59. | 1.8 | 100 |
| 13 | The inheritance of anther extrusion in hexaploid wheat and its relationship to *Fusarium* head blight resistance and deoxynivalenol content. Plant Breeding, 2010, 129, 149-155. | 1.9 | 98 |
| 14 | Molecular characterization of CIMMYT maize inbred lines with genotyping-by-sequencing SNPs. Theoretical and Applied Genetics, 2016, 129, 753-765. | 3.6 | 94 |
| 15 | Quantitative Trait Loci Controlling Fusarium Head Blight Resistance and Low Deoxynivalenol Content in Hexaploid Wheat Population from 'Arina' and NK93604. Crop Science, 2007, 47, 294-303. | 1.8 | 89 |
| 16 | Comparison of Kompetitive Allele Specific PCR (KASP) and genotyping by sequencing (GBS) for quality control analysis in maize. BMC Genomics, 2015, 16, 908. | 2.8 | 89 |
| 17 | The genetic dissection of quantitative traits in crops. Electronic Journal of Biotechnology, 2010, 13, 0-0. | 2.2 | 89 |
| 18 | Genome‐wide Association for Plant Height and Flowering Time across 15 Tropical Maize Populations under Managed Drought Stress and Well‐Watered Conditions in Sub‐Saharan Africa. Crop Science, 2016, 56, 2365-2378. | 1.8 | 88 |

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| 19 | Genetic Variation and Population Structure of Oryza glaberrima and Development of a Mini-Core Collection Using DArTseq. Frontiers in Plant Science, 2017, 8, 1748. | 3.6 | 71 |
| 20 | Improving Maize Grain Yield under Drought Stress and Non‐stress Environments in Sub‐Saharan Africa using Marker‐Assisted Recurrent Selection. Crop Science, 2016, 56, 344-353. | 1.8 | 70 |
| 21 | Quality control genotyping for assessment of genetic identity and purity in diverse tropical maize inbred lines. Theoretical and Applied Genetics, 2012, 125, 1487-1501. | 3.6 | 68 |
| 22 | QTLs associated with agronomic traits in the Attila Ã— CDC Go spring wheat population evaluated under conventional management. PLoS ONE, 2017, 12, e0171528. | 2.5 | 68 |
| 23 | Quantitative Trait Loci Mapping and Molecular Breeding for Developing Stress Resilient Maize for Sub‐Saharan Africa. Crop Science, 2015, 55, 1449-1459. | 1.8 | 61 |
| 24 | Fine mapping of Msv1, a major QTL for resistance to Maize Streak Virus leads to development of production markers for breeding pipelines. Theoretical and Applied Genetics, 2015, 128, 1839-1854. | 3.6 | 61 |
| 25 | Effect of source germplasm and season on the in vivo haploid induction rate in tropical maize. Euphytica, 2011, 180, 219-226. | 1.2 | 59 |
| 26 | Ecogeographical distribution of wild, weedy and cultivated Sorghum bicolor (L.) Moench in Kenya: implications for conservation and crop-to-wild gene flow. Genetic Resources and Crop Evolution, 2010, 57, 243-253. | 1.6 | 49 |
| 27 | Genetic structure and relationships within and between cultivated and wild sorghum (Sorghum) Tj ETQq1 1 0.784314 rgBT /Overlock 2011, 122, 989-1004. | 3.6 | 48 |
| 28 | A Genomic Selection Index Applied to Simulated and Real Data. G3: Genes, Genomes, Genetics, 2015, 5, 2155-2164. | 1.8 | 42 |
| 29 | QTLs Associated with Agronomic Traits in the Cutler Ã— AC Barrie Spring Wheat Mapping Population Using Single Nucleotide Polymorphic Markers. PLoS ONE, 2016, 11, e0160623. | 2.5 | 36 |
| 30 | Genetic variation and population structure of maize inbred lines adapted to the mid-altitude sub-humid maize agro-ecology of Ethiopia using single nucleotide polymorphic (SNP) markers. BMC Genomics, 2017, 18, 777. | 2.8 | 36 |
| 31 | Two Major Resistance Quantitative Trait Loci are Required to Counteract the Increased Susceptibility to Fusarium Head Blight of the <i>Rht‐D1b</i> Dwarfing Gene in Wheat. Crop Science, 2011, 51, 2430-2438. | 1.8 | 35 |
| 32 | Genetic relationships among ten endod types as revealed by a combination of morphological, RAPD and AFLP markers. Hereditas, 2002, 137, 149-156. | 1.4 | 34 |
| 33 | Genetic distance among doubled haploid maize lines and their testcross performance under drought stress and non-stress conditions. Euphytica, 2013, 192, 379-392. | 1.2 | 34 |
| 34 | Medicinal use and social status of the soap berry endod (Phytolacca dodecandra) in Ethiopia. Journal of Ethnopharmacology, 2003, 85, 269-277. | 4.1 | 32 |
| 35 | Molecular profiling of an interspecific rice population derived from a cross between WAB 56-104 (Oryza sativa) and CG 14 (Oryza glaberrima). African Journal of Biotechnology, 2007, 6, 2014-2022. | 0.6 | 30 |
| 36 | Mapping QTLs Controlling Agronomic Traits in the 'Attila' Ã— 'CDC Go' Spring Wheat Population under Organic Management using 90K SNP Array. Crop Science, 2017, 57, 365-377. | 1.8 | 30 |

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|---|---------|-----|-----------|
| 37 | Genome-wide association mapping of genomic regions associated with phenotypic traits in Canadian western spring wheat. Molecular Breeding, 2017, 37, 1. | 2.1 | 30 |
| 38 | Discovery and validation of genomic regions associated with resistance to maize lethal necrosis in four biparental populations. Molecular Breeding, 2018, 38, 66. | 2.1 | 29 |
| 39 | Comparison of multivariate methods for the analysis of genetic resources and adaptation in Phytolacca dodecandra using RAPD. Theoretical and Applied Genetics, 2000, 101, 1145-1154. | 3.6 | 28 |
| 40 | Leaf Tissue Sampling and DNA Extraction Protocols. Methods in Molecular Biology, 2014, 1115, 53-67. | 0.9 | 27 |
| 41 | Relationships between heterosis, genetic distances and specific combining ability among CIMMYT and Zimbabwe developed maize inbred lines under stress and optimal conditions. Euphytica, 2015, 204, 635-647. | 1.2 | 27 |
| 42 | Assessment of Genetic Variation and Population Structure of Diverse Rice Genotypes Adapted to Lowland and Upland Ecologies in Africa Using SNPs. Frontiers in Plant Science, 2018, 9, 446. | 3.6 | 27 |
| 43 | Population Structure and Genomewide Association Analysis of Resistance to Disease and Insensitivity to Ptr Toxins in Canadian Spring Wheat Using 90K SNP Array. Crop Science, 2017, 57, 1522-1539. | 1.8 | 24 |
| 44 | Physical mapping of QTL associated with agronomic and end-use quality traits in spring wheat under conventional and organic management systems. Theoretical and Applied Genetics, 2021, 134, 3699-3719. | 3.6 | 23 |
| 45 | Development of species diagnostic SNP markers for quality control genotyping in four rice (Oryza L.) species. Molecular Breeding, 2018, 38, 131. | 2.1 | 22 |
| 46 | Local scale patterns of gene flow and genetic diversity in a crop–wild–weedy complex of sorghum (Sorghum bicolor (L.) Moench) under traditional agricultural field conditions in Kenya. Conservation Genetics, 2012, 13, 1059-1071. | 1.5 | 21 |
| 47 | Genetic relationships and structure among open-pollinated maize varieties adapted to eastern and southern Africa using microsatellite markers. Molecular Breeding, 2014, 34, 1423-1435. | 2.1 | 21 |
| 48 | Mapping of QTLs associated with resistance to common bunt, tan spot, leaf rust, and stripe rust in a spring wheat population. Molecular Breeding, 2017, 37, 1. | 2.1 | 21 |
| 49 | QTL Mapping in Three Rice Populations Uncovers Major Genomic Regions Associated with African Rice Gall Midge Resistance. PLoS ONE, 2016, 11, e0160749. | 2.5 | 19 |
| 50 | Performance and grain yield stability of maize populations developed using marker-assisted recurrent selection and pedigree selection procedures. Euphytica, 2016, 208, 285-297. | 1.2 | 18 |
| 51 | Comparisons of molecular diversity indices, selective sweeps and population structure of African rice with its wild progenitor and Asian rice. Theoretical and Applied Genetics, 2019, 132, 1145-1158. | 3.6 | 16 |
| 52 | Mapping QTL Associated with Stripe Rust, Leaf Rust, and Leaf Spotting in a Canadian Spring Wheat Population. Crop Science, 2019, 59, 650-658. | 1.8 | 15 |
| 53 | Genetic purity and patterns of relationships among tropical highland adapted quality protein and normal maize inbred lines using microsatellite markers. Euphytica, 2015, 204, 49-61. | 1.2 | 14 |
| 54 | Molecular diversity and selective sweeps in maize inbred lines adapted to African highlands. Scientific Reports, 2019, 9, 13490. | 3.3 | 14 |

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|---|---------|-----|-----------|
| 55 | Comparisons of sampling methods for assessing intra- and inter-accession genetic diversity in three rice species using genotyping by sequencing. Scientific Reports, 2020, 10, 13995. | 3.3 | 13 |
| 56 | Physical Mapping of QTL in Four Spring Wheat Populations under Conventional and Organic Management Systems. I. Earliness. Plants, 2021, 10, 853. | 3.5 | 13 |
| 57 | Genomic Predictions for Common Bunt, FHB, Stripe Rust, Leaf Rust, and Leaf Spotting Resistance in Spring Wheat. Genes, 2022, 13, 565. | 2.4 | 13 |
| 58 | Title is missing!. Genetic Resources and Crop Evolution, 2003, 50, 649-661. | 1.6 | 12 |
| 59 | Resistance of tropical maize genotypes to the larger grain borer. Journal of Pest Science, 2012, 85, 267-275. | 3.7 | 11 |
| 60 | Allelic variation and effects of 16 candidate genes on disease resistance in western Canadian spring wheat cultivars. Molecular Breeding, 2017, 37, 1. | 2.1 | 11 |
| 61 | Analysis of Genetic Diversity and Structure in Ethiopian Populations of Phytolacca Dodecandra Using RAPD. Hereditas, 2004, 135, 51-60. | 1.4 | 10 |
| 62 | Genetic Diversity among Selected Elite CIMMYT Maize Hybrids in East and Southern Africa. Crop Science, 2017, 57, 2395-2404. | 1.8 | 10 |
| 63 | Genetic Relationships among Rice Varieties Based On Expressed Sequence Tags and Microsatellite Markers. Asian Journal of Plant Sciences, 2006, 5, 429-437. | 0.4 | 10 |
| 64 | Genome-based prediction of agronomic traits in spring wheat under conventional and organic management systems. Theoretical and Applied Genetics, 2021, 135, 537. | 3.6 | 10 |
| 65 | Genetic diversity and selective sweeps in historical and modern Canadian spring wheat cultivars using the 90K SNP array. Scientific Reports, 2021, 11, 23773. | 3.3 | 10 |
| 66 | Comparison of Weighted and Unweighted Stageâ€Wise Analysis for Genomeâ€Wide Association Studies and Genomic Selection. Crop Science, 2019, 59, 2572-2584. | 1.8 | 9 |
| 67 | Phenotypic performance and associated QTL of â€˜Peaceâ€™ Ã— â€˜CDC Stanleyâ€™ mapping population under conventional and organic management systems. Crop Science, 2021, 61, 3469-3483. | 1.8 | 8 |
| 68 | Analysis of unigenes involved in lateral root development in Bupleurum chinense and B. scorzonerifolium. Planta, 2021, 253, 128. | 3.2 | 7 |
| 69 | Parental genome contribution in maize DH lines derived from six backcross populations using genotyping by sequencing. Euphytica, 2015, 202, 129-139. | 1.2 | 6 |
| 70 | Assessment of the genetic diversity and pattern of relationship of West African sorghum accessions using microsatellite markers. African Journal of Biotechnology, 2014, 13, 1503-1514. | 0.6 | 5 |
| 71 | Genomeâ€wide association mapping of agronomic traits and grain characteristics in spring wheat under conventional and organic management systems. Crop Science, 0, , . | 1.8 | 5 |
| 72 | Biotechnology Success Stories by the Consultative Group on International Agriculture Research (CGIAR) System. Science Policy Reports, 2014, , 95-114. | 0.1 | 4 |

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|---|---------|----|-----------|
| 73 | Comparison of single-trait and multi-trait genomic predictions on agronomic and disease resistance traits in spring wheat. Theoretical and Applied Genetics, 2022, 135, 2747-2767. | 3.6 | 4 |
| 74 | Genomic Prediction Accuracy of Stripe Rust in Six Spring Wheat Populations by Modeling Genotype by Environment Interaction. Plants, 2022, 11, 1736. | 3.5 | 3 |
| 75 | Patterns of phenotypic variation in endod (Phytolacca dodecandra) from Ethiopia. African Journal of Biotechnology, 2004, 3, 32-39. | 0.6 | 1 |
| 76 | Rotational diversity effects in a triticale-based cropping system. Cereal Research Communications, 2018, 46, 717-728. | 1.6 | 1 |