

# Kassa Semagn

## List of Publications by Year in descending order

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76  
papers

4,742  
citations

147801

31  
h-index

106344

65  
g-index

77  
all docs

77  
docs citations

77  
times ranked

4707  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic Predictions for Common Bunt, FHB, Stripe Rust, Leaf Rust, and Leaf Spotting Resistance in Spring Wheat. <i>Genes</i> , 2022, 13, 565.	2.4	13
2	Comparison of single-trait and multi-trait genomic predictions on agronomic and disease resistance traits in spring wheat. <i>Theoretical and Applied Genetics</i> , 2022, 135, 2747-2767.	3.6	4
3	Genomic Prediction Accuracy of Stripe Rust in Six Spring Wheat Populations by Modeling Genotype by Environment Interaction. <i>Plants</i> , 2022, 11, 1736.	3.5	3
4	Physical Mapping of QTL in Four Spring Wheat Populations under Conventional and Organic Management Systems. I. Earliness. <i>Plants</i> , 2021, 10, 853.	3.5	13
5	Analysis of unigenes involved in lateral root development in <i>Bupleurum chinense</i> and <i>B. scorzonerifolium</i> . <i>Planta</i> , 2021, 253, 128.	3.2	7
6	Phenotypic performance and associated QTL of "Peace" – "CDC Stanley" mapping population under conventional and organic management systems. <i>Crop Science</i> , 2021, 61, 3469-3483.	1.8	8
7	Physical mapping of QTL associated with agronomic and end-use quality traits in spring wheat under conventional and organic management systems. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3699-3719.	3.6	23
8	Genome-based prediction of agronomic traits in spring wheat under conventional and organic management systems. <i>Theoretical and Applied Genetics</i> , 2021, 135, 537.	3.6	10
9	Genetic diversity and selective sweeps in historical and modern Canadian spring wheat cultivars using the 90K SNP array. <i>Scientific Reports</i> , 2021, 11, 23773.	3.3	10
10	Comparisons of sampling methods for assessing intra- and inter-accession genetic diversity in three rice species using genotyping by sequencing. <i>Scientific Reports</i> , 2020, 10, 13995.	3.3	13
11	Comparison of Weighted and Unweighted Stage-Wise Analysis for Genome-Wide Association Studies and Genomic Selection. <i>Crop Science</i> , 2019, 59, 2572-2584.	1.8	9
12	Molecular diversity and selective sweeps in maize inbred lines adapted to African highlands. <i>Scientific Reports</i> , 2019, 9, 13490.	3.3	14
13	Mapping QTL Associated with Stripe Rust, Leaf Rust, and Leaf Spotting in a Canadian Spring Wheat Population. <i>Crop Science</i> , 2019, 59, 650-658.	1.8	15
14	Comparisons of molecular diversity indices, selective sweeps and population structure of African rice with its wild progenitor and Asian rice. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1145-1158.	3.6	16
15	Rotational diversity effects in a triticale-based cropping system. <i>Cereal Research Communications</i> , 2018, 46, 717-728.	1.6	1
16	Development of species diagnostic SNP markers for quality control genotyping in four rice ( <i>Oryza L.</i> ) species. <i>Molecular Breeding</i> , 2018, 38, 131.	2.1	22
17	Assessment of Genetic Variation and Population Structure of Diverse Rice Genotypes Adapted to Lowland and Upland Ecologies in Africa Using SNPs. <i>Frontiers in Plant Science</i> , 2018, 9, 446.	3.6	27
18	Discovery and validation of genomic regions associated with resistance to maize lethal necrosis in four biparental populations. <i>Molecular Breeding</i> , 2018, 38, 66.	2.1	29

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19	Mapping QTLs Controlling Agronomic Traits in the "Attila"™ – "CDC Go"™ Spring Wheat Population under Organic Management using 90K SNP Array. <i>Crop Science</i> , 2017, 57, 365-377.	1.8	30
20	Allelic variation and effects of 16 candidate genes on disease resistance in western Canadian spring wheat cultivars. <i>Molecular Breeding</i> , 2017, 37, 1.	2.1	11
21	Genome-wide association mapping of genomic regions associated with phenotypic traits in Canadian western spring wheat. <i>Molecular Breeding</i> , 2017, 37, 1.	2.1	30
22	Mapping of QTLs associated with resistance to common bunt, tan spot, leaf rust, and stripe rust in a spring wheat population. <i>Molecular Breeding</i> , 2017, 37, 1.	2.1	21
23	Genetic Variation and Population Structure of <i>Oryza glaberrima</i> and Development of a Mini-Core Collection Using DArTseq. <i>Frontiers in Plant Science</i> , 2017, 8, 1748.	3.6	71
24	Effect of Trait Heritability, Training Population Size and Marker Density on Genomic Prediction Accuracy Estimation in 22 bi-parental Tropical Maize Populations. <i>Frontiers in Plant Science</i> , 2017, 8, 1916.	3.6	145
25	Genetic Diversity among Selected Elite CIMMYT Maize Hybrids in East and Southern Africa. <i>Crop Science</i> , 2017, 57, 2395-2404.	1.8	10
26	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. <i>BMC Genomics</i> , 2017, 18, 777.	2.8	36
27	Population Structure and Genomewide Association Analysis of Resistance to Disease and Insensitivity to Ptr Toxins in Canadian Spring Wheat Using 90K SNP Array. <i>Crop Science</i> , 2017, 57, 1522-1539.	1.8	24
28	QTLs associated with agronomic traits in the Attila – CDC Go spring wheat population evaluated under conventional management. <i>PLoS ONE</i> , 2017, 12, e0171528.	2.5	68
29	QTLs Associated with Agronomic Traits in the Cutler – AC Barrie Spring Wheat Mapping Population Using Single Nucleotide Polymorphic Markers. <i>PLoS ONE</i> , 2016, 11, e0160623.	2.5	36
30	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. <i>Crop Science</i> , 2016, 56, 2365-2378.	1.8	88
31	Improving Maize Grain Yield under Drought Stress and Non-stress Environments in Sub-Saharan Africa using Marker-Assisted Recurrent Selection. <i>Crop Science</i> , 2016, 56, 344-353.	1.8	70
32	Performance and grain yield stability of maize populations developed using marker-assisted recurrent selection and pedigree selection procedures. <i>Euphytica</i> , 2016, 208, 285-297.	1.2	18
33	Molecular characterization of CIMMYT maize inbred lines with genotyping-by-sequencing SNPs. <i>Theoretical and Applied Genetics</i> , 2016, 129, 753-765.	3.6	94
34	QTL Mapping in Three Rice Populations Uncovers Major Genomic Regions Associated with African Rice Gall Midge Resistance. <i>PLoS ONE</i> , 2016, 11, e0160749.	2.5	19
35	Genetic Gains in Grain Yield Through Genomic Selection in Eight Bi-parental Maize Populations under Drought Stress. <i>Crop Science</i> , 2015, 55, 154-163.	1.8	253
36	Comparison of Kompetitive Allele Specific PCR (KASP) and genotyping by sequencing (GBS) for quality control analysis in maize. <i>BMC Genomics</i> , 2015, 16, 908.	2.8	89

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37	Quantitative Trait Loci Mapping and Molecular Breeding for Developing Stress Resilient Maize for Sub-Saharan Africa. <i>Crop Science</i> , 2015, 55, 1449-1459.	1.8	61
38	A Genomic Selection Index Applied to Simulated and Real Data. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2155-2164.	1.8	42
39	Relationships between heterosis, genetic distances and specific combining ability among CIMMYT and Zimbabwe developed maize inbred lines under stress and optimal conditions. <i>Euphytica</i> , 2015, 204, 635-647.	1.2	27
40	Fine mapping of Msv1, a major QTL for resistance to Maize Streak Virus leads to development of production markers for breeding pipelines. <i>Theoretical and Applied Genetics</i> , 2015, 128, 1839-1854.	3.6	61
41	Genome-wide association and genomic prediction of resistance to maize lethal necrosis disease in tropical maize germplasm. <i>Theoretical and Applied Genetics</i> , 2015, 128, 1957-1968.	3.6	145
42	Genomic prediction in biparental tropical maize populations in water-stressed and well-watered environments using low-density and GBS SNPs. <i>Heredity</i> , 2015, 114, 291-299.	2.6	187
43	Genetic purity and patterns of relationships among tropical highland adapted quality protein and normal maize inbred lines using microsatellite markers. <i>Euphytica</i> , 2015, 204, 49-61.	1.2	14
44	High-resolution genetic mapping of maize pan-genome sequence anchors. <i>Nature Communications</i> , 2015, 6, 6914.	12.8	213
45	Parental genome contribution in maize DH lines derived from six backcross populations using genotyping by sequencing. <i>Euphytica</i> , 2015, 202, 129-139.	1.2	6
46	Assessment of the genetic diversity and pattern of relationship of West African sorghum accessions using microsatellite markers. <i>African Journal of Biotechnology</i> , 2014, 13, 1503-1514.	0.6	5
47	Optimal Design of Preliminary Yield Trials with Genome-Wide Markers. <i>Crop Science</i> , 2014, 54, 48-59.	1.8	100
48	Biotechnology Success Stories by the Consultative Group on International Agriculture Research (CGIAR) System. <i>Science Policy Reports</i> , 2014, , 95-114.	0.1	4
49	Single nucleotide polymorphism genotyping using Kompetitive Allele Specific PCR (KASP): overview of the technology and its application in crop improvement. <i>Molecular Breeding</i> , 2014, 33, 1-14.	2.1	784
50	Leaf Tissue Sampling and DNA Extraction Protocols. <i>Methods in Molecular Biology</i> , 2014, 1115, 53-67.	0.9	27
51	Genetic relationships and structure among open-pollinated maize varieties adapted to eastern and southern Africa using microsatellite markers. <i>Molecular Breeding</i> , 2014, 34, 1423-1435.	2.1	21
52	Genetic distance among doubled haploid maize lines and their testcross performance under drought stress and non-stress conditions. <i>Euphytica</i> , 2013, 192, 379-392.	1.2	34
53	Meta-analyses of QTL for grain yield and anthesis silking interval in 18 maize populations evaluated under water-stressed and well-watered environments. <i>BMC Genomics</i> , 2013, 14, 313.	2.8	129
54	Genomic Prediction in Maize Breeding Populations with Genotyping-by-Sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1903-1926.	1.8	235

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55	Effectiveness of Genomic Prediction of Maize Hybrid Performance in Different Breeding Populations and Environments. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 1427-1436.	1.8	242
56	Quality control genotyping for assessment of genetic identity and purity in diverse tropical maize inbred lines. <i>Theoretical and Applied Genetics</i> , 2012, 125, 1487-1501.	3.6	68
57	Molecular characterization of diverse CIMMYT maize inbred lines from eastern and southern Africa using single nucleotide polymorphic markers. <i>BMC Genomics</i> , 2012, 13, 113.	2.8	109
58	Local scale patterns of gene flow and genetic diversity in a crop-wild-weedy complex of sorghum ( <i>Sorghum bicolor</i> (L.) Moench) under traditional agricultural field conditions in Kenya. <i>Conservation Genetics</i> , 2012, 13, 1059-1071.	1.5	21
59	Resistance of tropical maize genotypes to the larger grain borer. <i>Journal of Pest Science</i> , 2012, 85, 267-275.	3.7	11
60	Effect of source germplasm and season on the in vivo haploid induction rate in tropical maize. <i>Euphytica</i> , 2011, 180, 219-226.	1.2	59
61	Genetic structure and relationships within and between cultivated and wild sorghum ( <i>Sorghum</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 2011, 122, 989-1004.	3.6	48
62	Two Major Resistance Quantitative Trait Loci are Required to Counteract the Increased Susceptibility to <i>Fusarium</i> Head Blight of the <i>Dwarfing</i> Gene in Wheat. <i>Crop Science</i> , 2011, 51, 2430-2438.	1.8	35
63	Ecogeographical distribution of wild, weedy and cultivated <i>Sorghum bicolor</i> (L.) Moench in Kenya: implications for conservation and crop-to-wild gene flow. <i>Genetic Resources and Crop Evolution</i> , 2010, 57, 243-253.	1.6	49
64	The inheritance of anther extrusion in hexaploid wheat and its relationship to <i>Fusarium</i> head blight resistance and deoxynivalenol content. <i>Plant Breeding</i> , 2010, 129, 149-155.	1.9	98
65	The genetic dissection of quantitative traits in crops. <i>Electronic Journal of Biotechnology</i> , 2010, 13, 0-0.	2.2	89
66	Quantitative Trait Loci Controlling <i>Fusarium</i> Head Blight Resistance and Low Deoxynivalenol Content in Hexaploid Wheat Population from 'Arina' and NK93604. <i>Crop Science</i> , 2007, 47, 294-303.	1.8	89
67	Molecular profiling of an interspecific rice population derived from a cross between WAB 56-104 ( <i>Oryza sativa</i> ) and CG 14 ( <i>Oryza glaberrima</i> ). <i>African Journal of Biotechnology</i> , 2007, 6, 2014-2022.	0.6	30
68	Distribution of DArT, AFLP, and SSR markers in a genetic linkage map of a doubled-haploid hexaploid wheat population. <i>Genome</i> , 2006, 49, 545-555.	2.0	152
69	Genetic Relationships among Rice Varieties Based On Expressed Sequence Tags and Microsatellite Markers. <i>Asian Journal of Plant Sciences</i> , 2006, 5, 429-437.	0.4	10
70	Patterns of phenotypic variation in endod ( <i>Phytolacca dodecandra</i> ) from Ethiopia. <i>African Journal of Biotechnology</i> , 2004, 3, 32-39.	0.6	1
71	Analysis of Genetic Diversity and Structure in Ethiopian Populations of <i>Phytolacca Dodecandra</i> Using RAPD. <i>Hereditas</i> , 2004, 135, 51-60.	1.4	10
72	Title is missing!. <i>Genetic Resources and Crop Evolution</i> , 2003, 50, 649-661.	1.6	12

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73	Medicinal use and social status of the soap berry endod ( <i>Phytolacca dodecandra</i> ) in Ethiopia. <i>Journal of Ethnopharmacology</i> , 2003, 85, 269-277.	4.1	32
74	Genetic relationships among ten endod types as revealed by a combination of morphological, RAPD and AFLP markers. <i>Hereditas</i> , 2002, 137, 149-156.	1.4	34
75	Comparison of multivariate methods for the analysis of genetic resources and adaptation in <i>Phytolacca dodecandra</i> using RAPD. <i>Theoretical and Applied Genetics</i> , 2000, 101, 1145-1154.	3.6	28
76	Genome-wide association mapping of agronomic traits and grain characteristics in spring wheat under conventional and organic management systems. <i>Crop Science</i> , 0, , .	1.8	5