

# Cinta Romay

## List of Publications by Year in descending order

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Version: 2024-02-01

49  
papers

4,611  
citations

304743

22  
h-index

206112

48  
g-index

60  
all docs

60  
docs citations

60  
times ranked

4825  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Genetic Architecture of Maize Flowering Time. <i>Science</i> , 2009, 325, 714-718.	12.6	1,284
2	Comprehensive genotyping of the USA national maize inbred seed bank. <i>Genome Biology</i> , 2013, 14, R55.	8.8	458
3	The Genetic Architecture Of Maize Height. <i>Genetics</i> , 2014, 196, 1337-1356.	2.9	329
4	A study of allelic diversity underlying flowering-time adaptation in maize landraces. <i>Nature Genetics</i> , 2017, 49, 476-480.	21.4	254
5	Novel Methods to Optimize Genotypic Imputation for Low Coverage, Next-Generation Sequence Data in Crop Plants. <i>Plant Genome</i> , 2014, 7, plantgenome2014.05.0023.	2.8	241
6	High-resolution genetic mapping of maize pan-genome sequence anchors. <i>Nature Communications</i> , 2015, 6, 6914.	12.8	213
7	Dysregulation of expression correlates with rare-allele burden and fitness loss in maize. <i>Nature</i> , 2018, 555, 520-523.	27.8	211
8	Construction of the third-generation <i>Zea mays</i> haplotype map. <i>GigaScience</i> , 2018, 7, 1-12.	6.4	191
9	Genomic estimation of complex traits reveals ancient maize adaptation to temperate North America. <i>Science</i> , 2017, 357, 512-515.	12.6	169
10	Genome-wide association analysis of seedling root development in maize ( <i>Zea mays</i> L.). <i>BMC Genomics</i> , 2015, 16, 47.	2.8	159
11	Identification of genetic variants associated with maize flowering time using an extremely large multi-genetic background population. <i>Plant Journal</i> , 2016, 86, 391-402.	5.7	122
12	The effect of artificial selection on phenotypic plasticity in maize. <i>Nature Communications</i> , 2017, 8, 1348.	12.8	105
13	Genome-wide association study of Fusarium ear rot disease in the U.S.A. maize inbred line collection. <i>BMC Plant Biology</i> , 2014, 14, 372.	3.6	85
14	The genetic architecture of teosinte catalyzed and constrained maize domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 5643-5652.	7.1	59
15	A sorghum practical haplotype graph facilitates genome-wide imputation and cost-effective genomic prediction. <i>Plant Genome</i> , 2020, 13, e20009.	2.8	54
16	The importance of dominance and genotype-by-environment interactions on grain yield variation in a large-scale public cooperative maize experiment. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	52
17	Utility of Climatic Information via Combining Ability Models to Improve Genomic Prediction for Yield Within the Genomes to Fields Maize Project. <i>Frontiers in Genetics</i> , 2020, 11, 592769.	2.3	44
18	Mapping of QTL for resistance to the Mediterranean corn borer attack using the intermated B73-AMo17 (IBM) population of maize. <i>Theoretical and Applied Genetics</i> , 2009, 119, 1451-1459.	3.6	42

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19	Maize genomes to fields (G2F): 2014–2017 field seasons: genotype, phenotype, climatic, soil, and inbred ear image datasets. <i>BMC Research Notes</i> , 2020, 13, 71.	1.4	38
20	Climatic and Genotypic Effects for Grain Yield in Maize under Stress Conditions. <i>Crop Science</i> , 2010, 50, 51-58.	1.8	36
21	Dominance Effects and Functional Enrichments Improve Prediction of Agronomic Traits in Hybrid Maize. <i>Genetics</i> , 2020, 215, 215-230.	2.9	35
22	Effect of Recurrent Selection on the Genetic Structure of Two Broad-Based Spanish Maize Populations. <i>Crop Science</i> , 2012, 52, 1493-1502.	1.8	29
23	Conserved noncoding sequences provide insights into regulatory sequence and loss of gene expression in maize. <i>Genome Research</i> , 2021, 31, 1245-1257.	5.5	29
24	The genetic architecture of the maize progenitor, teosinte, and how it was altered during maize domestication. <i>PLoS Genetics</i> , 2020, 16, e1008791.	3.5	27
25	Diverse Chromosomal Locations of Quantitative Trait Loci for Tolerance to <i>Maize chlorotic mottle virus</i> in Five Maize Populations. <i>Phytopathology</i> , 2018, 108, 748-758.	2.2	26
26	Maize Genomes to Fields: 2014 and 2015 field season genotype, phenotype, environment, and inbred ear image datasets. <i>BMC Research Notes</i> , 2018, 11, 452.	1.4	25
27	Stomatal conductance, xylem water transport, and root traits underpin improved performance under drought and well-watered conditions across a diverse panel of maize inbred lines. <i>Field Crops Research</i> , 2019, 234, 119-128.	5.1	24
28	Relative utility of agronomic, phenological, and morphological traits for assessing genotype-by-environment interaction in maize inbreds. <i>Crop Science</i> , 2020, 60, 62-81.	1.8	21
29	Three Cycles of Full-Sib Reciprocal Recurrent Selection in Two Spanish Maize Populations. <i>Crop Science</i> , 2011, 51, 1016-1022.	1.8	19
30	Genetic Relationship Between Maize Resistance to Corn Borer Attack and Yield. <i>Crop Science</i> , 2012, 52, 1176-1180.	1.8	18
31	Evaluation of European maize ( <i>Zea mays</i> L.) germplasm under cold conditions. <i>Genetic Resources and Crop Evolution</i> , 2010, 57, 329-335.	1.6	16
32	Coregulation of ribosomal RNA with hundreds of genes contributes to phenotypic variation. <i>Genome Research</i> , 2018, 28, 1555-1565.	5.5	16
33	Unoccupied aerial systems discovered overlooked loci capturing the variation of entire growing period in maize. <i>Plant Genome</i> , 2021, 14, e20102.	2.8	16
34	Maize for bread under organic agriculture. <i>Spanish Journal of Agricultural Research</i> , 2008, 6, 241.	0.6	14
35	Adaptation of super-sweet maize to cold conditions: mutant-by-genotype interaction. <i>Journal of Agricultural Science</i> , 2010, 148, 401-405.	1.3	10
36	Genetic and environmental factors reducing the incidence of the storage pest <i>Sitotroga cerealella</i> in maize. <i>Entomologia Experimentalis Et Applicata</i> , 2008, 128, 421-428.	1.4	9

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37	Genomic regions affecting fitness of the sweet corn mutant sugary1. <i>Journal of Agricultural Science</i> , 2013, 151, 396-406.	1.3	7
38	Genome-wide imputation using the practical haplotype graph in the heterozygous crop cassava. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	7
39	Identification of miRNA-eQTLs in maize mature leaf by GWAS. <i>BMC Genomics</i> , 2020, 21, 689.	2.8	6
40	Rapid, Affordable, and Scalable Genotyping for Germplasm Exploration in Maize. <i>Compendium of Plant Genomes</i> , 2018, , 31-46.	0.5	6
41	Causes of agronomic differences between synthetics developed by the random and convergent cross methods. <i>Field Crops Research</i> , 2009, 110, 229-234.	5.1	5
42	Domestication reshaped the genetic basis of inbreeding depression in a maize landrace compared to its wild relative, teosinte. <i>PLoS Genetics</i> , 2021, 17, e1009797.	3.5	5
43	A multiple alignment workflow shows the effect of repeat masking and parameter tuning on alignment in plants. <i>Plant Genome</i> , 2022, 15, e20204.	2.8	5
44	Joint analysis of days to flowering reveals independent temperate adaptations in maize. <i>Heredity</i> , 2021, 126, 929-941.	2.6	4
45	Genome-wide analysis of deletions in maize population reveals abundant genetic diversity and functional impact. <i>Theoretical and Applied Genetics</i> , 2021, 135, 273.	3.6	4
46	Effect of selection on the heterozygosity of inbred lines of maize. <i>Molecular Breeding</i> , 2007, 20, 117-129.	2.1	3
47	Effect of Visual Selection During the Development of Inbred Lines of Maize. <i>Crop Science</i> , 2012, 52, 2538-2545.	1.8	2
48	Eighteen cycles of recurrent mass selection for early flowering in two maize synthetics. <i>Euphytica</i> , 2019, 215, 1.	1.2	2
49	A conserved genetic architecture among populations of the maize progenitor, teosinte, was radically altered by domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	1