

Resource Summary Report

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AGI

RRID:SCR_007203

Type: Tool

Proper Citation

AGI (RRID:SCR_007203)

Resource Information

URL: <http://www.genome.arizona.edu/>

Proper Citation: AGI (RRID:SCR_007203)

Description: Their primary focus is in the area of structural, evolutionary and functional genomics of crop plants. AGI is divided into 5 Centers each lead by a Center Leader and a senior Manager (BAC Library Construction Center, BAC/EST Resource Center, Sequencing & Physical Mapping Center (including: production sequencing and fingerprinting, and sequence finishing), Bioinformatics Center and the Evolutionary and Functional Genomics Center). AGI is housed in the state of the art Thomas W. Keating Bioresearch Building on the northeast part of campus near the Medical School. AGI currently employees about 30 scientists and is primarily funded through federal grants, private contracts, and the Bud Antle Endowed Chair in Plant Molecular Genetics. Sponsors: AGI is supported by Bio5, Plant Sciences, National Science Foundation, National Institutes oh Health, and USDA.

Abbreviations: AGI

Synonyms: Arizona Genomics Institute, The Arizona Genomics Institute

Resource Type: topical portal, disease-related portal, portal, research forum portal, data or information resource

Keywords: genomics, structural, evolutionary, functional, genome, crop, plant, bac, est, resource, physical, sequencing, fingerprinting, bioinformatics, evoluntionary

Resource Name: AGI

Resource ID: SCR_007203

Alternate IDs: nif-0000-30120

Record Creation Time: 20220129T080240+0000

Ratings and Alerts

No rating or validation information has been found for AGI.

No alerts have been found for AGI.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 18 mentions in open access literature.

Listed below are recent publications. The full list is available at [nidm-terms](#) .

Ma X, et al. (2024) Seagrass genomes reveal ancient polyploidy and adaptations to the marine environment. *Nature plants*, 10(2), 240.

Huang Y, et al. (2024) A complete reference genome for the soybean cv. Jack. *Plant communications*, 5(2), 100765.

Crump LS, et al. (2024) Targeting Tryptophan Catabolism in Ovarian Cancer to Attenuate Macrophage Infiltration and PD-L1 Expression. *Cancer research communications*, 4(3), 822.

Bicknell R, et al. (2023) Genetic mapping of the LOSS OF PARTHENOGENESIS locus in *Pilosella piloselloides* and the evolution of apomixis in the Lactuceae. *Frontiers in plant science*, 14, 1239191.

Liu X, et al. (2016) Semi-Rolled Leaf2 modulates rice leaf rolling by regulating abaxial side cell differentiation. *Journal of experimental botany*, 67(8), 2139.

Christopoulou M, et al. (2015) Genome-Wide Architecture of Disease Resistance Genes in Lettuce. *G3 (Bethesda, Md.)*, 5(12), 2655.

Budot BO, et al. (2014) Suppression of cell wall-related genes associated with stunting of *Oryza glaberrima* infected with Rice tungro spherical virus. *Frontiers in microbiology*, 5, 26.

Jacquemin J, et al. (2014) Fifteen million years of evolution in the *Oryza* genus shows extensive gene family expansion. *Molecular plant*, 7(4), 642.

Ogiso-Tanaka E, et al. (2013) Natural variation of the RICE FLOWERING LOCUS T 1 contributes to flowering time divergence in rice. *PloS one*, 8(10), e75959.

Magbanua ZV, et al. (2011) Adventures in the enormous: a 1.8 million clone BAC library for the 21.7 Gb genome of loblolly pine. *PloS one*, 6(1), e16214.

Itoh Y, et al. (2011) Karyotypic polymorphism of the zebra finch Z chromosome. *Chromosoma*, 120(3), 255.

Balakrishnan CN, et al. (2010) Gene duplication and fragmentation in the zebra finch major histocompatibility complex. *BMC biology*, 8, 29.

Itoh Y, et al. (2009) Molecular cloning and characterization of the germline-restricted chromosome sequence in the zebra finch. *Chromosoma*, 118(4), 527.

Nah G, et al. (2009) Comparative sequence analysis of the SALT OVERLY SENSITIVE1 orthologous region in *Thellungiella halophila* and *Arabidopsis thaliana*. *Genomics*, 94(3), 196.

Lawrence CJ, et al. (2008) MaizeGDB: The maize model organism database for basic, translational, and applied research. *International journal of plant genomics*, 2008, 496957.

Foolad MR, et al. (2007) Genome mapping and molecular breeding of tomato. *International journal of plant genomics*, 2007, 64358.

Kelleher ES, et al. (2007) Gene duplication and adaptive evolution of digestive proteases in *Drosophila arizonae* female reproductive tracts. *PLoS genetics*, 3(8), e148.

Miyake T, et al. (2004) BAC libraries and comparative genomics of aquatic chordate species. *Comparative biochemistry and physiology. Toxicology & pharmacology : CBP*, 138(3), 233.