

Resource Summary Report

Generated by PRECISE-TBI on Jul 30, 2026

BGI; Shenzhen; China

RRID:SCR_011114

Type: Tool

Proper Citation

BGI; Shenzhen; China (RRID:SCR_011114)

Resource Information

URL: <http://www.genomics.cn/en/>

Proper Citation: BGI; Shenzhen; China (RRID:SCR_011114)

Description: Citizen-managed, non-profit research institution that uses genomics to benefit the human race. BGI (which includes both private non-profit research institutes and sequencing application commercial units) and its affiliated offshoots, BGI Americas and BGI Europe, have established partnerships and collaborations with leading academic and government research institutions as well as global biotechnology and pharmaceutical companies, to support a variety of healthcare, agricultural, environmental and related applications. BGI currently comprises of 4 regions: BGI China (Mainland), BGI Asia Pacific, BGI Americas (North and South America) and BGI Europe (Europe and Africa). Relying on advanced high-throughput sequencing technology, a highly efficient data analysis capability, uniquely rich biological resources, and a multidisciplinary scientific research system, BGI can provide innovative support for global communities, novel opportunities for researchers, and a regionally tailored application services in the fields of healthcare, agriculture and the environment.

Abbreviations: BGI

Synonyms: Beijing Genomics Institute

Resource Type: institution

Resource Name: BGI; Shenzhen; China

Resource ID: SCR_011114

Alternate IDs: nlx_73602

Record Creation Time: 20220129T080302+0000

Record Last Update: 20260725T190709+0000

Ratings and Alerts

No rating or validation information has been found for BGI; Shenzhen; China.

No alerts have been found for BGI; Shenzhen; China.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

Fujiwara T, et al. (2023) Evolution of genome space occupation in ferns: linking genome diversity and species richness. *Annals of botany*, 131(1), 59.

Chandrasegaran P, et al. (2023) Modelling host- *Trypanosoma brucei gambiense* interactions in vitro using human induced pluripotent stem cell-derived cortical brain organoids. *F1000Research*, 12, 437.

Wu C, et al. (2023) Prediction of cellular targets in diabetic kidney diseases with single-cell transcriptomic analysis of db/db mouse kidneys. *Journal of cell communication and signaling*, 17(1), 169.

Santiago-Carvalho I, et al. (2023) T cell-specific P2RX7 favors lung parenchymal CD4+ T??cell accumulation in response to severe lung infections. *Cell reports*, 42(11), 113448.

Zhang H, et al. (2021) Effect of trachea stiffness on tumor distribution in papillary thyroid microcarcinoma. *Oncology letters*, 22(1), 518.

Sharma P, et al. (2021) Improvements in the sequencing and assembly of plant genomes. *GigaByte (Hong Kong, China)*, 2021, gigabyte24.

Welgemoed T, et al. (2020) De novo Assembly of Transcriptomes From a B73 Maize Line Introgressed With a QTL for Resistance to Gray Leaf Spot Disease Reveals a Candidate Allele of a Lectin Receptor-Like Kinase. *Frontiers in plant science*, 11, 191.

Human MP, et al. (2020) Time-Course RNAseq Reveals *Exserohilum turcicum* Effectors and Pathogenicity Determinants. *Frontiers in microbiology*, 11, 360.

Zhang C, et al. (2018) Long non-coding RNAs of switchgrass (*Panicum virgatum* L.) in multiple dehydration stresses. *BMC plant biology*, 18(1), 79.

Martin G, et al. (2017) Evolution of the Banana Genome (*Musa acuminata*) Is Impacted by Large Chromosomal Translocations. *Molecular biology and evolution*, 34(9), 2140.

Wang J, et al. (2017) Mutation of *Arabidopsis* SMC4 identifies condensin as a corepressor of pericentromeric transposons and conditionally expressed genes. *Genes &*

development, 31(15), 1601.

Donovan PD, et al. (2016) Identification of Non-Coding RNAs in the *Candida parapsilosis* Species Group. *PloS one*, 11(9), e0163235.

Tello J, et al. (2015) Polymorphisms and minihaplotypes in the VvNAC26 gene associate with berry size variation in grapevine. *BMC plant biology*, 15, 253.

Hu D, et al. (2014) Whole genome wide expression profiles on germination of *Verticillium dahliae* microsclerotia. *PloS one*, 9(6), e100046.

Wu BH, et al. (2014) Genome-wide transcriptional profiles of the berry skin of two red grape cultivars (*Vitis vinifera*) in which anthocyanin synthesis is sunlight-dependent or -independent. *PloS one*, 9(8), e105959.

Kelly S, et al. (2014) A draft genome for the African crocodilian trypanosome *Trypanosoma grayi*. *Scientific data*, 1, 140024.