# Resource Summary Report

Generated by NIF on May 5, 2025

## Golden Helix Incorporated

RRID:SCR_012191
Type: Tool

### Proper Citation

Golden Helix Incorporated (RRID:SCR_012191)

### Resource Information

**URL:** http://goldenhelix.com/

**Proper Citation:** Golden Helix Incorporated (RRID:SCR_012191)

**Description:** Specializes in sequence and array-based SNP and copy number analysis, genetic association software, and analytic services. Their technologies empower scientists to determine the genetic causes of disease, transform drug discovery, develop genetic diagnostics, and advance the quest for personalized medicine.

**Abbreviations:** Golden Helix

**Synonyms:** Golden Helix Inc., GoldenHelix.com

**Resource Type:** commercial organization

**Keywords:** resource, portal, analysis, software

**Funding:**

**Availability:** Available to external user

**Resource Name:** Golden Helix Incorporated

**Resource ID:** SCR_012191

**Alternate IDs:** SciEx_10349

**Old URLs:** http://www.goldenhelix.com/Services, http://www.scienceexchange.com/facilities/golden-helix-inc

**Record Creation Time:** 20220129T080308+0000

**Record Last Update:** 20250420T014608+0000

## Ratings and Alerts

No rating or validation information has been found for Golden Helix Incorporated.

No alerts have been found for Golden Helix Incorporated.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 134 mentions in open access literature.

**Listed below are recent publications.** The full list is available at NIF.

Reshadmanesh A, et al. (2024) First Case of Macrocephaly, Dysmorphic Facies, and Psychomotor Retardation Harboring Co-inherited Variants in HERC1 and PMP22 Genes from Iran: Two Novel Variants. Archives of Iranian medicine, 27(12), 700.

Contreras-Méndez LA, et al. (2024) The Anti-Müllerian Hormone as Endocrine and Molecular Marker Associated with Reproductive Performance in Holstein Dairy Cows Exposed to Heat Stress. Animals : an open access journal from MDPI, 14(2).

Šimon M, et al. (2024) Whole genome sequencing of mouse lines divergently selected for fatness (FLI) and leanness (FHI) revealed several genetic variants as candidates for novel obesity genes. Genes & genomics, 46(5), 557.

Ngo KJ, et al. (2024) Lysosomal genes contribute to Parkinson's disease near agriculture with high intensity pesticide use. NPJ Parkinson's disease, 10(1), 87.

Šimon M, et al. (2023) Genome-wide screening for genetic variants in polyadenylation signal (PAS) sites in mouse selection lines for fatness and leanness. Mammalian genome : official journal of the International Mammalian Genome Society, 34(1), 12.

Manzanero BR, et al. (2023) Genomic and evolutionary relationships among wild and cultivated blueberry species. BMC plant biology, 23(1), 126.

Bennett TM, et al. (2023) Whole-exome sequencing prioritizes candidate genes for hereditary cataract in the Emory mouse mutant. G3 (Bethesda, Md.), 13(5).

Ricci C, et al. (2023) Evaluation of an institutional series of low-grade oncocytic tumor (LOT)

of the kidney and review of the mutational landscape of LOT. Virchows Archiv : an international journal of pathology, 483(5), 687.

Finzel JA, et al. (2023) Field demonstration analyzing the implementation of individual animal electronic identification and genetic testing in western range sheep flocks. PloS one, 18(8), e0290281.

Liu D, et al. (2023) Early Introduction and Community Transmission of SARS-CoV-2 Omicron Variant, New York, New York, USA. Emerging infectious diseases, 29(2), 371.

Duggirala N, et al. (2023) Spinocerebellar ataxia type 14 (SCA14) in an Argentinian family: a case report. Journal of medical case reports, 17(1), 168.

Jensen MR, et al. (2023) TINF2 is a major susceptibility gene in Danish patients with multiple primary melanoma. HGG advances, 4(4), 100225.

Wang F, et al. (2022) Genome-Wide Association Analysis to Search for New Loci Associated with Lifelong Premature Ejaculation Risk in Chinese Male Han Population. The world journal of men's health, 40(2), 330.

Muzammal M, et al. (2022) A novel protein truncating mutation in L2HGDH causes L-2-hydroxyglutaric aciduria in a consanguineous Pakistani family. Metabolic brain disease, 37(1), 243.

Verheyen S, et al. (2022) Novel subtype of mucopolysaccharidosis caused by arylsulfatase K (ARSK) deficiency. Journal of medical genetics, 59(10), 957.

Mhoswa L, et al. (2022) Genome-wide association study identifies SNP markers and putative candidate genes for terpene traits important for Leptocybe invasa resistance in Eucalyptus grandis. G3 (Bethesda, Md.), 12(4).

Wiedemann A, et al. (2022) Clinical, phenotypic and genetic landscape of case reports with genetically proven inherited disorders of vitamin B12 metabolism: A meta-analysis. Cell reports. Medicine, 3(7), 100670.

Vogt G, et al. (2022) Biallelic truncating variants in ATP9A cause a novel neurodevelopmental disorder involving postnatal microcephaly and failure to thrive. Journal of medical genetics, 59(7), 662.

Estrada-Reyes ZM, et al. (2022) Copy number variant-based genome wide association study reveals immune-related genes associated with parasite resistance in a heritage sheep breed from the United States. Parasite immunology, 44(11), e12943.

Wang F, et al. (2022) Genomic temporal heterogeneity of circulating tumour DNA in unresectable metastatic colorectal cancer under first-line treatment. Gut, 71(7), 1340.