

Resource Summary Report

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MAPINSPECT

RRID:SCR_009277

Type: Tool

Proper Citation

MAPINSPECT (RRID:SCR_009277)

Resource Information

URL: <http://www.dpw.wau.nl/pv/PUB/MapComp/>

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Description: Software application that can be used to compare linkage maps obtained from different sources/populations/etc.. It will draw the linkage maps and look for common marker names, these are then connected in the drawing with dashed lines. All neighboring maps are compared in this way. Images can be printed and saved. Orders of the MAPs (ie which map is compared with which other map) can be changed and maps can be flipped (right mouse button). remark: MapComp bears close relationships with the GGT software package (entry from Genetic Analysis Software), THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: MAPINSPECT

Synonyms: GGT

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, delphi pascal, ms-window (32-bit)

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: MAPINSPECT

Resource ID: SCR_009277

Alternate IDs: nlx_154458

Record Creation Time: 20220129T080252+0000

Record Last Update: 20260829T183107+0000

Ratings and Alerts

No rating or validation information has been found for MAPINSPECT.

No alerts have been found for MAPINSPECT.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 324 mentions in open access literature.

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

Li M, et al. (2025) Genome-wide characterization and expression analysis of LBD transcription factors in *Ziziphus jujuba* var. *spinosa*: putative roles in tissue development and abiotic stress adaptation. *Frontiers in plant science*, 16, 1602440.

You SH, et al. (2025) Genome-wide analysis of OPR family genes in *Vitis vinifera* and the role of VvOPR1 in copper, zinc tolerance. *Frontiers in plant science*, 16, 1509472.

Li M, et al. (2025) Genome-wide identification and characterization of WRKYs family involved in responses to *Cylindrocarpon destructans* in *Panax notoginseng*. *BMC genomics*, 26(1), 104.

Wu R, et al. (2024) The DBB Family in *Populus trichocarpa*: Identification, Characterization, Evolution and Expression Profiles. *Molecules* (Basel, Switzerland), 29(8).

Lv WB, et al. (2024) CDPK protein in cotton: genomic-wide identification, expression analysis, and conferring resistance to heat stress. *BMC plant biology*, 24(1), 842.

Zhang J, et al. (2024) Genome expression analysis of basic helix-loop-helix transcription factors in Sea buckthorn (*Hippophae rhamnoides* L.). *Frontiers in plant science*, 15, 1487960.

Wang YH, et al. (2024) Comprehensive analysis of B3 family genes in pearl millet (*Pennisetum glaucum*) and the negative regulator role of PgRAV-04 in drought tolerance. *Frontiers in plant science*, 15, 1400301.

Jha DK, et al. (2024) "Genome-wide identification of bZIP gene family in Pearl millet and transcriptional profiling under abiotic stress, phytohormonal treatments; and functional characterization of PgbZIP9". *Frontiers in plant science*, 15, 1352040.

Yin W, et al. (2024) Genome-wide identification and expression analysis of the CONSTANS-like family in potato (*Solanum tuberosum* L.). *Frontiers in genetics*, 15, 1390411.

Liu H, et al. (2023) Identification of the Absciscic Acid-, Stress-, and Ripening-Induced (ASR) Family Involved in the Adaptation of *Tetragonia tetragonoides* (Pall.) Kuntze to

Saline-Alkaline and Drought Habitats. International journal of molecular sciences, 24(21).

Chanwala J, et al. (2023) MYB Transcription Factor Family in Pearl Millet: Genome-Wide Identification, Evolutionary Progression and Expression Analysis under Abiotic Stress and Phytohormone Treatments. Plants (Basel, Switzerland), 12(2).

Fan T, et al. (2023) The LHT Gene Family in Rice: Molecular Characterization, Transport Functions and Expression Analysis. Plants (Basel, Switzerland), 12(4).

Xu L, et al. (2023) A chromosome-level genome assembly of radish (*Raphanus sativus* L.) reveals insights into genome adaptation and differential bolting regulation. Plant biotechnology journal, 21(5), 990.

Dai WS, et al. (2023) Genome-wide identification and comparative expression profiling of the WRKY transcription factor family in two Citrus species with different *Candidatus Liberibacter asiaticus* susceptibility. BMC plant biology, 23(1), 159.

Wu R, et al. (2023) The G2-Like gene family in *Populus trichocarpa*: identification, evolution and expression profiles. BMC genomic data, 24(1), 37.

Han J, et al. (2023) Genome-Wide Identification of 2-Oxoglutarate and Fe (II)-Dependent Dioxygenase (2ODD-C) Family Genes and Expression Profiles under Different Abiotic Stresses in *Camellia sinensis* (L.). Plants (Basel, Switzerland), 12(6).

Ling C, et al. (2023) Genome-Wide Identification of HSF Gene Family in Kiwifruit and the Function of AeHSFA2b in Salt Tolerance. International journal of molecular sciences, 24(21).

Wang Q, et al. (2022) Genome-wide characterization of Histone gene family and expression profiling during microspore development in radish (*Raphanus sativus* L.). Gene, 815, 146180.

Dong C, et al. (2022) Genome-wide identification of expansin in *Fragaria vesca* and expression profiling analysis of the FvEXPs in different fruit development. Gene, 814, 146162.

Zhang Y, et al. (2022) Whole-genome analysis of CGS, SAHH, SAMS gene families in five Rosaceae species and their expression analysis in *Pyrus bretschneideri*. PeerJ, 10, e13086.