

Resource Summary Report

Generated by [kravitz2](#) on Aug 2, 2026

PRINTS

RRID:SCR_003412

Type: Tool

Proper Citation

PRINTS (RRID:SCR_003412)

Resource Information

URL: <http://www.bioinf.man.ac.uk/dbbrowser/PRINTS/>

Proper Citation: PRINTS (RRID:SCR_003412)

Description: Compendium of protein fingerprints. Diagnostic fingerprint database.

Abbreviations: PRINTS

Resource Type: database, data or information resource

Keywords: compedium, protein, fingerprint, diagnostic, database, FASEB list

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: PRINTS

Resource ID: SCR_003412

Alternate IDs: nif-0000-03338

Alternate URLs: <http://130.88.97.239/PRINTS/index.php>

Record Creation Time: 20220129T080218+0000

Record Last Update: 20260803T040357+0000

Ratings and Alerts

No rating or validation information has been found for PRINTS.

No alerts have been found for PRINTS.

Data and Source Information

Usage and Citation Metrics

We found 395 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Mu W, et al. (2025) The haplotype-resolved T2T genome for *Bauhinia* ?? *blakeana* sheds light on the genetic basis of flower heterosis. *GigaScience*, 14.

Zhang RG, et al. (2025) Reticulate allopolyploidy and subsequent dysploidy drive evolution and diversification in the cotton family. *Nature communications*, 16(1), 7480.

Costa VA, et al. (2025) Limited similarity in microbial composition among coral reef fishes from the Great Barrier Reef, Australia. *FEMS microbiology ecology*, 101(3).

Jaggi KE, et al. (2025) A pangenome reveals LTR repeat dynamics as a major driver of genome evolution in *Chenopodium*. *The plant genome*, 18(1), e70010.

Xiao HX, et al. (2025) High quality chromosome level genome assembly of *Camellia fascicularis*, an endangered plant in China. *Scientific data*, 12(1), 1573.

Arantes LS, et al. (2025) Haplotype-resolved reference genomes of the sea turtle clade unveil ultra-syntenic genomes with hotspots of divergence. *GigaScience*, 14.

He J, et al. (2025) Chromosome-level genome assembly of stem borer *Batocera rufomaculata* using PacBio HiFi and Hi-C sequencing. *Scientific data*, 12(1), 1099.

Liu F, et al. (2025) Role of carbohydrate-active enzymes in brown planthopper virulence and adaptability. *Frontiers in plant science*, 16, 1554498.

Xu S, et al. (2025) Multi-omics analysis of yolk and allantoic fluid in chicken embryonic development and sexual differentiation. *Poultry science*, 104(8), 105349.

Chai J, et al. (2025) Multi-Omics Analysis of Chronic Heat Stress-Induced Biological Effects, Liver Injury, and Heat Tolerance Mechanisms via Oxidative and Anti-Inflammatory Pathways in Early-Pregnancy Sows. *Antioxidants (Basel, Switzerland)*, 14(6).

Fu C, et al. (2025) Haplotype-resolved chromosomal-level genome assembly of *Prunus mahaleb*. *Scientific data*, 12(1), 805.

He Y, et al. (2025) Autophagy is involved in the toxicity of the biocontrol agent GC16 against *Tetranychus pueraricola* (Acari: Tetranychidae) based on transcriptomic and proteomic analyses. *BMC genomics*, 26(1), 119.

Shi Y, et al. (2025) Chromosome-level genome assembly of the traditional medicinal plant *Lindera aggregata*. *Scientific data*, 12(1), 565.

Ng DYM, et al. (2025) Surveillance of coronaviruses in wild aquatic birds in Hong Kong: expanded genetic diversity and discovery of novel subgenus in the Deltacoronavirus. *Virus*

evolution, 11(1), veaf049.

Chen F, et al. (2025) Data-independent acquisition-based blood proteomics unveils predictive biomarkers for neonatal necrotizing enterocolitis. *Analytical and bioanalytical chemistry*, 417(1), 199.

Kariba R, et al. (2025) Draft genome sequence of Kei apple, an underutilized African tree crop. *Scientific data*, 12(1), 70.

Cheng L, et al. (2025) Genome assembly of *Stewartia sinensis* reveals origin and evolution of orphan genes in Theaceae. *Communications biology*, 8(1), 354.

Mo F, et al. (2025) mKmer: an unbiased K-mer embedding of microbiomic single-microbe RNA sequencing data. *Briefings in bioinformatics*, 26(3).

Chen Y, et al. (2025) An improved chromosomal-scale genome assembly of the Tanaka's snailfish (*Liparis tanakae*). *Scientific data*, 12(1), 965.

Sun YS, et al. (2025) Convergent musk biosynthesis across host and microbiota in musk deer and muskrat. *Zoological research*, 46(3), 505.