

Resource Summary Report

Generated by [dkNET](#) on Sep 20, 2026

ANGSD

RRID:SCR_021865

Type: Tool

Proper Citation

ANGSD (RRID:SCR_021865)

Resource Information

URL: <https://github.com/ANGSD/angsd>

Proper Citation: ANGSD (RRID:SCR_021865)

Description: Software tool for analysis of next generation sequencing data. Calculates various summary statistics, and performs association mapping and population genetic analyses utilizing full information in next generation sequencing data by working directly on raw sequencing data or by using genotype likelihoods.

Synonyms: Analysis of Next Generation Sequencing Data

Resource Type: data analysis software, data processing software, software application, software resource

Defining Citation: [DOI:10.1186/s12859-014-0356-4](https://doi.org/10.1186/s12859-014-0356-4)

Keywords: analysing NGS data, next generation sequencing data analysis, raw sequencing data, genotype likelihoods

Availability: Free, Available for download, Freely available

Resource Name: ANGSD

Resource ID: SCR_021865

Alternate URLs: <http://www.popgen.dk/angsd/index.php/ANGSD>

License: GPL v2

Record Creation Time: 20220129T080357+0000

Record Last Update: 20260919T195459+0000

Ratings and Alerts

No rating or validation information has been found for ANGSD.

No alerts have been found for ANGSD.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 47 mentions in open access literature.

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

Zhao X, et al. (2026) Tracing bronze to iron age population dynamics in Northwest Xinjiang using ancient time-series genomic data. *Genome biology*, 27(1), 33.

Barajas JM, et al. (2026) Tandem Duplications in UBTF Create XPO1-Dependent Nuclear Export Signals that Reveal a Leukemic Therapeutic Dependency. *Blood cancer discovery*, 7(1), 51.

Ketchum RN, et al. (2026) Genomic signatures of speciation and adaptation in the ctenophore *Mnemiopsis*. *BMC biology*, 24(1).

Cajigas Gandia A, et al. (2026) Transcriptomic genotyping elucidates the population structure and demographic history of the endangered poison frog *Oophaga vicentei* (Anura: Dendrobatidae). *BMC genomics*, 27(1).

Xu Y, et al. (2026) Reconstructing the west-east genetic division in Indonesia using ancient genomes. *iScience*, 29(6), 115974.

Denis H, et al. (2026) Contrasting population structures of reef-building corals and their algal symbionts inform adaptive potential across the western Pacific. *Current biology : CB*, 36(11), 2808.

Oriowo TO, et al. (2025) A chromosome-level, haplotype-resolved genome assembly and annotation for the Eurasian minnow (Leuciscidae: Phoxinus phoxinus) provide evidence of haplotype diversity. *GigaScience*, 14.

Wolf M, et al. (2025) Ocean-Wide Conservation Genomics of Blue Whales Suggest New Northern Hemisphere Subspecies. *Molecular ecology*, 34(2), e17619.

Xiao H, et al. (2025) Impacts of reproductive systems on grapevine genome and breeding. *Nature communications*, 16(1), 2031.

Giacomino K, et al. (2025) Physical exercises to prevent and rehabilitate hospital-associated disability in hospitalised older people: A protocol for a living systematic review with network meta-analysis. *F1000Research*, 14, 414.

Li H, et al. (2025) Ancient genomes shed light on the genetic history of the Iron Age to historical central Xinjiang, northwest China. *BMC biology*, 23(1), 93.

Baird RB, et al. (2025) Faster adaptation but slower divergence of X chromosomes under paternal genome elimination. *Nature communications*, 16(1), 5288.

Xiong J, et al. (2025) The genomic history of East Asian Middle Neolithic millet- and rice-agricultural populations. *Cell genomics*, 100976.

Fang H, et al. (2025) Dynamic history of the Central Plain and Haidai region inferred from Late Neolithic to Iron Age ancient human genomes. *Cell reports*, 44(2), 115262.

Zou Y, et al. (2025) Ancient genomes from the Yellow River Bend reveal long-distance population interactions between the Central Plains, Steppe, and southern China. *Cell reports*, 44(8), 116034.

Marques CI, et al. (2025) Physiological plasticity in zebra finch color varieties mitigates DNA damage under oxidative stress. *iScience*, 28(7), 112937.

Talavera A, et al. (2024) Genomic insights into the Montseny brook newt (*Calotriton arnoldi*), a Critically Endangered glacial relict. *iScience*, 27(1), 108665.

Nebenf??hr M, et al. (2024) High-speed whole-genome sequencing of a Whippet: Rapid chromosome-level assembly and annotation of an extremely fast dog's genome. *GigaByte* (Hong Kong, China), 2024, gigabyte134.

Shen Y, et al. (2024) Genomic insights into endangerment and conservation of the garlic-fruit tree (*Malania oleifera*), a plant species with extremely small populations. *GigaScience*, 13.

Cai L, et al. (2024) The chromosome-scale genome of *Magnolia sinica* (Magnoliaceae) provides insights into the conservation of plant species with extremely small populations (PSESP). *GigaScience*, 13.