

Resource Summary Report

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NextPolish

RRID:SCR_025232

Type: Tool

Proper Citation

NextPolish (RRID:SCR_025232)

Resource Information

URL: <https://github.com/Nextomics/NextPolish>

Proper Citation: NextPolish (RRID:SCR_025232)

Description: Software tool to fix base errors SNV/Indel in genome generated by noisy reads. Used to correct error bases in reference genome.

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

Keywords: fix base errors, SNV/Indel, genome, noisy reads, correct error bases, reference genome,

Funding:

Availability: Free, Available for download, Freely available

Resource Name: NextPolish

Resource ID: SCR_025232

License: GNU GPL v3.0

Record Creation Time: 20240409T053245+0000

Record Last Update: 20250501T081800+0000

Ratings and Alerts

No rating or validation information has been found for NextPolish.

No alerts have been found for NextPolish.

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 [FDI Lab - SciCrunch.org](#).

Yang G, et al. (2025) Chromosome-level genome assembly of *Megachile sculpturalis* Smith (Hymenoptera, Apoidea, Megachilidae). *Scientific data*, 12(1), 46.

Liu C, et al. (2025) A chromosome-scale genome assembly of the pioneer plant *Stylosanthes angustifolia*: insights into genome evolution and drought adaptation. *GigaScience*, 14.

Chen H, et al. (2024) Chromosome-level *Alstonia scholaris* genome unveils evolutionary insights into biosynthesis of monoterpenoid indole alkaloids. *iScience*, 27(5), 109599.

Kim KD, et al. (2024) Chromosome-level genome assembly of milk thistle (*Silybum marianum* (L.) Gaertn.). *Scientific data*, 11(1), 342.

Tang R, et al. (2024) A ghost moth olfactory prototype of the lepidopteran sex communication. *GigaScience*, 13.

Huang W, et al. (2024) De novo genome assembly and population genomics of a shrub tree *Barthea barthei* (Hance) Krass provide insights into the adaptive color variations. *Frontiers in plant science*, 15, 1365686.

Zhang T, et al. (2024) A chromosome-level genome reveals genome evolution and molecular basis of anthraquinone biosynthesis in *Rheum palmatum*. *BMC plant biology*, 24(1), 261.

Doellman MM, et al. (2024) Rethinking asexuality: the enigmatic case of functional sexual genes in *Lepraria* (Stereocaulaceae). *BMC genomics*, 25(1), 1003.

Shen R, et al. (2024) Chromosome-level genome assembly of the snakefly *Mongoloraphidia duomilia* (Raphidioptera: Raphidiidae). *Scientific data*, 11(1), 579.

Wang XP, et al. (2024) Insights into the divergence of the photosynthetic LH1 complex obtained from structural analysis of the unusual photocomplexes of *Roseospirillum parvum*. *Communications biology*, 7(1), 1658.

Xu X, et al. (2024) Three genome assemblies of *Opsariichthys bidens* from Yangtze River,

Pearl River and Qiantang River basins. *Scientific data*, 11(1), 1110.

Shang H, et al. (2024) Genome assembly of *Stephania longa* provides insight into cepharanthine biosynthesis. *Frontiers in plant science*, 15, 1414636.

Luo L, et al. (2024) The chromosome-level genomes of the herbal magnoliids *Warburgia ugandensis* and *Saururus chinensis*. *Scientific data*, 11(1), 554.

Wang Q, et al. (2024) Comparative genomic analyses provide insight into the pathogenicity of three *Pseudomonas syringae* pv. *actinidiae* strains from Anhui Province, China. *BMC genomics*, 25(1), 461.

Ge X, et al. (2024) Chromosome-scale genome assemblies of *Himalopsyche anomala* and *Eubasilissa splendida* (Insecta: Trichoptera). *Scientific data*, 11(1), 267.

Gao YF, et al. (2024) Chromosome-level genome assembly of the Japanese sawyer beetle *Monochamus alternatus*. *Scientific data*, 11(1), 199.

Ferrari RR, et al. (2024) The nuclear and mitochondrial genome assemblies of *Tetragonisca angustula* (Apidae: Meliponini), a tiny yet remarkable pollinator in the Neotropics. *BMC genomics*, 25(1), 587.

Yang S, et al. (2024) Genomic exploration of the endangered oriental stork, *Ciconia boyciana*, sheds light on migration adaptation and future conservation. *GigaScience*, 13.

Yang Y, et al. (2024) A chromosome-level genome assembly of Chinese quince (*Pseudocydonia sinensis*). *Frontiers in plant science*, 15, 1368861.

Wang Q, et al. (2024) A consensus genome of sika deer (*Cervus nippon*) and transcriptome analysis provided novel insights on the regulation mechanism of transcript factor in antler development. *BMC genomics*, 25(1), 617.