

Resource Summary Report

Generated by SPARC SAWG on Sep 17, 2026

DIYA

RRID:SCR_012066

Type: Tool

Proper Citation

DIYA (RRID:SCR_012066)

Resource Information

URL: <http://sourceforge.net/projects/diyyg/>

Proper Citation: DIYA (RRID:SCR_012066)

Description: A modular and configurable open source pipeline software, written in Perl, used for the rapid annotation of bacterial genome sequences.

Synonyms: Do-It-Yourself Annotator

Resource Type: software resource

Defining Citation: [PMID:19254921](#)

Keywords: standalone software, c++, java, perl, python

Availability: GNU General Public License

Resource Name: DIYA

Resource ID: SCR_012066

Alternate IDs: OMICS_04221

Record Creation Time: 20220129T080308+0000

Record Last Update: 20260912T195744+0000

Ratings and Alerts

No rating or validation information has been found for DIYA.

No alerts have been found for DIYA.

Data and Source Information

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Gu Y, et al. (2021) Improving clinical utility of GAD65 autoantibodies by electrochemiluminescence assay and clinical phenotype when identifying autoimmune adult-onset diabetes. *Diabetologia*, 64(9), 2052.

Pal R, et al. (2020) Knowledge, attitudes and practices towards COVID-19 among young adults with Type 1 Diabetes Mellitus amid the nationwide lockdown in India: A cross-sectional survey. *Diabetes research and clinical practice*, 166, 108344.

Clawson ML, et al. (2020) Differences between predicted outer membrane proteins of genotype 1 and 2???Mannheimia haemolytica. *BMC microbiology*, 20(1), 250.

Kampfraath AA, et al. (2019) Genome expansion of an obligate parthenogenesis-associated Wolbachia poses an exception to the symbiont reduction model. *BMC genomics*, 20(1), 106.

Dickey AM, et al. (2016) Large genomic differences between *Moraxella bovoculi* isolates acquired from the eyes of cattle with infectious bovine keratoconjunctivitis versus the deep nasopharynx of asymptomatic cattle. *Veterinary research*, 47, 31.

Tamarit D, et al. (2015) Functionally Structured Genomes in *Lactobacillus kunkeei* Colonizing the Honey Crop and Food Products of Honeybees and Stingless Bees. *Genome biology and evolution*, 7(6), 1455.

Gottlieb Y, et al. (2015) Distinctive Genome Reduction Rates Revealed by Genomic Analyses of Two *Coxiella*-Like Endosymbionts in Ticks. *Genome biology and evolution*, 7(6), 1779.

Yan X, et al. (2015) Genome sequencing and comparative genomics provides insights on the evolutionary dynamics and pathogenic potential of different H-serotypes of Shiga toxin-producing *Escherichia coli* O104. *BMC microbiology*, 15, 83.

Lee CC, et al. (2013) GI-POP: a combinational annotation and genomic island prediction pipeline for ongoing microbial genome projects. *Gene*, 518(1), 114.

Zwick ME, et al. (2012) Genomic characterization of the *Bacillus cereus* sensu lato species: backdrop to the evolution of *Bacillus anthracis*. *Genome research*, 22(8), 1512.