

Resource Summary Report

Generated by T1D on Jul 31, 2026

SolexaQA

RRID:SCR_005421

Type: Tool

Proper Citation

SolexaQA (RRID:SCR_005421)

Resource Information

URL: <http://solexaqa.sourceforge.net/>

Proper Citation: SolexaQA (RRID:SCR_005421)

Description: Software package to calculate sequence quality statistics and create visual representations of data quality for Illumina's second-generation sequencing technology.

Abbreviations: SolexaQA

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

Defining Citation: [PMID:20875133](#)

Keywords: bio.tools

Availability: Acknowledgement requested

Resource Name: SolexaQA

Resource ID: SCR_005421

Alternate IDs: biotools:solexaqa, OMICS_01078

Alternate URLs: <https://bio.tools/solexaqa>

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260731T042709+0000

Ratings and Alerts

No rating or validation information has been found for SolexaQA.

No alerts have been found for SolexaQA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 291 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Pei X, et al. (2025) Transcriptomic analysis of the anti-tumor effects of leflunomide in prolactinoma. *Scientific reports*, 15(1), 11703.

Chen Q, et al. (2025) Gut microbiota analysis in children with autism spectrum disorder and their family members. *Scientific reports*, 15(1), 44282.

Qin Q, et al. (2025) Oral microbiome between patients with non-obstructive and obstructive hypertrophic cardiomyopathy. *Chinese medical journal*, 138(18), 2308.

Rivas-Santisteban J, et al. (2025) Picoplankton nitrogen guilds in the tropical and subtropical oceans: From the surface to the deep. *PloS one*, 20(11), e0335222.

Li F, et al. (2025) Prevotella copri-mediated caffeine metabolism involves ferroptosis of osteoblasts in osteoarthritis. *Microbiology spectrum*, 13(6), e0157524.

Ha YH, et al. (2025) Genotyping-by-sequencing reveals low genetic diversity and peripheral isolation in Southern populations of *Sophora koreensis*, a Korean endemic shrub. *Scientific reports*, 15(1), 17996.

Lee HS, et al. (2025) Temperature-Photoperiod Interaction in Rice Phenology for Climate Adaptation: Insights Into Glycerate-Associated Metabolic Responses. *Physiologia plantarum*, 177(4), e70368.

Parwin N, et al. (2025) Metagenomic analysis of microbiome spatial dynamics in urban river confluence affected by city wastewater. *Genomics & informatics*, 23(1), 27.

Dong X, et al. (2024) The conservation of allelic DNA methylation and its relationship with imprinting in maize. *Journal of experimental botany*, 75(5), 1376.

Kim WJ, et al. (2024) Genome-Wide Association Study for Agronomic Traits in Gamma-Ray-Derived Mutant Kenaf (*Hibiscus cannabinus* L.). *Plants (Basel, Switzerland)*, 13(2).

Maitre A, et al. (2024) Differential interactions of *Rickettsia* species with tick microbiota in *Rh. sanguineus* and *Rh. turanicus*. *Scientific reports*, 14(1), 20674.

Kim JM, et al. (2024) Differentially Expressed Genes Related to Isoflavone Biosynthesis in a Soybean Mutant Revealed by a Comparative Transcriptomic Analysis. *Plants (Basel, Switzerland)*, 13(5).

Ramos-Barbero MD, et al. (2024) Experimental evolution at ecological scales allows linking of viral genotypes to specific host strains. *The ISME journal*, 18(1).

Babalola OO, et al. (2024) High-throughput metagenomic assessment of Congo Cave microbiome-A South African limestone cave. *Data in brief*, 54, 110381.

Zeng Y, et al. (2024) Characteristics of gut microbiota and serum metabolism in patients with atopic dermatitis. *Skin research and technology : official journal of International Society for Bioengineering and the Skin (ISBS) [and] International Society for Digital Imaging of Skin (ISDIS) [and] International Society for Skin Imaging (ISSI)*, 30(7), e13792.

Cho MS, et al. (2024) Phylogenetic relationships and genetic diversity of the Korean endemic *Phedimus latiovalifolius* (Crassulaceae) and its close relatives. *Scientific reports*, 14(1), 16255.

Viladomat Jasso M, et al. (2024) Metagenomic insight into taxonomic composition, environmental filtering and functional redundancy for shaping worldwide modern non-lithifying microbial mats. *PeerJ*, 12, e17412.

Lemieux-Labont V, et al. (2024) *Pseudogymnoascus destructans* invasion stage impacts the skin microbial functions of highly vulnerable *Myotis lucifugus*. *FEMS microbiology ecology*, 100(11).

Angom RS, et al. (2024) Forward genetic screen using a gene-breaking trap approach identifies a novel role of *grin2bb*-associated RNA transcript (*grin2bbART*) in zebrafish heart function. *Frontiers in cell and developmental biology*, 12, 1339292.

Feng X, et al. (2024) Genomic evidence for rediploidization and adaptive evolution following the whole-genome triplication. *Nature communications*, 15(1), 1635.