

Resource Summary Report

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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 analysis software, data processing software, data visualization software, sequence analysis software, software application, software resource

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: 20260829T182220+0000

Ratings and Alerts

No rating or validation information has been found for SolexaQA.

No alerts have been found for SorexQA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 297 mentions in open access literature.

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

Smith KF, et al. (2026) Risk of ciguatoxins is shaped by Gambierdiscus community structure. PloS one, 21(1), e0341899.

Tang J, et al. (2026) Bifidobacterium Infantis Promotes FOSL1-Mediated Transcriptional Repression of VDR to Accelerate Autoimmune Pancreatitis Progression Through Activation of Oxidative Stress. Inflammation, 49(1), 61.

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.

Kim G, et al. (2025) Three distinct genetic lineages of Trichonephila clavata based on mitochondrial COI and genome-wide SNPs on the Korean Peninsula. Scientific reports, 15(1), 41911.

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.

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

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

Guo S, et al. (2025) Novel probiotic Lactobacillus helveticus WIS02 alleviates diabetes through multi-pronged regulation of glycolipid metabolism, pancreatic protection and gut microbiota remodeling. Frontiers in microbiology, 16, 1735605.

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).

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).

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

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.

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).