Resource Summary Report

Generated by dkNET on May 19, 2025

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

Defining Citation: PMID:20875133

Keywords: bio.tools

Funding:

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: 20250517T055709+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 283 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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).

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).

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

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

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

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.

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.

Yi L, et al. (2024) Characterization of the complete chloroplast genome sequence of Camellia tetracocca (Theaceae). Mitochondrial DNA. Part B, Resources, 9(4), 461.

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.

Kalaipandian S, et al. (2023) Transcriptome Analysis of Heat Shock Factor C2a Over-Expressing Wheat Roots Reveals Ferroptosis-like Cell Death in Heat Stress Recovery. International journal of molecular sciences, 24(4).

Yu J, et al. (2023) Unveiling the early life core microbiome of the sea cucumber Apostichopus japonicus and the unexpected abundance of the growth-promoting Sulfitobacter. Animal microbiome, 5(1), 54.

Kibegwa FM, et al. (2023) Diversity and functional analysis of rumen and fecal microbial communities associated with dietary changes in crossbreed dairy cattle. PloS one, 18(1), e0274371.

Xu W, et al. (2023) Strain-level screening of human gut microbes identifies Blautia producta as a new anti-hyperlipidemic probiotic. Gut microbes, 15(1), 2228045.

Wang X, et al. (2023) Analysis of Genetic Diversity in Adzuki Beans (Vigna angularis): Insights into Environmental Adaptation and Early Breeding Strategies for Yield Improvement. Plants (Basel, Switzerland), 12(24).

Gao S, et al. (2023) Fine mapping of a Fusarium crown rot resistant locus on chromosome arm 6HL in barley by exploiting near isogenic lines, transcriptome profiling, and a large near isogenic line-derived population. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 136(6), 137.

Raza A, et al. (2023) A genetic locus complements resistance to Bordetella pertussis-induced histamine sensitization. Communications biology, 6(1), 244.