

Resource Summary Report

Generated by [RRID](#) on Sep 10, 2026

Q-Value Software

RRID:SCR_008538

Type: Tool

Proper Citation

Q-Value Software (RRID:SCR_008538)

Resource Information

URL: <http://genomine.org/qvalue/>

Proper Citation: Q-Value Software (RRID:SCR_008538)

Description: Features: * This software takes a list of p-values resulting from the simultaneous testing of many hypotheses and estimates their q-values. A point-and-click interface is now available! * The q-value of a test measures the proportion of false positives incurred (called the false discovery rate) when that particular test is called significant. * A short tutorial on q-values and false discovery rates is provided with the manual. * Various plots are automatically generated, allowing one to make sensible significance cut-offs. * Several mathematical results have recently been shown on the conservative accuracy of the estimated q-values from this software. * The software can be applied to problems in genomics, brain imaging, astrophysics, and data mining. This research was supported in part by a National Science Foundation graduate research fellowship.

Synonyms: Q-Value Software

Resource Type: software resource

Resource Name: Q-Value Software

Resource ID: SCR_008538

Alternate IDs: nif-0000-31382

Record Creation Time: 20220129T080248+0000

Record Last Update: 20260905T132624+0000

Ratings and Alerts

No rating or validation information has been found for Q-Value Software.

No alerts have been found for Q-Value Software.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Filippou P, et al. (2021) Systems biology reveals key tissue-specific metabolic and transcriptional signatures involved in the response of *Medicago truncatula* plant genotypes to salt stress. *Computational and structural biotechnology journal*, 19, 2133.

Pellegrini M, et al. (2016) Protein complex prediction for large protein protein interaction networks with the Core&Peel method. *BMC bioinformatics*, 17(Suppl 12), 372.

Szoboszlay M, et al. (2016) The Effect of Root Exudate 7,4'-Dihydroxyflavone and Naringenin on Soil Bacterial Community Structure. *PloS one*, 11(1), e0146555.

Liu YZ, et al. (2009) Genome-wide association analyses identify SPOCK as a key novel gene underlying age at menarche. *PLoS genetics*, 5(3), e1000420.

Crawford NP, et al. (2005) Evaluation of SLC11A1 as an inflammatory bowel disease candidate gene. *BMC medical genetics*, 6, 10.