# **Resource Summary Report**

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# **Q Squared Solutions Expression Analysis**

RRID:SCR\_012497 Type: Tool

### **Proper Citation**

Q Squared Solutions Expression Analysis (RRID:SCR\_012497)

## **Resource Information**

URL: https://www.q2labsolutions.com/genomics-laboratories

**Proper Citation:** Q Squared Solutions Expression Analysis (RRID:SCR\_012497)

**Description:** Core provides whole genome to focused set gene expression and genotyping assays along with DNA sequencings services, sequence enrichment technologies and bioinformatics support. Platforms utilized include Affymetrix GeneChip, Agilent Sure Select, Fluidigm Access Arrays, Illumina BeadChip, iScan, Genome Analyzer and Hi-Seq, RainDance Technologies RDT 1000 and, the Pacific Biosciences PacBio RS. Expression Analysis offers solutions for challenging specimens such as whole blood and FFPE tissues, as well as nucleic acid isolation and data analysis services.

Abbreviations: Q2 Solutions, EA, Q squared solutions, Q2, Q squared

**Synonyms:** Q2 Solutions Expression Analysis, Q 2 Solutions Expression Analysis, Q 2 Expression Analysis

**Resource Type:** commercial organization, service resource, core facility, access service resource

Keywords: genomic, genotyping, DNA sequencing,

Funding:

Availability: Available to external user

Resource Name: Q Squared Solutions Expression Analysis

Resource ID: SCR\_012497

Alternate IDs: SciEx\_366

Alternate URLs: http://www.scienceexchange.com/facilities/expression-analysis

**Record Creation Time:** 20220129T080310+0000

Record Last Update: 20250420T014613+0000

#### **Ratings and Alerts**

No rating or validation information has been found for Q Squared Solutions Expression Analysis.

No alerts have been found for Q Squared Solutions Expression Analysis.

# Data and Source Information

Source: SciCrunch Registry

### **Usage and Citation Metrics**

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

Iqbal M, et al. (2013) Expression of HMA4 cDNAs of the zinc hyperaccumulator Noccaea caerulescens from endogenous NcHMA4 promoters does not complement the zinc-deficiency phenotype of the Arabidopsis thaliana hma2hma4 double mutant. Frontiers in plant science, 4, 404.