Resource Summary Report

Generated by RRID on Aug 11, 2026

NASCs International Affymetrix Service

RRID:SCR_012825
Type: Tool

Proper Citation

NASCs International Affymetrix Service (RRID:SCR_012825)

Resource Information

URL: http://affymetrix.arabidopsis.info

Proper Citation: NASCs International Affymetrix Service (RRID:SCR_012825)

Description: The NASC International Affymetrix Service is a commercial website that provides transcripomics services for a fee. This data is available for any available species, any consortium chip, and any kind of experiment. The website also provides open source and free Xspecies software and techniques that can be (examples) used to perform GeneChip transcriptomics experiments on species for which no current Affymetrix chip exists.

Synonyms: NASCarrays

Resource Type: data or information resource, database

Keywords: FASEB list

Resource Name: NASCs International Affymetrix Service

Resource ID: SCR_012825

Alternate IDs: nif-0000-03176

Record Creation Time: 20220129T080312+0000

Record Last Update: 20260811T043445+0000

Ratings and Alerts

No rating or validation information has been found for NASCs International Affymetrix Service.

No alerts have been found for NASCs International Affymetrix Service.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 44 mentions in open access literature.

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

Liebsch D, et al. (2022) Metabolic control of arginine and ornithine levels paces the progression of leaf senescence. Plant physiology, 189(4), 1943.

Torres Acosta JA, et al. (2019) Zearalenone and ß-Zearalenol But Not Their Glucosides Inhibit Heat Shock Protein 90 ATPase Activity. Frontiers in pharmacology, 10, 1160.

Faria-Blanc N, et al. (2018) A Transcriptomic Analysis of Xylan Mutants Does Not Support the Existence of a Secondary Cell Wall Integrity System in Arabidopsis. Frontiers in plant science, 9, 384.

Nelson SK, et al. (2017) Transcriptional mechanisms associated with seed dormancy and dormancy loss in the gibberellin-insensitive sly1-2 mutant of Arabidopsis thaliana. PloS one, 12(6), e0179143.

Rodríguez-Celma J, et al. (2016) Systems-wide analysis of manganese deficiency-induced changes in gene activity of Arabidopsis roots. Scientific reports, 6, 35846.

Salazar-Henao JE, et al. (2016) Discriminative gene co-expression network analysis uncovers novel modules involved in the formation of phosphate deficiency-induced root hairs in Arabidopsis. Scientific reports, 6, 26820.

Armengot L, et al. (2016) The Protein Kinase CK2 Mediates Cross-Talk between Auxin- and Salicylic Acid-Signaling Pathways in the Regulation of PINOID Transcription. PloS one, 11(6), e0157168.

Hoehenwarter W, et al. (2016) Comparative expression profiling reveals a role of the root apoplast in local phosphate response. BMC plant biology, 16, 106.

Li W, et al. (2015) Re-analysis of RNA-seq transcriptome data reveals new aspects of gene activity in Arabidopsis root hairs. Frontiers in plant science, 6, 421.

Mortimer JC, et al. (2015) An unusual xylan in Arabidopsis primary cell walls is synthesised by GUX3, IRX9L, IRX10L and IRX14. The Plant journal : for cell and molecular biology, 83(3), 413.

Bush SJ, et al. (2015) Lineage-specific sequence evolution and exon edge conservation partially explain the relationship between evolutionary rate and expression level in A. thaliana. Molecular ecology, 24(12), 3093.

Eastmond PJ, et al. (2015) Arabidopsis uses two gluconeogenic gateways for organic acids to fuel seedling establishment. Nature communications, 6, 6659.

Chen CY, et al. (2015) The paralogous R3 MYB proteins CAPRICE, TRIPTYCHON and ENHANCER OF TRY AND CPC1 play pleiotropic and partly non-redundant roles in the phosphate starvation response of Arabidopsis roots. Journal of experimental botany, 66(15), 4821.

Li W, et al. (2015) Genome-wide analysis of overlapping genes regulated by iron deficiency and phosphate starvation reveals new interactions in Arabidopsis roots. BMC research notes, 8, 555.

Baima S, et al. (2014) Negative feedback regulation of auxin signaling by ATHB8/ACL5-BUD2 transcription module. Molecular plant, 7(6), 1006.

Schmitz J, et al. (2014) The essential role of sugar metabolism in the acclimation response of Arabidopsis thaliana to high light intensities. Journal of experimental botany, 65(6), 1619.

Chen L, et al. (2014) Correcting for differential transcript coverage reveals a strong relationship between alternative splicing and organism complexity. Molecular biology and evolution, 31(6), 1402.

Lan P, et al. (2013) A digital compendium of genes mediating the reversible phosphorylation of proteins in fe-deficient Arabidopsis roots. Frontiers in plant science, 4, 173.

Amirak E, et al. (2013) p90 ribosomal S6 kinases play a significant role in early gene regulation in the cardiomyocyte response to G(q)-protein-coupled receptor stimuli, endothelin-1 and ?(1)-adrenergic receptor agonists. The Biochemical journal, 450(2), 351.

Rodríguez-Celma J, et al. (2013) The transcriptional response of Arabidopsis leaves to Fe deficiency. Frontiers in plant science, 4, 276.