Resource Summary Report

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Affymetrix Power Tools

RRID:SCR_008401
Type: Tool

Proper Citation

Affymetrix Power Tools (RRID:SCR_008401)

Resource Information

URL: http://www.affymetrix.com/support/developer/powertools/apt_archive.affx

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Description: Affymetrix Power Tools (APT) are a set of cross-platform command line programs that implement algorithms for analyzing and working with Affymetrix GeneChip arrays. APT programs are intended for power users who prefer programs that can be utilized in scripting environments and are sophisticated enough to handle the complexity of extra features and functionality. APT provides platform for developing and deploying new algorithms without waiting for the GUI implementations. This resource is supported by Affymetrix, Inc.

Synonyms: APT

Resource Type: software resource

Keywords: Affymetrix, Inc., Genomics, Clinical, Study, Bioinformatic, Windows, MacOS, Linux, resource, Data, Normalization, Sequence, Annotation, Gene, Expression, Pattern, Motif, Inference, Toolkit, Model, Fitting, Algorithm

Resource Name: Affymetrix Power Tools

Resource ID: SCR_008401

Alternate IDs: nif-0000-30070

Alternate URLs:
https://www.affymetrix.com/support/developer/powertools/changelog/install.html, https://media.affymetrix.com/support/developer/powertools/changelog/index.html

Old URLs:
http://www.affymetrix.com/partners_programs/programs/developer/tools/powertools.affx

Record Creation Time: 20220129T080247+0000

Record Last Update: 20260808T185908+0000

Ratings and Alerts

No rating or validation information has been found for Affymetrix Power Tools.

No alerts have been found for Affymetrix Power Tools.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 32 mentions in open access literature.

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

Hofvander J, et al. (2026) Transcriptomic Subgroups in Soft Tissue Tumors Correlate with Morphologic Subtype, Genomic Features, and Outcome. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(9), 1825.

Wong H, et al. (2026) An Analytic Framework Characterizes the Biological Processes That Shape Copy Number-Based Genome Instability Patterns in Breast Cancer. Cancer research, 86(13), 3344.

Sharma NK, et al. (2025) Genome wide landscaping of copy number variations for horse inter-breed variability. Animal biotechnology, 36(1), 2446251.

Ahn R, et al. (2021) Large-Scale Imputation of KIR Copy Number and HLA Alleles in North American and European Psoriasis Case-Control Cohorts Reveals Association of Inhibitory KIR2DL2 With Psoriasis. Frontiers in immunology, 12, 684326.

Nuechterlein N, et al. (2021) Machine learning modeling of genome-wide copy number alteration signatures reliably predicts IDH mutational status in adult diffuse glioma. Acta neuropathologica communications, 9(1), 191.

Kikuchi M, et al. (2020) Disruption of a RAC1-centred network is associated with Alzheimer's disease pathology and causes age-dependent neurodegeneration. Human molecular genetics, 29(5), 817.

Mathias C, et al. (2020) Frequency of the TP53 R337H variant in sporadic breast cancer and its impact on genomic instability. Scientific reports, 10(1), 16614.

Mock JR, et al. (2019) Transcriptional analysis of Foxp3+ Tregs and functions of two identified molecules during resolution of ALI. JCI insight, 4(6).

Nanki K, et al. (2018) Divergent Routes toward Wnt and R-spondin Niche Independency during Human Gastric Carcinogenesis. Cell, 174(4), 856.

Zhang SY, et al. (2018) Inborn Errors of RNA Lariat Metabolism in Humans with Brainstem Viral Infection. Cell, 172(5), 952.

Delahaye-Duriez A, et al. (2016) Rare and common epilepsies converge on a shared gene regulatory network providing opportunities for novel antiepileptic drug discovery. Genome biology, 17(1), 245.

Zerbo O, et al. (2016) Maternal mid-pregnancy C-reactive protein and risk of autism spectrum disorders: the early markers for autism study. Translational psychiatry, 6(4), e783.

Priest HD, et al. (2014) Analysis of global gene expression in Brachypodium distachyon reveals extensive network plasticity in response to abiotic stress. PloS one, 9(1), e87499.

Booher RN, et al. (2014) MCL1 and BCL-xL levels in solid tumors are predictive of dinaciclib-induced apoptosis. PloS one, 9(10), e108371.

Trabzuni D, et al. (2013) Fine-mapping, gene expression and splicing analysis of the disease associated LRRK2 locus. PloS one, 8(8), e70724.

Lenz M, et al. (2013) PhysioSpace: relating gene expression experiments from heterogeneous sources using shared physiological processes. PloS one, 8(10), e77627.

Willmann CA, et al. (2013) To clone or not to clone? Induced pluripotent stem cells can be generated in bulk culture. PloS one, 8(5), e65324.

Boisson B, et al. (2013) An ACT1 mutation selectively abolishes interleukin-17 responses in humans with chronic mucocutaneous candidiasis. Immunity, 39(4), 676.

Syed YA, et al. (2013) Inhibition of phosphodiesterase-4 promotes oligodendrocyte precursor cell differentiation and enhances CNS remyelination. EMBO molecular medicine, 5(12), 1918.

Li C, et al. (2012) Comparative analyses reveal potential uses of Brachypodium distachyon as a model for cold stress responses in temperate grasses. BMC plant biology, 12, 65.