

**Affymetrix 大麦表达谱芯片服务****Affymetrix GeneChip Barley Genome Array**

芯片介绍: Affymetrix 大麦基因组芯片芯片信息来自 NCBI/GenBank 数据库, 包含大约 400,000 条大麦 EST。

**Agilent Barley 大麦基因组芯片**

安捷伦最新推出的大麦全基因组表达谱芯片所用的序列信息源于 WormBase、RefSeq、Unigene、Ensembl、UCSC 和 TIGR 等知名数据库, 代表了超过 43,000 个大麦基因和转录本。对研究者而言, 这意味着他们可以方便地利用高质量的微阵列分析, 在全基因组水平对未知基因的生物功能获得新发现。

| Feature               | Specification   |
|-----------------------|---|
| Product Number        | G2519F  |
| Design ID             | 021623  |
| Slide Format          | 4 x 44K   |
| Microarrays / Slide   | 4   |
| Slides / Kit          | 1   |
| Microarrays / Kit     | 4   |
| Features / Microarray | 45,018  |
| Genes / Microarray    | ~42,034   |
| Content Source        | RefSeq (Release 31), Sep 2008<br>Unigene (Build 52), Feb 2008<br>TIGR Plant Transcript Assemblies (Release 2), Jul 2008<br>TIGR Gene Indices (Release 10), Sep 2006 |

Vitamin E biosynthesis: functional characterization of the monocot homogentisate geranylgeranyl transferase

Yang, W. *et al.* Plant Journal 65(2), 206-17, 2011 [PubMed](#)

Transcriptome Analysis of the Vernalization Response in Barley (*Hordeum vulgare*) Seedlings

Greenup, A. G. *et al.* Plos One 6(3), NPG, 2011 [PubMed](#)

Quantitative and Qualitative Stem Rust Resistance Factors in Barley Are Associated with Transcriptional Suppression of Defense Regulons

Moscou, M. J. *et al.* Plos Genetics 7(7), NPG, 2011 [PubMed](#)

Significance of Light, Sugar, and Amino Acid Supply for Diurnal Gene Regulation in Developing Barley Caryopses(1[W][OA])

Mangelsen, E. *et al.* Plant Physiology 153(1), 14-33, 2010 [PubMed](#)

ODDSOC2 is a MADS box floral repressor that is down-regulated by vernalization in temperate cereals (1[W][OA])

Greenup, A. G. *et al.* Plant Physiology 153(3), 1062-73, 2010 [PubMed](#)

An informative set of SNP markers for molecular characterisation of Australian barley germplasm

Hayden, M. J. *et al.* Crop & Pasture Science 61(1), 70-83, 2010 [PubMed](#)

An eQTL Analysis of Partial Resistance to Puccinia hordei in Barley

Chen, X. W. *et al.* Plos One 5(1), NPG, 2010 [PubMed](#)

eTranscriptome analysis of a barley breeding program examines gene expression diversity and reveals target genes for malting quality improvement

Munoz-Amatriain, M. *et al.* BMC Genomics 11(), NPG, 2010 [PubMed](#)

Combining quantitative trait loci analyses and microarray data: An empirical likelihood approach

Wang, D. *et al.* Computational Statistics & Data Analysis 53(5 Sp Iss SI), 1661-73, 2009 [PubMed](#)

Development of 5006 Full-Length cDNAs in Barley: A Tool for Accessing Cereal Genomics Resources

Sato, K. *et al.* DNA Research 16(2), 81-9, 2009 [PubMed](#)

The genetics of barley low-tillering mutants: absent lower laterals (als)

Dabbert, T. *et al.* Theoretical and Applied Genetics 118(7), 1351-60, 2009 [PubMed](#)

Barley elicits a similar early basal defence response during host and non-host interactions with Polymyxa root parasites

McGrann, G. R. D. *et al.* European Journal of Plant Pathology 123(1), 5-15, 2009 [PubMed](#)

Blufensin1 Negatively Impacts Basal Defense in Response to Barley Powdery Mildew

Meng, Y. *et al.* Plant Physiology 149(1), 271-85, 2009 [PubMed](#)

A pathway-specific microarray analysis highlights the complex and co-ordinated transcriptional networks of the developing grain of field-grown barley

Hansen, M. *et al.* Journal of Experimental Botany 60(1), 153-67, 2009 [PubMed](#)

Time course analysis of gene expression over 24 hours in Fe-deficient barley roots

Nagasaka, S. *et al.* Plant Molecular Biology 69(5), 621-31, 2009 [PubMed](#)

Structure-function analysis of the barley genome: the gene-rich region of chromosome 2HL

Chen, A. *et al.* Functional & Integrative Genomics 9(1), 67-79, 2009 [PubMed](#)

Microarray analysis of the interaction between the aphid *Rhopalosiphum padi* and host plants reveals both differences and similarities between susceptible and partially resistant barley lines

Delp, G. *et al.* Molecular Genetics and Genomics 281(3), 233-48, 2009 [PubMed](#)

Differentially expressed genes during malting and correlation with malting quality phenotypes in barley (*Hordeum vulgare* L.)

Lapitan, N. L. V. *et al.* Theoretical and Applied Genetics 118(5), 937-52, 2009 [PubMed](#)

Linkage mapping of putative regulator genes of barley grain development characterized by expression profiling

Pietsch, C. *et al.* BMC Plant Biology 9(), NPG, 2009 [PubMed](#)

Gene expression profiling of tolerant barley in response to *Diuraphis noxia* (Hemiptera: Aphididae) feeding

Gutsche, A. *et al.* Bulletin of Entomological Research 99(2), 163-73, 2009 [PubMed](#)

A roadmap for zinc trafficking in the developing barley grain based on laser capture microdissection and gene expression profiling

Tauris, B. *et al.* Journal of Experimental Botany 60(4), 1333-47, 2009 [PubMed](#)

Robust Detection and Genotyping of Single Feature Polymorphisms from Gene Expression Data

Wang, M. H. *et al.* Plos Computational Biology 5(3), NPG, 2009 [PubMed](#)

Microarray Analysis of Late Response to Boron Toxicity in Barley (*Hordeum vulgare* L.) Leaves

Oez, M. T. *et al.* Turkish Journal of Agriculture and Forestry 33(2), 191-202, 2009 [PubMed](#)

Anatomical and Transcriptomic Studies of the Coleorhiza Reveal the Importance of This Tissue in Regulating Dormancy in Barley

Barrero, J. M. *et al.* Plant Physiology 150(2), 1006-21, 2009 [PubMed](#)

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Analysis of the (1,3)-beta-D-glucan synthase gene family of barley  
Schober, M. S. *et al.* *Phytochemistry* 70(6), 713-20, 2009 [PubMed](#)

Identification and characterization of barley RNA-directed RNA polymerases  
Madsen, C. T. *et al.* *Biochimica Et Biophysica Acta-Genes and Cell Regulation*  
*Mechanisms* 1789(5), 375-85, 2009 [PubMed](#)

Microspore embryogenesis: assignment of genes to embryo formation and green vs.  
albino plant production  
Munoz-Amatriain, M. *et al.* *Functional & Integrative Genomics* 9(3), 311-23, 2009 [PubMed](#)

A high-density transcript linkage map of barley derived from a single population  
Sato, K. *et al.* *Heredity* 103(2), 110-7, 2009 [PubMed](#)