

ARRAYS >

Data Sheet

GeneChip[®] *Pseudomonas aeruginosa* Genome Array

Pseudomonas aeruginosa is an opportunistic pathogen associated with a wide variety of human infections. The GeneChip® Pseudomonas aeruginosa Genome Array serves as an important tool in studying gene functions of this clinically relevant bacterium. Pseudomonas aeruginosa (P. aeruginosa) is responsible for many nosocomial (hospital-acquired) infections and can cause persistent infections in patients with cancer, severe burns, or other immunecompromising conditions. P. aeruginosa can cause particularly virulent and chronic lung infections in individuals afflicted with cystic fibrosis (CF), a common genetic disorder that currently affects over 30,000 people in the United States. P. aeruginosa is the most common bacterial infection found in the lungs of CF patients and leads to progressive lung disease, which is also the leading cause of death among these individuals.

Because P. aeruginosa forms biofilms under laboratory conditions, it has been used as a model to study quorum sensing and cell signaling in gram-negative bacteria. These properties and its pathogenicity have made P. aeruginosa a key target in the development of new anti-bacterial drugs. Its disease-causing properties are not restricted to mammalian organisms. P. aeruginosa has been shown to be pathogenic in the worm Caenorhabditis elegans and plant Arabidopsis thaliana. P. aeruginosa utilizes common pathogenicity pathways between animals and plants¹. Its ability to survive in a wide variety of environments also makes the P. aeruginosa genome a source for identifying novel transport and utilization pathways for metabolites.

The *P. aeruginosa* genome, which is relatively large for a prokaryote, contains over 6.3 million base pairs and 5,570 predicted open reading frames (ORFs). This genome is comprehensively represented on the GeneChip® *P. aeruginosa* Genome Array, which contains probes to over 5,500 ORFs. The sequence information on this array was developed, in collaboration with the Cystic Fibrosis Foundation, from the initial publication of the *P. aeruginosa* sequence².

Applications

With the *P. aeruginosa* Genome Array, specific genes can be studied to understand the role of individual genes in processes such as antibiotic resistance, biofilm formation³, and host-pathogen interaction.

The *P. aeruginosa* Genome Array includes probe sets to intergenic sequences which may lead to the identification of new genes.

In addition to sequences from the *P. aeruginosa* strain PAO1, the array also includes unique sequences from other strains to broaden the research possibilities with the array. Genes encoding serological determinants and pathogenicity islands⁴ are included on the array and have proven useful in genotyping *P. aeruginosa* strains isolated from human infections originating from different tissues.

Assay

The sample preparation for this array utilizes reverse transcriptase and random hexamers for cDNA synthesis. A unique hybridization protocol has been developed to accommodate the relatively high GC content of the *P. aeruginosa* genome.

Array Content

The GeneChip *P. aeruginosa* Genome Array contains probe sets for over 5,500 ORFs from the PAO1 strain of *P. aeruginosa*, 199 probe sets corresponding to 100 intergenic sequences, and 117 additional genes from *P. aeruginosa* strains other than PAO1.

During the design process, the *P. aeruginosa* sequences were pruned against the GeneChip Human Genome U95 Genome Array, facilitating experiments on the *P. aeruginosa* samples isolated from human tissues.

Critical Specifications

| Number of arrays in set | One |
|------------------------------|---|
| Array format | Midi |
| Feature size | 20 µm |
| Oligonucleotide probe length | 25-mer |
| Probe pairs/sequence | ~13 |
| Control sequences included | Poly-A controls: |
| | dap, lys, phe, and trp from B. subtilis |
| Detection sensitivity | ~1 copy/cell* |

*Expected performance based on the detection of unlabeled controls spiked into total RNA and carried through the cDNA labeling protocol. This sensitivity is based on the assumption that *P. aeruginosa* content is similar to *E. coli* cells which contain approximately 100 fg total RNA per cell, and mRNA accounts for approximately 2% of total RNA.

Supporting Products

| Part # | Product Name | Description |
|--------|---|-----------------------------|
| 900542 | GeneChip® DNA Labeling Reagent | Sufficient for 30 reactions |
| 900301 | Control Oligo B2, 3nM | Sufficient for 30 reactions |
| 900433 | GeneChip [®] Eukaryotic Poly-A RNA Control Kit | Approximately 100 reactions |
| | | |

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REFERENCES:

- 1. L.G. Rahme, *et al. Proc Acad Sci USA* **97**(16): 8815-21 (August 1, 2000).
- 2. C. Stover, et al. Nature 406: 959-964
- (August 21, 2000).
- M. Whiteley, *et al. Nature* **413**: 860-864 (October 25, 2001).
- 4. X. Liang, et al. J Bacteriol **183**(3): 843-853 (Feb. 2001).

Ordering Information

GeneChip[®] *P. aeruginosa* Genome Array

| 900339 | Contains 5 GeneChip | |
|--------|-----------------------------|--|
| | P. aeruginosa Genome Arrays | |
| 900340 | Contains 30 GeneChip | |
| | P. aeruginosa Genome Arrays | |

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