eArray 5.0 and Beyond
Print what you want, when you want it.

http://earray.chem.agilent.com

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Agilent Technologies
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Session Summary

- Each Module is about 15 minutes
- Live demonstration
- Q&A at the end of each Module

Module 1: The Basics
- The eArray Paradigms
- Array Creation Workflow

Module 2: Upload Probes
Creating a microarray design by uploading probes

Module 3: GE Probe Design
Creating a microarray design from Target Sequence.

Module 4: CGH/ChIP HD Search
Create from HD CHIP/CGH Database Probes
Module 1: The Basics
Basic Features

eArray is a secure, web-based application that allows you to:

• Create custom microarray designs
• Work collaboratively with others and share designs
• Search High Definition (HD) CGH/LA Databases
• Access all Agilent Catalog Content
• Design Custom Probes for Gene Expression (GE)
• Check the Quality of GE probes Developed by 3rd parties.
• Support High Density Array formats – (1 X 244 K, 2 X 105 K, 4 X 44 K)

...for Free!
Module 1: The Basics

The Content Paradigm

Agilent Probe 001
Agilent Probe 002
Agilent Probe 003

Probes
Your Probe 001
Your Probe 002
Your Probe 003
Your Probe 004
Your Probe 005
Your Probe 006

Probe Groups

Microarray Designs

Microarray Sets

Your WorkGroup
Module 1: The Basics
The Workgroup Paradigm: Workgroups

Agilent Domain

- Agilent Catalog
- HD CGH Probe Database
- HD ChiP Probe Database

“Superadmin”

Your WorkGroup

- Admin
- Users
- Probes, Probe Groups, Microarray Designs

Other WorkGroup
Module 1: The Basics
The Workgroup Paradigm: Collaborations

Agilent Domain

- Agilent Catalog
- HD CGH Probe Database
- HD ChiP Probe Database

“Superadmin”

Your WorkGroup

- Admin
- Users
- Probes, Probe Groups, Microarray Designs

Collaboration Space

Probes, Probe Groups, Microarray Designs

Other WorkGroup

Agilent Technologies
Module 1: The Basics
The Workflow

eArray provides an easy way of managing the array creation process.
Module 1: The Basics
New UI Paradigm

Application Views: Users can select between applications, where each view shows only functionality for the current application.
Module 1: The Basics

New UI Paradigm

Content Bar- Provides access to functionality surrounding the basic concepts in eArray.
Module 1: The Basics
New UI Paradigm

Search – Allows you to search for Microarrays, Probes, or Probe Groups in your account.
Module 1: The Basics
New UI Paradigm

Design Wizards – Takes you through the most common scenarios for creating a microarray design, from start to finish.
Module 1: The Basics
Finished

End of Module 1
Do you have any questions?
Module 2: Creating a microarray design from Uploaded Probes

The Process

1. Design Probes
2. Search Agilent Probes
3. Create Probe Groups
4. Upload Probes
5. Create Microarray Designs
6. Download Design Files
7. Submit to Manufacture
8. Order Arrays
Module 2: Creating a microarray design from Uploaded Probes

File Formats

0. Creating the Probe File

1. Probe Parameter and File Details
2. Preview Uploaded Probes
3. Define Design
4. Layout probes and Create Design
5. Print Arrays

The first step in creating a design from uploaded probes is to create the probe file. The probe file serves as the vehicle for getting the probes into your account, and in many respects is the most difficult because you need to make sure that it is formatted correctly.

This step is numbered ‘0’ because it is the first step in the process, and because it is not a part of the eArray design wizard flow.

The file is “tab-delimited”, and should be saved with the extension ‘.txt’ or ‘.tdt’. You can use a text editor program like Microsoft notepad to create it. Optionally, you can use MS Excel to define the rows and columns of the file.

Minimal Format

Use this format if you only have probe IDs and sequence.

- Header defining the columns is optional
- Probe IDs can be up to 15 characters.
- Probe IDs should be unique
- Probe Sequence can be 25-60bp long.
- A <tab> character is between columns

Example

<table>
<thead>
<tr>
<th>ProbeID</th>
<th>Sequence</th>
</tr>
</thead>
<tbody>
<tr>
<td>C_52_P616047</td>
<td>TGTCGGACTGTCCTCAGGCAACCAACGGAGACGAGGAGCTCACAGCAG</td>
</tr>
<tr>
<td>C_51_P288390</td>
<td>CCCTGGAGTCGCAAACGGAGATGCTAGTGCCATATTTTATTTTATTTTTGCTATAACAGCAAAAAGAACATGGGACAG</td>
</tr>
<tr>
<td>C_52_P276815</td>
<td>TCTCAGCTTCTGAGGACTGAGCTACCTCTTCTGCTATAACAGCAAAAAGAACATGGGACAG</td>
</tr>
<tr>
<td>C_52_P363216</td>
<td>CAGATCAGTGAGCAAGCTCTAGGATGTTCCAACATGACCTCAGCAGTTTGTGCTATAACAGCAAAAAGAACATGGGACAG</td>
</tr>
<tr>
<td>C_52_P594049</td>
<td>GAACAGTCTGAGGGAAGATGGGAGCTGAGGCTTCTTCTGCTATAACAGCAAAAAGAACATGGGACAG</td>
</tr>
<tr>
<td>C_52_P429944</td>
<td>TATCAGTCTGAGGGAAGATGGGAGCTGAGGCTTCTTCTGCTATAACAGCAAAAAGAACATGGGACAG</td>
</tr>
<tr>
<td>C_51_P111704</td>
<td>CCTCAGCTTCTGAGGGAAGATGGGAGCTGAGGCTTCTTCTGCTATAACAGCAAAAAGAACATGGGACAG</td>
</tr>
<tr>
<td>C_51_P343489</td>
<td>TATCAGTCTGAGGGAAGATGGGAGCTGAGGCTTCTTCTGCTATAACAGCAAAAAGAACATGGGACAG</td>
</tr>
<tr>
<td>C_51_P237245</td>
<td>TATCAGTCTGAGGGAAGATGGGAGCTGAGGCTTCTTCTGCTATAACAGCAAAAAGAACATGGGACAG</td>
</tr>
<tr>
<td>C_52_P593965</td>
<td>AGGGACTGACAGGTGGGCACAGAGAGTTTCAGGAATGCTGAGGGAAGATGGGAGCTGAGGCTTCTTCTGCTATAACAGCAAAAAGAACATGGGACAG</td>
</tr>
</tbody>
</table>
### Module 2: Creating a microarray design from Uploaded Probes

#### Save States

<table>
<thead>
<tr>
<th>How do you want to save and create your Design?</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Draft</strong> Saves the design, allowing only you to make changes to it before completing.</td>
</tr>
<tr>
<td><strong>Review</strong> Saves the design, enabling users in your Workgroup to make versions of the design before completing.</td>
</tr>
<tr>
<td><strong>Complete</strong> Saves the design. This design cannot be edited, and can it <strong>cannot</strong> be ordered.</td>
</tr>
<tr>
<td><strong>Submit</strong> Saves the design, this design cannot be edited, and is <strong>available for ordering.</strong></td>
</tr>
</tbody>
</table>

[Save] [Cancel]

Available December 10, 2007
Module 2: Creating a microarray design from Uploaded Probes

Demo
Module 2: Creating a microarray design from Uploaded Probes

Finished

End of Module 2

Do you have any questions?
Module 3: Creating a microarray design from Target Sequence

Overview

Comments:

- Same probe design algorithms used for Agilent Catalog content.
- Uses thermodynamic principles of duplex formation.
- “Tm Matched” probe design for prokaryotic organisms.
- Probes between 25-60mers.

Things to Keep in Mind:

- “Garbage in Garbage out”
- eArray GE probe design is “Gene Centric”
- Algorithm optimized for 3’ biased 60mers.
Module 3: Creating a microarray design from Target Sequence
Probe Design Process

Input Sequence

Preprocessing

Masking

Candidate Probes

Output Probes

Similarity Search

Hyperlink to process
Module 3: Creating a microarray design from Target Sequence

FASTA Format

The file is should be saved as a .txt file, and can contain multiple FASTA formatted-sequences.

You can also reference the sequence in eArray if you know the Genbank Accession Numbers.

Example

>gi|124028520|ref|NM_001080547.1| Homo sapiens spleen focus forming virus (SFFV) proviral integration oncogene spi1 (SPI1), transcript variant 1, mRNA

GACTATCTCCAGGCGAGCGCCCTTCTGATAAAATCAGGAACTTGTGCTGGCCCTGCAATGTCAAGGGAGGGGGCTCACCCAGGGCTCCTGTAGCTCAGGGGGCAGGCCTGAGCCCTGCACCCGCCCCACGACCGTCCAGCCCCTGACGGGGCACCCCATCCTGAGGGGCTCTGCATTGGCCCCACCCCAACCGAGGCAGGGATCTGACCGACTCGGAGCCCGGCTGGATGTTACAGGCGTGCAAAATGGAAGGGTTTCCCCTCGTCCCCCTCAGCCATTCAGAAAGACCTGTTGCCCTATGTACACCGGATCTATACCAAACCGAAGCAGATATTACCCCTATCTCAGCAGTGATGGGAAGGCCAGACGTATCCGCTACCCACCACCCACGCAGTGCAAGCGAGTTTGAGACTGCTGAGCCCGCCGCTCGCTGATACCCGCCAGCGCTGCGACAGCGACGCGCCACGCTGCTGGAGACCTCTCCTGCTGCGAGCGCCCGCGCGCGCGAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC

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Module 3: Creating a microarray design from Target Sequence

FASTA Format

0. Creating the FASTA File

1. Select Method
2. Select Parameters
3. Define Targets
4. Define Design
5. Layout Probes and Submit Design
6. Print Arrays

You can also reference the sequence in eArray if you know the Genbank Accession Numbers.

The file should be saved as a .txt file, and can contain multiple FASTA formatted-sequences.

Example

>gi|124028520|ref|NM_001080547.1| Homo sapiens spleen focus forming virus (SFFV) proviral integration oncogene sp1 (SPI1), transcript variant 1, mRNA

GACTATCTCCAGCGGAGGCCCTTCCATAGTAAATACAGGAACCTGTGCTGACCCTGCAATGTCAAGGGAGGGGGCTCACCCAGGGCTCCTGTAGCTCAGGGGGCAGGCCTGAGCCCTGCACCCGCCCCACGACCGTCAGCCACCTGACGGGGCACCCCATCCTGAGGGGCTCTGCATTGGCCCCACCGAGGCAGGGGATCTGAGCCGACTCGGAGCCCGGCTGGATGTTACAGGCGTGCAAAATGGAAGGGTTTCCCCTCGTCCCCCTCATTCATCAGAAAGACCTGCTTGCCTATGACACGGATCTATACCAACGCCAAACGCACGAGTATTACCCCTATCTCAGCAGTAGTGAGGAAGCCATAGGACCATTACTGGGACTTCCACCCCCACCACGTGACAGGAGTTCGAGGCTCCCGAGCAGGACTGTGGCGGGCCGGGCCTCGCCTCACCCGCCCCCTCCCCCCACTCCAGGCCCTCCACATCCCGCTTCGCTCCCTCCAGGACTCCACCCCGCCTCCCGGACGCCAGCTGGGCTGTCAGACCCCACCGGGGCAACCTTGCAAAGGACGACCCGGGGTACTGCCTTGGGAGTCTCAAGTCCGTATGTAATCAGATCTCCCCTCTCACCCCTCCCACCCATTAACCTCCTCCCAAAAAAACAAGTAAAGTTATTCTCAAT
Module 3: Creating a microarray design from Target Sequence Demo
Module 3: Creating a microarray design from Target Sequence
FASTA Format

End of Module 3
Do you have any questions?
Module 4: Create from HD CHIP/CGH Database Probes
Chromosomal Location Format

0. Creating File

1. HD Probe Search Details
2. HD Probe Search Submission
3. Create Probe Group
4. Define Design
5. Layout Probes and Submit Design
6. Print Arrays

You can also use Agilent Probe IDs if you have them!

The file is should be saved as a .txt file, and can contain multiple chromosomal locations in the following format:

- chr3:27739533-27739583
- chr9:122350069-122350129
- chrX:149512474-149512534
- chr5:176629952-176629999
- chr16:3751779-3751834
- chr17:2632341-2632386
- chr17:2848887-2848936
Module 4: Create from HD CHIP/CGH Database Probes

Database Summary

Comparative Genomic Hybridization (CGH) HD Database:

<table>
<thead>
<tr>
<th>Species</th>
<th>Probe#</th>
<th>Density</th>
<th>Build Annotation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Human</td>
<td>8.4 Million</td>
<td>200 bp</td>
<td>NCBI Build 36</td>
</tr>
<tr>
<td>Mouse</td>
<td>7.2 Million</td>
<td>200 bp</td>
<td>NCBI Build 36</td>
</tr>
<tr>
<td>Rat</td>
<td>6.9 Million</td>
<td>200 bp</td>
<td>UCSC Rn4</td>
</tr>
</tbody>
</table>

Chromatin Immuno-precipitation (ChIP) HD Database:

<table>
<thead>
<tr>
<th>Species</th>
<th>Probe#</th>
<th>Density</th>
<th>Build Annotation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Human</td>
<td>23.8 Million</td>
<td>&lt;100 bp</td>
<td>NCBI Build 36</td>
</tr>
<tr>
<td>Mouse</td>
<td>27.4 Million</td>
<td>&lt;100 bp</td>
<td>NCBI Build 36</td>
</tr>
<tr>
<td>Rat</td>
<td>22.1 Million</td>
<td>&lt;100 bp</td>
<td>UCSC Rn4</td>
</tr>
</tbody>
</table>

In addition to - A. gambiae; A. thaliana; C. elegans; D. melanogaster; S. cerevisiae (~ 1.0 M each)
End of Module 4

Do you have any questions?
The End

Do you have any questions?

http://earray.chem.agilent.com