

eArray 5.0 and

Beyond

Print what you want,
when you want it.

<http://earray.chem.agilent.com>

Charlie Nelson
Agilent Technologies
November 7, 2007





eArray 5.0 – Overview

Session Summary

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

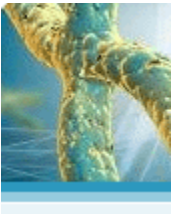
Basic Features

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)

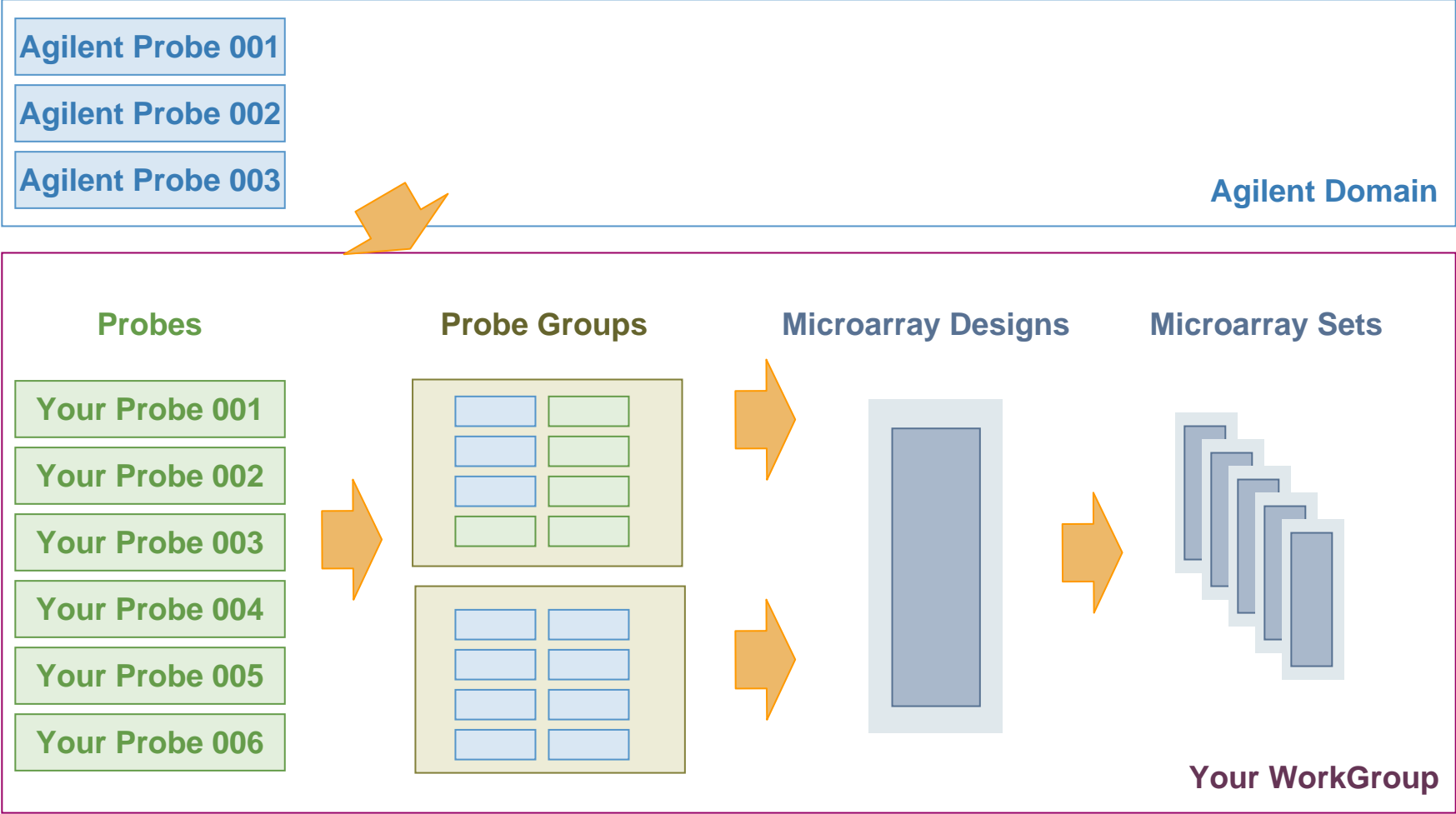
...for Free!

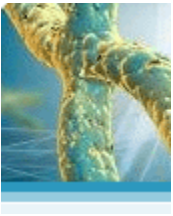




Module 1: The Basics

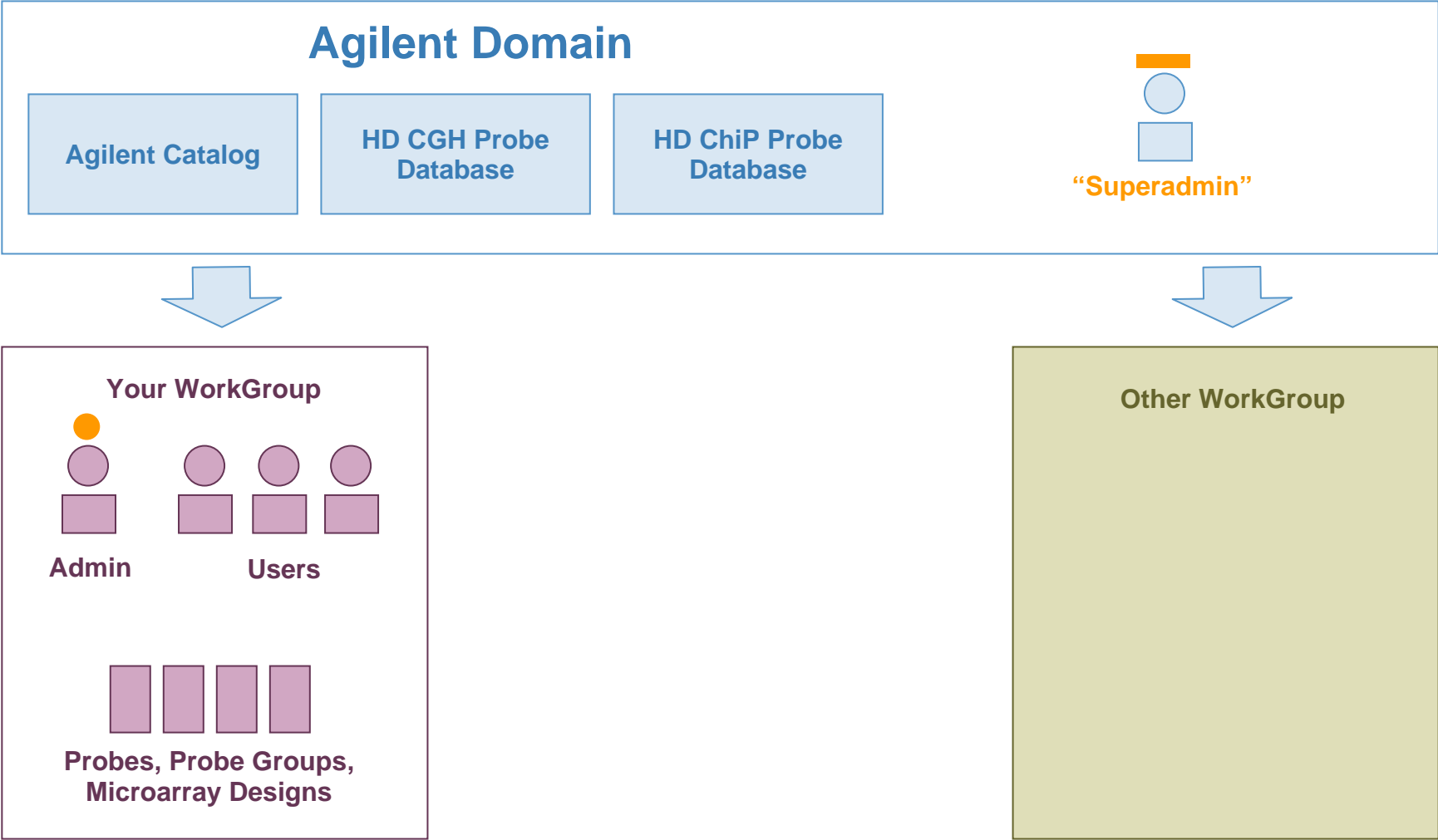
The Content Paradigm

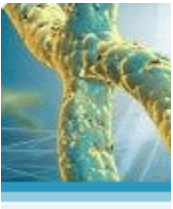




Module 1: The Basics

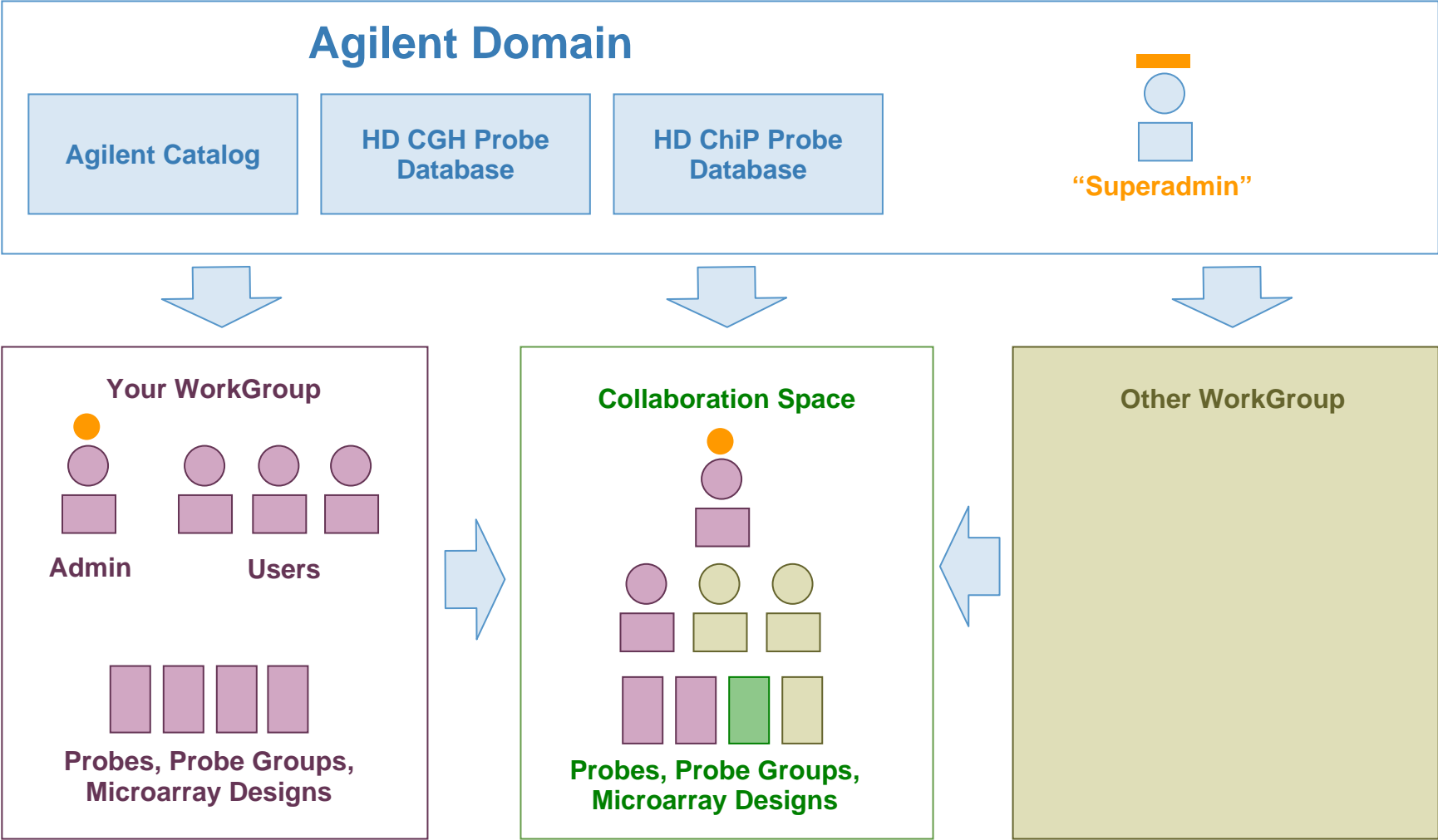
The Workgroup Paradigm: Workgroups





Module 1: The Basics

The Workgroup Paradigm: Collaborations

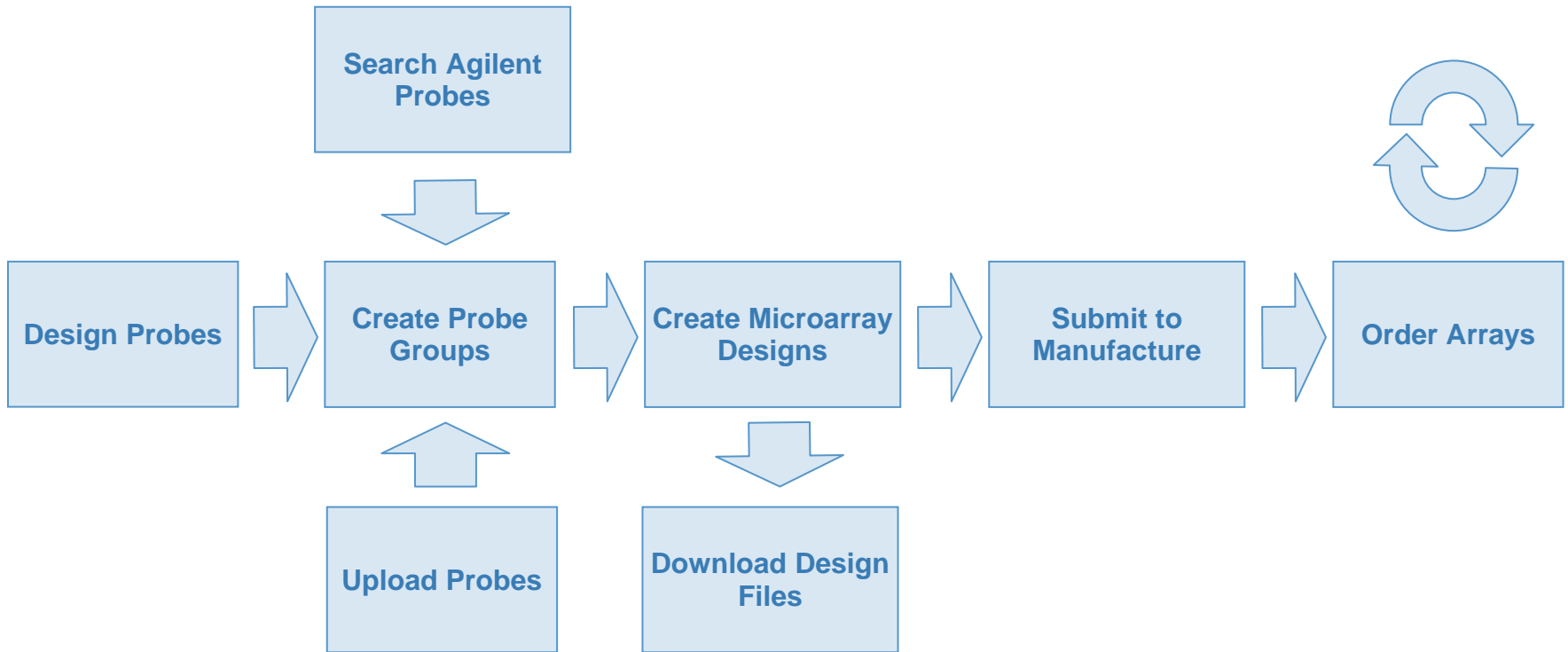




Module 1: The Basics


The Workflow

eArray provides an easy way of managing the array creation process.



Module 1: The Basics

New UI Paradigm


Help | Logout

Workspace Collaboration
Welcome Charlie Nelson (Agilent)
[Help](#)

Home
Microarray
Probe Group
Probes
My Account
Master Data
OF Functions
Site Maintenance

Application Type: Expression [Switch Application Type](#)

Search

Microarray
 Probe Group
 Simple Probe

Microarray Name:

Species: [Select and Add](#)

Design Number: [Upload](#)

Search
Reset

Create Design Wizards

[Refresh](#) [View All](#)

- Create a Microarray Design by Uploading Probes [Info](#)
- Create a Microarray Design from Existing ProbeGroup(s) [Info](#)
- Create a Microarray Design from Target Transcripts [Info](#)

Next >>

Search Results: 6 matching results found

Wizard Name	Status	Created Date	Action
MAD_Uploaded_Probes_Liumkai	Probes Uploaded Failed	05-Nov-2007	Delete
MAD_Uploaded_Probes_For Shukla	Probes Uploaded	05-Nov-2007	Continue Delete

Pending Jobs

[Refresh](#) [View All](#)

Search Results: 0 matching results found

My Designs

[Refresh](#) [View All](#)

Search Results: 10 matching results found

Name	Created Date	Action
testlist	05-Nov-2007	Order Download
gigidi	05-Nov-2007	Order Download
Test Design	03-Nov-2007	Order Download

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Module 1: The Basics

New UI Paradigm

Application Views- Users can select between applications, where each view shows only functionality for the current application

The screenshot displays the Agilent Technologies eArray application interface. At the top left is the Agilent Technologies eArray logo. The top right corner contains 'Help | Logout' and a user greeting 'Welcome Charlie Nelson (Agilent)'. Below the logo are two tabs: 'Workspace' and 'Collaboration'. A main navigation bar includes 'Home', 'Microarray', 'Probe Group', 'Probes', 'My Account', 'Master Data', 'OF Functions', and 'Site Maintenance'. A secondary navigation bar on the right shows 'Application Type: Expression' with a 'Switch Application Type' link and a 'Help' link. The main content area is divided into four panels: 1. 'Search' panel with radio buttons for 'Microarray', 'Probe Group', and 'Simple Probe', and input fields for 'Microarray Name', 'Species', and 'Design Number'. 2. 'Create Design Wizards' panel with three radio button options and a 'Next >>' button. 3. 'Pending Jobs' panel showing 'Search Results: 0 matching results found'. 4. 'My Designs' panel showing 'Search Results: 10 matching results found' and a table of design entries.

Agilent Technologies
eArray

Help | Logout
Welcome Charlie Nelson (Agilent)

Workspace Collaboration

Home Microarray Probe Group Probes My Account Master Data OF Functions Site Maintenance

Application Type: **Expression** [Switch Application Type](#) [Help](#)

Search

Microarray Probe Group Simple Probe

Microarray Name:

Species: [Select and Add](#)

Design Number: [Upload](#)

Create Design Wizards [Refresh](#) [View All](#)

Create a Microarray Design by Uploading Probes [Info](#)

Create a Microarray Design from Existing ProbeGroup(s) [Info](#)

Create a Microarray Design from Target Transcripts [Info](#)

Search Results: 6 matching results found

Wizard Name	Status	Created Date	Action
MAD_Uploaded_Probes_Liumkai	Probes Uploaded Failed	05-Nov-2007	Delete
MAD_Uploaded_Probes_For Shukla	Probes Uploaded	05-Nov-2007	Continue Delete

Pending Jobs [Refresh](#) [View All](#)

Search Results: 0 matching results found

My Designs [Refresh](#) [View All](#)

Search Results: 10 matching results found

Name	Created Date	Action
testlist	05-Nov-2007	Order Download
gigoi	05-Nov-2007	Order Download
Test Design	03-Nov-2007	Order Download

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Module 1: The Basics

New UI Paradigm

Content Bar- Provides access to functionality surrounding the basic concepts in eArray.

The screenshot displays the Agilent Technologies eArray application interface. At the top left is the Agilent Technologies eArray logo. The top right corner contains 'Help | Logout' and 'Welcome Charlie Nelson (Agilent)'. Below the logo is a navigation bar with tabs for 'Workspace' and 'Collaboration'. A content bar below the navigation bar contains links for 'Home', 'Microarray', 'Probe Group', 'Probes', 'My Account', 'Master Data', 'OF Functions', and 'Site Maintenance'. The 'Application Type' is set to 'Expression', with a link to 'Switch Application Type'. The main content area is divided into four panels: 1. Search: Includes radio buttons for 'Microarray', 'Probe Group', and 'Simple Probe'. It has input fields for 'Microarray Name', 'Species', and 'Design Number', with 'Select and Add' and 'Upload' links. 'Search' and 'Reset' buttons are at the bottom. 2. Create Design Wizards: Includes radio buttons for three wizard options: 'Create a Microarray Design by Uploading Probes', 'Create a Microarray Design from Existing ProbeGroup(s)', and 'Create a Microarray Design from Target Transcripts'. A 'Next >>' button is on the right. 3. Search Results: 6 matching results found. A table with columns 'Wizard Name', 'Status', 'Created Date', and 'Action'. 4. Pending Jobs: Search Results: 0 matching results found. 5. My Designs: Search Results: 10 matching results found. A table with columns 'Name', 'Created Date', and 'Action'. At the bottom, there are links for 'eArray Contact/Support', 'Site Information', 'eArray Terms of Use', and 'FAQ', followed by a copyright notice: '@ Copyright Agilent Technologies, Inc. 2002-2007'.

Agilent Technologies
eArray

Help | Logout
Welcome Charlie Nelson (Agilent)
Help

Workspace Collaboration

Home Microarray Probe Group Probes My Account Master Data OF Functions Site Maintenance

Application Type: Expression [Switch Application Type](#)

Search

Microarray Probe Group Simple Probe

Microarray Name:

Species: [Select and Add](#)

Design Number: [Upload](#)

Create Design Wizards [Refresh](#) [View All](#)

Create a Microarray Design by Uploading Probes [Info](#)

Create a Microarray Design from Existing ProbeGroup(s) [Info](#)

Create a Microarray Design from Target Transcripts [Info](#)

Search Results: 6 matching results found

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MAD_Uploaded_Probes_Liumkai	Probes Uploaded Failed	05-Nov-2007	Delete
MAD_Uploaded_Probes_For Shukla	Probes Uploaded	05-Nov-2007	Continue Delete

Pending Jobs [Refresh](#) [View All](#)

Search Results: 0 matching results found

My Designs [Refresh](#) [View All](#)

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Test Design	03-Nov-2007	Order Download

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Module 1: The Basics

New UI Paradigm

Search – Allows you to search for Microarrays, Probes, or Probe Groups in your account.

The screenshot displays the Agilent Technologies eArray application interface. At the top, there is a navigation bar with the Agilent Technologies logo and 'eArray' branding. The user is logged in as 'Charlie Nelson (Agilent)'. The main navigation menu includes 'Home', 'Microarray', 'Probe Group', 'Probes', 'My Account', 'Master Data', 'OF Functions', and 'Site Maintenance'. The 'Application Type' is set to 'Expression'. The main content area is divided into several sections:

- Search:** A search form with radio buttons for 'Microarray' (selected), 'Probe Group', and 'Simple Probe'. It includes input fields for 'Microarray Name', 'Species', and 'Design Number', along with 'Search' and 'Reset' buttons.
- Create Design Wizards:** A section with three radio buttons: 'Create a Microarray Design by Uploading Probes', 'Create a Microarray Design from Existing ProbeGroup(s)', and 'Create a Microarray Design from Target Transcripts'. A 'Next >>' button is present.
- Search Results:** A table showing 6 matching results found. The table has columns for Wizard Name, Status, Created Date, and Action.
- Pending Jobs:** A section showing 0 matching results found.
- My Designs:** A section showing 10 matching results found. The table has columns for Name, Created Date, and Action.

At the bottom, there is a footer with links for 'eArray Contact/Support', 'Site Information', 'eArray Terms of Use', and 'FAQ', along with a copyright notice for Agilent Technologies, Inc. 2002-2007.

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.

The screenshot displays the Agilent Technologies eArray application interface. The top navigation bar includes the Agilent Technologies logo, 'eArray', and user information: 'Welcome Charlie Nelson (Agilent)'. Below this is a secondary navigation bar with tabs for 'Workspace' and 'Collaboration'. A main navigation bar contains links for 'Home', 'Microarray', 'Probe Group', 'Probes', 'My Account', 'Master Data', 'OF Functions', and 'Site Maintenance'. The 'Application Type' is set to 'Expression'.

The main content area is divided into several sections:

- Search:** A search form with radio buttons for 'Microarray' (selected), 'Probe Group', and 'Simple Probe'. It includes input fields for 'Microarray Name', 'Species', and 'Design Number', along with 'Search' and 'Reset' buttons.
- Create Design Wizards:** This section is highlighted with an orange border. It contains three radio button options:
 - Create a Microarray Design by Uploading Probes [Info](#)
 - Create a Microarray Design from Existing ProbeGroup(s) [Info](#)
 - Create a Microarray Design from Target Transcripts [Info](#)
 A 'Next >>' button is located at the bottom right of this section. Below the options is a table of search results:

Wizard Name	Status	Created Date	Action
MAD_Uploaded_Probes_Liumkai	Probes Uploaded Failed	05-Nov-2007	Delete
MAD_Uploaded_Probes_For Shukla	Probes Uploaded	05-Nov-2007	Continue Delete
- Pending Jobs:** A section showing 'Search Results: 0 matching results found'.
- My Designs:** A section showing 'Search Results: 10 matching results found' and a table:

Name	Created Date	Action
testlist	05-Nov-2007	Order Download
gigigi	05-Nov-2007	Order Download
Test Design	03-Nov-2007	Order Download

At the bottom of the page, there is a footer with links for 'eArray Contact/Support', 'Site Information', 'eArray Terms of Use', and 'FAQ', followed by the copyright notice: '@ Copyright Agilent Technologies, Inc. 2002-2007'.

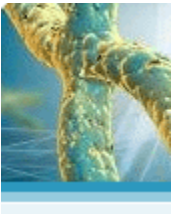


Module 1: The Basics

Finished

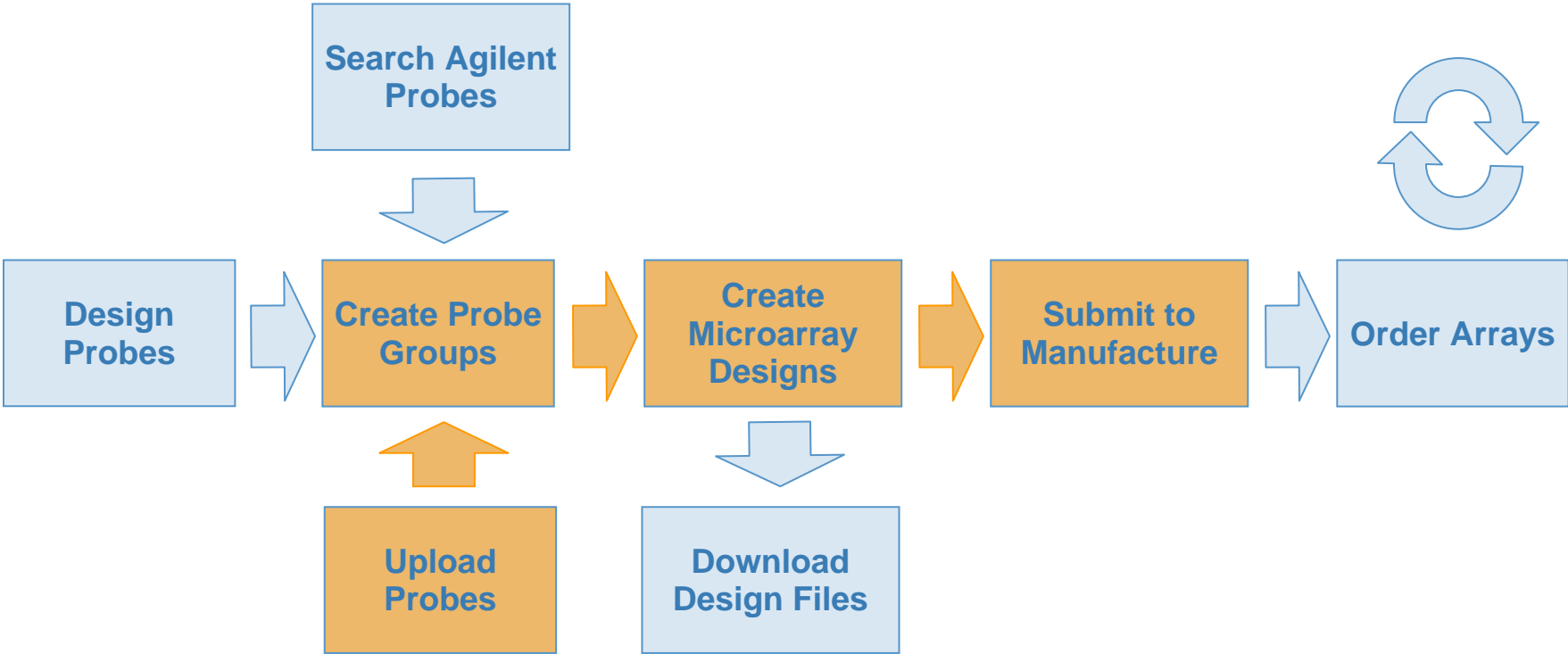
End of Module 1

Do you have any questions?



Module 2: Creating a microarray design from Uploaded Probes

The Process



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

ProbeID	Sequence
C_52_P616047	TGTCCGAAGTGTCTCAGTGCCAACCAACGGAATGGCGAAGAACGGCAGTGAAGCAGA
C_51_P288390	CCCTGAGTCCACATGCACACCTCAGCAGCCTATATTTATTTGTTTCTGGTTTAGCCTCAA
C_52_P276815	TCTCATCATTGTACGAGAAGTTTCTTCATAAGCACTATAGACAAAAACAATGGGGGAAGA
C_52_P363216	CAGATGATGTAGCAAGCCTTAGGATGGTTCATGATCAGTAGGAAGCAAATCTAAGACC
C_52_P594049	GAAACAGCTGGAGGGGAGAAGTGGGCAGTGCTGCTCTTTGCACTGTTTTGTTTTGTTTT
C_52_P429944	TATCATTCTGAGCCAGCTTCCACTTATTCTTGGTCCAAAGAGCAGTTTGTTCCATGTGG
C_51_P111704	CCTACATTTTTATTCTTACAGGGTGCTAAATTCTCCCTCAATAGTAATTAGATTAGCAG
C_51_P343489	TAGGGGTCAACATGGCCCCATTGAGCTCCCTACACTGCCAGTCCCTATTACCAATCCCTGT
C_51_P237245	AGTGGACATTCTAGAGTTATACTGTAGTAGCCAGAAATCTTAATTGACTGTTTCAGTCAT
C_52_P593965	AGGGACTGACAGGTGGGCACAGAGAATTTTCAGAAATATTAACCTTAAATCTCACCAGAT



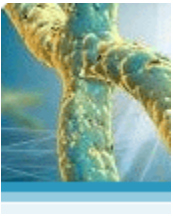
Module 2: Creating a microarray design from Uploaded Probes

Save States

How do you want to save and create your Design?

- Draft** Saves the design, allowing only you to make changes to it before completing. [More](#)
- Review** Saves the design, enabling users in your Workgroup to make versions of the design before completing. [More](#)
- Complete** Saves the design. This design cannot be edited, and can it **cannot** be ordered. [More](#)
- Submit** Saves the design, this design cannot be edited, and is **available for ordering**. [Order Checklist](#) [More](#)

Available December 10, 2007



Module 2: Creating a microarray design from Uploaded Probes

Demo

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

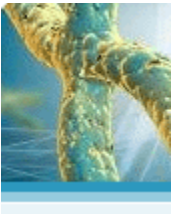
Comments:

- 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:

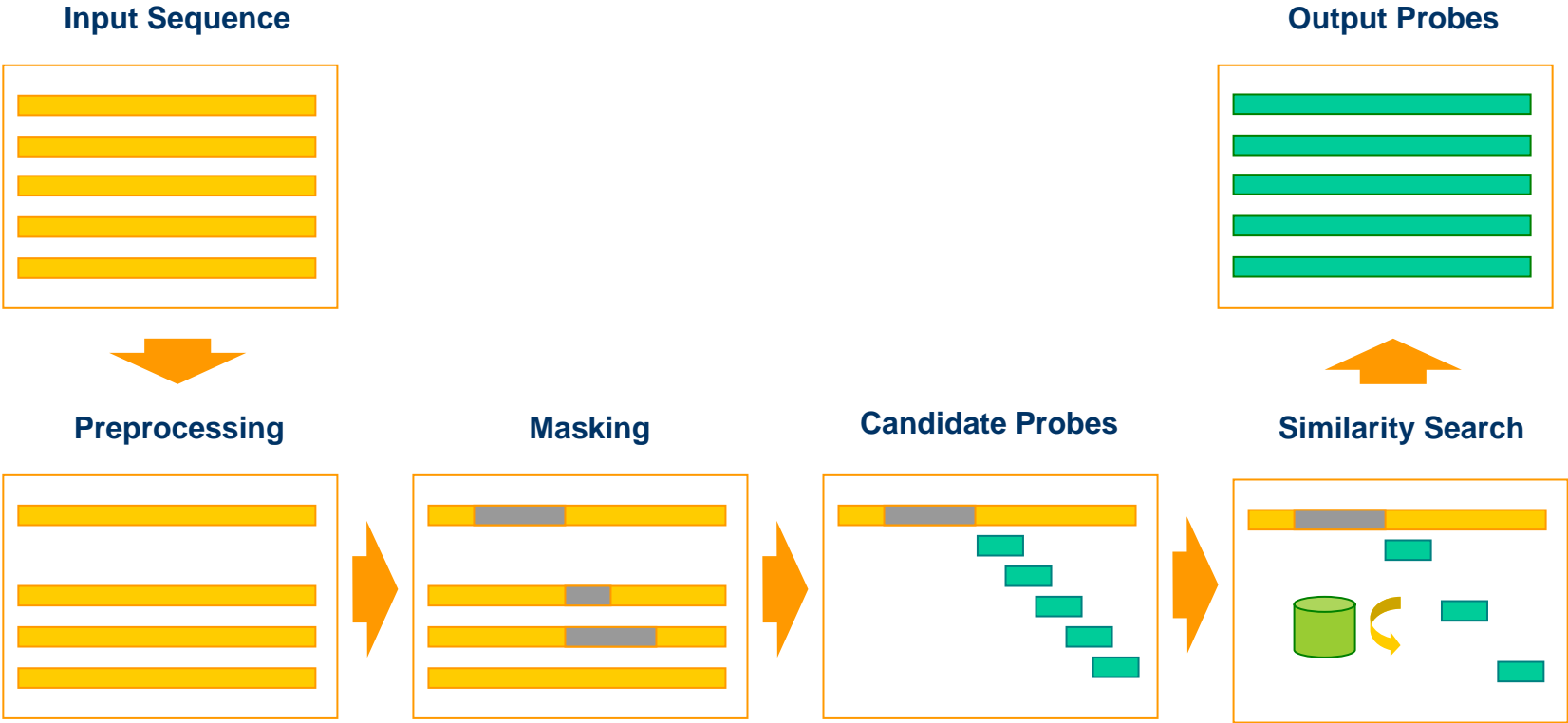
- “Garbage in Garbage out”
- eArray GE probe design is “Gene Centric”
- Algorithm optimized for 3’ biased 60mers.



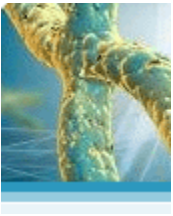


Module 3: Creating a microarray design from Target Sequence

Probe Design Process



[Hyperlink to process](#)



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

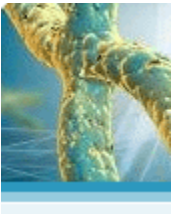
You can also reference the sequence in eArray if you know the Genbank Accession Numbers.

Example

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

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

```
GACTATCTCCCAGCGGCAGGCCCTTCGATAAAATCAGGAACTTGTGCTGGCCCTGCAATGTCAAGGGAG
GGGGCTCACCCAGGGCTCCTGTAGCTCAGGGGGCAGGCCCTGAGCCCTGCACCCGCCCCACGACCGTC
CAGCCCCTGACGGGGCACCCATCCTGAGGGGCTCTGCATTGGCCCCACCGAGGCAGGGGATCTGA
CCGACTCGGAGCCCGGCTGGATGTTACAGGCGTGCAAAATGGAAGGGTTTCCCCTCGTCCCCCCTCAG
CCATCAGAAGACCTGGTGCCCTATGACACGGATCTATACCAACGCCAAACGCACGAGTATTACCCCTATC
TCAGCAGTGATGGGGAGAGCCATAGCGACCATTACTGGGACTTCCACCCCCACCACGTGCACAGCGAG
TTCGAGAGCTTCGCCGAGAACAACCTTCACGGAGCTCCAGAGCGTGCAGCCCCCGCAGCTGCAGCAGCT
CTACCGCCACATGGAGCTGGAGAGAAGGTGAAGAAGAAGCTCACCTACCAGTTCAGCGGCGAAGTGCT
GGGCCGCGGGGGCCTGGCCGAGCGGGCGCCACCCGCCCACTGAGCCCGCAGCCCCCGCCGGGCCCC
GCCAGGCCTCCCCGCTGGCCATAGCATTAAAGCCCTCGCCCGGCCCGACACAGGGAGGACGCTCCCG
GGGCCAGAGGCAGGACTGTGGCGGGCCGGGCTCGCCTACCCGCCCCCTCCCCCACTCCAGGCC
CCCTCCACATCCCGCTTCGCCTCCCTCCAGGACTCCACCCCGGCTCCCGGACGCCAGCTGGGCGTCAG
ACCCACCGGGGCAACCTTGCAGAGGACGACCCGGGGTACTGCCTTGGGAGTCTCAAGTCCGTATGTA
AATCAGATCTCCCTCTCACCCCTCCCACCCATTAACCTCCTCCCAAAAAACAAGTAAAGTTATTCTCAAT
CCATCAAAAAAAAAAAAAAAAAAAAA
```



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.

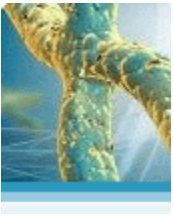
Example

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

ProbeID is the text string after the '>', and before the first <space>

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

```
GACTATCTCCCAGCGGCAGGCCCTTCGATAAAATCAGGAACCTTGCTGGCCCTGCAATGTCAAGGGAG
GGGGCTACCCAGGGCTCCTGTAGCTCAGGGGGCAGGCCCTGAGCCCTGCACCCGCCCCACGACCGTC
CAGCCCCTGACGGGGCACCCATCCTGAGGGGCTCTGCATTGGCCCCACCGAGGCAGGGGATCTGA
CCGACTCGGAGCCCGGCTGGATGTTACAGGCGTGCAAAATGGAAGGGTTTCCCCTCGTCCCCCTCAG
CCATCAGAAGACCTGGTGCCCTATGACACGGATCTATACCAACGCCAAACGCACGAGTATTACCCCTATC
TCAGCAGTGATGGGGAGAGCCATAGCGACCATTACTGGGACTTCCACCCCCACCACGTGCACAGCGAG
TTCGAGAGCTTCGCCGAGAACAACCTTCACGGAGCTCCAGAGCGTGCAGCCCCCGCAGCTGCAGCAGCT
CTACCGCCACATGGAGCTGGAGAGAAGGTGAAGAAGAAGCTCACCTACCAGTTCAGCGGCGAAGTGCT
GGGCCGCGGGGGCCTGGCCGAGCGGGCCACCCGCCCACTGAGCCCGCAGCCCCCGCCGGGCCCC
GCCAGGCCTCCCCGCTGGCCATAGCATTAAAGCCCTCGCCCCGGCCCGACACAGGGAGGACGCTCCCG
GGGCCAGAGGCAGGACTGTGGCGGGCCGGGCTCGCCTACCCGCCCCCTCCCCCACTCCAGGCC
CCCTCCACATCCCGCTTCGCCTCCCTCCAGGACTCCACCCCGGCTCCCGGACGCCAGCTGGGCGTCAG
ACCCACCCGGGGCAACCTTGACAGAGGACACCCGGGGTACTGCCTTGGGAGTCTCAAGTCCGTATGTA
AATCAGATCTCCCTCTCACCCCTCCCACCCATTAACCTCCTCCCAAAAAACAAGTAAAGTTATTCTCAAT
CCATCAAAAAAAAAAAAAAAAAAAAA
```



Module 3: Creating a microarray design from Target Sequence

Demo

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!

Example

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

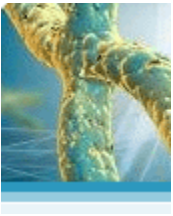
Comparative Genomic Hybridization (CGH) HD Database:

Species	Probe#	Density	Build Annotation
Human	8.4 Million	200 bp	NCBI Build 36
Mouse	7.2 Million	200 bp	NCBI Build 36
Rat	6.9 Million	200 bp	UCSC Rn4

Chromatin Immuno-precipitation (ChIP) HD Database:

Species	Probe#	Density	Build Annotation
Human	23.8 Million	<100 bp	NCBI Build 36
Mouse	27.4 Million	<100 bp	NCBI Build 36
Rat	22.1 Million	<100 bp	UCSC Rn4

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



Module 4: Create from HD CHIP/CGH Database Probes

Demo

Demo

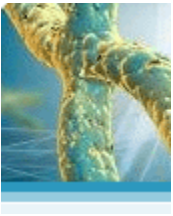


Module 4: Create from HD CHIP/CGH Database Probes

Database Summary

End of Module 4

Do you have any questions?



The End

Do you have any questions?

<http://earray.chem.agilent.com>