

**A QuickStart Guide  
for the Creation and  
Ordering of  
SureSelect Target  
Enrichment Oligo Sets  
without the Wizard**

Using **eArray**,  
a free web-based  
design tool

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# Getting Started

## Access eArray

- Access eArray at: <https://earray.chem.agilent.com/earray/>
- Log in to eArray, if this is your first time visiting, click **Request for Registration**

Agilent Technologies  
eArray

Guest View | Login Page | Help

### User Login

Login Name:

Remember my login name

Password:

**LOGIN**

[Forgot Password](#)

[Request for Registration](#)

### Important Links

- [Catalog Gene Lists](#)
- [Published Designs](#)
- [eArray Product Page](#)
- [System Requirements](#)

### Additional Information

- [Frequently asked questions](#)
- [Information on how to do common tasks](#)
- [Download DNA Analytics 4.0](#)
- [Download GeneSpring GX](#)

### News and Alerts

**Welcome to eArray 5.4!!**

[Get 15% off your first time eArray design order here](#)

The Login Name is the e-mail address used to register

# Getting Started

## Confirm Application Type

- Confirm that the Application Type is **TargetEnrichment**

The screenshot shows the Agilent Technologies eArray web application. At the top right, the user is logged in as 'Demo User (Agilent Marketing)'. The 'Application Type' is displayed as 'TargetEnrichment' with a link to 'Switch Application Type'. The main content area is divided into four panels:

- Search:** Includes input fields for Library Name, Species, and ELID, with 'Search' and 'Reset' buttons.
- Library Wizards:** Offers options to create a library from bait upload, existing bait groups, or bait tiling, with a 'Next >>' button.
- Pending Jobs:** Shows a table with one job: 'BaitTiling' (Job Name: Demo\_BaitTiling, Status: Bait Design Completed, Created Date: 27-Jan-2009).
- My Libraries:** Shows a table with two libraries: 'Demo\_BaitTiling\_Library2' and 'Demo\_BaitTiling\_Library', both created on 28-Jan-2009.

At the bottom, there is a note about downloading files and a footer with contact information and copyright notice: '© Copyright Agilent Technologies, Inc. 2002-2009'.

If necessary, select **Switch Application Type** to select Target Enrichment

This close-up shows the 'Select View Type' dropdown menu. The current selection is 'TargetEnrichment'. Other options in the list include Expression, ChIP, CGH, DNACapture, and microRNA. A 'Change' button is visible next to the dropdown.

# Getting Started

## Select Method

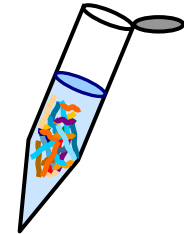
- Choose between two methods for creating a SureSelect Target Enrichment Set

	Benefits	Caveats	When to Use
<b>Following the Wizard*</b>	<ul style="list-style-type: none"><li>• Easy, stream-lined method</li><li>• The Wizard takes the user from initiation of design to submission</li></ul>	<ul style="list-style-type: none"><li>• The user will only be able to download the library details after the library is completed</li><li>• The user will not have access to a "fate" file</li></ul>	When a simple or straightforward design is planned
<b>Independent of the Wizard</b>	<ul style="list-style-type: none"><li>• User can download additional files, including a Fate file that lists the # of baits tiled for each target interval</li><li>• User can fine-tune the design, creating and combining multiple bait groups with a variety of parameter settings</li><li>• User can easily track the success of bait tiling for individual targets during the process of design</li></ul>	<ul style="list-style-type: none"><li>• User will not be guided by a Wizard</li></ul>	When iterations may be desired to get an optimal design for a target set

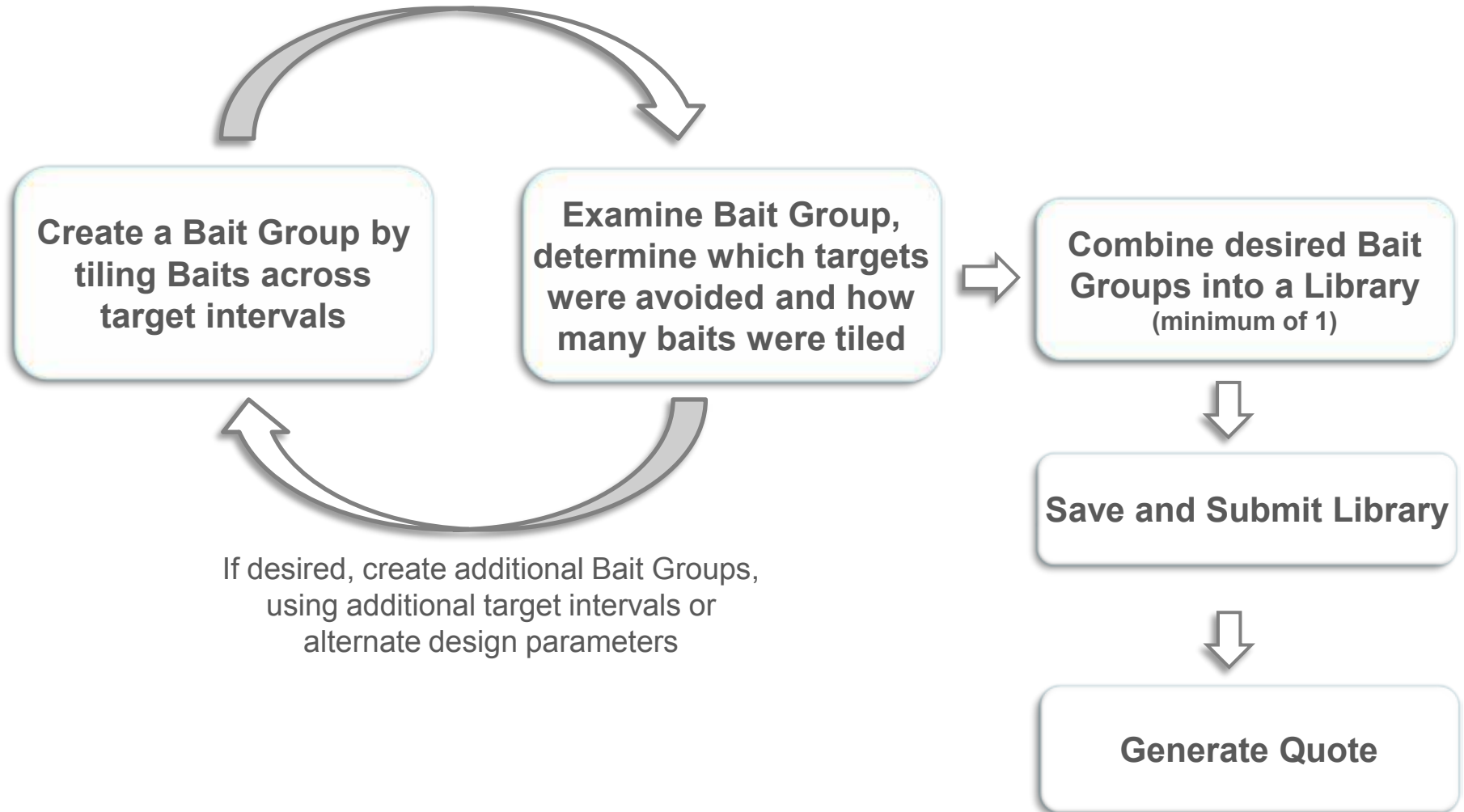
**\* This tutorial guides the user on how to create a design independent of the Wizard. If desired, please see the tutorial on how to create a design with the Wizard.**

# Terms and Definitions

- **Bait:**
  - A single oligo sequence of pre-determined length (120 bp) that complements a targeted region of the genome
- **Bait Group:**
  - Consists of a group of Baits designed to complement a single or set of targeted intervals
  - May be formed from baits generated within eArray, baits uploaded into eArray, or bait search results within eArray
- **Library:**
  - Consists of one or more Bait Groups
  - Represents the set of oligos that will be produced for the kit



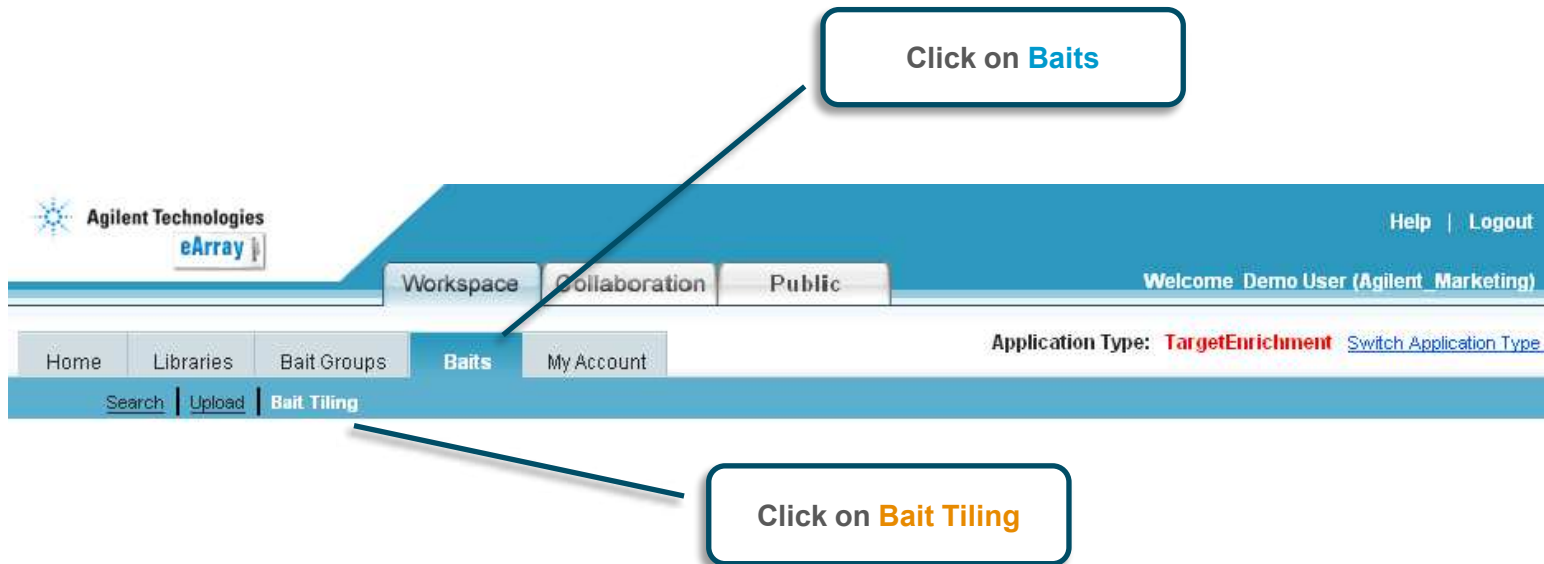
# Workflow Summary



# Create a Bait Group

## Design Baits

- To create a Bait Group, go to the **Baits** page, and select **Bait Tiling**



- This will bring you to the page where you can define design parameters for a Bait Group



# Create a Bait Group

## Design Options

1. Enter a name for the design job.

2. **Design Strategy:** To use the parameters previously optimized for general bait tiling, leave the checkmark on this option. To change the parameters, uncheck this option. The next slide describes the parameter changes that can be applied.

3. **Species:** Select the species for which the target intervals were designed. The Genome Build will then automatically be populated by eArray.

Home Libraries Bait Groups Baits My Account

Application Type: **TargetEnrichment** [Switch Application Type](#)

Search Upload Bait Tiling

Design Options		Target Details	
Design Job Name	First Bait Group	Species	H. sapiens
Sequencing Technology <a href="#">Info</a>	Illumina	Genome Build	H. sapiens, UCSC hg18, NCBI Build 36, Marc
Sequencing Protocol <a href="#">Info</a>	end-sequencing	Genomic Target Intervals <a href="#">Info</a>	chrX:100003816-100003948   chrX:1000 <a href="#">Upload</a>
Design Strategy <a href="#">Info</a>	<input checked="" type="checkbox"/> Use Optimized Parameters <input type="radio"/> Centered <input type="radio"/> Justified	Genomic Avoid Intervals	<input checked="" type="checkbox"/> Avoid Standard Repeat Masked Regions <a href="#">Info</a> <input type="checkbox"/> Custom Avoid Intervals <a href="#">Info</a> <a href="#">Upload</a>
Bait Length	120 bp		
Bait Tiling Frequency <a href="#">Info</a>	2x		
Allowed overlap into avoid regions <a href="#">Info</a>	20 bp		
<a href="#">Submit</a> <a href="#">Cancel</a>			

4. **Genomic Target Intervals:** Either type in or upload the genomic intervals for the targets to be enriched. Examples are provided on a later slide.

5. **Genomic Avoid Intervals:**

- Choose to avoid the standard repeat masked regions by leaving a checkmark next to this option (based on the UCSC RepeatMasker track).
- Add additional intervals to avoid with the baits by typing those intervals in or uploading them in the same format as the target intervals.

6. **Submit:** Select Submit when Options and Details are completed.

# Create a Bait Group

## Design Strategy

**1. Change the parameters:** To be able to change these parameters, first remove the checkbox from the “Use Optimized Parameters” option.

Design Strategy [Info](#)  Use Optimized Parameters

Centered  Justified

Bait Length  bp

Bait Tiling Frequency [Info](#)

Allowed overlap into avoid regions [Info](#)  bp

### 5. Allowed overlap into avoid regions:

Centered baits may overlap with regions adjacent to the target. In case the targets are adjacent to Avoid Regions, enter the acceptable amount of overlap with these in bp. To ensure that there is no overlap in any Avoid Regions, select '0 bp'.

### 2. Centered versus Justified: (see next slide for visuals)

#### Centered:

Baits are centered, and evenly distributed, across each target region. Baits may overlap to regions outside of the target.

**Why use this?** This is the method tested most extensively.

#### Justified:

Baits are first tiled across the target. If baits extend past the target interval, all baits are shifted inward so that there will be no overlap with adjacent but un-targeted genomic regions.

**Why use this?** If it is desired to avoid having baits to any region adjacent to targets, for example, if sequencing cDNA.

**3. Bait Length:** Currently, 120 bp is available as the only bait length option. All baits will be designed to be 120 bp in length.

### 4. Bait Tiling Frequency:

Options include 2X, 3X, 4X, and 5X and indicate the amount of bait overlap. Tiling frequency is not enforced at target edges. Increasing the frequency will lead to the ability to cover fewer or smaller regions in a library.

#### 2X Tiling:



#### 3X Tiling:



#### 4X Tiling:



#### 5X Tiling:



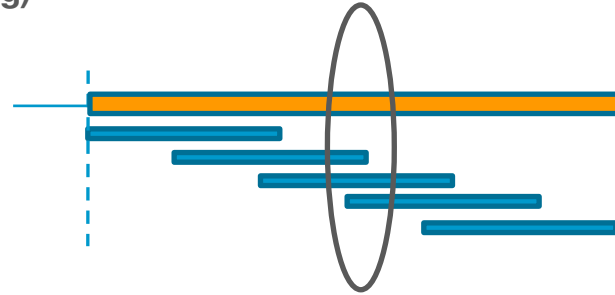
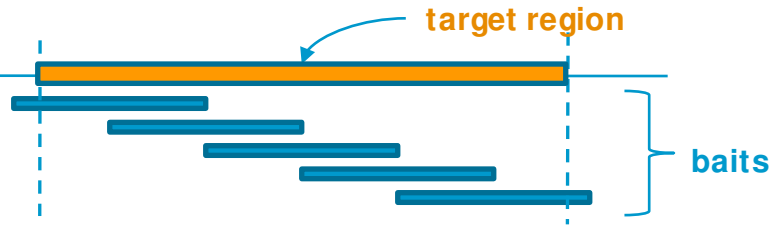
# Create a Bait Group

## Centered versus Justified

### Centered

### Justified

(a) Target region is large (example of 2x tiling)



Centered baits extend past interval boundaries, but have even coverage across entire region  
Justified baits do not extend past boundaries, but may have uneven coverage (eg, see circle where regions have both 2x and 3x tiling)

(b) Target region is 2 times the bait length



Design is the same for Centered and Justified

(c) Target region is shorter than the bait length



Design is the same for Centered and Justified

# Create a Bait Group

## Formats for describing Target Intervals

Target Details	
Species	H. sapiens
Genome Build	H. sapiens, UCSC hg18, NCBI Build 36, Marc
Genomic Target Intervals <a href="#">Info</a>	chrX:100003816-100003948   chrX:1000
	<input type="button" value="Upload"/>

### Option 1: Type in the genomic intervals to be targeted.

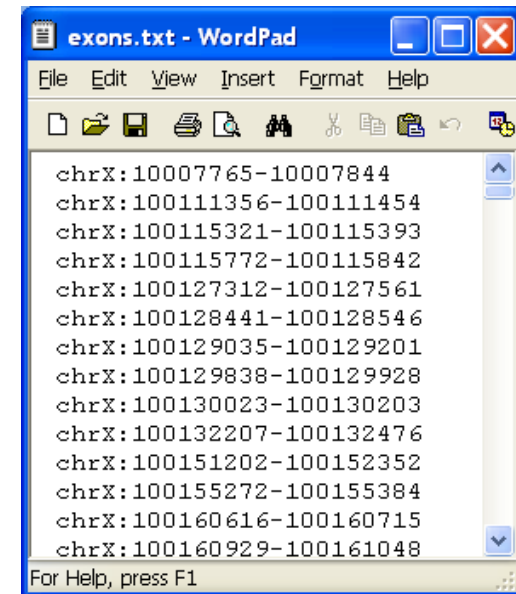
The format for typing in the intervals is as follows:

```
chrX:100003816-100003948|chrX:100004037-100004218|chrX:100004314-100004465|chrX:100004329-100004465|chrX:100004804-100004888
```

Each interval should be separated by the | character. If there is a long list of intervals, it would be better to use option 2.

### Option 2: Upload a file that includes the genomic intervals to be targeted:

The format for uploading the intervals is as follows:



```
exons.txt - WordPad
File Edit View Insert Format Help
chrX:10007765-10007844
chrX:100111356-100111454
chrX:100115321-100115393
chrX:100115772-100115842
chrX:100127312-100127561
chrX:100128441-100128546
chrX:100129035-100129201
chrX:100129838-100129928
chrX:100130023-100130203
chrX:100132207-100132476
chrX:100151202-100152352
chrX:100155272-100155384
chrX:100160616-100160715
chrX:100160929-100161048
For Help, press F1
```

Each interval should be presented on a separate line, and the file should be saved as a text file.

When using this option, select **Upload**, **Browse** to find the saved file, and then select **Upload File**.

# Create a Bait Group

## Check Bait Group Status

- The status of your Bait Group can be viewed in the Pending Jobs quadrant on the [Home](#) page (see left), or at the bottom of the [Baits](#) page (see right)
- To continue, you must be on the [Baits](#) page

The screenshot shows the 'Home' page of the Agilent Technologies eArray application. The navigation bar includes 'Home', 'Libraries', 'Bait Groups', 'Baits', and 'My Account'. The 'Search' section has radio buttons for 'Libraries', 'Bait Groups', and 'Baits'. Below this are input fields for 'Library Name', 'Species', and 'ELID', with 'Select and Add' and 'Upload' buttons. The 'Pending Jobs' section is circled in blue and shows a search result for 'Bait Tiling' with a status of 'Completed'.

Job Type	Job Name	Status	Created Date	Job Position	Action
Bait Tiling	FirstBaitGroup	Bait Design Completed	05-Feb-2009		

The screenshot shows the 'Baits' page of the Agilent Technologies eArray application. The navigation bar includes 'Workspace', 'Collaboration', and 'Public'. The 'Design Options' section includes fields for 'Design Job Name', 'Sequencing Technology' (Illumina), 'Sequencing Protocol' (end-sequencing), 'Design Strategy' (Use Optimized Parameters), 'Bait Length' (130 bp), 'Bait Tiling Frequency' (2x), and 'Allowed overlap into avoid regions' (20 bp). The 'Target Details' section includes 'Species' (H. sapiens), 'Genome Build' (H. sapiens. UCSC hg18. NCBI Build 36. Marc), and 'Genomic Target Intervals'. The 'Pending Jobs' section is circled in blue and shows a search result for 'Bait Tiling' with a status of 'Completed'.

Job ID	Job Name	Status	Design Type	Creation Date	Position in Queue	Actions
B407162395	FirstBaitGroup	Completed	Bait Tiling	05-Feb-2009	NA	Delete   View Design   Download   Create Bait Group

**Note:- Your design results will be removed from the system 2 weeks after design completion!**

# Create a Bait Group

## View Design Details (I)

- To view the Bait Group design, click on **View Design** on the **Baits** page

The screenshot shows the Agilent Technologies eArray web interface. The top navigation bar includes 'Workspace', 'Collaboration', and 'Public' tabs. The user is logged in as 'Demo User (Agilent\_Marketing)'. The main navigation bar shows 'Home', 'Libraries', 'Bait Groups', 'Baits', and 'My Account'. The 'Baits' section is active, and the 'Application Type' is set to 'TargetEnrichment'. Below the navigation, there are buttons for 'Search', 'Upload', and 'Bait Tiling'. The main content area is divided into two panels: 'Design Options' and 'Target Details'. The 'Design Options' panel includes fields for 'Design Job Name', 'Sequencing Technology' (Illumina), 'Sequencing Protocol' (end-sequencing), 'Design Strategy' (Use Optimized Parameters), 'Bait Length' (120 bp), 'Bait Tiling Frequency' (2x), and 'Allowed overlap into avoid regions' (20 bp). The 'Target Details' panel includes 'Species' (H. sapiens), 'Genome Build' (H. sapiens, UCSC hg18, NCBI Build 36, Marc), 'Genomic Target Intervals', and 'Genomic Avoid Intervals' (Avoid Standard Repeat Masked Regions). There are 'Submit' and 'Cancel' buttons at the bottom of the 'Design Options' panel.

If you have difficulty downloading the desired file, hold down the <Ctrl> key until a File Download dialog box appears. This bypasses pop-up blocking software.

Search Results: 1 matching results found

[Refresh](#)

Job ID	Job Name	Status	Design Type	Creation Date	Position in Queue	Actions
BI407162395	FirstBaitGroup	Completed	BaitTiling	05-Feb-2009	NA	<a href="#">Delete</a> <a href="#">View Design</a> <a href="#">Download</a> <a href="#">Create Bait Group</a>

[Refresh](#)

If you have difficulty downloading the desired file, hold down the <Ctrl> key until a File Download dialog box appears. This bypasses pop-up blocking software.

**Note:- Your design results will be removed from the system 2 weeks after design completion!**

# Create a Bait Group

## View Design Details (II)

- Toggle between Design Summary, Design Details, Target Fate, and Bed File to view the details of the bait design (only the first 100 lines will be presented).

Design Summary	Design Details	Target Fate	Bed File
Number of Input Targets : 8423			
Number of Valid Targets : 8423			
Number of Baits per Targets : 4.86			
Number of Targets with Baits Designed : 8081			
Number of Baits : 40931			
Number of Baits removed due to avoids : 2311			
Standard Deviation of Bait Length : 0.0			
Mean of Bait Length : 120.0			
Minimum Bait Length : 120			
Maximum Bait Length : 120			

First 100 lines of Bait Tiling Design Details for "B407149254"

Design Summary	Design Details	Target Fate	Bed File
Target ID	Genomic Location	Sequence	Bait Length
chrX:140476646-140476911	chrX:140476619-140476938	CTCCTCACAGAGCCTCGGCCAGCTTAAGCTCCACCGGTATCAAGCCGCCCTCAGAGGAGGCTCTCCCTCTCTGACCCCAAGTCGCGACCTCAGTGAACATCCGCCCCCAA	120
chrX:46989025-46989267	chrX:46989026-46989145	AGATGACAGAGGAGGATAAAGATGACCTCCCTCGGCCCTCAACTGGGGCCAGCTCCGAGACCTCAAGCCAGGACAGCTGGGCCAGCTCTGGAGTCAGCAACAGGTCCTCTCT	120
chrX:46989025-46989267	chrX:46989026-46989205	CCCTAGCCAGAGCAGCTGGGCCAGCTCTGGAGTCAGCAACAGGTCCTCTCTCTGAGCAATTGCTTGGACATCTCAGTGGCCCCAAGCCAGGACGCAAGCAAGCTCTTAC	120

First 100 lines of Bait Tiling Design Details for "B407149254"

Design Summary	Design Details	Target Fate	Bed File
Target ID	Status	Target Length	Bait Generated
TARGET:chrX:140476646-140476911	Pass	66	1
TARGET:chrX:46989025-46989267	Pass	243	5
TARGET:chrX:24001129-24001301	Pass	173	3

First 100 lines of Bait Tiling Design Details for "B407149254"

Design Summary	Design Details	Target Fate	Bed File		
Chromosome	Chromosome Start	Chromosome Stop	Bait Name	Score	Strand
chrX	140476619	140476938	B407149254_0	1000	+
chrX	046989026	046989145	B407149254_2	1000	+
chrX	046989026	046989205	B407149254_3	1000	+
chrX	046989206	046989325	B407149254_5	1000	+

# Create a Bait Group

## Download the Design (I)

- To download the design results files, click on **Download** on the **Baits** page.
- It may be necessary to hold down the Ctrl key until the File Download dialog box appears

Agilent Technologies eArray

Help | Logout

Workspace Collaboration Public Welcome Demo User (Agilent Marketing)

Home Libraries Bait Groups **Baits** My Account Application Type: TargetEnrichment Switch Application Type

Search Upload Bait Tiling

**Design Options**

Design Job Name

Sequencing Technology Info Illumina

Sequencing Protocol Info end-sequencing

Design Strategy Info  Use Optimized Parameters  
 Centered  Justified

Bait Length 120 bp

Bait Tiling Frequency Info 2x

Allowed overlap into avoid regions Info 20 bp

Submit Cancel

**Target Details**

Species H. sapiens

Genome Build H. sapiens, UCSC hg18, NCBI Build 36, Marc

Genomic Target Intervals Info Upload

Genomic Avoid Intervals  Avoid Standard Repeat Masked Regions Info  
 Custom Avoid Intervals Info Upload

If you have difficulty downloading the desired file, hold down the <Ctrl> key until a File Download dialog box appears. This bypasses pop-up blocking software.

Search Results: 1 matching results found

Refresh

Job ID	Job Name	Status	Design Type	Creation Date	Position in Queue	Actions
BL407162395	FirstBaitGroup	Completed	BaitTiling	05-Feb-2009	NA	Delete   View Design   <b>Download</b>   Create Bait Group

Refresh



# Create a Bait Group

## Download the Design (II)

There are four files included in the downloaded zip:

Example of a Fate file:

	A	B	C	D	E
1	<b>TargetID</b>	<b>Status</b>	<b>Target Length</b>	<b>Baits Generated</b>	
2	TARGET:chrX:148476846-148476911	Pass	66	1	
3	TARGET:chrX:46989025-46989267	Pass	243	5	
4	TARGET:chrX:24001129-24001301	Pass	173	3	
5	TARGET:chrX:152694536-152694863	Pass	328	5	

Example of a BED file:

```
browser position
track name=BaitTiling description="" visibility=2 color=0,128,0 useScore=1
chrX 148476819 148476938 BI407162395_0 1000 +
chrX 046989026 046989145 BI407162395_2 1000 +
chrX 046989086 046989205 BI407162395_3 1000 +
```

Example of a Summary file:

	A	B	C
1	numInputTargets	8423	
2	numValidTargets	8423	
3	numBaitPerTarget	4.86	
4	numTargetsWithBait	8081	
5	numBaits	40931	
6	numBaitsRemovedDueToAvoids	2311	
7	lengthSD	0	
8	lengthMean	120	
9	lengthMin	120	
10	lengthMax	120	

Example of a TDT (tab delimited table) file:

	A	B	C	D
1	<b>TargetID</b>	<b>BaitLocation</b>	<b>Sequence</b>	<b>BaitLength</b>
2	chrX:148476846-148476911	chrX:148476819-148476938	CTCCTCACAGAGCCTCC	120
3	chrX:46989025-46989267	chrX:46989026-46989145	AGATGACGAGGAGGAT	120
4	chrX:46989025-46989267	chrX:46989086-46989205	CCCTGAGCCAGAGCAG	120
5	chrX:46989025-46989267	chrX:46989026-46989145	CCTCCAGAGCCTCAAG	120

# Create Bait Group

## Create Bait Group

Once satisfied with the Bait Group Design, select **Create Bait Group**

Check the status of the Bait Group creation in the Pending Jobs quadrant of the **Home** page

The screenshot shows the 'Design Options' and 'Target Details' sections of the Agilent Technologies eArray application. The 'Design Options' section includes fields for Design Job Name, Sequencing Technology (Illumina), Sequencing Protocol (end-sequencing), Design Strategy (Use Optimized Parameters), Bait Length (120 bp), Bait Tiling Frequency (2x), and Allowed overlap into avoid regions (20 bp). The 'Target Details' section includes Species (H. sapiens), Genome Build (H. sapiens, UCSC hg18, NCBI Build 36, Marc), Genomic Target Intervals, and Genomic Avoid Intervals (Avoid Standard Repeat Masked Regions). A 'Submit' button is visible at the bottom of the design options.

If you have difficulty downloading the desired file, hold down the <Ctrl> key until a File Download dialog box appears. This bypasses pop-up blocking software.

Search Results: 1 matching results found

Job ID	Job Name	Status	Design Type	Creation Date	Position in Queue	Actions
BH07162395	FirstBaitGroup	Completed	BaitTiling	05-Feb-2009	NA	<a href="#">Delete</a>   <a href="#">View Design</a>   <a href="#">Download</a>   <a href="#">Create Bait Group</a>

The screenshot shows the 'Pending Jobs' quadrant of the Agilent Technologies eArray application. It includes a search bar and a table of pending jobs. The table has columns for Job Type, Job Name, Status, Created Date, Job Position, and Action. A blue circle highlights the 'Create Bait Group' link in the Actions column for the first job.

Search Results: 2 matching results found

Job Type	Job Name	Status	Created Date	Job Position	Action
BaitUpload	ID407167887	Upload Processing	05-Feb-2009		
BaitTiling	FirstBaitGroup	Bait Design Completed	05-Feb-2009		

While waiting for the Bait Group to be created, design additional Bait Groups, if desired

# Examine Bait Group

## Look for Missed Targets

- Open the [BaitTiling\\_fate](#) file in Excel
- Sort the file for **Status** to identify invalid (failed) genomic coordinates
  - These are targets for which the genomic coordinates could not be correctly assigned
- Sort the file for **Baits Generated** to identify targets for which no baits were assigned
  - In this example, according to the [BaitTiling\\_sum](#) file (left):  $8423 - 8081 = 342$  targets were not assigned baits; these can be viewed on the right in the [BaitTiling\\_fate](#) file

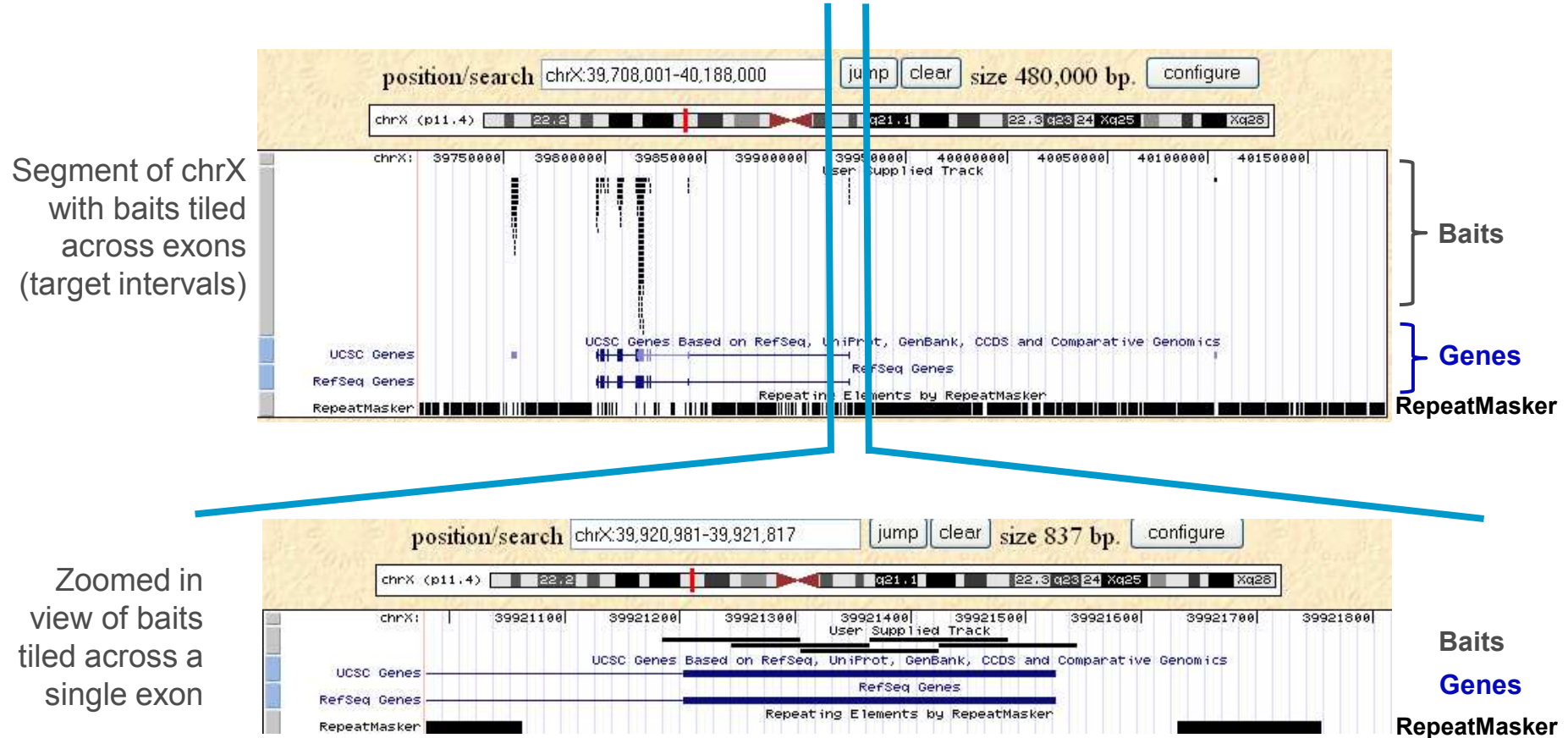
	A	B	C
1	numInputTargets	8423	
2	numValidTargets	8423	
3	numBaitPerTarget	4.86	
4	numTargetsWithBait	8081	
5	numBaits	40931	
6	numBaitsRemovedDueToAvoids	2311	
7	lengthSD	0	
8	lengthMean	120	
9	lengthMin	120	
10	lengthMax	120	

	A	B	C	D
1	<b>TargetID</b>	<b>Status</b>	<b>Target Length</b>	<b>Baits Generated</b>
2	TARGET:chrX:114947632-114949510	Pass	1879	0
3	TARGET:chrX:101598384-101598491	Pass	108	0
4	TARGET:chrX:103060664-103060787	Pass	124	0
5	TARGET:chrX:52260569-52260678	Pass	110	0
6	TARGET:chrX:154002692-154004543	Pass	1852	0
7	TARGET:chrX:134674851-134675089	Pass	239	0
8	TARGET:chrX:49190972-49191088	Pass	117	0
9	TARGET:chrX:135213958-135214032	Pass	75	0
10	TARGET:chrX:52397077-52397187	Pass	111	0

# Examine Bait Group

## View Design in UCSC Browser

- The BED file can be uploaded into the UCSC browser as an easy method to visualize the probes tiled across targets of interest



# Examine Bait Group

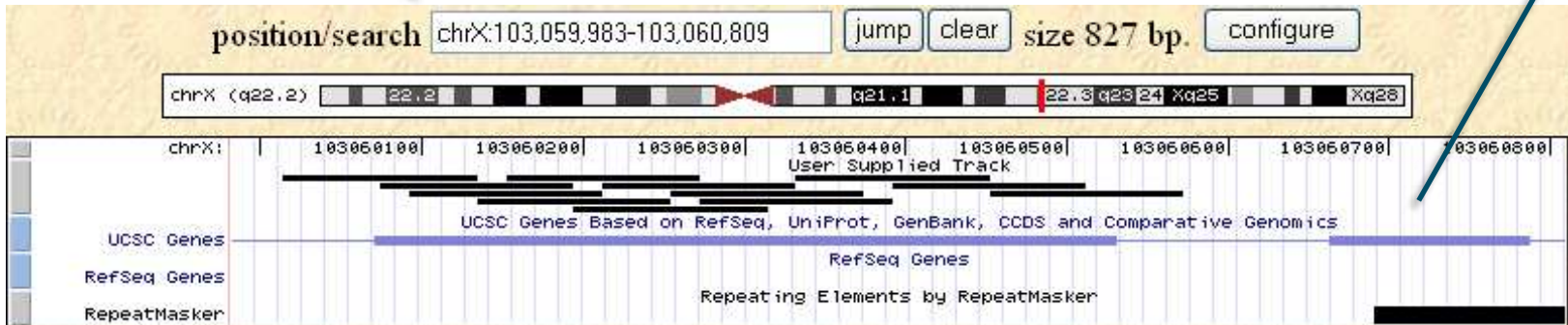
## Identify Targets for Potential Re-Tiling

1. Select targets not assigned baits in the Fate file.

2. Upload BED file to the UCSC browser, and zoom in on the target to identify the reason that it was provided zero baits.

3. In this example, the exon on the right is covered by a section identified as "repeats" by the RepeatMasker track, and design parameters had specified to avoid these regions. Therefore, this target received zero baits.

	A	B	C	D	E
1	<b>TargetID</b>	<b>Status</b>	<b>Target Length</b>	<b>Baits Generated</b>	
2	TARGET:chrX:114947632-114949510	Pass	1879	0	
3	TARGET:chrX:101598384-101598491	Pass	108	0	
4	TARGET:chrX:103060664-103060787	Pass	124	0	
5	TARGET:chrX:52260569-52260678	Pass	110	0	



If the target is still desired, it is possible to create a new, additional Bait Group for this target with new design parameters that allow repeat regions. Both Bait Groups can later be included in the final library.

# Complete Design for all Bait Groups

- Before proceeding to create the Library, complete the design for all Bait Groups that might be included in that Library
- Reasons for using multiple Bait Groups include:
  - To use different design options for different targets
  - To include Bait Groups from previous projects
  - To maintain separate Bait Groups based on target types; for example, a Bait Group of chrX exons, a Bait Group for Kinases, and so on

Search Results: 2 matching results found

Refresh

Job ID	Job Name	Status	Design Type	Creation Date	Position in Queue	Actions
BI407194606	SecondBaitGroup	In Queue	BaitTiling	06-Feb-2009	Job 1 of 1	<a href="#">Delete</a>
BI407162395	FirstBaitGroup	Completed	BaitTiling	05-Feb-2009	NA	<a href="#">Delete</a>   <a href="#">View Design</a>   <a href="#">Download</a>

Refresh



# Create the Library

## Select Bait Groups to Include in the Library

1. Go to the **Bait Groups** page, and select **Browse BaitGroup**

2. Place a check next to any Bait Groups that should be included in the Library

Home Libraries **Bait Groups** Baits My Account

Application Type: **TargetEnrichment** [Switch Application Type](#)

Search | **Browse BaitGroup**

**Browse WorkGroup by Category**

— Category

**Browse Catalog by Category**

Category

- Applications
- Species

**Browse by Folder**

ROOT

- AgilentCatalog
- Agilent\_Marketing

**View Bait Group**

Status: Select

Search Results: 5 matching results found

<input type="checkbox"/>	Bait Group Name	No.of Baits	Length	Folder	Status	Created Date	Actions
<input type="checkbox"/>	Demo_BaitTiling	33910	120	Agilent_Marketing	Locked	28-Jan-2009	<a href="#">Copy</a>   <a href="#">View</a>   <a href="#">Delete</a>   <a href="#">Download</a>
<input checked="" type="checkbox"/>	FirstBaitGroup	40931	120	Agilent_Marketing	Incomplete	05-Feb-2009	<a href="#">Copy</a>   <a href="#">Edit</a>   <a href="#">View</a>   <a href="#">Delete</a>   <a href="#">Download</a>
<input checked="" type="checkbox"/>	SecondBaitGroup	81	120	Agilent_Marketing	Incomplete	06-Feb-2009	<a href="#">Copy</a>   <a href="#">Edit</a>   <a href="#">View</a>   <a href="#">Delete</a>   <a href="#">Download</a>
<input type="checkbox"/>	Wizard_Demo	19466	120	Agilent_Marketing	Incomplete	28-Jan-2009	<a href="#">Copy</a>   <a href="#">Edit</a>   <a href="#">View</a>   <a href="#">Delete</a>   <a href="#">Download</a>
<input type="checkbox"/>	Wizard_Demo_Job	40931	120	Agilent_Marketing	Locked	04-Feb-2009	<a href="#">Copy</a>   <a href="#">View</a>   <a href="#">Delete</a>   <a href="#">Download</a>

3. Select **Create Library**

# Create the Library

## Select the Species

Home Libraries **Bait Groups** Baits My Account

Search | Browse BaitGroup

Select Species : Select Species

E.Coli  
F. heteroclitus  
F. neoformans  
G. aculeatus  
G. gallus  
G. hirsutum  
G. max  
G. moniliformis  
G. raimondii  
H. annus  
H. magnipapillata  
**H. sapiens**  
H. vulgare  
L. corniculatus  
L. esculentum  
L. japonicus  
L. sativa  
M. domestica  
M. fascicularis  
M. grisea  
M. mulatta  
M. musculus  
M. tectiformis  
M. truncatula  
N. crassa  
N. tabacum  
O. aries  
O. cuniculus  
O. latipes  
O. mykiss

Next Back

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1. Select the species

2. Select  
Next



# Create the Library

## Define the Library

1. Provide a name for the library

2. Set the length for the baits

3. Provide a Description, Keywords, and Comments

4. View the Library statistics

Home Libraries Bait Groups Baits My Account Application Type: **TargetEnrichment** [Switch Application Type](#)

Search Create Library Browse Library Notification Request for Quote

**Create Library :**

Library Name:	GF_Demo_Feb09	Length:	120	Number of Available Features:	16668
Status:	Draft	Library Size:	1 X 55K <a href="#">Show Details</a>	Number of Agilent Controls:	70
Folder:	Agilent_Marketing	Control Grid:	<a href="#">IS-57750-1-V1</a> <a href="#">Hs</a> <a href="#">55K</a> <a href="#">TE</a> <a href="#">120</a>	Number of User Controls:	0
Species:	H. sapiens	Number of Libraries:	1	Percentage Filled:	71.13766 %
Attachment:	<a href="#">+</a>	Total Number of Features:	57750	Percentage Feature Occupied:	71.13766 %
Description:	Demo	Keywords:	Demo	Comments:	This is a Demo

**Bait Group Details**

Select	Bait Group name	Control Type	Replicate
<input checked="" type="checkbox"/>	<a href="#">SecondBaitGroup</a>		1
<input checked="" type="checkbox"/>	<a href="#">FirstBaitGroup</a>		1

[Remove](#) [Add](#)

[Create](#) [Reset](#) [Cancel](#)

5. Set the Control Type for each Bait Group. If these are not controls, leave the Control Type blank.

6. Determine the number of replicates desired per Bait Group. Use the Percentage Filled statistic above to help decide on replicate #, and to monitor the effect of changing the #.

7. Click **Create**

# Create the Library

## Review Library Details and Submit as Complete

### 1. Review the Library Details

If desired, replicate #s can be edited at this time

### 2. Determine the status for the Library

If the library is to be submitted, it must be set as Complete.

Status:

Draft ▼  
Draft  
Review  
Complete

The screenshot displays the 'Edit Library' page for 'GP\_Demo\_Feb09'. The 'Status' dropdown is set to 'Complete'. The 'Bait Group Details' table shows two bait groups, 'SecondBaitGroup' and 'FirstBaitGroup', each with a 'Replicate' value of 1. At the bottom, there are 'Save', 'Reset', and 'Cancel' buttons. A callout box points to the 'Save' button with the instruction '3. Click Save'.

Select	Bait Group name	Control Type	Replicate
<input type="checkbox"/>	SecondBaitGroup		1
<input type="checkbox"/>	FirstBaitGroup		1

3. Click **Save**

# Create the Library

## Finalize Submission

1. Provide a comment and click **Yes**

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Home Libraries Bait Groups Baits My Account

Search Create Library Browse Library Notification Request for Quote

Warning : You are about to complete this Library. Once saved no changes can be made.

Please type comments here: : This is a Demo

Are you sure you want to continue ?

Yes No

2. Provide a comment in the next window and click on **Design check list**

Home Libraries Bait Groups Baits My Account

Search Create Library Browse Library Notification Request for Quote

Warning : You are about to submit this Library. Once saved no changes can be made.

Please type comments here: : This is a Demo

Are you sure you want to continue ?

Design check list

Yes No

3. Read and check off the Design check list, and click **Done**

Design check list

- Evaluate the complete platform's footprint for your application (Library Design Checklist 8)
- Include the necessary controls not already incorporated by the design?
- Include the appropriate built-in test and the appropriate control and potential failures?
- Check the quality and location, height, etc. of all new included parts in the library?
- For your intended use, include only those required parts for which you assume full test responsibility?
- Include the appropriate built-in test with the correct tests?
- Add all the required features to the library you created?
- Include the required technical specifications and be responsible for them?
- Enter in a separate section with your corresponding equipment, kits, and protocols?

Other and select the "Default" button in the next step. This step is required for your library to be submitted for approval for the purpose of getting the kit order. To enable testing, an eArray protocol must be created to create and debug you with your device.

By clicking the "Done" button below, you are certifying that you have reviewed your Design Checklist. Design Checklist 8 items and files selected and approved for the checklist above. Submission of the checklist, you are responsible for your design's fitness for a particular purpose.

By clicking the "Done" button, you are also certifying as representative for an Agilent representative to contact you. If you are not the kit order for you and you are not an Agilent representative, you are responsible for your design's fitness for a particular purpose.

If needed, contact the Agilent Design Checklist team at [designchecklist@agilent.com](mailto:designchecklist@agilent.com) for more information. If you are not the kit order for you and you are not an Agilent representative, you are responsible for your design's fitness for a particular purpose.

Done Cancel

4. Click **Yes** to finalize the submission of the Library, making it available for getting a quote.  
This is not a kit order, this is only a submission so that the kit can be ordered.

# Generate a Quote

## Select Library

1. Select Browse Library on the [Libraries](#) page to find the Library

The screenshot shows the Agilent eArray web interface. The top navigation bar includes 'Workspace', 'Collaboration', and 'Public'. The main content area is titled 'Browse Library' and features a search bar with 'Design Format' and 'Status' dropdowns. Below the search bar, it displays 'Search Results: 4 matching results found'. A table lists the following libraries:

<input type="checkbox"/>	Library Name	Folder Name	Status	Created Date	Length	Actions
<input type="checkbox"/>	Demo_BatTilingLibrary	Agilent_Marketing	Submitted	26-Jan-2009	120	<a href="#">View</a>   <a href="#">Quote</a>   <a href="#">Download</a>   <a href="#">Change Control Table</a>
<input type="checkbox"/>	Demo_BatTiling_Library2	Agilent_Marketing	Submitted	20-Jan-2009	120	<a href="#">View</a>   <a href="#">Quote</a>   <a href="#">Download</a>   <a href="#">Change Control Table</a>
<input type="checkbox"/>	Demo_Vizard_Library	Agilent_Marketing	Submitted	05-Feb-2009	120	<a href="#">View</a>   <a href="#">Quote</a>   <a href="#">Download</a>   <a href="#">Change Control Table</a>
<input checked="" type="checkbox"/>	QP_Demo_Feb06	Agilent_Marketing	Submitted	06-Feb-2009	120	<a href="#">View</a>   <a href="#">Quote</a>   <a href="#">Download</a>   <a href="#">Change Control Table</a>

A blue arrow points from the 'Quote' link in the 'QP\_Demo\_Feb06' row to a callout box.

2. Click on **Quote**

# Generate a Quote

## Describe Order

**Agilent Technologies**  
eArray

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Home Libraries Bait Groups Baits My Account

Search Create Library Browse Library Notification Request for Quote

**Request for Quote**

**Library Details**

Library Name: GP\_Demo\_Feb09  
ELID: 0228501

**Quote Details**

Quantity [Info](#) :

Reaction Size [Info](#) : 50 ▾

Sequencing Technology [Info](#) : Illumina ▾

Sequencing Protocol [Info](#) : end-sequencing ▾

**Customer Details**

Workgroup Name: Agilent Technologies  
Company Name: Internal  
Company Number: Internal

Next Cancel

1. Determine the number of Libraries desired

2. Determine the number reactions per library:  
A reaction size of 50 means that a single Library can be used for capture with 50 DNA samples

3. Determine the sequencing technology and protocol

4. Click **Next**

# Generate a Quote

## Review and Submit Quote

Agilent Technologies  
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Workspace Collaboration Public

Home Libraries Bait Groups Baits My Account

Search Create Library Browse Library Notification Request for Quote

### Request for Quote

Library Details	
Library Name:	GP_Demo_Feb09
ELID:	0228501
Part Number:	G3360C

Quote Details	
Quantity <a href="#">Info</a> :	1
Sequencing Protocol <a href="#">Info</a> :	end-sequencing
Sequencing Technology <a href="#">Info</a> :	Illumina(Optional 001)

Customer Details	
Workgroup Name:	Agilent Technologies
Company Name:	Internal
Company Number:	Internal

Request for Quote submission complete

Thank you. Your request for quote has been submitted.  
You will receive an email re-confirming this request for quote.  
You will also be contacted by an Agilent sales representative.

Home

Your quote is placed successfully

CLOSE

Print Cancel Edit Quote Request Submit

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Click **Submit**