



# Probe Match Manual

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*Probe Match is a tool for aligning query sequences with Affymetrix probe sequences.*

## Alignment Program

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The alignment program used in this tool is an implementation of a perfect match algorithm. It iterates over each position in a query sequence, searching Affymetrix probe sequences for perfect match similarities at the subset between the current position and 25 bases downstream in the query. The design type of the probe determines its orientation when performing the alignment. For sense probes, the reverse complement of the probe is aligned to the query. For antisense, the probe itself is used.

## Performing a Query

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You can enter query sequences in the appropriate text field, or upload a FASTA file with query sequences. It is important to note the file to be uploaded cannot exceed 20 KB in size. You can select the GeneChip® array against which you would like to query. You also have the option of performing the search with reverse complement of the query sequence.

**Search for perfect matches between your query sequence and Affymetrix® probe sequences.**

**Select array to query**

**Against**

- AtGenome1
- ATH1-121501
- C. elegans
- DrosGenome1
- E. coli
- HG-Focus
- HG-U133**
- HG-U95
- Hu35K
- HuGeneFL
- MG-U74
- Mu11K
- P. aeruginosa
- RG-U34

**Enter a name for Query Sequence**

mySequence

**Enter DNA sequence in plain text or FASTA format:**

```
cggtgccagagcaagogaattgtggggccagattatocccagccattgccaccacta
cagca
```

**Or Upload Sequence(s) in FASTA File:**

**Search with Reverse Complement of Query**

**perform query**

**Figure 1**  
Probe Match query window

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## Viewing Results

The results of the query are presented in a summary table describing which probe sets the query matched. This page provides hyperlinks to the probe set name, which provides access to the full target record available in the NetAffx™ Analysis Center. You can use the hyperlinks in the column **# Probes Matching Query** to view the details of the query result, and follow the hyperlinks in the column **Base Position of Probes in Consensus** to access the probe sequence information.

### Search results for HG-U133

#### Query 'mySequence' (60 bases)

Array	Probe Set	Probe Set Description	# Probes Matching Query Out Of Total Probes In Probe Set	Base Position Of Probes In Consensus
HG-U133A	1294_at	L13852 FEATURE= DEFINITION=HUME1URP Homo sapiens ubiquitin-activating enzyme E1 related protein mRNA, complete cds	2/16 (View Alignment)	2688, 2694

**Figure 2**  
Probe Match query results

The result page shows the details of the query result with the list of probes (identified by serial order) matching the query. The start and the stop positions with the relevant probe sequences are displayed in this page. This page also shows the alignment of the query against the probes.

### Search results for HG-U133

#### Matched Probes For: HG-U133A 1294\_at

Serial Order	Query Start	Query Stop	Probe Location in Affymetrix Consensus/Exemplar	Probe Sequence(5'-3')
1	1	25	2688	CGTGCCCGAGGCAAGCGAATTGTGGGCCAGATTATCCCGOCATTGOCROCACTACAGCA
2	7	31	2694	CGAGGCAAGCGAATTGTGGGCCAG

#### Alignment

```

Query 1 CGTGCCCGAGGCAAGCGAATTGTGGGCCAGATTATCCCGOCATTGOCROCACTACAGCA 60
Hit 1  CGTGCCCGAGGCAAGCGAATTGTGG-----
Hit 2  -----CGAGGCAAGCGAATTGTGGGCCAG-----
    
```

#### Query 'mySequence' (60 bases)

**CGTGCCCGAGGCAAGCGAATTGTGGGCCAGATTATCCCGOCATTGOCROCACTACAGCA**

**Figure 3**  
Probe Match detailed query results