

Q01. Which browser is suitable for your web service?

We have tested our software using the following browsers:

- (1) Mozilla *Firefox* 2.0.x (Linux and Windows)
- (2) Microsoft *Internet Explorer* 7.0.x (Windows)
- (3) Google *Chrome* 1.0.x (Windows)

Q02. What happens after I upload my sequence file in FASTA format?

webGMAP
A public web service for cDNA-genome mapping

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GMAP Configuration and Execution
GMAP Result To DB
GMAP Result Exploration

Upload a Sequence File in FASTA Format

Project Name: guest@muohio.edu_081230_044635

A. Requirement for your fasta file

- The max file size allowed is **1 MB**.
- If there are more than 100 sequence reads inside your fasta file, we will only process the first 100.
- File name should not contain space or other special characters like ' \ / , # \$ * ^ *) (+ .

B. A sample Fasta file for download and then upload

- Rice.fasta
- Arabidopsis.fasta
- Chlamy.fasta

C. Upload File: Browse...
Reset Submit

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When a user upload his/her sequence file in FASTA format, a WebGMAP project will be created and a specific project name (*e.g.*, guest@muohio.edu_081230_044635) will be associated uniquely with the uploaded file. Within one project, you can only conduct cDNA-genome mapping once, by selecting your desired genome and specifying GMAP parameter settings. Obviously, the project name is the backbone of all database operations and user interface accessing in the future. *Users can create unlimited projects dependent on their needs, but they have to upload a FASTA sequence file for each project.*

Q03. What if I want to reuse the same sequence file and conduct cDNA-genome mapping using different genomes or parameter settings?

You have to upload your sequence file multiple times and create different projects. Consequently, each of these projects is associated with the same sequence file you uploaded. See Q02 for explanation.

Q04. Within the same sequence file, can I put cDNA or EST sequences from different species?

You can do whatever you want. However, it is recommended that you should put cDNA or EST sequences from the same species together as one single sequence file. Then, you can take advantage of cDNA-genome mapping options we provide: intra-species versus inter-species (see **Q05** for details).

Q05. What is intra-species or inter-species cDNA-genome mapping?

Currently, we provide the genomes of *Arabidopsis thaliana*, *Oryza sativa* and *Chlamydomonas reinhardtii* for mapping. If you have cDNA or EST sequences that are from the same species, you should select “intra-species” mapping. Otherwise, you need to choose “inter-species” mapping (or cross-species mapping).

What happens behind the scene is that we adopt different filtration conditions for inter-species and inter-species mapping results:

(1) For intra-species mapping, only the hits that satisfy the following criteria are the valid hits.

- (1.1) minimum matched query length=50 (nt)
- (1.2) minimum matched query identity=60 (%)
- (1.3) minimum matched coverage of query sequence=30 (%)

(2) For inter-species mapping, only the hits that satisfy the following criteria are the valid hits.

- (2.1) minimum matched query length=30 (nt)
- (2.2) minimum matched query identity=30 (%)
- (2.3) minimum matched coverage of query sequence=10 (%)

Please keep in mind that in most cases, GMAP will not produce bad mapping results, such as identity of 30%. In the near future, we will allow users to set up the filtration for their valid cDNA-genome mapping hits.

Q06. I got the raw GMAP result file. However, when I clicked “GMAP Result To DB” to proceed, I was told that no hit has been saved successfully into the database. Why?

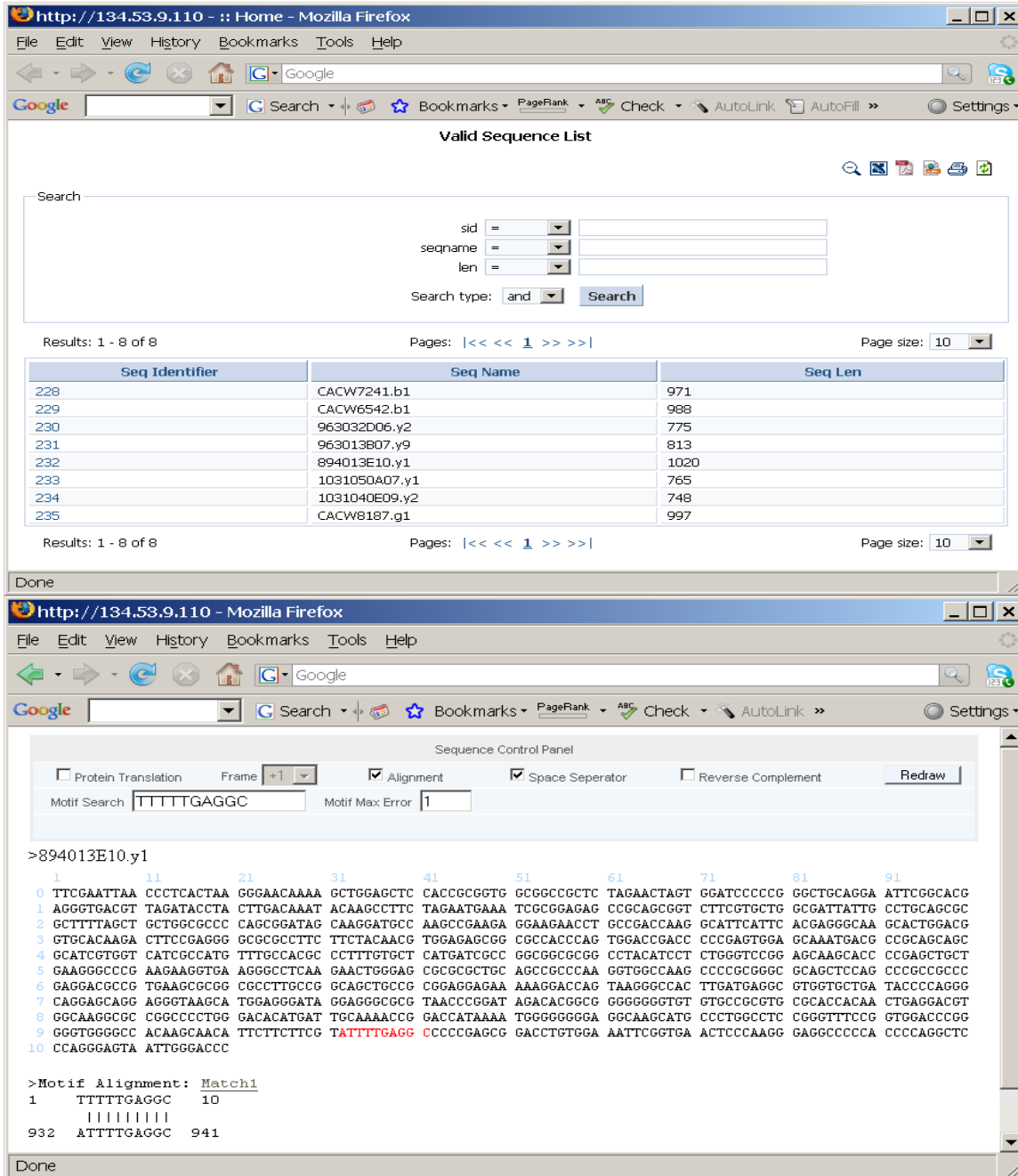
That is the intra-species or inter-species filtration we established (See **Q05** for details). We only save the valid GMAP hits into our database for further exploration.

Q07. In my sequence file, can I put amino acid sequences instead of nucleotide sequences?

At this moment, our web service can only handle DNA sequences, not amino acid sequences.

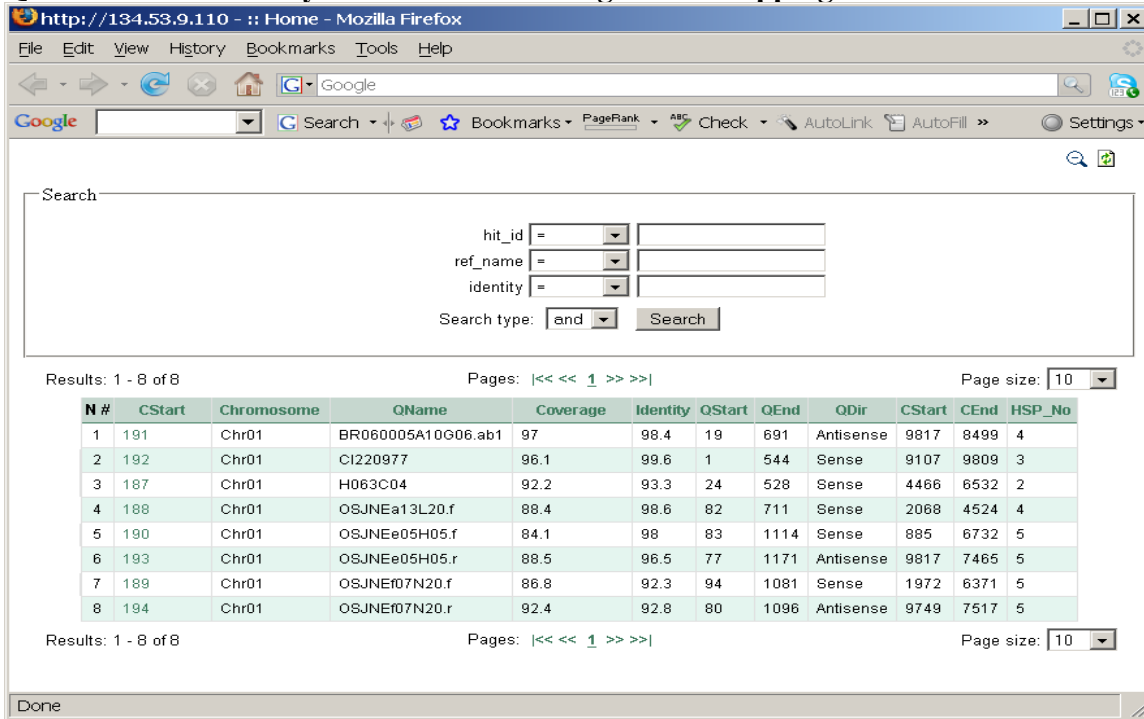
Q08. What is the main functionality of your sequence viewer?

As you can see in the figures below, you can easily search, filter and order your sequences by their names or lengths, as well as their SeqID, the internal identifier designated by us.



For each individual sequence, you can do 6-frame translations, reverse complement the sequence, or use space separator to track nucleotide positional information. Moreover, we provide fuzzy motif detection that allows users to search a given motif in the sequence, and if existing, we provide sequence alignments for the detected motif(s) in the sequence.

Q09. How can we use your interface to navigate the mapping results?



We provide users a tabulated view for their GMAP results. Again, a user can search, filter and order their results easily. By clicking the CStart number, a graphic interface will be



