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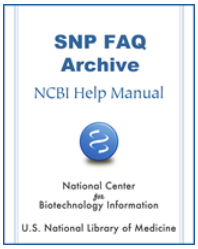
NLM Citation: SNP FAQ Archive [Internet]. Bethesda (MD): National Center for Biotechnology Information (US); 2005-. Searching for SNP Primer Sequences. 2005 Jul 7 [Updated 2014 Feb 25].
Bookshelf URL: https://www.ncbi.nlm.nih.gov/books/



Searching for SNP Primer Sequences

Created: July 7, 2005; Updated: February 25, 2014.

I'm trying to design primers for gene GRIN2A, but the SNP flanking sequences are formatted in lower case letters. How do I find my primers?

The sequence in lowercase format is in that format because it has been identified by RepeatMasker as being a low-complexity or repetitive element. This means that you will have to search further out 5' and 3' to your SNP for good primers.

First of all, scroll down to the FASTA sequence section of your refSNP record, and look further out (beyond your lowercase nucleotides) on the sequence – if you find sufficient 3' and 5' sequence that is not lowercase, then you could use this sequence to search for primer sequences.

If you want to see even more flanking sequence (beyond the sequence given in the refSNP record), then do the following (I will use GRIN2A as an example):

1. Search for the gene name (GRIN2A) on Entrez Gene
2. Click on the blue text that says "Links" located on the far to the right of the GRIN2A result (I'm using the first result in this example)to activate a drop down menu, and select "SNP: GeneView" to see a gene model report
3. Click on the reference contig (NT_010393.15) link located in the yellow highlighted portion of the screen. This will take you to the contig record.
4. Once you are looking at the contig record, scroll down the screen until you see a list of variations (and their corresponding refSNP numbers) that is located on this contig. The position for a particular variation is located immediately to the left of the word "variation" in this list of variations.
5. Once you have located the variation position, scroll down further on this record to see the actual contig sequence. You can then determine the position of your SNP on the sequence.
6. Once this is done, you'll have to use software (like Repeatmasker) to find low-complexity or repetitive elements in the flanking sequence; then you can search for your primers. (**4/15/07**)

How do I find primer sequence in dbSNP that will allow me to amplify a SNP locus?

dbSNP doesn't provide primers sequence for SNPs, but each SNP submission, however, contains flanking sequence (FASTA sequence usually between 100-500bp) that could be used to design primers:

1. Search for your SNPs using Entrez SNP.
2. Once you have some refSNP numbers of interest, go to the "Display" drop-down menu located just under the tabs near the top of the Entrez SNP page, and select "FASTA", and the FASTA flanking sequence of your SNPs will be displayed.

(**08/01/08**)

dbSNP doesn't provide the sequence of primers. Each SNP submission, however, contains flanking sequence (FASTA sequence usually between 100-500bp) that could be used to design primers. Here is an example of such flanking sequence. **(12/16/05)**

How do I use dbSNP to determine what primers were used for each mouse SNP?

dbSNP does not contain SNP primer information. I recommend that you contact the submitter for this information. We do have plans to capture this information in the future. **(2/3/05)**

I couldn't find PCR primer information for SNPs in dbSNP using the submission report links or LinkOuts in the submission reports, so how do I find them?

When a dbSNP submitter submits an STS primer or provides an STS accession, we link to dbSTS to show the primer information, for example, ss3.

Click on view Detail in dbSTS.

About 300,000 of the submitted SNPs (of a total 8.6 million) have STS information.

You can also search for primers by using the Map Viewer with both the variation and the STS tracks turned on. First, locate the SNP of interest, then use the adjacent STS map to find the STS, and then get the STS accession and primer information by using the uniSTS page.

Here is an example using rs2665.

Go to Map Viewer (click on chromosome 9), find the variation, and then click on STS D9S1131, which takes you to the uniSTS page. Clicking on the GenBank accession number will take you to the GenBank record, where you will find the primer information.

How do I find the rs numbers for two primer sequences? The primers are not attaching very well, and I'd like to extend them.

Try BLASTing the flanking (primer) sequences against dbSNP to see if there are any matching rs numbers. If there are, use the flanking sequence included in the SNP record of the rs number that matches your primer. **(11/15/05)**

I have been searching dbSNP using a SNP accession number (2979099) to find information on primers and assay conditions. I can't find them. Can you help me?

Go to the dbSNP homepage and select Search by IDs, then enter the prefix "ss" next to the accession number (2979099) in the search box. You will then be taken to the Submitted SNP(ss) Details page for that accession number. To view the details of the experiment, locate the ASSAY section, and click on the link that follows the method "PROTOCOL_1".

How do I get the chromosome positions of microsatellite primers?

You can get the chromosome positions from the "Chromosome Report" using Batch Query.

Commercial Primer Synthesis Firms

Can you give me a recommendation for a primer synthesis firm?

dbSNP does not provide recommendations for commercial entities (primer synthesis companies). You can try searching online for the terms "DNA primer design" for companies offering design and synthesis services. Some of these companies have their own custom software for designing and ordering primers. (**10/14/08**)