



Errors that Occur While Searching

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Unable to Find an rs Number

I am simply trying to find a list of soybean SNP sequences — Is this possible? I just can't figure out your web site.

You can find the soybean SNPs using the "New Batches" search:

1. Go to the dbSNP Home page, look at the left blue side bar, and click on "Search" to release a menu of search options.
2. Click on "New Batches"
3. When you get to the "New Batches" [dialogue page](#), select "soybean_3847:Glycine max" from the "organism" drop-down menu, and select "Variation submissions (SNP)" from the "Batch Type" drop-down menu.
4. Click the "Search Batch" button at the bottom of the pane. You will be taken to the only [two submissions](#) currently in dbSNP.

(07/14/08)

Human minor histocompatibility antigen HA-2 does not appear in dbSNP under the MYO1G gene, despite its SNP having been published 7 years ago. Could you please update dbSNP to include this?

In general, dbSNP does not mine publications for input, and the variations in dbSNP are submitted by submitters directly to dbSNP. If you would like the SNP mentioned in this publication to be included in dbSNP, go to the [Variation Batch Submission](#) page. Here you can submit variations described in a publication not authored by you, but you must be able to describe the variations using [HGVS nomenclature](#). You will see that the submission template has a field for the inclusion of the PubMed ID number, so that the original reference for the variation will be linked to the submission. You can also submit a single variation from the literature using the [Human Variation: Search, Annotate, Submit](#) site. (03/05/08)

Why was rs2228570 withdrawn from dbSNP? I can't find it using Entrez SNP.

rs2228570 has not been withdrawn from dbSNP; however, it does not map to the genome assemblies, which may be due to the fact that this SNP was derived from cDNA. Since rs2228570 does not map to the genome assemblies, you won't see it in Entrez SNP. I can tell you that rs2228570 is located in NM_000376. Future releases of Entrez SNP will include all SNPs —those that map to genome assemblies, and those that don't.

(2/16/07)

I'm using GenBank to analyze the variations in *Rattus norvegicus*. When I double-click on a specific variation icon, I get the following message: "rs8149781 is not in dbSNP". The rs number is correct, so how is this possible?

The annotation on the *Rattus norvegicus* assembly is temporarily more current than the dbSNP public webpages. As soon as NCBI human assembly build 34 is made public, we will release dbSNP build 117. Once that happens, the dbSNP links in the GenBank annotation will be active.

Sorry for the confusion. dbSNP is working toward a more flexible data structure that will allow us to release public data in a more timely fashion so that these synchronization issues can be resolved

Unable to find SNPs for Specific Organism

I can't tell if you have horse SNPs in the db or not. If I query dbSNP for horse or txid9796, I get no results, yet there is a directory for horse on the SNP FTP site.

Search for horse using the “New Batch” search.

1. Go to the dbSNP Home page, look at the left blue side bar, and click on “Search” to release a menu of search options.
2. Click on “New Batches”
3. When you get to the “New Batches” dialogue page, select “Horse_9796: Equus caballus” from the “organism” drop-down menu, and select “Variation submissions (SNP)” from the “Batch Type” drop-down menu.
4. Click the “Search Batch” button at the bottom of the pane. You will be taken to the [submissions](#) currently in dbSNP.

You could also find horse SNPs using the dbSNP [Summary page](#). You will find "Equus caballus" toward the bottom. (07/18/08)

Errors using Specific Search Terms

Why does the "[ACC]" term used in SNP searches return the following error message: “The following term was not found: AC019340[ACC]”?

We only index sequence accession numbers (NT and NM) that have SNPs mapped directly to them, and do not project them onto BAC clone sequences (ie. AC000120). (3/6/07)

Is there a bad link to the SNP records for NRP2 (human neuropilin 2)? When I key RP2 into the Entrez SNP search box, it takes me to NELL2, a completely different gene.

By keying only “RP2” into the search box, you are telling Entrez to search not just the gene name field but all fields that contain “RP2”; so you end up with 1465 records, most of which do not pertain to your gene of interest. If you key in “RP2[Gene Name]” into the Entrez SNP search box, then Entrez SNP will retrieve only those SNP records that contain RP2 in the “Gene Name” field (352 records).

Errors using Specific Search Filters

When I search for human SNPs and limit the results to chromosome 22, with non-synonymous coding and OMIM links, I got 346 records without OMIM links.

Your original query was ((“Homo sapiens”[Organism] AND (“snp omim”[Filter] OR “snp structure”[Filter])) AND “coding nonsynonymous”[Function class]) AND 22[CHR]).

These request limits specify that the results must have OMIM, **or** must have structure; the results therefore, can have either OMIM or have structure — they don’t have to have both OMIM and structure.

If you change the query to: ((“Homo sapiens”[Organism] AND (“snp omim”[Filter] AND “snp structure”[Filter])) AND “coding nonsynonymous”[Function class]) AND 22[CHR]), your results will include both OMIM and structure. (3/29/06)

Errors Searching with rs or ss Numbers

If I query all fields of dbSNP for a submitted SNP (ss) number that I submitted using the home page default search, I do not get a result, yet if I query a an older version of the dbSNP home page, the ss number I queried for is found.

Although your SNP was submitted in the latest build cycle, it missed the refSNP (rs) clustering process of the new build (in this case b125), which means your SNP has an ss number, but no rs number. You couldn't find your ss number because Entrez SNP indexes only refSNP (rs) numbers. Also, B125 had numerous internal BLAST pipeline changes; so many ss numbers were not clustered. In the future, we hope to get all ss numbers clustered before a new build — so this should not be a problem again. (1/4/06)

I entered dbSNP rs numbers for a region and got back 129 entries. When I looked a few of them up, they were returned as “not found”, although I know there are data for them.

Please try entering only the number and the “uid” field without the “rs” prefix (i.e., 10168104[uid]).

Runtime Error Message while Using Entrez SNP

I am using Entrez SNP on Internet Explorer and get an error message that reads: “A runtime error has occurred. Do you wish to debug? Line:71 Error: 'undefined' is null or not an object [Yes] [No].” This occurs during searches using any chromosome number.

You must have tried to get access while the binary applications were being updated. You should change your URL to specify the [CHR] field to search for SNPs by chromosome. [Here's an example.](#)

[Additional fields and examples](#) are shown on the Entrez SNP site.

Errors using Entrez Batch upload

I am trying to retrieve allele frequencies for 2500 SNPs, and would like to get a text file with the results directly, but I get an error when I try a BATCH upload.

Try using the [non-Entrez Batch query](#) service and requesting the genotype xml report which include allele frequency. We'll look into the generating a simpler frequency report. (03/26/08)