



eSearch (Programmatic Searches)

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

Will the HGVS based variation search you are testing also be available through eutils?

Yes, it should also be available through eutils once we have finished developing the resource (9/27/07)

How do I programmatically search for SNPs submitted by Sue Povey?

You can search by submitter handle using eSearch and retrieve with eFetch.(7/27/07)

How do I extract information from dbSNP by using eutils and specifying the chromosome position interval?

Use the following eSearch query: "100000:200000[Base Position] AND "1"[CHR] AND txid9606". See [example](#).

You can also get the result using eFetch. (7/9/07)

Discrepancies Between Esearch Results and Direct SQL Queries

If I query eSearch for all SNPs that hit on chromosome 1 in the 1 to 6000 bp range, I get 11 hits, but if I search our local MSSQL directly, I get 115 hits. Why the difference? How do I get the same results that I got from Entrez by using a direct SQL query, and vice versa?

The answer to your first question is that Entrez only returns SNPs that clearly map once to the current genome build, while a direct SQL query will deliver SNPs that map more than once.

To get the same results that are returned by Entrez by using a direct SQL query, that is, to get an refSNP (rs) number with "clear", or as we call it, a "unique" map hit, please see the Database Dictionary description for [SNPContigLoc](#), and for [SNPMAPIInfo](#) (look for the weight information in SNPMAPIInfo).

To get the same results that were delivered by SQL using an Entrez query is not really possible. When a SNP maps to multiple locations on multiple chromosomes, Entrez indexes the SNP as chrMulti. So if I use your example of finding SNPs with hits on chromosome1 in the 1:6000 bp range, you will find in SNPContigLoc all SNPs (including those with weight higher than 1) that hit in the 1:6000 range.

But if you use Entrez, however, you will find only weight 1 SNPs (weight 1 represents SNPs that align at exactly one locus) that hit chromosome 1 in the 1:6000 range. SNPs that are weight 2 (weight 2 represents SNPs that align at two loci on same chromosome) are not indexed in Entrez, so you will not find the same number of SNPs that hit chromosome 1 in the 1:6000 range using Entrez as you do using a direct SQL query. (8/27/07)