



## Submission Using dbSNP's online Clinical/LSDB Submission Resources

Created: June 6, 2005; Updated: June 15, 2010.

### Is it possible for me to submit human SNPs that are not available in dbSNP, but are described in research articles I've read?

Yes, you can now submit previously published human variations described in a publication not authored by you to a new resource called [Human Variation: Annotate and Submit Batch Data](#). You must, however, be able to describe the variations using [HGVS nomenclature](#). You will see that the submission template for this resource 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. **Please Note:** these online submission resources do not take submissions from other species. (06/11/08)

### Will the Clinical/LSDB submission resources allow me to annotate an existing human SNP record that I did not originally submit?

Yes, you can now annotate existing human SNP records using two new resources. One is called the [Human Variation: Search, Annotate, Submit](#) site, where you can submit a single variation or annotation to a single variation, and the other is the [Human Variation: Annotate and Submit Batch Data](#) site, where you can submit a number of annotations or variations simultaneously.

Both of these resources allow you to submit phenotypic data for an existing SNP in the "Comments" section of each respective submission form. You can also submit a "Linkout" URL that will point to this variant on your organization's website, as well as OMIM IDs, Allelic Variant IDs, and other associated PubMed IDs (in addition to the primary PubMed ID for the variant's original publication). **Please Note:** these online submission resources do not take annotations or submissions for SNPs of other species. (07/10/08)

### I have some phenotypic data I'd like to annotate to an existing SNP. If I can do this, where do I submit this data?

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## Submission using the Human Variation: Search, Annotate, Submit Site

**I have to submit SNPs discovered by my group, but do not have any of the sequence data for the variations — just the position on a reference sequence.**

There are three ways you can submit:

1. If you do not have the sequence data, but have a GenBank accession and a position as reference, you can send this information to dbSNP submissions, and we can use this information to get the sequence from GenBank.
2. You can now submit batches of SNPs yourself using dbSNP's [Human Variation: Annotate and Submit Batch Data](#) site, although you must be able to describe the variations using [HGVS nomenclature](#) in order to submit them. Click on the “submission help” link located at the upper right corner of the page for help getting started.
3. Finally, if you want to submit you variations one at a time, you can use the [Human Variation: Search, Annotate, Submit](#) site. Here is an example of how this resource might be used for a submission: if you query using NM\_000212.2:c.176T>C as your search term, you will find that [rs5918](#) has already been assigned to that location. You can then add value that SNP by providing the URL to your database. (04/30/08)

**When I submit human variations or annotate existing ones using either the online human variation single or batch submission, can I submit more than one publication per variation?**

Yes, multiple publications can be associated with a human variant submitted from Human Variation [Single](#) or [Batch](#) submission.

If you have more than one publication you would like associated with a variation, place the multiple PubMed uids you have for the variant (separated by semicolons) in the PubMed ID section of the single or Batch submission forms.(07/31/08)

## Submission using the Variation Batch Submission Site

**I have to submit SNPs discovered by my group, but do not have any of the sequence data for the variations — just the position on a reference sequence.**

There are three ways you can submit:

1. If you do not have the sequence data, but have a GenBank accession and a position as reference, you can send this information to dbSNP submissions, and we can use this information to get the sequence from GenBank.
2. You can now submit batches of SNPs yourself using dbSNP's [Human Variation: Annotate and Submit Batch Data](#) site, although you must be able to describe the variations using [HGVS nomenclature](#) in order to submit them. Click on the “submission help” link located at the upper right corner of the page for help getting started.
3. Finally, if you want to submit you variations one at a time, you can use the [Human Variation: Search, Annotate, Submit](#) site . Here is an example of how this resource might be used for a submission: if you query using NM\_000212.2:c.176T>C as your search term, you will find that [rs5918](#) has already been assigned to that location. You can then add value that SNP by providing the URL to your database. (04/30/08)

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