



## Batch Submissions and Large Submissions to dbSNP

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

**How long would you expect submission processing for a list of ~ 5000 SNPs to take? It seems to be taking a long time (>10 minutes).**

Submission processing shouldn't take more than 30 seconds. I just tested the system using 10,000 SNPs and it took less than 10 seconds. Make sure you have javacript turned on in your browser. Please contact dbSNP at [snp-admin@ncbi.nlm.nih.gov](mailto:snp-admin@ncbi.nlm.nih.gov) if you're still having a problem with it, and we'll try to find out where the problem is. (8/22/06)

**I need to submit some SNPs located within pseudogenes (caused by a premature stop codon), as well as SNPs not located in pseudogenes. Can I submit them in the same batch?**

Yes, you can assign batches based on your preference. (12/14/05)

**I want to send a large amount of data to dbSNP. Is there another submission channel besides email?**

Contact SNPdev at [snp-admin@ncbi.nlm.nih.gov](mailto:snp-admin@ncbi.nlm.nih.gov), and we'll set up an FTP account for you to upload the submission file to our site. Your account information will be sent to you once the account has been set up.

**I want to submit data on several SNP assays. Do I have to submit the assays, SNPs, and the allele frequencies in one batch or in separate submissions?**

You can submit the assays, SNPs, and the allele frequencies simultaneously. The submission only has to have one SNPASSAY header as long as the same assay method is used for all the SNPs.

All of the SNPs found in the assay should be below their corresponding SNPASSAY header.

To submit the allele frequencies, you can use your local SNP identifier during submission.

You can submit all of the SNPs and the allele frequencies as a single batch.

**When I submit a single sequence that contains multiple SNPs, do I submit each SNP individually under the same batch number?**

Submit each SNP individually under the same batch number. You can submit the same flanking sequence for each SNP.

Example of two adjacent SNPs:

```
tcccgttttc tgcgtggtgg tgtgggggga acttcctcag gcctctccgc agt[C/T][A/G]tgccctc  
ctcccgtaca cagcaagatg cgctccctaaa ctcccggggg aattagact
```

dbSNP submission format:

```
SNP:TNFRSF5-000324A  
ACCESSION:AY504960  
SAMPLESIZE:180
```

INDHMZYDET: YES  
GENENAME: TNFRSF5  
LOCUSID: 958  
LENGTH: 511  
5'\_ASSAY: gccttcccgttttctgcgtggtggtgtggggggaacttcctcaggcctctccgcagt  
OBSERVED: C/T  
3'\_ASSAY: atgcctcctcccgtacacagcaagatgcgtccctaaactcccgggggaattagact  
||  
SNP: TNFRSF5-000324B  
ACCESSION: AY504960  
SAMPLESIZE: 180  
INDHMZYDET: YES  
GENENAME: TNFRSF5  
LOCUSID: 958  
LENGTH: 511  
5'\_ASSAY: gccttcccgttttctgcgtggtggtgtggggggaacttcctcaggcctctccgcagtc  
OBSERVED: A/G  
3'\_ASSAY: tgcctcctcccgtacacagcaagatgcgtccctaaactcccgggggaattagact