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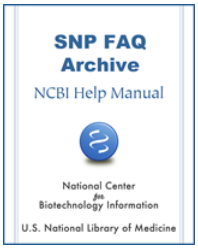
**NLM Citation:** SNP FAQ Archive [Internet]. Bethesda (MD): National Center for Biotechnology Information (US); 2005-. Citing dbSNP in a Publication. 2005 Jul 7 [Updated 2010 Jun 15].
**Bookshelf URL:** https://www.ncbi.nlm.nih.gov/books/




# Citing dbSNP in a Publication

Created: July 7, 2005; Updated: June 15, 2010.

**How do I cite dbSNP as a NCBI Resource?**

Sherry ST, Ward MH, Kholodov M, Baker J, Phan L, Smigielski EM, Sirotkin K. dbSNP: the NCBI database of genetic variation. Nucleic Acids Res. 2001 Jan 1;29(1):308-11.

**How do I cite dbSNP database as a whole for a specific build?**

Database of Single Nucleotide Polymorphisms (dbSNP). Bethesda (MD): National Center for Biotechnology Information, National Library of Medicine. (dbSNP Build ID: {build ID}).
Available from: http://www.ncbi.nlm.nih.gov/SNP/

**How do I cite a single or a range of Submitted SNP (ss) or Reference SNP (rs) entries?**

Database of Single Nucleotide Polymorphisms (dbSNP). Bethesda (MD): National Center for Biotechnology Information, National Library of Medicine. dbSNP accession:{ss1 or ss1 – ss100}, (dbSNP Build ID: {build ID}). Available from: http://www.ncbi.nlm.nih.gov/SNP/

**I was wondering if NCBI has some universal recommendations concerning the reporting of new SNPs for our publication. Should we use HGVS standards?**

I don't know specific NCBI policy on offering "universal recommendations" to publishers about their citation policies, but I will point out that dbSNP identifiers [submitted SNP (ss) number; refSNP (rs) number] are stable and unique identifiers within the NCBI dbSNP database, and that they provide flanking sequence context and alleles for a specific variation.

The issue of requiring use of HGVS nomenclature as you have asked is useful when all the information pieces are available (i.e. accessioned sequence records, gene annotation, functional analysis). Many polymorphism discovery projects, however, occur before such organized knowledge is available for a new species genome, and the rs number/ss number paradigm has been sufficient to describe sequence variations at this minimal level of detail.

I would say use HGVS standards when available, but use the rs numbers and ss numbers as well. This will encourage submission of the variation data to a public repository since using HGVS alone does not guarantee that the variation is in a public database. (**8/14/07**)