



Choosing a Submission Format

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What formats are available for dbSNP Submissions?

dbSNP will process submissions submitted on our new dbSNP Variant Call Format (VCF) or on our existing Flat File format.

Which format is better for submitting to dbSNP and why?

Although the Flat File format has the benefit of familiarity through long-standing use, we prefer that users now submit their data using the new dbSNP VCF submission format since:

1. VCF is very flexible and can be altered to fit the requirements of the data being submitted:
 - a. VCF can be used to submit many kinds of common variations as well as their associated genotypes and annotation.
 - b. VCF format can be used to submit both large and small scale submissions over multiple populations
2. VCF allows a submitter to submit an “asserted position”* as a means to locate variations, which allows for much greater accuracy in variation mapping than does flanking sequence.

*Note: An “asserted position” is a statement, or assertion, based on experimental evidence that a variant is located at a particular position.