

## Genome-wide Association Studies (GWAS)

The NIH is interested in advancing genome-wide association studies (GWAS) to identify common genetic factors that influence health and disease. Whole genome information, when combined with clinical and other phenotype data, offers the potential for increased understanding of basic biological processes affecting human health, improvement in the prediction of disease and patient care, and ultimately the realization of the promise of personalized medicine.

GWAS are defined as “any study of genetic variation across the entire human genome that is designed to identify genetic associations with observable traits (such as blood pressure or weight), or the presence or absence of a disease or condition”.

All investigators who receive NIH funds to conduct genome-wide analysis of genetic variation in a study population are expected to include in their protocol, a description of how the PI will submit the study data to the NIH GWAS repository and how confidentiality of the data will be maintained.

Investigators submitting GWAS data are expected to:

- Provide descriptive information about their studies;
- Submit coded genotypic and phenotypic data to the NIH GWAS data repository; and
- Submit certification by the Institutional Official(s) of the responsible submitting institution that it has reviewed and approved submission to the NIH, noting any limitations on data use based on the relevant informed consents and providing assurance that all data are submitted to the NIH in accord with applicable laws and regulations and that the identities of research participants will not be disclosed to the NIH GWAS data repository. Investigators should contact the IRB director to obtain the certification.

Click here to view a template:

[http://www.usc.edu/admin/provost/oprs/private/docs/oprs/GWAS\\_IO\\_Memo.pdf](http://www.usc.edu/admin/provost/oprs/private/docs/oprs/GWAS_IO_Memo.pdf)