

NIH Study Registration Information (SRI) Form for the Database of Genotypes and Phenotypes (dbGaP)

Complete this form so that NIH can consider your data submission to dbGaP or to another controlled-access data repository via dbGaP. Once completed, this form must be submitted to both the [Genomic Program Administrator \(GPA\)](#) and the Program Officer (PO)/Program Director at the NIH institute/center/office (ICO) that funded the data generation. (If submitting data that were generated without NIH funding, submit this completed form to the GPA at the ICO that most closely aligns with the submitted data for consideration.)

For any question on this form with multiple fields, list only one entry per field. If more space is needed for any question, write “Please see attachment” in the field, and add an attachment with the needed information.

Additional requirements to submit data:

- To submit this form, the PI for this study must have either NIH staff credentials or an eRA Commons account associated with the submitting institution. More information about registering yourself or your institution in eRA Commons can be found here: <https://www.era.nih.gov/eracommons-timeline.htm>.
- To submit data to NIH, the PI for this study must also have completed an [Institutional Certification](#) at the appropriate time. For example, for data subject to the [Genomic Data Sharing Policy](#), NIH-funded investigators must submit the Institutional Certification to the relevant NIH PO by Just-in-Time, prior to the issuance of an award.
- In some cases, additional registration information may be needed, as directed by the GPA, PO, and/or NIH repository staff.

OMB control Number: 0925-0670

Expiration Date: March 31, 2026

Public reporting burden for this collection of information is estimated to be about an hour per response including the time to complete the form and submit data. An agency may not conduct or sponsor, and a person is not required to respond to, a collection of information unless it displays a currently valid OMB control number. Send comments regarding this burden estimate or any other aspect of this collection of information, including suggestions for reducing this burden, to: NIH, Project Clearance Branch, 6705 Rockledge Drive, MSC 7974, Bethesda, MD 20892-7974, ATTN: PRA (0925-0670). Do not return the completed form to this address.

Study Registration Information

1 – Basic study information

Study name ¹

Click or tap here to enter text.

Provide a brief, detailed description of the original study (summarizing the design, methods, and principal findings) and data that will be available through dbGaP.

Any description with copyrighted material (even if not yet published) must include the following: "Reprinted from [Article Citation], with permission from [Publisher]."

Click or tap here to enter text.

Are the data sourced from multiple sites?

 Yes No*If yes: Number of sites* ²

Click or tap here to enter text.

Is there a target data release date? ³ Yes No*If yes: Target date (YYYY-MM-DD)* ⁴

Click or tap here to enter text.

Estimated number of study participants

Click or tap here to enter text.

Provide the suggested Acknowledgement Statement to accompany the dataset. ⁵

*Example Acknowledgement Statements are provided at the end of this form. Consider citing a specific publication that comprehensively describes the origin of the dataset, sources of support, or collaborators who provided subjects/samples. **Include grant or accession numbers associated with the NIH funding or data sources used for the dataset.***

Click or tap here to enter text.

Form continues on the next page

2 – Personnel information

Submitting PI name	Click or tap here to enter text.
Submitting PI email	Click or tap here to enter text.
Submitting PI institution	Click or tap here to enter text.
Submitting PI eRA account username associated with this institution ⁶	Click or tap here to enter text.
Main data submitter name ⁷	Click or tap here to enter text.
Main data submitter email ⁷	Click or tap here to enter text.

3 – NIH funding & support information associated with the data generation

Main NIH ICO funding/aligned with the study	Click or tap here to enter text.
Main NIH grant/Z number for the study	Click or tap here to enter text.
Main GPA associated with the study/grant ⁸	Click or tap here to enter text.
Main PO associated with the study/grant ⁶	Click or tap here to enter text.

Additional NIH grant/Z number(s) for the study, *if applicable*

Click or tap here to enter text.	Click or tap here to enter text.	Click or tap here to enter text.
Click or tap here to enter text.	Click or tap here to enter text.	Click or tap here to enter text.

Additional NIH ICO(s) funding/aligned with the study, *if applicable*

Click or tap here to enter text.
Click or tap here to enter text.
Click or tap here to enter text.

4 – Study data information

There are **nine (9)** questions in this section. For these questions, indicate whether the listed types of data are being submitted. For all data types being submitted (i.e., those marked “Yes”) that require further information, mark the appropriate checkboxes below that data type.

1. Subjects and samples	<input type="checkbox"/> Yes	<input type="checkbox"/> No
<i>If yes: Mark all that apply.</i>		
<input type="checkbox"/> Germline	<input type="checkbox"/> Tumor/Normal	<input type="checkbox"/> DNA
<input type="checkbox"/> Mitochondria	<input type="checkbox"/> Microbiome	<input type="checkbox"/> From repository

Form continues on the next page

2. Phenotype	<input type="checkbox"/> Yes	<input type="checkbox"/> No
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3. Molecular ⁹	<input type="checkbox"/> Yes	<input type="checkbox"/> No
<i>If yes: Mark all that apply.</i>		
<input type="checkbox"/> Sequence-based Multi Sample Genotype Files	<input type="checkbox"/> Array-based Multi Sample Genotype Files	
<input type="checkbox"/> Single Sample Genotype Files derived from Sequencing	<input type="checkbox"/> Imputed Genotypes (e.g., IMPUTE)	
<input type="checkbox"/> Tumor / Normal Variations / Somatic SNV (.MAF)	<input type="checkbox"/> CNV calls from microarray	
<input type="checkbox"/> Methylation Array Data or Summaries	<input type="checkbox"/> Expression Array Data or Summaries	
<input type="checkbox"/> CNV calls derived from Sequencing	<input type="checkbox"/> Other: Click or tap here to enter text.	
4. Links to public NCBI databases	<input type="checkbox"/> Yes	<input type="checkbox"/> No
<i>If yes: Mark all that apply.</i>		
<input type="checkbox"/> GEO	<input type="checkbox"/> SRA	<input type="checkbox"/> Genbank
		<input type="checkbox"/> Trace
5. Sequence	<input type="checkbox"/> Yes	<input type="checkbox"/> No
<i>If yes: Select one of the following.</i>		
<input type="checkbox"/> Cloud Data Storage for Sequence Data	<input type="checkbox"/> NCBI Storage for Sequence Data	
<i>If yes: Mark all that apply.</i>		
<input type="checkbox"/> Whole or targeted genome	<input type="checkbox"/> Whole or targeted exome	
<input type="checkbox"/> RNASeq – Whole or targeted transcriptome	<input type="checkbox"/> Methylation/Epigenomic Marks	
<input type="checkbox"/> Microbiome sequence (e.g., Metagenome, 16s rRNA, 18s rRNA, ITS)	<input type="checkbox"/> Other: Click or tap here to enter text.	
6. Association Analysis	<input type="checkbox"/> Yes	<input type="checkbox"/> No
• <i>If yes: Mark all checkboxes that apply.</i>		
<input type="checkbox"/> SNP Based Association Results	<input type="checkbox"/> Gene Based Association Results	
7. Documents	<input type="checkbox"/> Yes	<input type="checkbox"/> No
<i>Form continues on the next page</i>		
8. Images	<input type="checkbox"/> Yes	<input type="checkbox"/> No

9. Other files not covered and/or any other notes about expected data

Click or tap here to enter text.

Endnotes

- ¹ Unless directed otherwise, the study name must match the name listed on the associated Institutional Certification.
- ² Unless directed otherwise, provide the *exact* number of sites under the study protocol where data were sourced. You may also be asked to provide an attachment to this form that lists all sites.
- ³ Please only answer “Yes” if you have a target date based on anticipated deadlines that apply to your project (e.g., for publications, grants, or personnel changes). Otherwise, mark “No” for this question.
- ⁴ Data are typically released 6–8 weeks after the final submission of error-free data. Coordinate with repository staff to determine a data submission timeline that makes sense for your study.
- ⁵ Unless directed otherwise, base the Acknowledgement Statement on the provided examples. Doing so facilitates backend automation processes to share the data.
- ⁶ NIH staff may leave this question blank.
- ⁷ This person will be NIH’s main contact for this submission, and they can approve the study for release. If the PI is the primary data submitter, these fields can be left blank.
- ⁸ If you do not know your GPA, or your GPA has changed, consult the [NIH Data Sharing website](#) to find the current list of GPAs for the ICO that funded/aligns with the study.
- ⁹ This data type does *not* include Next Generation Sequencing (NGS).

*End of form
Additional supporting materials on the next page*

Example Acknowledgement Statements

Example 1: General template

Funding for [study name] was provided by [funding source]. Additional support with [part of study] was provided by [support source]. Additional data used for this study were obtained from [data source].

Example 2: Study with NIH funding

Funding for the Environmental & eXome Age-related Major Phenotypes with Longitudinal Effects (EXAMPLE) Study was provided through the NIH External Grant (E.G.) Initiative (U00 XX000000), with additional funding support for sequencing provided by the National Human Genome Research Institute (NHGRI). Assistance with data cleaning was provided by the National Center for Biotechnology Information (NCBI). Support for the collection of datasets and samples was provided by the Fourth International STANdardization of Collected Exomes Consortium (4INSTANCE, U00 XX000000). Genetic data used for this study were obtained from dbGaP through dbGaP accession number phs000000.v1.p.

Example 3: Study with non-NIH funding

Funding for the Environmental & eXome Age-related Major Phenotypes with Longitudinal Effects (EXAMPLE) Study was provided through the Foundation for Organized Research (FOR) and International Network of Scientific & Technological, And Computing Enhancements (INSTANCE). Additional funding support for the study was provided by the University of College Medical Center, City, State. Additional genetic data used for this study were obtained from the International Biobank.

Example 4: Childhood Cancer Data Initiative

This project has been funded, in whole or in part, by the National Cancer Institute's Childhood Cancer Data Initiative (CCDI) and the XXXXX to generate and share data with the research community under grants No. U01CAXXXXXX and APP XXXXXX. Approved Users of the data are expected to acknowledge the funding sources listed here and the NCI's Cancer Research Data Commons (<https://datacommons.cancer.gov/>).

- **Suggested Acknowledgement Statement for Secondary Users:** The results analyzed and <published or shown> here are based in whole or in part analyzing the study phsXXXXXX and were accessed from the NCI's Cancer Research Data Commons (<https://datacommons.cancer.gov/>).