

Legacy System

dbGaP Registration and Data Submission System

Online forms

This document provides screenshots of the legacy system

**Submitting Investigator can choose to enter some parts
of the SRI Form into the online Legacy Registration
System**

Section updated to be consistent with the data type section of the SRI form

6. Association Analysis	<input checked="" type="radio"/> yes <input type="radio"/> no <input checked="" type="checkbox"/> SNP Based Association Results <input type="checkbox"/> Gene Based Association Results
7. Documents	<input checked="" type="radio"/> yes <input type="radio"/> no
8. Images	<input checked="" type="radio"/> yes <input type="radio"/> no
9. Other files not covered and / or any other notes about expected data	<input type="text"/>

Feedback

* Include analyses for this study in CADA: Yes No

Sequence Read Archive (SRA)

* Sequence Read Archive submission is expected:
 Yes No

* Expected storage location for Sequence Data:
 NCBI Google Cloud Amazon Cloud

Principal Investigator (PI)

First Name: Last Name: Email: NIH grant or Contract #: Account Type:

PI institution:

I understand that this PI (NED:GPA_DOU) will have streamlined access

PI Assistant/Submitter:
 First Name: Last Name: Email: Account Type:

Feedback

Certification

Controlled Access or Unrestricted

No Submission Certification Yet

Provisional Submission Certification

Submission Certification verified by IC

Study is prior to the GWAS policy or is cleared for submission by the sponsoring IC

Program Officer (PO) assigned to this study

No PO is assigned to this study

First Name: Last Name: Email: NED#:

Feedback

Info: Study "Test 02102026" has been created successfully.

Manage Study

Registration Status: **Incomplete**

Processing Status: [open](#)

Test 02102026

Study Registration Information [View](#)

Admin. IC: NHGRI
Primary GPA: [redacted]
PI: Jane Doe (NIH)
NIH administration: NIGMS, NHGRI
NIH funding: NIGMS, NHGRI

Target data delivery: 2026-02-20
Target public release: 2026-03-10
Submission certification: not yet
Release Type: Controlled access
Submission expected for:

- Subjects and Samples
- Phenotype
- Molecular (not NGC)
- Links to public NCBI databases
- Sequence
- Association Analysis
- Documents
- Images

Include analyses in CADA: yes
Est. study participants: 1
SRA submission is expected: yes
Data submission to dbGaP is expected: yes



Sequence Read Archive (SRA)

Title	Comment	Accession

Policy [View](#)

Research statement: display
Public summary: display
Years until renewal: 1

DAR appendices: none
Weeks to cancel request: 8
Acknowledgement Statement:

INSTRUCTIONS: This study has not provided a suggested acknowledgement statement. However, Approved Users are expected to acknowledge the Submitting Investigator(s) who submitted data from the original study to an NIH-designated data repository, the primary funding organization that supported the Submitting Investigator(s), and the NIH-designated data repository (e.g., dbGaP). The acknowledgment statement should include the dbGaP accession number to the specific version of the dataset(s) analyzed.

Consent Groups (0) [View](#)

[Back to studies list](#)

[History](#)



DRAFT | DRAFT | DRAFT

DRAFT | DRAFT | DRAFT

Once the study is registered, the Submitting Investigator is sent the Submission Portal to submit data to dbGaP

OMB control Number: 0925-0670

Expiration Date: March 31, 2026

Public reporting burden for this collection of information is estimated to be about one hour per response including the time gathering and maintaining the information needed, adding information to this part of the study registration and uploading the 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.

Submission Portal

dbGaP Studies

[Home](#) [Submissions](#) [Objects](#) [Groups](#) [Accounts](#) [Templates](#) [Stats](#) [My profile](#)

Study Id	Study Name	Submitter	IC	Study short-name	phs accession	Files Updated	Last Updated	Study status
65008	MoTrPAC Multiomics Dataset – Adult Humans – Restricted Access	Shruti Marwaha	NIDDK		phs004523.v1.p1	None	2026-02-18 17:15	View study status
59562	Human GPR15 deficiency reveals CD8+ T regulatory cell-macrophage crosstalk in intestinal inflammation	Yu Zhang	NIAID	GPR15_Deficiency_IBD	phs003950.v1.p1	2026-02-04 11:58	2026-02-18 16:32	View study status
65470	Interrogating gene regulation during human cortical development	Yashodara Abeykoon	NIMH		phs004522.v1.p1	None	2026-02-18 16:16	View study status
64362	Tissue Collection and Characterization: Longitudinal Senescence Analysis		None		.v1	None	2026-02-18 16:04	View study status
65559	Liver Study Collection		None		.v1	None	2026-02-18 14:23	View study status
57380	A091401 Randomized Phase II Study of Nivolumab With or Without Ipilimumab in Patients With Metastatic or Unresectable Sarcoma	Paige Fuentes	NCI	A091401	phs003785.v1.p1	2026-02-18 13:55	2026-02-18 14:16	View study status

Submitting Investigator can click on the registered study to enter required information for data submission

The Genetics of Telework Stress (Example Study)

Study Data Outline [?](#)

Consent group registered for this study [?](#)

Consent Group Title	Consent Group Abbreviation
Disease-Specific (Allergy, IRB, PUB, COL, NPU, MDS, GSO, RD)	DS-ALERG-IRB-PUB-COL-NPU-MDS-GSO-RD
General Research Use	GRU

Required fields are marked with * asterisk

Please review all questions and select all data types that will be provided by you or another submitter as part of this study

Required information provided by the Submitting Investigator for data submission

Study data type	Study data outline provided at registration	Select 'Yes' if this data type will be provided						
<p>* 1. Subject IDs, Sample IDs, and Consents ?</p> <table border="1"> <thead> <tr> <th>Subject Consent ?</th> <th>Subject Sample Mapping ?</th> </tr> </thead> <tbody> <tr> <td>2a_SubjectConsent_DS.txt</td> <td>3a_SSM_DS.txt</td> </tr> <tr> <td>2b_SubjectConsent_DD.xlsx</td> <td>3b_SSM_DD.xlsx</td> </tr> </tbody> </table> <p>* Pedigree: Are the relationships of the subjects known? ?</p>	Subject Consent ?	Subject Sample Mapping ?	2a_SubjectConsent_DS.txt	3a_SSM_DS.txt	2b_SubjectConsent_DD.xlsx	3b_SSM_DD.xlsx	Yes	<p><input checked="" type="radio"/> Yes <input type="radio"/> No</p> <p><input type="radio"/> Yes <input checked="" type="radio"/> No</p>
Subject Consent ?	Subject Sample Mapping ?							
2a_SubjectConsent_DS.txt	3a_SSM_DS.txt							
2b_SubjectConsent_DD.xlsx	3b_SSM_DD.xlsx							
<p>* 2. Phenotypes and Attributes ?</p> <table border="1"> <thead> <tr> <th>Subject Phenotypes</th> <th>Sample Attributes</th> </tr> </thead> <tbody> <tr> <td>5a_SubjectPhenotypes_DS.txt</td> <td>6a_SampleAttributes_DS.txt</td> </tr> <tr> <td>5b_SubjectPhenotypes_DD.xlsx</td> <td>6b_SampleAttributes_DD.xlsx</td> </tr> </tbody> </table>	Subject Phenotypes	Sample Attributes	5a_SubjectPhenotypes_DS.txt	6a_SampleAttributes_DS.txt	5b_SubjectPhenotypes_DD.xlsx	6b_SampleAttributes_DD.xlsx	Yes	<p><input checked="" type="radio"/> Yes <input type="radio"/> No</p>
Subject Phenotypes	Sample Attributes							
5a_SubjectPhenotypes_DS.txt	6a_SampleAttributes_DS.txt							
5b_SubjectPhenotypes_DD.xlsx	6b_SampleAttributes_DD.xlsx							
<p>* 3. Molecular (DOES NOT include high throughput sequencing data such as BAM, CRAM, and FASTQ) ?</p>	No	<p><input checked="" type="radio"/> Yes <input type="radio"/> No</p> <p>Genome Build</p> <p>GRCh38 <input type="text"/></p> <p>Array Name</p> <p>Illumina 1M <input type="text"/></p> <p>* Select at least one</p> <p><input type="checkbox"/> Sequence-based genotypes (multi-sample vcf)</p> <p><input type="checkbox"/> Sequence-based genotypes (single sample vcf)</p> <p><input type="checkbox"/> CNV derived from sequence (vcf)</p> <p><input checked="" type="checkbox"/> SNP array (PLINK and/or raw data)</p>						

Required information provided by the Submitting Investigator for data submission

- SNP array (PLINK and/or raw data)
- CNV calls from array (PLINK and/or raw data)
- Imputed genotypes
- Tumor / Normal variations / Somatic SNV (maf)
- Methylation array or summaries
- Expression array or summaries
- Other

*** Other description**

test data for sdo change email

Describe this data

<p>* 4. Links to public NCBI databases ?</p>	<p>No</p>	<p><input type="radio"/> Yes <input checked="" type="radio"/> No</p>
<p>* 5. Sequence ?</p>	<p>Yes</p>	<p><input checked="" type="radio"/> Yes <input type="radio"/> No</p> <p>Please select one option</p> <p><input checked="" type="radio"/> NCBI Storage (SRA)</p> <p><input type="radio"/> Cloud Storage (External Data Sources including Trusted Partners)</p> <p>* Select at least one</p> <p>* <input checked="" type="checkbox"/> Whole or Targeted Genome</p> <p><input type="checkbox"/> Whole or Targeted Exome</p> <p><input type="checkbox"/> RNASeq - Whole or targeted transcriptome</p> <p><input type="checkbox"/> MethylSeq / Epigenomic Marks</p> <p><input type="checkbox"/> Microbiome sequence (Metagenome, 16S rRNA, 18S rRNA, ITS)</p> <p><input type="checkbox"/> Other</p>
<p>* 6. Association Analysis ?</p>	<p>No</p>	<p><input type="radio"/> Yes <input checked="" type="radio"/> No</p>
<p>* 7. Documents (protocols, questionnaires, consent forms, etc) ?</p>	<p>No</p>	<p><input type="radio"/> Yes <input checked="" type="radio"/> No</p>
<p>* 8. Medical Images ?</p>	<p>No</p>	<p><input type="radio"/> Yes <input checked="" type="radio"/> No</p>
<p>9. Other files not covered and/or any notes about study outline</p>		<p></p>

Submit

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