

funding.identifier	author.name	infectiousAgent	MeasurementTechnique	Data Repositories
HHSN272201200031C1*	MaPHIC	<i>Plasmodium cynomolgi</i>	Animal Data, Genomics, Immunological Assay, Lipidomics, Metabolomics, Proteomics	PlasmoDB, GEO, ImmPort, MassIVE, Metabolights, PRIDE
U01AI111598**	FluDyNeMo	Influenza A, Human, H1N1	Immunological Assay, Microbiome Sequencing, Pathology, Transcriptomics	Synapse
U19AI106754**	FluOMICS	Influenza A, Avian (Including H5N1), Influenza A, Human, H1N1, Influenza A, Human, H3N2	Genomics, Metabolomics, Proteomics, Software, Transcriptomics	GEO, MassIVE, Figshare, PI Website
U19AI106761**	Omics4TB	<i>Mycobacterium tuberculosis</i> , Other	Genomics, Software, Transcriptomics	MTB Network Portal, Macrophage Network Portal, GEO
U19AI106772**	OmicsLHV	Influenza A, Avian (Including H5N1), MERS-CoV, Ebola Virus, Influenza A, Human, H1N1, West Nile Virus, Other	Genomics, Lipidomics, Metabolomics, Proteomics, Transcriptomics	GEO, MassIVE
U01AI124255***	Systems biology of <i>Clostridium difficile</i> infection	<i>Clostridium difficile</i> ; Gram-Positive Bacteria; Microbiome/Microbiota	Software, Genomics, Transcriptomics, Metagenomics, Microbiome Sequencing	SRA
U01AI124275***	Systems Biology of Microbiome-mediated Resilience to Antibiotic-resistant Pathogens	Microbiome/Microbiota	Metadata, Metagenomics, Microbiome Sequencing	Figshare, SRA
U01AI124290***	Decoding Antibiotic-induced Susceptibility to <i>Clostridium difficile</i> Infection	<i>Clostridium difficile</i> ; Microbiome/Microbiota	Genomics, Transcriptomics, Microbiome Sequencing	NCBI, SRA, Mothur

U01AI124302***	Predicting the emergence of antibiotic resistance through multi-omics approaches and Immune System-surveillance	<i>Acinetobacter</i> , <i>Escherichia coli</i> , <i>Klebsiella</i> , <i>Pseudomonas aeruginosa</i> , <i>Salmonella</i> , <i>Staphylococcus aureus</i> , <i>Streptococcus pneumoniae</i>	Transposon Sequencing, Genomics, Transcriptomics, Software	SRA, NCBI
U01AI124316***	Systems Biology Approach to Redefine Susceptibility Testing and Treatment of MDR Pathogens in the Context of Host Immunity	<i>Acinetobacter</i> , <i>Enterococcus</i> , <i>Escherichia coli</i> , Gram-Negative Bacteria, <i>Pseudomonas aeruginosa</i> , <i>Salmonella</i> , <i>Staphylococcus aureus</i>	Acinetobacter, Bacteriology Assay, Genomics, Metabolomics, Transcriptomics	MassIVE, SRA
U01AI124319***	Systems Immunobiology of Antibiotic-Persistent MRSA Infection	<i>Staphylococcus aureus</i>	Reduced-Representation Bisulfite Sequencing	GEO
U19AI135972****	FluOMICS: The Next Generation	Influenza A, Avian (Including H5N1); Influenza A, Human, H1N1; SARS-CoV-2	Transcriptomics; Software	GEO, PI Website
U19AI135976****	Omics4TB	<i>Mycobacterium tuberculosis</i> ; <i>Mycobacterium</i> , Other	Genomics; Metabolomics; Transcriptomics; Software	SRA, GEO, NCBI
U19AI135990****	HPMI	<i>Mycobacterium tuberculosis</i> ; SARS-CoV-2	Proteomics; Software; Crispr Ko Screens	Pride, NDEx, EMBD, Mendele, Cytoscape
U19AI135995****	CViSB	Ebola Virus; Lassa Fever Virus; SARS-CoV-2	Genomics; Immunological Assay; Metadata; Virology Assay; Software	CViSB Website, Publication
U19AI135964****	SCRIPT	<i>Acinetobacter</i> ; Gram-Positive Bacteria; <i>Pseudomonas aeruginosa</i> ; Microbiome/Microbiota; SARS-CoV-2	Genomics; Metabolomics; Transcriptomics; Software; Metagenomics; Microbiome Sequencing	GenBank, Figshare, SRA, NCBI, GISAID, PI Website, GEO, Manuscript, Publication, Website

Table 5. Overview of 345 datasets available in the DDE (as of 12 July 2022). Datasets are grouped by grant number and derived from multiple iterations of the Systems Biology Program for Infectious Diseases. * [AI-11-038](#) (Contract⁶⁰); ** AI-12-027 (U01/U19 grants⁶¹); *** [AI-14-064](#) (U01 grants⁶²); **** [AI-16-080](#) (U19 grants⁶³). Code to dynamically generate this table is available at <https://github.com/Hughes-Lab/niid-schema-publication/blob/main/figures-code/Table%203%20-%20Datasets%20by%20Grant.qmd> (DOI 10.5281/zenodo.6816052).