



# QUARTERLY REPORT SPRING 2023

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# WHERE WE ARE NOW

## MISSION & VISION

The Undiagnosed Diseases Network (UDN) is a research study that is funded by the National Institutes of Health Common Fund with the purpose of bringing together clinical and research experts from across the United States to solve the most challenging medical mysteries using advanced technologies.

Through this study, we hope to both help individual patients and families living with the burden of undiagnosed diseases, and contribute to the understanding of how the human body works.

## CURRENT STATUS

UDN sites continue to evaluate participants and support research into undiagnosed and rare conditions. Since NIH Common Fund support for the UDN is ramping down, we are working on sustainability strategies, including the development of a foundation, to support the work of the network. We aim to make the transition from the current UDN to a sustainable model seamless and smooth for patients and families. If you are interested in partnering with the UDN on sustainability efforts, please contact [UDN@hms.harvard.edu](mailto:UDN@hms.harvard.edu).

# RECENT PUBLICATIONS

Exome/Genome Sequencing in Undiagnosed Syndromes ([PMID: 36706750](#))

Undiagnosed diseases: Needs and opportunities in 20 countries participating in the Undiagnosed Diseases Network International ([PMID: 36935719](#))

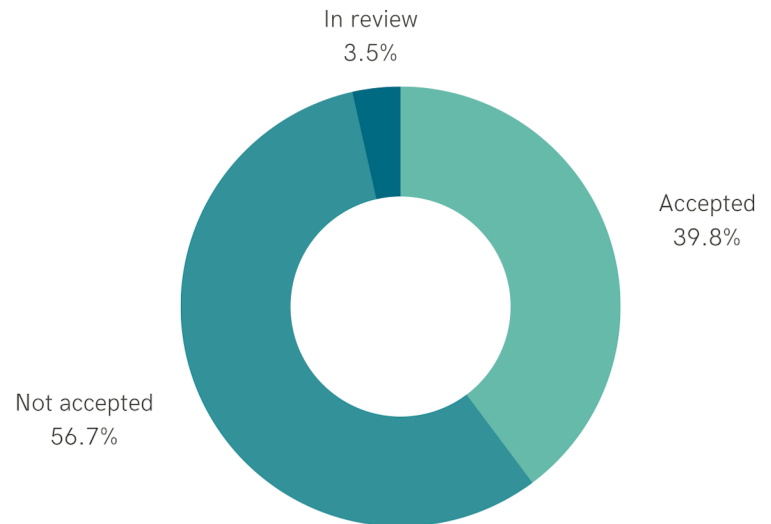
H4C5 missense variant leads to a neurodevelopmental phenotype overlapping with Angelman syndrome ([PMID: 36987712](#))

Bi-allelic ATG4D variants are associated with a neurodevelopmental disorder characterized by speech and motor impairment ([PMID: 36765070](#))

Bi-allelic SNAPC4 variants dysregulate global alternative splicing and lead to neuroregression and progressive spastic paraparesis ([PMID: 36965478](#))

# LATEST NUMBERS

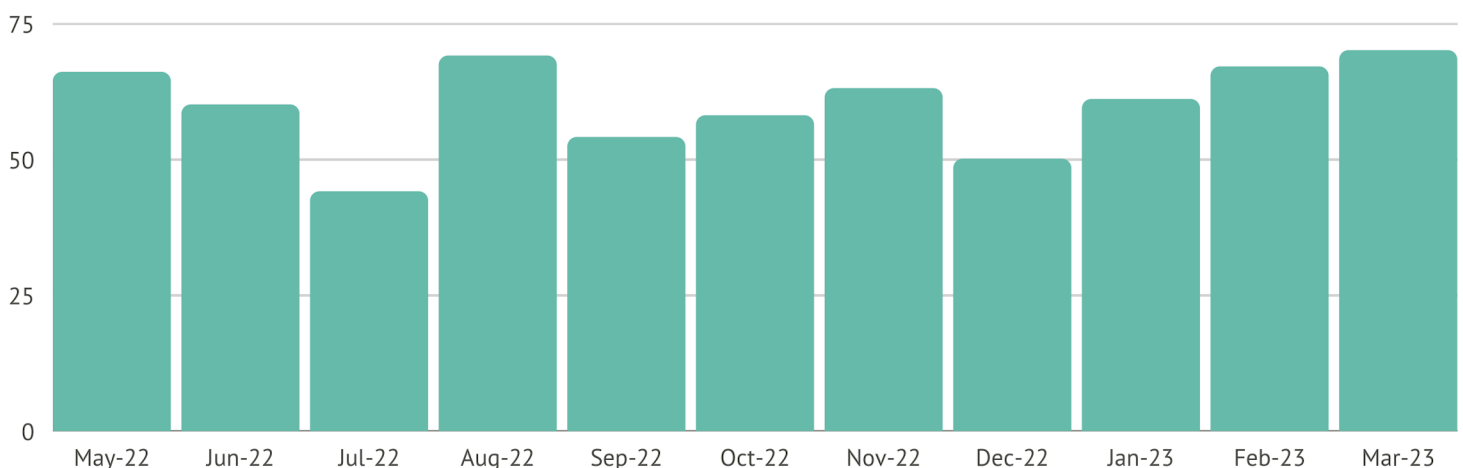
Of 6,376 applications received, 2,535 have been accepted, representing all US states, the District of Columbia, and more than 25 countries. Currently, there are 227 applications undergoing review. Applicants are not accepted for a variety of reasons, including lack of objective findings. Applicants who are not accepted may receive recommendations for additional tests or evaluations during the review process.



Applicants present with a wide variety of symptoms, with neurologic symptoms being the most common clinical presentation (40%).

The small majority of applicants are female (53%), and 40% are under 18 years old. Of the applicants accepted for participation in the study, 50% are female, and 61% are under 18 years old. The majority of applicants (83%) and accepted participants (79%) identify as Non-Hispanic white.

## APPLICATIONS PER MONTH



# EVALUATION PROCESS

As part of the UDN evaluation process, multiple specialists are consulted to provide input on each individual case. Often, participants are evaluated by these specialists at one of the 12 UDN clinical sites. In cases where participants are not able to travel to a UDN site, telehealth visits may be performed. To date, 2,165 evaluations have been completed.



# DIAGNOSES

Providing diagnoses to participants is a central goal of the UDN. Thus far, 678 certain or highly likely diagnoses (in 653 participants) have been identified. The majority of diagnoses (81%) have been made through exome or genome sequencing. Other diagnoses have been made primarily based on clinical grounds (6%) or directed clinical testing based on phenotype (9%). The remaining 4% of diagnoses were identified through a genome-wide assay such as chromosomal microarray or karyotype.

53

CONDITIONS HAVE  
BEEN NEWLY  
DESCRIBED

98

DIAGNOSES HAVE  
BEEN MADE BASED  
ON CLINICAL  
GROUNDS OR  
THROUGH DIRECTED  
CLINICAL TESTING

23

PARTICIPANTS HAVE  
MORE THAN ONE  
DIAGNOSIS

# EXOME SEQUENCING

469 participants (231 children and 238 adults) have undergone exome sequencing. The most common symptom category for participants undergoing exome sequencing is neurology (46%).

# 33%

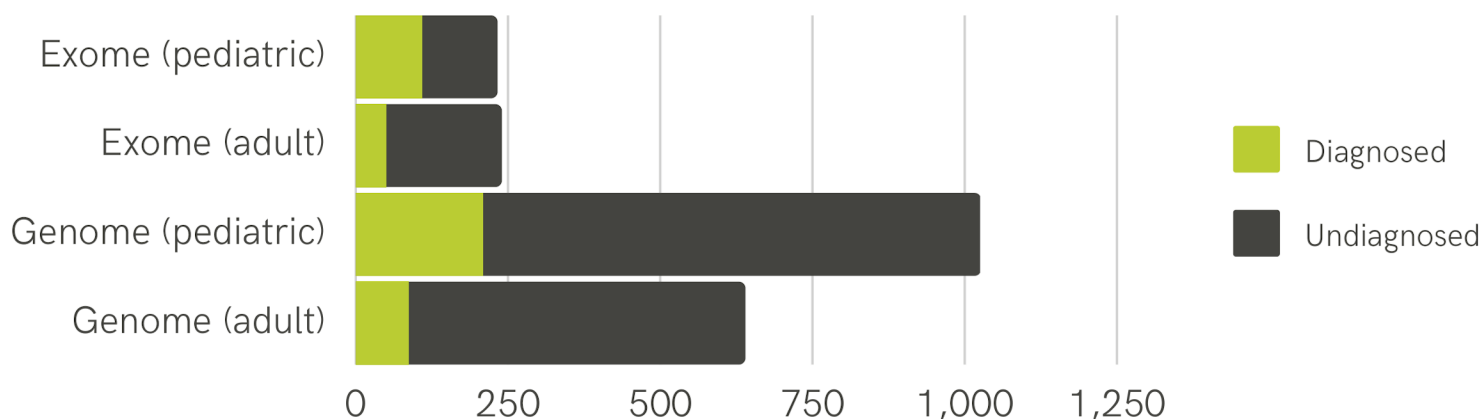
OF PARTICIPANTS WHO UNDERWENT EXOME SEQUENCING HAVE AT LEAST ONE DIAGNOSIS MADE THROUGH SEQUENCING

# 18%

OF PARTICIPANTS WHO UNDERWENT GENOME SEQUENCING HAVE AT LEAST ONE DIAGNOSIS MADE THROUGH SEQUENCING

# GENOME SEQUENCING

1,663 participants (1025 children and 638 adults) have undergone genome sequencing. Many of these participants had non-diagnostic exome sequencing prior to enrollment in the UDN. The most common symptom category for participants undergoing genome sequencing is neurology (49%).



## MODEL ORGANISMS

The Model Organisms Screening Center (MOSC) is composed of two centers that use fruit fly (*Drosophila melanogaster*), nematode worm (*C. elegans*) and zebrafish (*Danio rerio*) genetics to evaluate the impact and function of genetic variants identified through the UDN.

455

VARIANTS EVALUATED BY  
THE MODEL ORGANISMS  
SCREENING CENTER

322

NUMBER OF PARTICIPANTS  
WITH METABOLOMICS  
ANALYSES COMPLETE

## METABOLOMICS

The Metabolomics Core provides comprehensive analytical methods, analyses, technologies, and metabolomics expertise to the UDN to aid in clinical diagnosis and investigate potential mechanisms underlying phenotypic changes in participants.

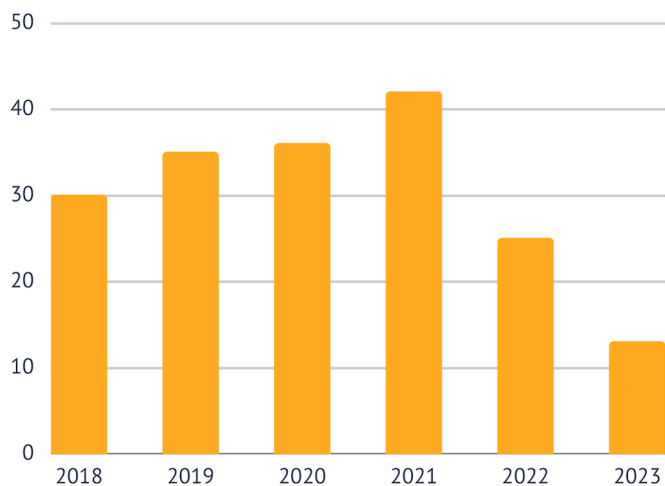
## RNA SEQUENCING

The UDN uses next-generation RNA sequencing methods to analyze the transcriptome of select UDN participants. RNA sequencing has the capability to quantify gene expression and can also facilitate the discovery of novel transcripts, identification of alternatively spliced genes, and detection of allele-specific expression.

651

NUMBER OF PARTICIPANTS  
WITH RNA SEQUENCING  
COMPLETE

# DATA SHARING



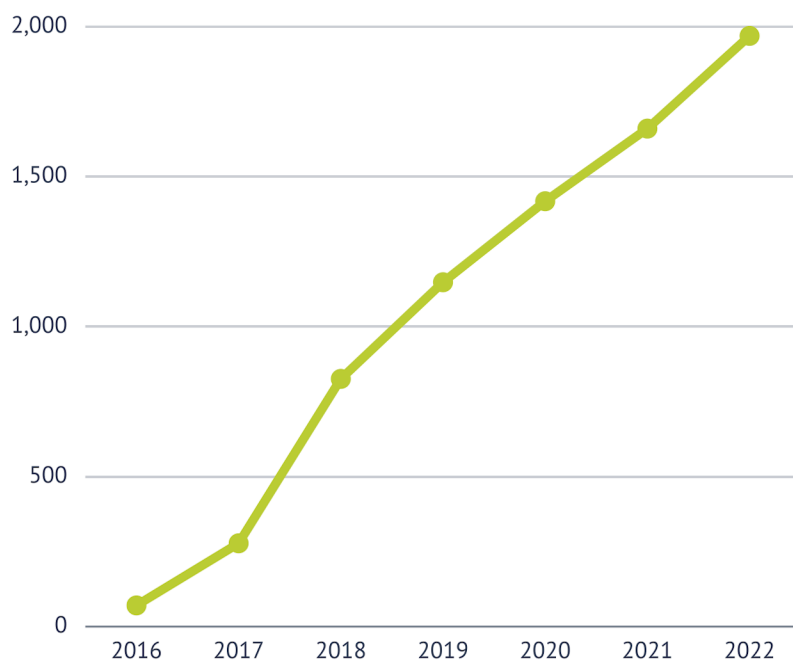
The UDN is committed to collecting and sharing data in useful, sustainable, and responsible ways. In addition to sharing data in relevant research repositories as described below, for those participants who would like to do so, the UDN shares their information via participant pages on the UDN website to identify other similar patients. Investigators also disseminate UDN research by publishing in the scientific literature. The graph on the left shows the number of UDN publications per year.

## GENOMIC DATA

Genomic data are shared in the database of Genotypes and Phenotypes (dbGaP) under accession phs001232.

## VARIANT-LEVEL DATA

Variant-level data are submitted to ClinVar, shared across the Matchmaker Exchange, and posted on the UDN website to facilitate collaborations and connections among researchers and families. The graph on the right shows the number of participant records shared across the Matchmaker Exchange over time.



# 647

VARIANT  
INTERPRETATIONS  
SUBMITTED TO CLINVAR

# 1991

RECORDS SHARED ACROSS  
MATCHMAKER EXCHANGE

# 211

PARTICIPANT PAGES  
PUBLISHED ON UDN  
WEBSITE