



# QUARTERLY REPORT WINTER 2021

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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

Despite significant challenges brought by COVID-19, the UDN continues to make progress towards its goals to provide diagnoses to patients and advance knowledge of rare disease. The UDN sites rapidly implemented new workflows, including protocols for remote work and telemedicine, to ensure continuity of UDN research activities. We look forward to continuing to make advances in rare and undiagnosed conditions in the coming months and years.

# RECENT PUBLICATIONS

Transcriptome-directed analysis for Mendelian disease diagnosis overcomes limitations of conventional genomic testing ([PMID: 33001864](#))

Clinical sites of the Undiagnosed Diseases Network: Unique contributions to genomic medicine and science ([PMID: 33093671](#))

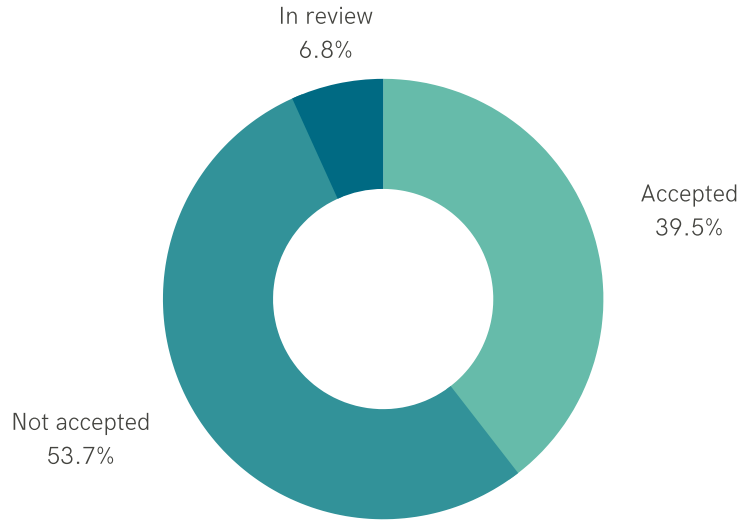
Somatic Mutations in *UBA1* and Severe Adult-Onset Autoinflammatory Disease ([PMID: 33108101](#))

Family genetic result communication in rare and undiagnosed disease communities: understanding the practice ([PMID: 33108040](#))

*BICRA*, a SWI/SNF Complex Member, Is Associated with BAF-Disorder Related Phenotypes in Humans and Model Organisms ([PMID: 33232675](#))

# LATEST NUMBERS

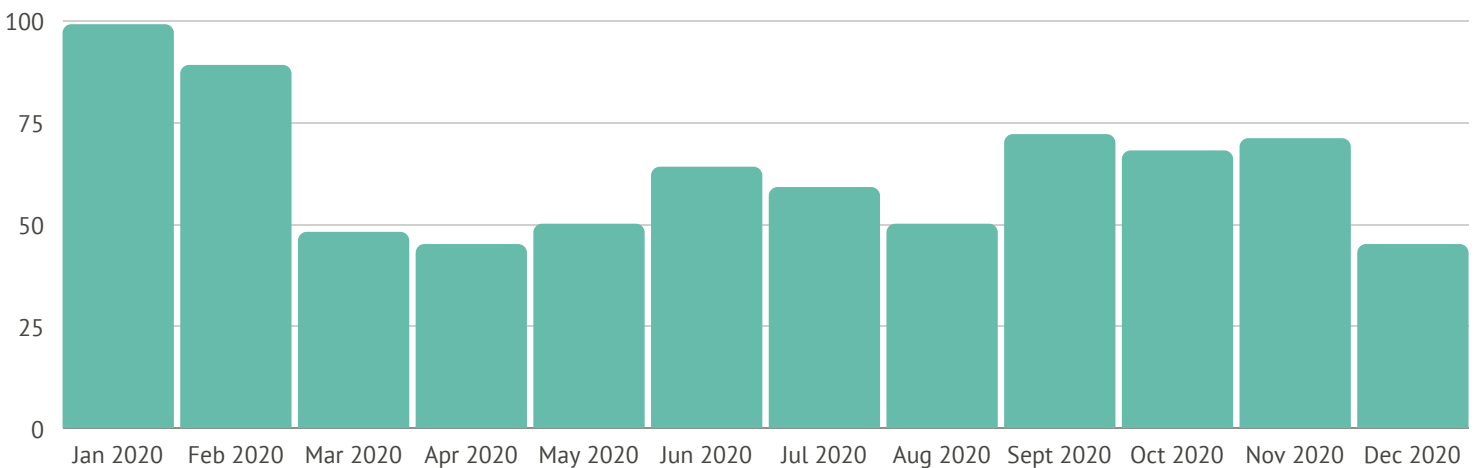
Of 4,752 applications received, 1,877 have been accepted, representing all US states, the District of Columbia, and more than 25 countries. Currently, there are 322 applications under medical record review. Applicants are not accepted for a variety of reasons, including lack of objective findings. Applicants 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 (52%), and 42% are under 18 years old. Of the applicants accepted for participation in the study, 49% are female, and 62% are under 18 years old. The majority of applicants (69%) and accepted participants (63%) 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, 1,473 evaluations have been completed.



# DIAGNOSES

Providing diagnoses to participants is a central goal of the UDN. Thus far, 454 certain or highly likely diagnoses 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 diagnoses were identified through a genome-wide assay such as chromosomal microarray or karyotype. Regarding the 81% of diagnoses made through exome or genome sequencing, multiple variant types were observed, including single nucleotide variants (85%) and copy number variants (7%).

# 30

CONDITIONS HAVE  
BEEN NEWLY  
DESCRIBED

# 70

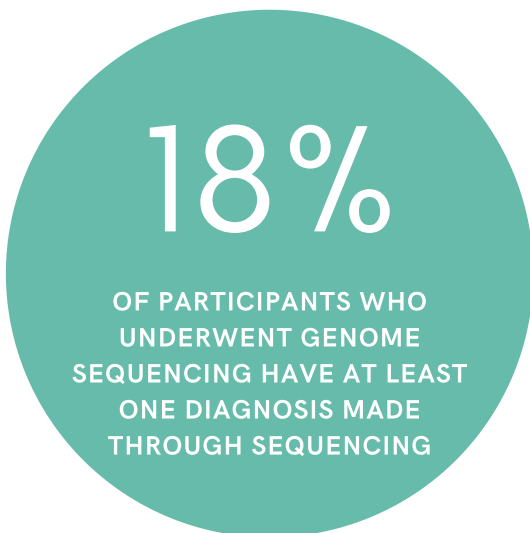
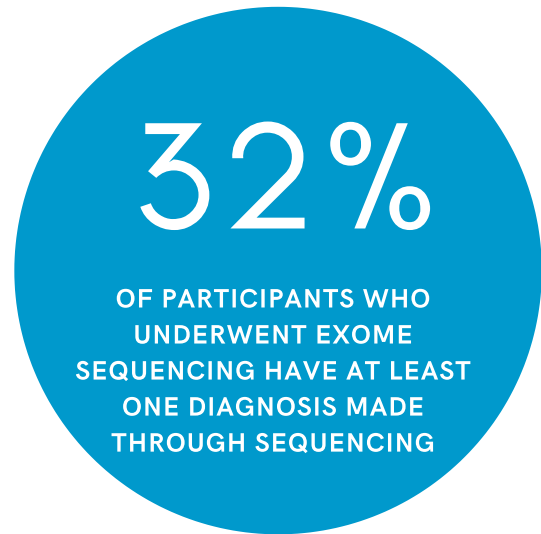
DIAGNOSES HAVE  
BEEN MADE BASED  
ON CLINICAL  
GROUNDS OR  
THROUGH DIRECTED  
CLINICAL TESTING

# 14

PARTICIPANTS HAVE  
MORE THAN ONE  
DIAGNOSIS

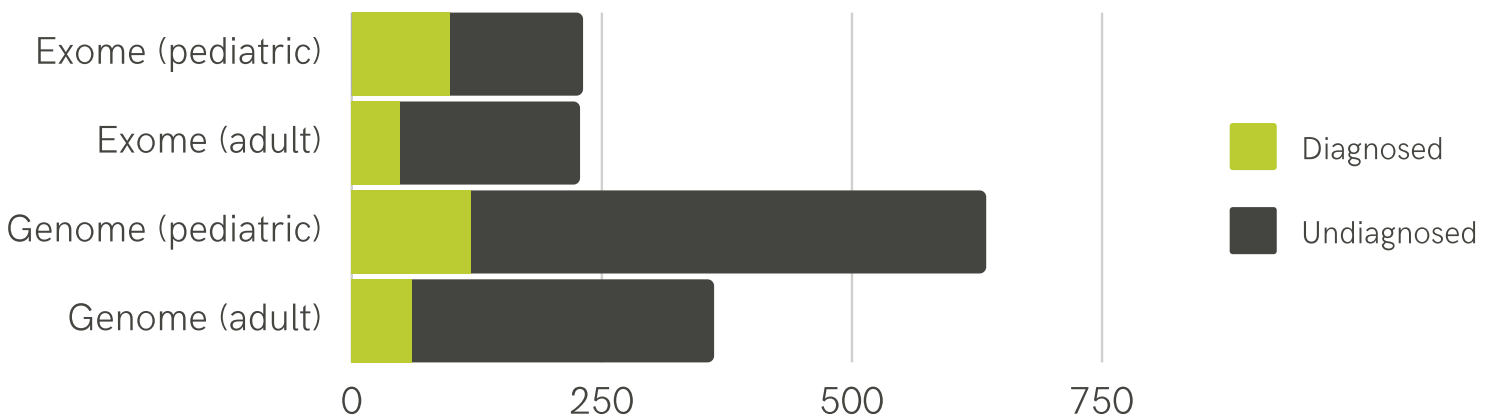
# EXOME SEQUENCING

457 participants (230 children and 227 adults) have undergone exome sequencing. The most common symptom category for participants undergoing exome sequencing is neurology (47%), followed by multiple congenital anomalies (9%).



# GENOME SEQUENCING

994 participants (633 children and 361 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 (51%), followed by multiple congenital anomalies (9%).



## 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.

321

VARIANTS EVALUATED BY  
THE MODEL ORGANISMS  
SCREENING CENTER

179

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.

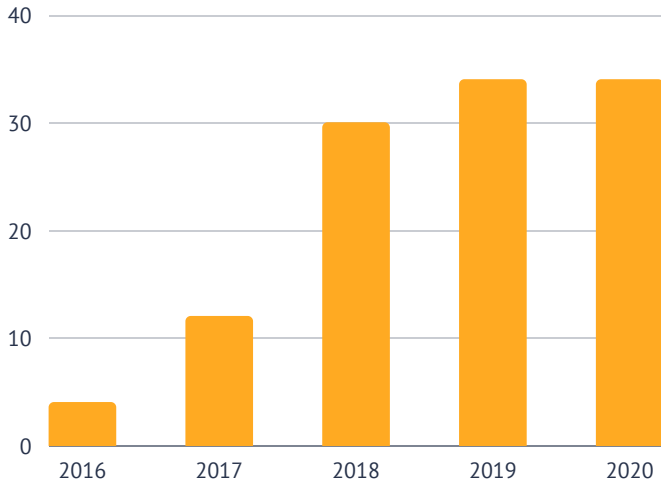
## RNA SEQUENCING

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.

407

NUMBER OF PARTICIPANTS  
WITH RNA SEQUENCING  
COMPLETE

# DATA SHARING



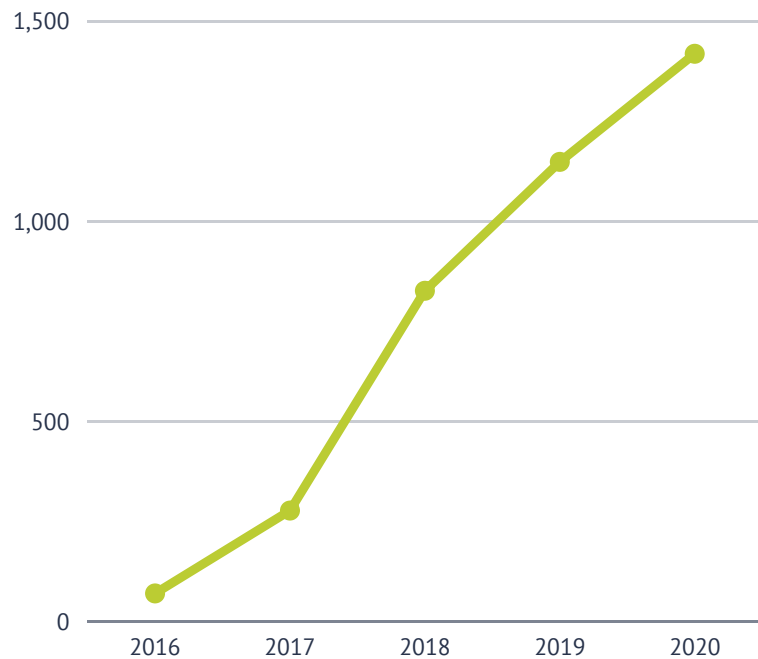
The UDN is committed to collecting and sharing data in useful, sustainable, and responsible ways. In addition to sharing data in relevant research repositories as described below, for those participants who would like to do so, the UDN shares their information via participant pages on the UDN website 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.



470

VARIANT INTERPRETATIONS SUBMITTED TO CLINVAR

1,419

RECORDS SHARED ACROSS MATCHMAKER EXCHANGE

176

PARTICIPANT PAGES PUBLISHED ON UDN WEBSITE