

**Referrer Information**

Physician:

UPIN/NPI:

Genetic Counselor:

Email:

Institution:

Address:

Phone:

Fax:

Additional reports to:

Address:

Phone:

Fax:

**Mandatory Signature**

I have confirmed that the patient has consented for the testing ordered and that two matching identifiers are present on each page of this requisition.

Signature:

Date:

**Patient Information (\*two of these identifiers MUST also appear on the sample tube)**

Legal Name\* (Last):

(First):

Preferred Name (Last):

(First):

Date of birth\* (mm/dd/yy):

Sex assigned at birth:

Gender:

Patient ID/MRN\*:

Patient Address:

**Billing Information (contact Billing Coordinator at 443-287-2486 prior to submitting)**

Billing contact:

Phone:

Fax:

Email:

Inpatient

Referring Center

MD Medicaid

Self-pay

Patient Insurance

Medicare

**Shipping Address: 1812 Ashland Ave, Sample Intake Rm 245, Baltimore, MD 21205**



Patient Information

Patient Name:

DOB:

Proband Sample Information

Test Selection

Proband-only  Duo  Trio  Quad

Include full sequence analysis and deletion testing of the mitochondrial genome

Sample Type

Whole Blood  Cord blood  
 Extracted DNA  Cleaned chorionic villi  
 Saliva  Cultured chorionic villi  
 Cultured skin fibroblasts\*  Cultured amniocytes  
 Other: \_\_\_\_\_

Collection Date:

Blood and saliva are **not** acceptable if the patient has:

- Received blood products <2 weeks before specimen collection. Exceptions are made for pRBC-only transfusions.
- Received an allogenic bone marrow or stem cell transplant. Cultured skin fibroblasts are the only accepted specimen type in this case.
- Active hematologic malignancy; cultured skin fibroblasts are the recommended sample type.

Contact the lab with specific questions or concerns.

Isolation or extraction of nucleic acids must be performed in a CLIA-certified laboratory or a laboratory meeting equivalent (or more stringent) requirements as determined by the College of American Pathologists (CAP) and/or the Centers for Medicare and Medicaid Services (CMS).

Family Information (if applicable)

Name (Last, First)	DOB	Relationship	Sample Type
<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="checkbox"/> Blood <input type="checkbox"/> Saliva
<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="checkbox"/> Blood <input type="checkbox"/> Saliva
<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="checkbox"/> Blood <input type="checkbox"/> Saliva

Collection Site(s)

Ethnicity

Black, African American, or of African descent  Native Hawaiian, Pacific Islander  
 East Asian  South Asian  
 Middle Eastern, Southwest Asian, North African  Southeast Asian  
 Hispanic, Latino/Latina/Latinx  White  
 Native American, Alaska Native, First Nations  Other: \_\_\_\_\_

**Patient Information**

Patient Name: \_\_\_\_\_

DOB: \_\_\_\_\_

**Phenotypic Information**

**Cancer**

\_\_\_ Type: \_\_\_\_\_

\_\_\_ Location: \_\_\_\_\_

\_\_\_ Age of onset: \_\_\_\_\_

**Developmental/Behavioral**

\_\_\_ Absent speech

\_\_\_ Aggressive behavior

\_\_\_ Anxiety

\_\_\_ Autistic Behavior

\_\_\_ Cognitive impairment

\_\_\_ Delayed speech & language development

\_\_\_ Developmental regression

\_\_\_ Gait disturbance

\_\_\_ Global developmental delay

\_\_\_ Hyperactivity

\_\_\_ Intellectual disability

\_\_\_ Learning disability

\_\_\_ Memory impairment

\_\_\_ Other: \_\_\_\_\_

**Cardiac**

\_\_\_ Amyloidosis

\_\_\_ Aortic root dilation

\_\_\_ Arrhythmia

\_\_\_ Atrial septal defect

\_\_\_ Bicuspid aortic valve

\_\_\_ Cardiomyopathy

\_\_\_ Coarctation of aorta

\_\_\_ Mitral valve prolapse

\_\_\_ Patent ductus arteriosus

\_\_\_ Prolonged QTc interval

\_\_\_ Sudden death

\_\_\_ Tetralogy of Fallot

\_\_\_ Ventricular septal defect

\_\_\_ Other: \_\_\_\_\_

**Ear Defects/Hearing Impairment**

\_\_\_ Ears (shape, placement)

\_\_\_ Conductive hearing impairment

\_\_\_ Sensorineural hearing impairment

\_\_\_ Other: \_\_\_\_\_

**Craniofacial/Dysmorphism**

\_\_\_ Dysmorphic features

\_\_\_ Asymmetry

\_\_\_ Brachycephaly

\_\_\_ Cleft lip and/or palate

\_\_\_ Coarse facial features

\_\_\_ Craniosynostosis

\_\_\_ Short neck

\_\_\_ Synophrys

\_\_\_ Other: \_\_\_\_\_



Patient Information

Patient Name:

DOB:

Phenotypic Information (continued)

Eye Defects/Vision

- Cataracts
- Coloboma
- Corneal opacity
- Ectopia lentis
- External ophthalmoplegia
- Microphthalmia/Anophthalmia
- Myopia
- Nystagmus
- Optic atrophy
- Ptosis
- Retinal detachment
- Retinitis pigmentosa
- Strabismus
- Other: \_\_\_\_\_

Endocrine

- Hypogonadism
- Delayed puberty
- Precocious puberty
- Diabetes
- Hyperinsulinism
- Hyperthyroidism
- Hypothyroidism
- Other: \_\_\_\_\_

Gastrointestinal/Abdominal

- Constipation
- Diaphragmatic hernia
- Diarrhea
- Duodenal stenosis/atresia
- Exocrine pancreatic insufficiency
- Failure to thrive
- Feeding difficulties
- Gastroesophageal reflux
- Hepatomegaly
- Heterotaxy
- Inflammatory bowel disease
- Intrahepatic biliary atresia
- Jaundice
- Nausea/Vomiting
- Pancreatitis
- Pyloric stenosis
- Splenomegaly
- Tracheoesophageal fistula
- Umbilical hernia
- Other: \_\_\_\_\_

**Patient Information**

Patient Name:

DOB:

**Phenotypic Information (continued)**

**Genitourinary**

- Ambiguous genitalia
- Cystic kidney disease
- Cryptorchidism
- Horseshoe kidney
- Hydronephrosis
- Hypospadias
- Inguinal hernia
- Micropenis
- Nephrolithiasis
- Renal agenesis
- Other: \_\_\_\_\_

**Growth**

- Abnormal fat distribution
- Failure to thrive
- Obesity
- Overgrowth
- Short stature
- Tall stature
- Macrocephaly
- Microcephaly
- Other: \_\_\_\_\_

**Hematologic/Immunologic**

- Allergic rhinitis
- Anemia
- Immunodeficiency
- Neutropenia
- Pancytopenia
- Recurrent infections
- Thrombocytopenia
- Other: \_\_\_\_\_

**Imaging Findings**

Specify or provide relevant imaging reports:

**Metabolic/Lab Findings**

Specify or provide relevant lab reports/values:



Patient Information

Patient Name:

DOB:

Phenotypic Information (continued)

Musculoskeletal

- |  |  |  |
|--|--|--|
| <input type="checkbox"/> Abnormal connective tissue            | <input type="checkbox"/> Ectrodactyly        | <input type="checkbox"/> Osteopenia          |
| <input type="checkbox"/> Abnormal form of the vertebral bodies | <input type="checkbox"/> Fatigue             | <input type="checkbox"/> Pectus deformity    |
| <input type="checkbox"/> Abnormality of the ribs               | <input type="checkbox"/> Hemihypertrophy     | <input type="checkbox"/> Polydactyly         |
| <input type="checkbox"/> Arachnodactyly                        | <input type="checkbox"/> Hypotonia           | <input type="checkbox"/> Recurrent fractures |
| <input type="checkbox"/> Arthrogryposis                        | <input type="checkbox"/> Joint hypermobility | <input type="checkbox"/> Rhabdomyolysis      |
| <input type="checkbox"/> Bruising susceptibility               | <input type="checkbox"/> Muscle weakness     | <input type="checkbox"/> Scoliosis           |
| <input type="checkbox"/> Camptodactyly                         | <input type="checkbox"/> Myopathic facies    | <input type="checkbox"/> Skeletal dysplasia  |
| <input type="checkbox"/> Clinodactyly                          | <input type="checkbox"/> Myopathy            | <input type="checkbox"/> Other: _____        |
| <input type="checkbox"/> Decreased muscle mass                 | <input type="checkbox"/> Osteoarthritis      |  |

Neurological

- |   |   |  |
|---|---|--|
| <input type="checkbox"/> Ataxia                     | <input type="checkbox"/> Dystonia         | <input type="checkbox"/> Peripheral neuropathy |
| <input type="checkbox"/> Cerebral palsy             | <input type="checkbox"/> Encephalopathy   | <input type="checkbox"/> Seizures              |
| <input type="checkbox"/> Chorea                     | <input type="checkbox"/> Headaches        | <input type="checkbox"/> Sensory neuropathy    |
| <input type="checkbox"/> Cortical Visual Impairment | <input type="checkbox"/> Hemiplegia       | <input type="checkbox"/> Spasticity            |
| <input type="checkbox"/> Dementia                   | <input type="checkbox"/> Infantile Spasms | <input type="checkbox"/> Stroke                |
| <input type="checkbox"/> Dysarthria                 | <input type="checkbox"/> Migraines        | <input type="checkbox"/> Tremors               |
| <input type="checkbox"/> Dyskinesia                 | <input type="checkbox"/> Myoclonus        | <input type="checkbox"/> Other: _____          |
| <input type="checkbox"/> Dysphasia                  | <input type="checkbox"/> Parkinsonism     |  |

**Patient Information**

Patient Name:

DOB:

**Phenotypic Information (continued)**

**Pre/Perinatal History**

- Increased NT/Cystic hygroma
- Intrauterine growth retardation
- Nonimmune hydrops fetalis
- Oligohydramnios
- Omphalocele
- Polyhydramnios
- Two vessel cord
- Prematurity
- Other: \_\_\_\_\_

**Respiratory**

- Asthma
- Hypoventilation
- Laryngomalacia
- Pneumothorax
- Pulmonary fibrosis
- Respiratory insufficiency
- Other: \_\_\_\_\_

**Skin/Hair**

- Abnormal blistering of the skin
- Abnormality of hair
- Abnormality of nail
- Abnormal skin pigmentation
- Abnormality of teeth
- Other: \_\_\_\_\_

**Structural Brain Abnormalities**

- Abnormal myelination
- Abnormality of basal ganglia
- Abnormality of brainstem
- Abnormality of periventricular white matter
- Abnormality of the corpus callosum
- Aplasia/hypoplasia of cerebellum/vermis
- Arnold Chiari malformation
- Encephalocele
- Heterotopia
- Holoprosencephaly
- Hydrocephalus/Ventriculomegaly
- Leukodystrophy
- Lissencephaly
- Pachygyria/Polymicrogyria
- Other: \_\_\_\_\_

**Vascular**

- Arterial aneurysm/dissection
- Arterial calcification
- Arterial tortuosity
- Arteriovenous malformation
- Epistaxis
- Lymphedema
- Pulmonary hypertension
- Other: \_\_\_\_\_

**Additional Clinical Information/ Genes of Interest/ Previously Reported Variants**

**My Choices - Patient**

**Secondary Findings Reported to Me**

Secondary findings are genetic changes that are likely to cause specific conditions other than the primary reason for testing in me/my child. Only conditions with clear management guidelines are included, and not every possible disease is covered. The DNA Diagnostic Laboratory largely follows the ACMG version 3 guidelines for reporting secondary findings. With respect to TTN-associated DCM, our current policy is to report truncating variants in the A-band alone.

- Yes, I would like secondary findings to be analyzed for me/my child.
- No, I would not like secondary findings to be analyzed for me/my child.

**Research**

De-identified clinical and genetic information may be used in academic case research and/or publications. The ordering provider may reach out to me to obtain additional information and/or photos. Additionally, if the results of clinical exome sequencing are negative, the ordering provider may re-contact me about follow-up research sequencing opportunities.

- Yes, I agree to my/my child's de-identified sample being used for research.
- No, I do not agree to my/my child's de-identified sample being used for research.

**Sequence Data Given to My Provider**

My provider can have a copy of the raw sequence data from my exome test (called a variant call file or VCF). My provider may request the raw data to further analyze genetic changes that may be associated with my/my child's primary medical concerns. This information will not be used for research purposes or shared with other providers or insurers unless otherwise discussed with me.

- Yes, I allow the lab to release my raw data to my referring provider.
- No, I do not allow the lab to release my raw data to my referring provider.

**Statement of Consent - Patient**

My ordering provider has reviewed OR I have read the Clinical Exome Sequencing Informed Consent document in its entirety. I have had the opportunity to ask questions of the provider about Exome Sequencing. I grant permission for the DNA Diagnostic Laboratory at Johns Hopkins University to perform clinical exome sequencing for me and/or my child. I have chosen to either opt-in or opt-out of receiving secondary findings, being re-contacted for research, and allowing my referring provider to request access to the VCF as detailed above. I understand the benefits, risks, and limitations of exome sequencing.

Patient Name (Print):

Signature:

Date:

Relationship to patient (if not self):



**My Choices - Family Member**

**Secondary Findings Reported to Me**

Secondary findings are genetic changes that are likely to cause specific conditions other than the primary reason for testing in me/my child. Only conditions with clear management guidelines are included, and not every possible disease is covered. The DNA Diagnostic Laboratory largely follows the ACMG version 3 guidelines for reporting secondary findings. With respect to TTN-associated DCM, our current policy is to report truncating variants in the A-band alone. I understand that my DNA will be analyzed for secondary findings only if a secondary finding is reported for the patient on this test.

- Yes, I would like secondary findings to be analyzed for me/my child.
- No, I would not like secondary findings to be analyzed for me/my child.

**Research**

De-identified clinical and genetic information may be used in academic case research and/or publications. The ordering provider may reach out to me to obtain additional information and/or photos. Additionally, if the results of clinical exome sequencing are negative, the ordering provider may re-contact me about follow-up research sequencing opportunities.

- Yes, I agree to my/my child's de-identified sample being used for research.
- No, I do not agree to my/my child's de-identified sample being used for research.

**Sequence Data Given to My Provider**

My provider can have a copy of the raw sequence data from my exome test (called a variant call file or VCF). My provider may request the raw data to further analyze genetic changes that may be associated with my/my child's primary medical concerns. This information will not be used for research purposes or shared with other providers or insurers unless otherwise discussed with me.

- Yes, I allow the lab to release my raw data to my referring provider.
- No, I do not allow the lab to release my raw data to my referring provider.

**Statement of Consent - Family Member**

My ordering provider has reviewed OR I have read the Clinical Exome Sequencing Informed Consent document in its entirety. I have had the opportunity to ask questions of the provider about Exome Sequencing. I grant permission for the DNA Diagnostic Laboratory at Johns Hopkins University to perform clinical exome sequencing for me and/or my child. I have chosen to either opt-in or opt-out of receiving secondary findings, being re-contacted for research, and allowing my referring provider to request access to the VCF as detailed above. I understand the benefits, risks, and limitations of exome sequencing.

Family Member Name (Print):

Signature:

Date:

Relationship to patient:



**My Choices - Family Member**

**Secondary Findings Reported to Me**

Secondary findings are genetic changes that are likely to cause specific conditions other than the primary reason for testing in me/my child. Only conditions with clear management guidelines are included, and not every possible disease is covered. The DNA Diagnostic Laboratory largely follows the ACMG version 3 guidelines for reporting secondary findings. With respect to TTN-associated DCM, our current policy is to report truncating variants in the A-band alone. I understand that my DNA will be analyzed for secondary findings only if a secondary finding is reported for the patient on this test.

- Yes, I would like secondary findings to be analyzed for me/my child.
- No, I would not like secondary findings to be analyzed for me/my child.

**Research**

De-identified clinical and genetic information may be used in academic case research and/or publications. The ordering provider may reach out to me to obtain additional information and/or photos. Additionally, if the results of clinical exome sequencing are negative, the ordering provider may re-contact me about follow-up research sequencing opportunities.

- Yes, I agree to my/my child's de-identified sample being used for research.
- No, I do not agree to my/my child's de-identified sample being used for research.

**Sequence Data Given to My Provider**

My provider can have a copy of the raw sequence data from my exome test (called a variant call file or VCF). My provider may request the raw data to further analyze genetic changes that may be associated with my/my child's primary medical concerns. This information will not be used for research purposes or shared with other providers or insurers unless otherwise discussed with me.

- Yes, I allow the lab to release my raw data to my referring provider.
- No, I do not allow the lab to release my raw data to my referring provider.

**Statement of Consent - Family Member**

My ordering provider has reviewed OR I have read the Clinical Exome Sequencing Informed Consent document in its entirety. I have had the opportunity to ask questions of the provider about Exome Sequencing. I grant permission for the DNA Diagnostic Laboratory at Johns Hopkins University to perform clinical exome sequencing for me and/or my child. I have chosen to either opt-in or opt-out of receiving secondary findings, being re-contacted for research, and allowing my referring provider to request access to the VCF as detailed above. I understand the benefits, risks, and limitations of exome sequencing.

Family Member Name (Print):

Signature:

Date:

Relationship to patient:

**My Choices - Family Member**

**Secondary Findings Reported to Me**

Secondary findings are genetic changes that are likely to cause specific conditions other than the primary reason for testing in me/my child. Only conditions with clear management guidelines are included, and not every possible disease is covered. The DNA Diagnostic Laboratory largely follows the ACMG version 3 guidelines for reporting secondary findings. With respect to TTN-associated DCM, our current policy is to report truncating variants in the A-band alone. I understand that my DNA will be analyzed for secondary findings only if a secondary finding is reported for the patient on this test.

- Yes, I would like secondary findings to be analyzed for me/my child.
- No, I would not like secondary findings to be analyzed for me/my child.

**Research**

De-identified clinical and genetic information may be used in academic case research and/or publications. The ordering provider may reach out to me to obtain additional information and/or photos. Additionally, if the results of clinical exome sequencing are negative, the ordering provider may re-contact me about follow-up research sequencing opportunities.

- Yes, I agree to my/my child's de-identified sample being used for research.
- No, I do not agree to my/my child's de-identified sample being used for research.

**Sequence Data Given to My Provider**

My provider can have a copy of the raw sequence data from my exome test (called a variant call file or VCF). My provider may request the raw data to further analyze genetic changes that may be associated with my/my child's primary medical concerns. This information will not be used for research purposes or shared with other providers or insurers unless otherwise discussed with me.

- Yes, I allow the lab to release my raw data to my referring provider.
- No, I do not allow the lab to release my raw data to my referring provider.

**Statement of Consent - Family Member**

My ordering provider has reviewed OR I have read the Clinical Exome Sequencing Informed Consent document in its entirety. I have had the opportunity to ask questions of the provider about Exome Sequencing. I grant permission for the DNA Diagnostic Laboratory at Johns Hopkins University to perform clinical exome sequencing for me and/or my child. I have chosen to either opt-in or opt-out of receiving secondary findings, being re-contacted for research, and allowing my referring provider to request access to the VCF as detailed above. I understand the benefits, risks, and limitations of exome sequencing.

Family Member Name (Print):

Signature:

Date:

Relationship to patient:



## Informed Consent

### Exome Sequencing

Exome sequencing is a genetic test that analyzes a patient's genetic material, or DNA. Genes are the instructions that tell cells and bodies how to grow and develop. They are made up of DNA. Changes in genes, or variants, may contribute to a patient's health concerns. All people have many changes in their genetic information. Only some of these variants are known to result in genetic conditions. Exome sequencing is able to analyze many genes at once to look for variants that may provide a genetic diagnosis. Understanding the cause of a patient's health concerns may provide insight into what can be expected for the patient in the future, whether other family members may be at risk for carrying the variant, and what the risk is for recurrence. Although exome sequencing is able to read through many genes, it is not able to read through the entirety of the patient's genetic information. The goal of exome sequencing is to identify a genetic cause for a patient's health concerns.

### Types of Results

There are several types of results that may be reported by exome sequencing:

- **POSITIVE:** A positive result indicates that a genetic change has been identified in a gene known to be responsible for a genetic condition. This may or may not provide a cause or diagnosis for the patient's health concerns. It is possible that this test may identify more than one genetic change. It is possible that other family members may carry the same genetic change.
- **NEGATIVE:** A negative result indicates that no known genetic cause for the patient's medical concerns was found. A negative result does not mean that there is not a genetic cause for the patient's health concerns. Future genetic testing may be able to identify additional genetic changes.
- **UNCERTAIN:** A variant of uncertain significance (VUS) indicates that a genetic change was identified in a gene, but that there is not yet enough information known about the consequences of a particular change or gene to determine whether it has health care significance. Testing of additional family members may be recommended to better understand the effect of an uncertain variant.

### Family Member Testing

Obtaining samples from the patient's biological family members may aid in the interpretation of exome sequencing results. If a genetic change is identified in a patient, the family member samples may be tested for the same change. This may indicate whether or not the change was inherited or de novo (new to the patient). Family member samples will only be analyzed in the event that a genetic change is identified in the patient.

### Secondary Findings

Exome sequencing analyzes many genes all at once. Accordingly, it is possible to find genetic changes in genes that are not related to the patient's primary health concerns. These results are called secondary findings. The American College of Medical Genetics and Genomics (ACMG) recommends that laboratories report such findings in genes that are known to cause specific actionable inherited conditions. Examples include hereditary cancer and heart syndromes, among others (please see attached table). Some of these conditions may not present until adulthood and may have a significant impact on the patient's and family member's healthcare and/or reproductive risk. If the patient is found to have a genetic change associated with one of these conditions, the family member's samples will be analyzed for the same change. A complete list of these genes will be provided to the patient/parent/guardian. Secondary findings will only be analyzed and reported if the patient/parent/guardian consents to receive them.

## Informed Consent (continued)

### Results Reporting

Results of exome sequencing will be reported to your ordering provider. Additionally, the provider may wish to get a copy of the raw sequence data, also known as the variant call file (VCF), after results are returned. Results that will be reported include positive results in the genes analyzed, variants of uncertain significance in the genes analyzed, and secondary findings if the patient/parent/guardian consents to receive them. A negative result does not rule out a disease-causing genetic change in the genes analyzed. Changes that are not believed to affect the patient's health will not be reported. Changes that are known to be risk-factors but not causative of disease may not be reported.

### Risks

It is possible that this test may result in an uncertain result or identify unexpected secondary findings. It is possible that this test may reveal unexpected familial relationships (i.e. consanguinity, non-paternity, etc.). Results of this test may affect the healthcare and/or reproductive decisions of both the patient and their family members. Results may also affect the patient's and/or family member's ability to buy life, disability, and long-term care insurance in the future. Additionally, it is possible that exome sequencing may not be covered in full by the patient's health insurance plan. Although unlikely, there is a possibility for laboratory error to occur. Genetic counseling is recommended prior to consent for exome sequencing and after results are returned.

### Limitations

Although exome sequencing analyzes many genes at once, it does not analyze all genes and all types of genetic changes. It is possible that this test may not identify the genetic change responsible for the patient's medical concerns. This test may identify a change in a gene, but does not have the ability to predict long-term prognosis. Interpretation of results is based on our current understanding of genetics. It is possible that results may change in the future upon reanalysis.

### Research

If the patient/parent/guardian provides permission, de-identified clinical and genetic information may be used in academic case reports and publications. The ordering provider may reach out to the patient/parent/guardian for additional information and/or photos. Additionally, if the results of the clinical exome sequencing are negative, the ordering provider may re-contact the patient/parent/guardian regarding follow-up research sequencing opportunities.

### Privacy Protections

The results of clinical exome sequencing will be released only to providers authorized by the patient/parent/guardian. In addition, The Genetic Information Nondiscrimination Act (GINA) protects most individuals from discrimination by employers and/or health insurers on the basis of genetic test results. In an attempt to better understand the field of genetics and variant interpretation, the DNA Diagnostic Laboratory may share de-identified genetic information in healthcare databases.