Blueprint Genetics

Autism Spectrum Disorders Panel

Test code: NE0101

Is a 75 gene panel that includes assessment of non-coding variants.

In addition, it also includes the maternally inherited mitochondrial genome.
Is ideal for patients with clinical diagnosis of autism.

Twin studies have indicated that the heritability of autism is over 90%. However, currently a genetic cause can be identified in 20% to 25% of children with autism. Single-gene disorders, in which neurologic findings are associated with autism spectrum disorder (ASD), can be identified in ~5% of ASD patients. As an example, *MECP2* pathogenic variants causing Rett syndrome have been reported in approximately 1% of children diagnosed with autism.

About Autism Spectrum Disorders

Autism spectrum disorder (ASD) is a neurodevelopmental disorder characterized by deficits in social communication, absence or delay in language development, and stereotyped or repetitive behaviors. Autism has many etiologies, as it has been documented in hundreds of neurologically based syndromes with multiple causes, outcomes, and treatment responses. Currently a genetic cause can be identified in 20% to 25% of children with autism. Single-gene disorders, in which neurologic findings are associated with autism spectrum disorder (ASD), can be identified in ~5% of ASD patients. Autism can be considered complex (i.e., presence of dysmorphic features and/or microcephaly) or essential (i.e., absence of physical abnormalities and microcephaly).

Availability

Results in 3-4 weeks

Gene set description

Genes in the Autism Spectrum Disorders Panel and their clinical significance

Gene	Associated phenotypes	Inheritance	ClinVar	HGMD
ADNP	Helsmoortel-van der Aa syndrome (Mental retardation, autosomal dominant 28)	AD	44	66
BCL11A	Dias-Logan syndrome	AD	20	29
C12ORF4	Developmental delay and seizures with or without movement abnormalities (DEDSM)	AR	1	5
CACNA1C*	Brugada syndrome, Timothy syndrome	AD	19	68
CC2D1A	Mental retardation, autosomal recessive 3	AR	3	7
CNOT3	Developmental delay and seizures with or without movement abnormalities (DEDSM)	AD	1	8
CNTN6	Developmental delay and seizures with or without movement abnormalities (DEDSM)	AD	2	41
COL4A3BP	Mental retardation, autosomal dominant 34	AD	6	7
CSNK2A1	Jeune asphyxiating thoracic dystrophy, Joubert syndrome 21		14	20

CTNND2	Developmental delay and seizures with or without movement abnormalities (DEDSM)	AD	7	35
DHCR7	Smith-Lemli-Opitz syndrome	AR	88	217
EHMT1	Kleefstra syndrome	AD	86	89
EN2	Autism	AD		2
FBXO11	Developmental delay and seizures with or without movement abnormalities (DEDSM)	AD	8	9
FOXP1	Mental retardation with language impairment and autistic features, Congenital heart malformations	AD	48	76
GAMT	Guanidinoacetate methyltransferase deficiency	AR	18	58
KMT2E		AD		4
KMT5B	Developmental delay and seizures with or without movement abnormalities (DEDSM), Autism spectrum disorder, overgrowth syndrome with intellectual disability	AD	9	14
MBOAT7	Mental retardation, autosomal recessive 57	AR	5	5
MECP2	Angelman-like syndrome, Autism, Rett syndrome, Encephalopathy, Mental retardation	XL	506	1039
MT-ATP6	Neuropathy, ataxia, and retinitis pigmentosa, Leber hereditary optic neuropathy, Ataxia and polyneuropathy, adult-onset, Cardiomyopathy, infantile hypertrophic, Leigh syndrome, Striatonigral degeneration, infantile, mitochondrial	Mitochondrial	19	
MT-ATP8	Cardiomyopathy, apical hypertrophic, and neuropathy, Cardiomyopathy, infantile hypertrophic	Mitochondrial	4	
MT-CO1	Myoglobinuria, recurrent, Leber hereditary optic neuropathy, Sideroblastic anemia, Cytochrome C oxidase deficiency	Mitochondrial	17	
MT-CO2	Cytochrome c oxidase deficiency	Mitochondrial	8	
MT-CO3	Cytochrome c oxidase deficiency, Leber hereditary optic neuropathy	Mitochondrial	9	
MT-CYB		Mitochondrial	69	
MT-ND1	Mitochondrial myopathy, encephalopathy, lactic acidosis, and stroke-like episodes, Leber hereditary optic neuropathy, Leber optic atrophy and dystonia	Mitochondrial	21	
MT-ND2	Leber hereditary optic neuropathy, Mitochondrial complex I deficiency	Mitochondrial	6	
MT-ND3	Leber optic atrophy and dystonia, Mitochondrial complex I deficiency	Mitochondrial	7	
MT-ND4	Leber hereditary optic neuropathy, Leber optic atrophy and dystonia, Mitochondrial complex I deficiency	Mitochondrial	11	
MT-ND4L	Leber hereditary optic neuropathy	Mitochondrial	2	
MT-ND5	Myoclonic epilepsy with ragged red fibers, Mitochondrial myopathy, encephalopathy, lactic acidosis, and stroke-like episodes, Leber hereditary optic neuropathy, Mitochondrial complex I deficiency	Mitochondrial	19	

MT-ND6	Mitochondrial myopathy, encephalopathy, lactic acidosis, and stroke-like episodes, Oncocytoma, Leber hereditary optic neuropathy, Leber optic atrophy and dystonia, Mitochondrial complex I deficiency	Mitochondrial	16
MT-RNR1	Deafness, mitochondrial	Mitochondrial	3
MT-RNR2	Chloramphenicol toxicity/resistance	Mitochondrial	2
MT-TA		Mitochondrial	4
MT-TC	Mitochondrial myopathy, encephalopathy, lactic acidosis, and stroke-like episodes	Mitochondrial	3
MT-TD		Mitochondrial	1
MT-TE	Diabetes-deafness syndrome, Mitochondrial myopathy, infantile, transient, Mitochondrial myopathy with diabetes	Mitochondrial	5
MT-TF	Myoclonic epilepsy with ragged red fibers, Nephropathy, tubulointerstitial, Encephalopathy, mitochondrial, Epilepsy, mitochondrial, Myopathy, mitochondrial, Mitochondrial encephalomyopathy with lactic acidosis and stroke-like episodes	Mitochondrial	7
MT-TG		Mitochondrial	3
MT-TH		Mitochondrial	4
MT-TI		Mitochondrial	7
MT-TK		Mitochondrial	5
MT-TL1	Cytochrome c oxidase deficiency, Myoclonic epilepsy with ragged red fibers, Mitochondrial myopathy, encephalopathy, lactic acidosis, and stroke-like episodes, Diabetes-deafness syndrome, Cyclic vomiting syndrome, SIDS, susceptibility to	Mitochondrial	14
MT-TL2	Mitochondrial multisystemic disorder, Progressive external ophthalmoplegia	Mitochondrial	5
MT-TM	Leigh syndrome, Mitochondrial multisystemic disorder	Mitochondrial	1
MT-TN	Progressive external ophthalmoplegia, Mitochondrial multisystemic disorder	Mitochondrial	3
MT-TP		Mitochondrial	2
MT-TQ	Mitochondrial multisystemic disorder	Mitochondrial	2
MT-TR	Encephalopathy, mitochondrial	Mitochondrial	2
MT-TS1	Myoclonic epilepsy with ragged red fibers, Mitochondrial myopathy, encephalopathy, lactic acidosis, and stroke-like episodes	Mitochondrial	10
MT-TS2	Mitochondrial multisystemic disorder	Mitochondrial	2
MT-TT		Mitochondrial	5
MT-TV	Hypertrophic cardiomyopathy (HCM), Leigh syndrome, Mitochondrial multisystemic disorder	Mitochondrial	3
MT-TW	Leigh syndrome, Myopathy, mitochondrial	Mitochondrial	8

MT-TY	Mitochondrial multisystemic disorder	Mitochondrial	4	
NBEA	Epilepsy	AD	3	13
NFIB	Macrocephaly	AD	17	2
NLGN3	Autism, Asperger syndrome	XL	2	10
NLGN4X	Autism, Asperger syndrome, Mental retardation	XL	7	35
NSD1	Sotos syndrome, Weaver syndrome, Beckwith-Wiedemann syndrome	AD	329	517
POGZ	Mental retardation, autosomal dominant 37 (White-Sutton syndrome)	AD	46	52
PTCHD1	Autism susceptibility, X-linked 4	XL	9	47
PTEN*	Bannayan-Riley-Ruvalcaba syndrome, Lhermitte-Duclos syndrome, Cowden syndrome	AD	435	638
RPL10	Autism	XL	4	5
SHANK3	Phelan-McDermid syndrome, Schizophrenia 15	AD	66	191
TBR1		AD	16	18
TCF20	Developmental delay and seizures with or without movement abnormalities (DEDSM)	AD	7	16
TRIP12	Intellectual disability	AD	14	32
TSC1	Lymphangioleiomyomatosis, Tuberous sclerosis	AD	177	372
TSC2	Lymphangioleiomyomatosis, Tuberous sclerosis	AD	396	1195
VAMP2		AD		
WASF1	Intellectual disability and seizures	AD	3	3
ZSWIM6	Acromelic frontonasal dysostosis	AD	4	2

*Some regions of the gene are duplicated in the genome. Read more.

The gene has suboptimal coverage (means <90% of the gene's target nucleotides are covered at >20x with mapping quality score (MQ>20) reads), and/or the gene has exons listed under Test limitations section that are not included in the panel as they are not sufficiently covered with high quality sequence reads.

The sensitivity to detect variants may be limited in genes marked with an asterisk (*) or number sign (#)

Gene refers to the HGNC approved gene symbol; Inheritance refers to inheritance patterns such as autosomal dominant (AD), autosomal recessive (AR), mitochondrial (mi), X-linked (XL), X-linked dominant (XLD) and X-linked recessive (XLR); ClinVar refers to the number of variants in the gene classified as pathogenic or likely pathogenic in this database (ClinVar); HGMD refers to the number of variants with possible disease association in the gene listed in Human Gene Mutation Database (HGMD). The list of associated, gene specific phenotypes are generated from CGD or Mitomap databases.

Non-coding disease causing variants covered by the panel

Gene	Genomic location HG19	HGVS	RefSeq	RS-number
EHMT1	Chr9:140678546	c.2382+1697T>G	NM_024757.4	rs786205602

GAMT	Chr19:1399508	c.391+15G>T	NM_138924.2	rs367567416
PTEN	Chr10:89622883–89623482			
PTEN	Chr10:89622988	c.-1239A>G	NM_000314.6	
PTEN	Chr10:89623049	c.-1178C>T	NM_000314.6	
PTEN	Chr10:89623056	c.-1171C>T	NM_000314.6	rs587779981
PTEN	Chr10:89623116	c.-1111A>G	NM_000314.6	
PTEN	Chr10:89623226	c.-1001T>C	NM_000314.4	
PTEN	Chr10:89623296	c.-931G>A	NM_000314.4	rs587781959
PTEN	Chr10:89623306	c.-921G>T	NM_000314.4	
PTEN	Chr10:89623331	c.-896T>C	NM_000314.4	
PTEN	Chr10:89623365	c.-862G>T	NM_000314.4	rs587776675
PTEN	Chr10:89623373	c.-854C>G	NM_000314.4	
PTEN	Chr10:89623392	c.-835C>T	NM_000314.4	rs587779994
PTEN	Chr10:89623428	c.-799G>C	NM_000314.4	rs587779992
PTEN	Chr10:89623462	c.-765G>A	NM_000314.4	
PTEN	Chr10:89690791	c.210-8dupT	NM_000314.4	
PTEN	Chr10:89692749	c.254-21G>C	NM_000314.4	
PTEN	Chr10:89725294	c.*65T>A	NM_000314.4	
PTEN	Chr10:89725304	c.*75_*92delTAATGGCAATAGGACATTinsCTATGGCAATAGGACATTG	NM_000314.4	
TSC1	Chr9:135800306	c.363+668G>A	NM_000368.4	
TSC2	Chr16:2098067	c.-30+1G>C	NM_000548.3	rs587778004
TSC2	Chr16:2106052	c.600-145C>T	NM_000548.3	
TSC2	Chr16:2107460	c.848+281C>T	NM_000548.3	rs45517132
TSC2	Chr16:2110656	c.976-15G>A	NM_000548.3	rs45517150
TSC2	Chr16:2127477	c.2838-122G>A	NM_000548.3	
TSC2	Chr16:2138031	c.5069-18A>G	NM_000548.3	rs45484794

Test Strengths

The strengths of this test include:

- CAP accredited laboratory
- CLIA-certified personnel performing clinical testing in a CLIA-certified laboratory
- Powerful sequencing technologies, advanced target enrichment methods and precision bioinformatics pipelines ensure superior analytical performance
- Careful construction of clinically effective and scientifically justified gene panels
- Some of the panels include the whole mitochondrial genome (please see the Panel Content section)
- Our Nucleus online portal providing transparent and easy access to quality and performance data at the patient level
- Our publicly available analytic validation demonstrating complete details of test performance
- ~2,000 non-coding disease causing variants in our clinical grade NGS assay for panels (please see 'Non-coding disease causing variants covered by this panel' in the Panel Content section)
- Our rigorous variant classification scheme

- Our systematic clinical interpretation workflow using proprietary software enabling accurate and traceable processing of NGS data
- Our comprehensive clinical statements

Test Limitations

Genes with partial, or whole gene, segmental duplications in the human genome are marked with an asterisk (*) if they overlap with the UCSC pseudogene regions. The technology may have limited sensitivity to detect variants in genes marked with these symbols (please see the Panel content table above).

This test does not detect the following:

- Complex inversions
- Gene conversions
- Balanced translocations
- Some of the panels include the whole mitochondrial genome but not all (please see the Panel Content section)
- Repeat expansion disorders unless specifically mentioned
- Non-coding variants deeper than ±20 base pairs from exon-intron boundary unless otherwise indicated (please see above Panel Content / non-coding variants covered by the panel).

This test may not reliably detect the following:

- Low level mosaicism in nuclear genes (variant with a minor allele fraction of 14.6% is detected with 90% probability)
- Stretches of mononucleotide repeats
- Low level heteroplasmy in mtDNA (>90% are detected at 5% level)
- Indels larger than 50bp
- Single exon deletions or duplications
- Variants within pseudogene regions/duplicated segments
- Some disease causing variants present in mtDNA are not detectable from blood, thus post-mitotic tissue such as skeletal muscle may be required for establishing molecular diagnosis.

The sensitivity of this test may be reduced if DNA is extracted by a laboratory other than Blueprint Genetics.

For additional information, please refer to the Test performance section and see our Analytic Validation.

Test performance

The Blueprint Genetics autism spectrum disorders panel covers classical genes associated with autism spectrum disorder, syndromic autism, Rett syndrome, Timothy syndrome, Smith-Lemli-Opitz syndrome and tuberous sclerosis complex. The genes on the panel have been carefully selected based on scientific literature, mutation databases and our experience.

Our panels are sliced from our high-quality whole exome sequencing data. Please see our sequencing and detection performance table for different types of alterations at the whole exome level (Table).

Assays have been validated for different starting materials including EDTA-blood, isolated DNA (no FFPE), saliva and dry blood spots (filter card) and all provide high-quality results. The diagnostic yield varies substantially depending on the assay used, referring healthcare professional, hospital and country. Blueprint Genetics' Plus Analysis (Seq+Del/Dup) maximizes the chance to find a molecular genetic diagnosis for your patient although Sequence Analysis or Del/Dup Analysis may be a cost-effective first line test if your patient's phenotype is suggestive of a specific mutation type.

The genes on the panel have been carefully selected based on scientific literature, mutation databases and our experience.

Our panels are sectioned from our high-quality, clinical grade NGS assay. Please see our sequencing and detection performance table for details regarding our ability to detect different types of alterations (Table).

	Sensitivity % (TP/(TP+FN)	Specificity %
Single nucleotide variants	99.89% (99,153/99,266)	>99.9999%
Insertions, deletions and indels by sequence analysis		
1-10 bps	99.2% (7,745/7,806)	>99.9999%
11-50 bps	99.13% (2,524/2,546)	>99.9999%
Copy number variants (exon level dels/dups)		
1 exon level deletion (heterozygous)	100% (20/20)	NA
1 exon level deletion (homozygous)	100% (5/5)	NA
1 exon level deletion (het or homo)	100% (25/25)	NA
2-7 exon level deletion (het or homo)	100% (44/44)	NA
1-9 exon level duplication (het or homo)	75% (6/8)	NA
Simulated CNV detection		
5 exons level deletion/duplication	98.7%	100.00%
Microdeletion/-duplication sdrs (large CNVs, n=37))		
Size range (0.1-47 Mb)	100% (25/25)	

The performance presented above reached by Blueprint Genetics high-quality, clinical grade NGS sequencing assay with the following coverage metrics

Mean sequencing depth	143X
Nucleotides with >20x sequencing coverage (%)	99.86%

Performance of Blueprint Genetics Mitochondrial Sequencing Assay.

	Sensitivity %	Specificity %
ANALYTIC VALIDATION (NA samples; n=4)		
Single nucleotide variants		
Heteroplasmic (45-100%)	100.0% (50/50)	100.0%
Heteroplasmic (35-45%)	100.0% (87/87)	100.0%
Heteroplasmic (25-35%)	100.0% (73/73)	100.0%
Heteroplasmic (15-25%)	100.0% (77/77)	100.0%
Heteroplasmic (10-15%)	100.0% (74/74)	100.0%
Heteroplasmic (5-10%)	100.0% (3/3)	100.0%

Heteroplasmic (<5%)	50.0% (2/4)	100.0%
CLINICAL VALIDATION (n=76 samples)		
All types		
Single nucleotide variants n=2026 SNVs		
Heteroplasmic (45-100%)	100.0% (1940/1940)	100.0%
Heteroplasmic (35-45%)	100.0% (4/4)	100.0%
Heteroplasmic (25-35%)	100.0% (3/3)	100.0%
Heteroplasmic (15-25%)	100.0% (3/3)	100.0%
Heteroplasmic (10-15%)	100.0% (9/9)	100.0%
Heteroplasmic (5-10%)	92.3% (12/13)	99.98%
Heteroplasmic (<5%)	88.9% (48/54)	99.93%
Insertions and deletions by sequence analysis n=40 indels		
Heteroplasmic (45-100%) 1-10bp	100.0% (32/32)	100.0%
Heteroplasmic (5-45%) 1-10bp	100.0% (3/3)	100.0%
Heteroplasmic (<5%) 1-10bp	100.0% (5/5)	99,997%
SIMULATION DATA /(mitomap mutations)		
Insertions, and deletions 1-24 bps by sequence analysis; n=17		
Homoplasmic (100%) 1-24bp	100.0% (17/17)	99.98%
Heteroplasmic (50%)	100.0% (17/17)	99.99%
Heteroplasmic (25%)	100.0% (17/17)	100.0%
Heteroplasmic (20%)	100.0% (17/17)	100.0%
Heteroplasmic (15%)	100.0% (17/17)	100.0%
Heteroplasmic (10%)	94.1% (16/17)	100.0%
Heteroplasmic (5%)	94.1% (16/17)	100.0%
Copy number variants (separate artifical mutations; n=1500)		
Homoplasmic (100%) 500 bp, 1kb, 5 kb	100.0%	100.0%
Heteroplasmic (50%) 500 bp, 1kb, 5 kb	100.0%	100.0%
Heteroplasmic (30%) 500 bp, 1kb, 5 kb	100.0%	100.0%
Heteroplasmic (20%) 500 bp, 1kb, 5 kb	99.7%	100.0%
Heteroplasmic (10%) 500 bp, 1kb, 5 kb	99.0%	100.0%

The performance presented above reached by following coverage metrics at assay level (n=66)		
	Mean of medians	Median of medians
Mean sequencing depth MQ0 (clinical)	18224X	17366X
Nucleotides with >1000x MQ0 sequencing coverage (%) (clinical)	100%	
rho zero cell line (=no mtDNA), mean sequencing depth	12X	

Bioinformatics

The target region for each gene includes coding exons and ±20 base pairs from the exon-intron boundary. In addition, the panel includes non-coding variants if listed above (Non-coding variants covered by the panel). Some regions of the gene(s) may be removed from the panel if specifically mentioned in the 'Test limitations" section above. The sequencing data generated in our laboratory is analyzed with our proprietary data analysis and annotation pipeline, integrating state-of-the art algorithms and industry-standard software solutions. Incorporation of rigorous quality control steps throughout the workflow of the pipeline ensures the consistency, validity and accuracy of results. Our pipeline is streamlined to maximize sensitivity without sacrificing specificity. We have incorporated a number of reference population databases and mutation databases such as, but not limited, to 1000 Genomes Project, gnomAD, ClinVar and HGMD into our clinical interpretation software to make the process effective and efficient. For missense variants, *in silico* variant prediction tools such as SIFT, PolyPhen, MutationTaster are used to assist with variant classification. Through our online ordering and statement reporting system, Nucleus, the customer has an access to details of the analysis, including patient specific sequencing metrics, a gene level coverage plot and a list of regions with inadequate coverage if present. This reflects our mission to build fully transparent diagnostics where customers have easy access to crucial details of the analysis process.

Clinical interpretation

We provide customers with the most comprehensive clinical report available on the market. Clinical interpretation requires a fundamental understanding of clinical genetics and genetic principles. At Blueprint Genetics, our PhD molecular geneticists, medical geneticists and clinical consultants prepare the clinical statement together by evaluating the identified variants in the context of the phenotypic information provided in the requisition form. Our goal is to provide clinically meaningful statements that are understandable for all medical professionals regardless of whether they have formal training in genetics.

Variant classification is the corner stone of clinical interpretation and resulting patient management decisions. Our classifications follow the ACMG guideline 2015.

The final step in the analysis of sequence variants is confirmation of variants classified as pathogenic or likely pathogenic using bi-directional Sanger sequencing. Variant(s) fulfilling the following criteria are not Sanger confirmed: the variant quality score is above the internal threshold for a true positive call, and visual check-up of the variant at IGV is in-line with the variant call. Reported variants of uncertain significance are confirmed with bi-directional Sanger sequencing only if the quality score is below our internally defined quality score for true positive call. Reported copy number variations with a size <10 exons are confirmed by orthogonal methods such as qPCR if the specific CNV has been seen less than three times at Blueprint Genetics.

Our clinical statement includes tables for sequencing and copy number variants that include basic variant information (genomic coordinates, HGVS nomenclature, zygosity, allele frequencies, in silico predictions, OMIM phenotypes and classification of the variant). In addition, the statement includes detailed descriptions of the variant, gene and phenotype(s) including the role of the specific gene in human disease, the mutation profile, information about the gene's variation in population cohorts and detailed information about related phenotypes. We also provide links to the references used, congress abstracts and mutation variant databases used to help our customers further evaluate the reported findings if desired. The conclusion summarizes all of the existing information and provides our rationale for the classification of the variant.

Identification of pathogenic or likely pathogenic variants in dominant disorders or their combinations in different alleles in recessive disorders are considered molecular confirmation of the clinical diagnosis. In these cases, family member testing can be used for risk stratification within the family. In the case of variants of uncertain significance (VUS), we do not recommend

family member risk stratification based on the VUS result. Furthermore, in the case of VUS, we do not recommend the use of genetic information in patient management or genetic counseling.

Our interpretation team analyzes millions of variants from thousands of individuals with rare diseases. Thus, our database, and our understanding of variants and related phenotypes, is growing by leaps and bounds. Our laboratory is therefore well positioned to re-classify previously reported variants as new information becomes available. If a variant previously reported by Blueprint Genetics is re-classified, our laboratory will issue a follow-up statement to the original ordering health care provider at no additional cost.

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ICD codes

Commonly used ICD-10 codes when ordering the Autism Spectrum Disorders Panel

ICD-10	Disease
F84.0	Developmental delay and seizures with or without movement abnormalities (DEDSM)
F84.2	Rett syndrome
E78.72	Smith-Lemli-Opitz syndrome
Q85.1	Tuberous sclerosis complex
H49.40	Progressive external ophthalmoplegia
G11.9	Hereditary ataxia
C94.2	Acute Megakaryoblastic Leukemia
K59.8	Chronic Intestinal Pseudoobstruction
T36.5	Adverse effect of aminoglycosides
G93.41	Metabolic Encephalopathy
H49.81	Kearns Sayre Syndrome
E88.42	MERFF Syndrome
H47.013	Nonarteritic Anterior Ischemic Optic Neuropathy
G60.2	Neuropathy in association with hereditary ataxia
G30	Alzheimer's Disease
G25.5	Chorea
G40	Epilepsy and recurrent seizures
I42	Cardiomyopathy
N26.9	Focal Segmental Glomerulosclerosis
G31.82	Leigh's Disease
H47.2	Leber's hereditary optic neuropathy

G71.3	Mitochondrial Myopathy
I42.1	Hypertrophic Cardiomyopathy
E11.9	Non-Insulin Dependent Diabetes Mellitus
Z86.74	Personal history of sudden cardiac arrest
H90.3	Sensorineural Hearing Loss

Accepted sample types

- EDTA blood, min. 1 ml
- Purified DNA, min. 3µg*
- Saliva (Oragene DNA OG-500 kit)

Label the sample tube with your patient's name, date of birth and the date of sample collection.

Note that we do not accept DNA samples isolated from formalin-fixed paraffin-embedded (FFPE) tissue.

Resources

- Autism BrainNet
- Autism Europe
- Autism Research Institute
- Autism Services Center
- Autism Society of America
- Autism Speaks
- GeneReviews - Autism Spectrum Disorders
- GeneReviews - Rett Syndrome
- GeneReviews - Smith-Lemli-Opitz Syndrome
- GeneReviews - Timothy Syndrome
- GeneReviews - Tuberous Sclerosis Complex
- Geneva Centre for Autism
- International Rett Syndrome Foundation
- NORD - Rett Syndrome
- NORD - Smith-Lemli-Opitz Syndrome
- NORD - Timothy Syndrome
- NORD - Tuberous Sclerosis
- Rett Syndrome Research Trust
- Siu AL et al. Screening forAutismSpectrumDisorderin Young Children: US Preventive Services Task Force Recommendation Statement. JAMA. 2016 Feb 16;315(7):691-6.
- Smith-Lemli-Opitz/RSH Foundation
- Tuberous Sclerosis Alliance
- Tuberous Sclerosis Association